Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Introduction to Clinical Genomics	Variant Analysis; Databases	This class describes how to access information about genes and their variants associated with diseases and the impact of variants on drug response and dosing guidelines. More…
Ingenuity Pathway Analysis	Metabolomics	More…
Gene Resources: From Transcription Factor Binding Sites to Function	Databases; Functional Analysis	This course describes how to obtain information about a human gene at all levels of the central dogma of life, genome, transcript and protein, and prediction of transcription factors regulating its expression. More…
Expression Data Analysis on Microarray and NGS in Partek	Expression Analysis	More…
Pathway Studio	Metabolomics; Functional Analysis	More…
CS101A Perl for Biologists, Level 1	Languages	Taught in the context of biological research, this course teaches biologists how to use the scripting language Perl to automate certain tasks. More…
CS101A Perl for Biologists, Level 2	Languages	Taught in the context of biological research, this course shows biologists how to use the scripting language Perl to automate certain tasks. It is a continuation of CS101A Perl for Biologists, Level 1 and covers advanced topics and projects. More…
CS103A Perl for Biologists, Level 3	Languages	Taught in the context of biological research, this course shows biologists how to use the scripting language Perl to automate certain tasks. It is a continuation of CS102A Perl for Biologists, Level 2 and covers advanced topics in regular expressions, objects, modules will be covered, along with tips and tricks to fine-tune programs and resolve bugs. More...
CS101B R for Biologists, Level 1	Languages	Taught in the context of biological research, this course helps biologists learn how to use the statistical scripting language R for data analysis. More...
CS101B R for Biologists, Level 2	Languages	Taught in the context of biological research, this course helps biologists understand the data analysis and visualization language R. It is a continuation of CS101B R for Biologists, Level 1 and covers advanced topics and projects. More…
CS101C MySQL for Biologists, Level 1	Languages; Databases	Taught in the context of biological research, this course teaches biologists how to use the database management system MySQL to store, manage and query biological information. More…
CS101D MATLAB for Biologists, Level 1	Languages	Taught in the context of biological research, this course helps biologists learn how to use the technical computing language MATLAB to automate certain tasks. More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
CS101E Python for Biologists, Level 1	Languages	This course teaches biologists how to use Python as a programming language to automate routine data management tasks in biological research and solve difficult data-related computational problems. Data could be DNA or amino acid sequence, microarray data, images, mass spectrometry data, LIMS data, or any other kind of biological information. More...
CS112A Image Processing for Biologists, Level 1	General Computing; Computer Science; Statistics	This course teaches biologists how to analyze and manipulate biological images, and extract meaningful information from them, using a variety of tools. For large quantities of images that need to be analyzed with the same algorithm, the course teaches how to automate these routine tasks and generate reports in a high throughput fashion. More...
BI231 NGS Data Analysis	Functional Analysis; Comparative Genomics; Variant Analysis; DNA Sequencing Technology	This course teaches biologists how to analyze data from Next Generation Sequencing (NGS) platforms. Topics to be covered include the description of sequencing strategies and platforms, experiment types, data formats, and command line tools for various workflows, such as quantification of transcripts, alternative splice forms, copy number variants, single nucleotide polymorphisms, etc. More...
BI201 Gene Expression Analysis	Expression Analysis	This course helps to demystify Affymetrix analysis so that any researcher can take the basic steps to go from a chip image to a list of genes that are up- or down-regulated in an experiment. Various tools will be covered, e.g. Affymetrix Expression Console (replacing GCOS), Microsoft Excel, MathWorks MATLAB, and free tools like R/Bioconductor and dChip. It is geared towards researchers who conduct microarray experiments to study genome-wide expression changes and understand the underlying mechanisms of gene regulation in samples of interest. More...
BI202 SNP Genotyping	Variant Analysis	This course helps to demystify Affymetrix analysis so that any researcher can take the basic steps to go from a chip image to genotypes, for each SNP, and to the copy number or linkage associated with the SNPs in given samples. Various tools will be covered, such as GCOS, GTYPE, BRLMM, CNAT, Excel, MATLAB, and free tools like dChip. It is geared towards researchers who conduct microarray-based SNP genotyping experiments to study genome-wide polymorphisms and then use the information for genotyping and linkage analysis. More...
BI203 dChip for Gene Expression and SNP Microarray Data Analysis	Expression Analysis; Variant Analysis	This course will teach the workings of the dChip application and cover topics such as importing arrays, performing normalization, model based expression calculations, gene and SNP filtering, clustering, linkage, LOH and copy number analysis. More…
MA101A Distributions, Tests and Graphics	Statistics	The various statistical distributions covered will help you know when assumptions can be made about a normal distribution and how to test whether or not these assumptions are true. Essential descriptive statistics are reviewed and then used in various situations to calculate background, noise, normalization and thresholding. Additionally, hypothesis testing is introduced so that you can assess groups of observations for a particular parameter and calculate whether or not the difference between groups is significant. Data visualization using various graphs will also be reviewed. Armed with these techniques, you will be able to better deal with the challenges of data analysis. Plus, you'll be able to understand and interpret data at a more fundamental level and draw the correct conclusions about them. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Introduction to Computational Microbial Genomics	Microbiology; Comparative Genomics; Functional Analysis	o DNA sequence and molecular structure o Principles of gene/operon architecture o Principles of genome organization o Methods for genome sequencing and characterization o Basics of genome sequence analysis o Genome sequence features o Applications/uses of microbial genome sequences More...
Next-Generation Sequencing	DNA Sequencing Technology	o DNA sequence and molecular structure o Principles of DNA sequencing o Sanger sequencing o Advantages of next-generation sequencing o Example: Illumina sequencing o Example: PacBio sequencing o Applications and uses of next-generation sequencing More…
Computational Sequence Analysis	Comparative Genomics	o DNA sequence file formats o DNA sequence file access and download o Sequence search applications o Multiple sequence alignment o Phylogenetic analysis o Three-dimensional protein sequence/structure analysis More…
Introduction to Bioinformatic Databases	Databases; Webtools	o Principles of biological databases o Database search utilities o Examples of bioinformatics databases o Health and disease related databases o Genome browser examples o Microbial genome sequence databases and tools o Metagenomic sequence databases and tools o Custom database design and implementation More...
Introduction to Computational Genomics	Comparative Genomics; Variant Analysis	o Genome sequence data and file formats o Sequence read quality control and trimming o Genome assembly: ab initio and reference o Read-to-genome mapping o SNP calling and validation o Gene and feature prediction More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Comparative Genomics	Comparative Genomics; Variant Analysis	o Principles of sequence homology and similarity o Sequence similarity and search algorithms o Local and global sequence alignment o Whole genome sequence comparison and alignment o Genome sequence and alignment visualization o Sequence clustering and orthologous group comparison o Core genome and accessory genome analysis o Applications of comparative genomics to molecular epidemiology More...
Genomic Approaches to Molecular Epidemiology and Typing	Comparative Genomics; Variant Analysis	o Principles of molecular epidemiology and typing o Pulse field gel electrophoresis and PulseNet o Multi-locus sequence typing o Ribosomal gene sequence typing o Whole genome sequence comparison o SNP based genome typing and characterization o Rationale genome-based design of novel typing methods More...

Clinical Metagenomics	Metagenomics	o Introduction to genomics and metagenomics
		o Review of next-generation sequencing methods
		o Principles of clinical metagenomics
		o Methods for sequence similarity searching
		  o Sequence comparison methods
		  o K-mer based methods
		o Supervised and unsupervised sequence characterization
		o Applications for sterile versus non-sterile sites
		o Clinical metagenomic case studies
		More...

Introduction to Scientific Computing	General Computing	o Introduction to the Unix/Linux compute environment o System administration and program installation o Command line operations o Shell scripting o Version control and code sharing o Computing in the cluster environment More…

High-Performance and Cluster Computing	HPC/Cloud	o Cluster environment and architecture
		o Cloud computing environment
		o Review of command line environment
		o Remote access to servers and cluster
		o Queuing systems and file management
		o Principles of threading and parallelization
		o Examples of parallel sequence analysis applications
		  o Assembly
		  o Sequence similarity searches
		More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Introduction to Sequence Data Manipulation	Comparative Genomics	o DNA file formats o Protein file formats o Alignment based formats o Miscellaneous commonly used formats o Conversion between formats: available tools and languages More…
Sequence Alignments	Comparative Genomics	o Small sequences: Pairwise & Multiple o Genome alignment o Alignment viewing o Editing alignments o Verifying goodness of alignments More…
Computational Phylogenetics	Phylogenomics	o Molecular evolution vs Phylogenetics o Genes phylogeny vs Species phylogeny o Tree representation: rooted vs unrooted o Distance-based methods (UPGMA, NJ) o Character-based methods (ML, MP) o Tree evaluation o Tree viewing and editing More…
MLST Based Molecular Epidemiology	Phylogenomics; Databases; Microbiology	o MLST basics o MLST databases and resources o Few examples o Other MLST based techniques: ribosomal MLST, gtMLST o Principles of creating your own MLST More…
Gene Prediction	Comparative Genomics; Functional Analysis	o Prediction basics: biology, underlying models o Prokaryotic gene prediction o Eukaryotic gene prediction (they have fungal division) o Promotor and regulatory elementary predictions More…
Introduction to NCBI	Databases; Webtools	o NCBI structure – site tour o Genbank, RefSeq o BLAST o Taxonomy o Genomes o SRA o Sequence submission More…
Protein Functional Annotation	Functional Analysis; Proteomics	o Functional annotation basics o Sequence homology and similarity o Sequence clustering based tools o Gene ontology based tools o Automated annotation pipelines o Pathway analysis More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Structural Bioinformatics	Functional Analysis; Proteomics	o Structure basics: hierarchy, determination of protein structure o Protein structure database o Visualization o Comparison o Classification Prediction techniques basics: Secondary structure prediction, tertiary structure prediction More…
Bioinformatics Programming Basics	General Computing; Languages	o Introduction of *nix based environment o Command line navigation o Introduction to program installations o Environment setting o Basic error debugging in installations o Redirection, shell scripting and pipelining More…
Genome Assembly	Comparative Genomics; Metagenomics	o DNA sequencing and its generations o Assembly problem o De novo assembly o Reference based assembly o Read to genome mapping o Metagenomic assembly More…
Genome Assembly I	Comparative Genomics	This advanced level bioinformatics sub-module provides participants with the opportunity to gain hands on experience in handling and assembly of next-generation sequencing (NGS) data. Course material includes bioinformatics aspects of sequencing basics, Illumina paired end sequencing, and de novo genome assembly. The module will involve a mix of graphical user interface (GUI) and command line tools such as FastQC, PRINSEQ, Velvet, SOAPdenovo2, QUAST and CISA among others. More...
Genome Assembly II	Comparative Genomics	This advanced level bioinformatics sub-module provides participants with the opportunity to gain hands on experience in the handling and analysis of next-generation sequencing (NGS) data. Course material includes bioinformatics aspects of sequencing basics, genome mapping and variant calling. Bioinformatics programs for which instruction will be provided include a mix of graphical user interface (GUI) and command line tools such as FastQC, PRINSEQ, BWA, SAMtools, BCFtools and IGV among others. More...
Perl for Bioinformatics Programming	Languages	This intermediate level bioinformatics module provides participants with the opportunity to gain hands on experience working with the Perl programming language, a commonly used tool in the analysis of biological data. Course material includes the basics of programming concepts and Perl, file access, handling and manipulation, searching and regular expressions and CPAN. More...
Introduction to Sequence Storage Formats		This basic level bioinformatics sub-module provides participants with the opportunity to gain hands on experience working with numerous sequence storage formats and their inter-conversions. The participants will receive instruction in basic command line Linux and gain experience working at the command line to perform the required tasks. Course material includes discussions and exercises on sequence read formats, mapping formats, variant formats, nucleotide and protein formats and alignment and tree formats. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Intermediate Bioinformatics Programming	Languages	This intermediate level bioinformatics sub-module provides participants with the opportunity to gain hands on experience working with the Perl programming language, a commonly used tool in the analysis of biological data. Course material includes the basics of programming concepts and Perl, file access, file handling and manipulation, loops, subroutines and modules. More...
Sequence Visualization		This intermediate level bioinformatics sub-module provides participants with the opportunity to gain hands on experience with sequence visualization. Course material includes discussions and exercises on the visualization of different types of sequences and analyses such as multiple sequence alignments, trees, read to genome mapping, genome alignments, circular genome visualization and network visualization. More...
Writing Functions in Python Programming	Languages	This is a module from the "Python for Biologists" course. It deals with functions and how to write and use them. It also introduces namespaces and the tuple data structure. More…
Pathway and Network Analysis of -Omics Data (2014)	Metabolomics; Functional Analysis	Many research programs often slow or stall after generating a gene list. The Canadian Bioinformatics Workshops at Bioinformatics.ca has developed a 3-day course covering the bioinformatics concepts and tools available for annotating and determining functional enrichment of a gene list and analyzing networks. The workshop is focused on the principles and concepts required for analyzing and conducting pathway analysis on a gene list from any organism, although focus will be on human and model Eukaryotic organisms. More…
Informatics for RNA-Seq Analysis (2014)	Expression Analysis	High-throughput sequencing of RNA libraries (RNA-seq) has become increasingly common and largely supplanted gene microarrays for transcriptome profiling. When processed appropriately, RNA-seq data has the potential to provide a considerably more detailed view of the transcriptome. The CBW has developed a 2-day course providing an introduction to RNA-seq data analysis followed by integrated tutorials demonstrating the use of popular RNA-seq analysis packages. More...
Introduction to Biopython	Languages	Understand what Biopython is and what it can do. Learn how to get Biopython running. Learn how to retrieve data records from NCBI. More…
Multiple Sequence Alignment and Phylogenetics	Phylogenomics	The overall course aim is to provide an introduction to the computation of quality Multiple Sequence Alignments (MSAs), primarily for phylogenetic analysis. More…
Flow Cytometry Data Analysis Using R (2013)	Laboratory; Metabolomics; Functional Analysis	With the underlying technology rapidly increasing in complexity, Flow Cytometry (FCM) data analysis is becoming more crucial for biological experiments. This workshop aims to provide participants some familiarity with the open source software environment R as an analysis tool for FCM data as they explore the fundamental concepts of taking their data to diagnosis and discovery. More...
Statistics and R for the Life Sciences	Statistics	Topics: • Distributions • Exploratory Data Analysis • Inference • Non-parametric statistics More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
UCSC Genome Browser	Webtools	Bioinformatics Tutorials Series (BITS) Short video tutorials from a collaboration of MIT Engineering and Science Libraries and Harvard's Countway Library. BIT 1.1: UCSC Genome Browser: Getting DNA Sequence (3:57) BIT 1.2: UCSC Genome Browser: Using Annotation Tracks (5:47) BIT 1.3: UCSC Genome Browser: Locating Intron-Exon Boundaries (4:56) BIT 1.4: UCSC Genome Browser: Searching with BLAT (6:14) More...
NCBI BLAST	Functional Analysis; Comparative Genomics	Bioinformatics Tutorials Series (BITS) Short video tutorials from a collaboration of MIT Engineering and Science Libraries and Harvard's Countway Library. BIT 2.1: BLAST Link (7:24) BIT 2.2: Do I Need BLAST? The Use of the Related Sequences Tool (6:53) BIT 2.3: Nucleotide BLAST (5:46) BIT 2.4: Nucleotide BLAST: Algorithm Comparison (6:14) More...
OMIM and OMIA	Databases; Webtools	Bioinformatics Tutorials Series (BITS) Short video tutorials from a collaboration of MIT Engineering and Science Libraries and Harvard's Countway Library. BIT 3.1: OMIM and OMIA (6:34) More...
Entrez Gene	Databases; Webtools	Bioinformatics Tutorials Series (BITS) Short video tutorials from a collaboration of MIT Engineering and Science Libraries and Harvard's Countway Library. BIT 3.2: Entrez Gene (5:35) More...
Coffee Break: Tutorials for NCBI Tools	Databases; Webtools	Coffee Break is a resource at NCBI that combines reports on recent biomedical discoveries with use of NCBI tools. The result is an interactive tutorial that tells a biological story. More…
Entrez Gene Tutorial	Databases; Webtools	This resource is a brief animated tour of a Entrez Gene record, from NIH. More…
NCBI YouTube	Databases; Webtools	This resource contains videos about NCBI tools. More…
Online Lectures on Bioinformatics	Comparative Genomics; Functional Analysis	1. Biological preliminaries 2. Analysis of individual sequences 3. Pairwise sequence comparison 4. Algorithms for the comparison of two sequences 5. Suboptimal Alignments 6. Variants of the dynamic programming algorithm 7. Practical Sections on Pairwise Alignments 8. Multiple sequence alignment 9. Algorithms for SP-optimal multiple alignments 10. Phylogenetic Trees and Multiple Alignments 11. Protein Structure More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
UCSC Genome Browser Workshop and Training Materials	Webtools	This webpage contains links to training materials (including a YouTube channel) on the UCSC Genome Browser, and a list of workshop locations/times. The workshop can be scheduled at your institution. More…
CLC Genomics	Comparative Genomics	Tutorials. More…
DNAStar	Comparative Genomics	Tutorials. More…
DNAStar SeqManNGen	Comparative Genomics; DNA Sequencing Technology	Tutorials. More…
Genomatix	Comparative Genomics; DNA Sequencing Technology	Help pages. More…
GeneSpring	Expression Analysis	GeneSpring Support Portal. More…
Golden Helix SVS	Variant Analysis	Tutorials. More…
Golden Helix VarSeq	Variant Analysis	Tutorials. More…
BIOBASE Archived Webinars	Variant Analysis; Databases	Archived webinars. More…
Ingenuity Pathway Analysis (2)	Metabolomics; Functional Analysis	Online training and webinars. More…
Metacore	Variant Analysis; Functional Analysis	This is a list of tips and archived webinars compiled by NIH. More…
Partek Genomics	Comparative Genomics; DNA Sequencing Technology	Tutorials. More…
Protein Lounge	Proteomics	Tutorials. More…
NCBI Training and Tutorials	Comparative Genomics; Webtools; Databases	This resource consists of training and tutorials for all NCBI tools. More…
NLM Georgia Biomedical Informatics Course	General Computing	This week-long survey course is designed to familiarize individuals with the application of computer technologies and information science in biomedicine and health science. More…
Data Analysis	Statistics	This course is an applied statistics course focusing on data analysis. The course will begin with an overview of how to organize, perform, and write-up data analyses. Then we will cover some of the most popular and widely used statistical methods. More...
Genomic Data Science Certificate	Online Certificate Program; Comparative Genomics; DNA Sequencing Technology	This Johns Hopkins specialization certificate is offered through Coursera. • Basic computational, biological, and statistical skills for analyzing big genomic data • Foundational tools for successfully engaging in this rapidly changing field • How to go from unprocessed next generation sequencing data to meaningful biological results More...
Introduction to Genomic Technologies	DNA Sequencing Technology	Course 1 in Genomic Data Science Certificate: Introduction to Genomic Technologies 1. The Central Dogma of Molecular Biology 2. How next generation sequencing works 3. Applications of next generation sequencing 4. Basic concepts in computing on next generation sequencing data 5. Basic concepts in statistics for next generation sequencing More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Genomic Data Science with Galaxy	Webtools	Course 2 in Genomic Data Science Certificate: Genomic Data Science with Galaxy 1. The challenge of reproducibility 2. Introduction to the Galaxy platform 3. Working with genomic Intervals 4. Galaxy Workflows 5. Annotation, Sharing, Publishing 6. Sequence Data Quality Control 7. ChIP-seq analysis with MACS 8. RNA-seq mapping and assembly 9. Galaxy on the cloud 10. Installing your own Galaxy More...
Command Line Tools for Genomic Data Science	General Computing; Languages	Course 3 in Genomic Data Science Certificate: Command Line Tools for Genomic Data Science 1. Unix commands 2. Sequences and genomic features 3. Alignment and sequence variation 4. Transcriptomics More…
Python for Genomic Data Science	Languages	Course 4 in Genomic Data Science Certificate: Python for Genomic Data Science 1. Introduction to Programming 2. Data structures 4. Defining and Using Functions 5. Modules and Packages 6. Reading and Writing Files 7. Interfacing with External Programs 8. Biopython More...
Algorithms for DNA Sequencing		Course 5 in Genomic Data Science Certificate: Algorithms for DNA Sequencing 1. Sequencing 2. Computational problems 3. Exact matching 4. Preprocessing 5. Approximate matching 6. De novo assembly More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Bioconductor for Genomic Data Science	Languages	Course 5 in Genomic Data Science Certificate: Bioconductor for Genomic Data Science 1. Introduction to Bioconductor 2. Introduction to common data structures 3. Getting data into Bioconductor 4. Data analysis using Bioconductor 5. Annotate your results using Bioconductor 6. Visualize your data using Bioconductor More...
Statistics for Genomic Data Science	Statistics	Course 6 in Genomic Data Science Certificate: Statistics for Genomic Data Science 1. Experimental desgin 2. Exploratory analysis/data processing 3. Statistical inference 4. Common mistakes to avoid More…
Bioinformatic Methods I	Comparative Genomics; Functional Analysis	This course focuses on employing existing bioinformatic resources – mainly web-based programs and databases – to access the wealth of data to answer questions relevant to the average biologist, and is highly hands-on. Topics covered include multiple sequence alignments, phylogenetics, gene expression data analysis, and protein interaction networks, in two separate parts. Bioinformatic Methods I deals with databases, BLAST, multiple sequence alignments, phylogenetics, selection analysis and metagenomics. More...
Bioinformatic Methods II	Comparative Genomics; Functional Analysis	This course focuses on employing existing bioinformatic resources – mainly web-based programs and databases – to access the wealth of data to answer questions relevant to the average biologist, and is highly hands-on. Topics covered include multiple sequence alignments, phylogenetics, gene expression data analysis, and protein interaction networks, in two separate parts. Bioinformatic Methods II covers motif searching, protein-protein interactions, structural bioinformatics, gene expression data analysis, and cis-element predictions. More...
Clustering Biological Data (Bioinformatics V)		To find genes implicated in the diauxic shift, we will learn about clustering algorithms that will divide yeast genes into distinct groups based on their patterns of regulatory behavior. A similar method can be applied to distinguish normal and tumor cells, an approach that led to diagnostic tests like MammaPrint for predicting the return of cancer after chemotherapy. We can also apply clustering algorithms to identify the genetic foundation of human population structure and discover which populations have contributed to your own genome. To do so, we will need to power up the clustering algorithms we encounter using a powerful computational approach called principal component analysis. More...
Deciphering Molecular Evolution (Bioinformatics IV)	Phylogenomics	The course will be based around the following biological questions, with the algorithmic ideas that we will use to solve them in parentheses: • Which Animal Gave Us SARS? (Evolutionary Tree Reconstruction) • Was T. rex Just a Big Chicken? (Computational Proteomics) More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Finding Hidden Messages in DNA (Bioinformatics I)	Phylogenomics	A genome may look like an incomprehensible string of the letters A, C, G, and T. Yet hidden in the three billion nucleotides of your genome is a secret language. This course offers an introduction to how we can start to understand this language by using algorithms to find hidden messages in DNA. What do these hidden messages say? More...
Assembling Genomes and Sequencing Antibiotics (Bioinformatics II)	Comparative Genomics	In "Finding Hidden Messages in DNA", we discussed how to separate some of the signal from the apparent noise of DNA sequences. But how do we know what the DNA sequence making up a genome is in the first place? • How Do We Assemble Genomes? (Graph Algorithms) • How Do We Sequence Antibiotics? (Brute Force Algorithms) More...
Comparing Genes, Proteins, and Genomes (Bioinformatics III)	Comparative Genomics	The course will be based around the following biological questions, with the algorithmic ideas that we will use to solve them in parentheses: • How Do We Compare Biological Sequences? (Dynamic Programming) • Are There Fragile Regions in the Human Genome? (Combinatorial Algorithms) More...
Finding Mutations in DNA and Proteins (Bioinformatics VI)	Variant Analysis	The course will be based around the following biological questions, with the algorithmic ideas that we will use to solve them in parentheses: • How Do We Locate Disease-Causing Mutations? (Combinatorial Pattern Matching) • Why Have Biologists Still Not Developed an HIV Vaccine? (Hidden Markov Models) More…
Algorithms, Biology, and Programming for Beginners	Statistics	The course will be based around the following biological questions, with the algorithmic ideas that we will use to solve them in parentheses: • Where Does DNA Replication Begin? (Algorithmic Warm-up) • How Do We Sequence Antibiotics? (Brute Force Algorithms) • Which DNA Patterns Act As Cellular Clocks? (Greedy and Randomized Algorithms) • How Do We Assemble Genomes? (Graph Algorithms) • How Do We Compare Biological Sequences? (Dynamic Programming Algorithms) • Are There Fragile Regions in the Human Genome? (Combinatorial Algorithms) • Which Animal Gave Us SARS? (Evolutionary Trees) • How Do We Locate Disease-Causing Mutations? (Combinatorial Pattern Matching) • How Did Yeast Become Such a Good Wine Brewer? (Clustering Algorithms) More...
20th Summer Institute in Statistical Genetics (SISG 2015)	Statistics; Variant Analysis; Expression Analysis; Phylogenomics; Metagenomics	The 20th Summer Institute in Statistical Genetics (SISG 2015) will be held at the University of Washington in Seattle, Washington during July 6-24, 2015. The Institute consists of a series of two-and-a-half day workshops designed to introduce geneticists to modern methods of statistical analysis and to introduce statisticians to the statistical challenges posed by modern genetic data. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

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Pacbio SMRT Portal Bootcamp	DNA Sequencing Technology	These training materials are from a course presented by the University of California, Davis. • Introduction to Amazon Web Services EC2 • SMRT-Sequencing, Assembly - lecture • SMRT-Portal Assembly, Alignment - exercises • Finishing circular assemblies - lecture More...
RNA-Seq and ChIP-Seq Analysis with Galaxy	Webtools; Expression Analysis	These training materials are from a course presented by the University of California, Davis. More…
Using the Linux Command Line for Analysis of High Throughput Sequence Data	General Computing; Languages; Expression Analysis; HPC/Cloud; Comparative Genomics	These training materials are from a course presented by the University of California, Davis. More…
Using Galaxy for Analysis of High Throughput Sequence Data	Webtools; Expression Analysis; Expression Analysis	These training materials are from a course presented by the University of California, Davis. More…
Bootcamp: Introduction to the Amazon Cloud for Galaxy and the Command-Line	HPC/Cloud; General Computing	These training materials are from a course presented by the University of California, Davis. More…
Bootcamp: Genome Assembly Using Next Generation Sequence Data	Comparative Genomics	These training materials are from a course presented by the University of California, Davis. More…
Bootcamp: Next Generation Sequence Alignment and Variant Discovery	DNA Sequencing Technology; Variant Analysis	These training materials are from a course presented by the University of California, Davis. More...
Bootcamp: Introduction to Next Generation Sequence Analysis with Galaxy	Webtools	These training materials are from a course presented by the University of California, Davis. More...
Bioinformatics Short Course 2013	Comparative Genomics; Expression Analysis	These training materials are from a course presented by the University of California, Davis. More…
RNA-Seq Workshop: From Pipette to P-Value!	Laboratory; Expression Analysis	These training materials are from a course presented by the University of California, Davis. More...
Bootcamp: Cloud Computing for Bioinformatics	HPC/Cloud; General Computing	These training materials are from a course presented by the University of California, Davis. More…
Bootcamp: Introduction to RNA-Seq	Expression Analysis	These training materials are from a course presented by the University of California, Davis. More...
Bootcamp: Introduction to Galaxy	Webtools; Functional Analysis	These training materials are from a course presented by the University of California, Davis. More…
Data Analysis & Visualization	Statistics; Expression Analysis	These training materials are from a course presented by the University of California, Davis. More...
Using the Linux Command Line for Analysis of High Throughput Sequence Data (2)	General Computing; Languages; Variant Analysis; DNA Sequencing Technology; HPC/Cloud	This workshop covers modern high throughput sequencing technologies, applications, and ancillary topics. More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Using Galaxy for Analysis of High Throughput Sequence Data (2)	Webtools; Variant Analysis; DNA Sequencing Technology; HPC/Cloud	This workshop covers modern high throughput sequencing technologies, applications, and ancillary topics. More...
Analyzing Next-Generation Sequencing Data	DNA Sequencing Technology; Variant Analysis; HPC/Cloud; Languages	This intensive two week summer course will introduce attendees with a strong biology background to the practice of analyzing short-read sequencing data from Illumina and other next-gen platforms. The first week will introduce students to computational thinking and large-scale data analysis on UNIX platforms. The second week will focus on mapping, assembly, and analysis of short-read data for resequencing, ChIP-seq, and RNAseq. More...
Next-Gen Sequence Analysis Workshop	DNA Sequencing Technology; Variant Analysis; HPC/Cloud; Languages	This intensive two week summer course will introduce attendees with a strong biology background to the practice of analyzing short-read sequencing data from Illumina and other next-gen platforms. The first week will introduce students to computational thinking and large-scale data analysis on UNIX platforms. The second week will focus on mapping, assembly, and analysis of short-read data for resequencing, ChIP-seq, and RNAseq. More...
2013 CEMI Workshop at Caltech (Microbial Bioinformatics)		This 2013 Caltech workshop was sponsored by CEMI, the Caltech Environmental Microbial Initiative. More…
Computational Science for Biologists	General Computing; Comparative Genomics	This 2013 Michigan State University (MSU) workshop was co-sponsored by BEACON (a National Science Foundation center at MSU) and iCER (Institute for Cyber-Enabled Research). More...
The Unix Shell	General Computing; Languages	The Unix shell has been around longer than most of its users have been alive. It has survived so long because it's a power tool that allows people to do complex things with just a few keystrokes. More importantly, it helps them combine existing programs in new ways and automate repetitive tasks so that they don't have to type the same things over and over again. Use of the shell is fundamental to using a wide range of other powerful tools and computing resources (including "high-performance computing" supercomputers). More...
Version Control with Git	Reproducible Research; General Computing	Version control is the lab notebook of the digital world: it's what professionals use to keep track of what they've done and to collaborate with other people. Every large software development project relies on it, and most programmers use it for their small jobs as well. And it isn't just for software: books, papers, small data sets, and anything that changes over time or needs to be shared can and should be stored in a version control system. In this lesson we use Git from the Unix Shell. More...
Using Databases and SQL	Databases	Text files are easiest to create, and work well with version control, but then we would have to build search and analysis tools ourselves. Spreadsheets are good for doing simple analyses, but they don't handle large or complex data sets well. Databases, however, include powerful tools for search and analysis, and can handle large, complex data sets. These lessons will show how to use a database to explore the expeditions' data. More...
Version Control with Mercurial	Reproducible Research; General Computing	More…
Programming with Python	Languages	These training materials are from a Software Carpentry course. The Software Carpentry Foundation is a non-profit volunteer organization whose members teach researchers basic software skills. More…
Programming with R	Languages	These training materials are from a Software Carpentry course. The Software Carpentry Foundation is a non-profit volunteer organization whose members teach researchers basic software skills. More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Programming with MATLAB	Languages	These training materials are from a Software Carpentry course. The Software Carpentry Foundation is a non-profit volunteer organization whose members teach researchers basic software skills. More...
ArrayExpress: Exploring Functional Genomics Data with ArrayExpress	Expression Analysis; Functional Analysis	This course will show you how to search, retrieve and interpret data from ArrayExpress, a repository of data from functional genomics experiments. ArrayExpress allows you to search and download this data. More...
ArrayExpress: Quick Tour	Expression Analysis; Functional Analysis	This quick tour provides a brief introduction to the EBI's functional genomics resource: ArrayExpress. More...
diXa Data Warehouse: Exploring Data From Toxicogenomics Studies	Databases; Metabolomics	The diXa data warehouse is a curated collection of toxicogenomics experiments, accessible through the diXa website. This course will show you how to use the diXa warehouse and what data is available. Topic: Gene Expression, Ontologies, Chemical biology More...
EBI: Next Generation Sequencing Practical Course	DNA Sequencing Technology	Here you will find a collection of video lectures from the 'Hands on training in Next-Generation Sequencing' course that took place at EMBL-EBI on 12-14 March 2012, available for you to watch in your own time. The workshop provides an introduction to Next Generation Sequencing (NGS) and addresses how to interpret the data and how the analysis is applied in Genomics. More...
EMBO Practical Course on Analysis of High-Throughput Sequencing Data	Expression Analysis	Here you will find a collection of materials including videos of lectures from the 'EMBO Practical Course on Analysis of High-Throughput Sequencing Data' that took place at EMBL-EBI on 23-29 October 2011. This course was aimed at advanced PhD students and post-doctoral researchers who are applying or planning to apply high throughput sequencing technologies and bioinformatics methods in their research. The aim of this course was to familiarize the participants with advanced data analysis methodologies and provide hands-on training on the latest analytical approaches. Topic: Gene Expression More...
Expression Atlas: Quick Tour	Expression Analysis; Databases	This extended quick tour provides a brief introduction to the Expression Atlas ("Atlas"). Topic: Gene Expression More...
Functional Genomics: An Introduction to EMBL-EBI Resources	Functional Analysis; Databases	This course will introduce the field of functional genomics and provide an overview of the major resources for this field at EMBL-EBI. Topic: Gene Expression More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Introduction to EMBL-EBI Resources: Bioinformatics Forum 2012	Webtools; Databases	This course is a collection of videos and slides from the EMBL-EBI's SME Bioinformatics Forum, which took place in Barcelona on 8-9 October 2012. The event was aimed at researchers working in small and medium-sized enterprises (SMEs) and will be of interest to anyone who would like to learn more about the core data resources available from EMBL-EBI. For an overview of the event, there is a summary on EMBL-EBI's SME Forum web pages and a full list of talks. Topic: DNA & RNA, Gene Expression, Ontologies, Proteins, Chemical biology More...
DGVa: Quick Tour	Databases	This quick tour provides a brief introduction to the DGVa, the EBI's Database of Genomic Variants archive. Topic: DNA & RNA More...
EBI Metagenomics Resource: Quick Tour	Metagenomics; Databases	This quick tour provides a brief introduction to the EBI Metagenomics resource, for archiving, analysing and integrating metagenomics data. Topic: DNA & RNA More...
EGA: Quick Tour	Functional Analysis; Databases	This Quick tour provides a brief introduction to the European Genome-phenome archive (EGA). Topic: DNA & RNA More...
Ensembl Genomes (Non-Chordates): Quick Tour	Databases	This quick tour provides a brief introduction to Ensembl Genomes, the non-chordate genome browser. Topic: DNA & RNA More...
Ensembl Tools: Webinar	Comparative Genomics	Emily Perry from the Ensembl Outreach Team presents this webinar on Ensembl tools, including the ever-popular Variant Effect Predictor (VEP), BLAST/BLAT and BioMart. This webinar took place on 22nd April 2015. Topic: DNA & RNA More...
Ensembl: Browsing Chordate Genomes	Webtools	This course focuses on chordate (mostly vertebrate) genomes on the Ensembl website at www.ensembl.org. It provides a quick beginner's guide to the overall structure of the Ensembl genome browser. Topic: DNA & RNA More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Ensembl: Filmed API Workshop	Databases	Ensembl runs API workshops worldwide, and for the first time we make one available online. Here you will find a collection of video lectures from the 'Ensembl API workshop' that took place at EMBL-EBI 22nd-24th May 2013, using Ensembl version 71. The exercises associated with the workshop are included to carry out at your leisure. Topic: DNA & RNA More...
Ensembl: Filmed Browser Workshop	Webtools	This workshop provides an introduction to Ensembl, what kind of data Ensembl has, and how to browse and export the data. Topic: DNA & RNA More...
Ensembl: Quick Tour	Webtools	This course provides a very short introduction to the Ensembl website for browsing chordate genomes. Topic: DNA & RNA More...
European Nucleotide Archive: Using the Primary Nucleotide Sequence Resource	Databases	This course will show you how to search and retrieve nucleotide sequence data from the European Nucleotide Archive (ENA). The ENA provides sequence assembly details and biological annotation, and uses versioning to track sequence changes. Topic: DNA & RNA More...
Genomics: An Introduction to the EBI Resources	Databases	This course will introduce the field of genomics and provide an overview of the different resources at the EBI which are related to this field. The course is aimed at graduates in the life sciences or related subjects, with an interest in using bioinformatics resources to solve problems related to genome biology. Topic: DNA & RNA More...
Introduction to Phylogenetics	Phylogenomics	This course provides a basic introduction to the field of phylogenetics, with an emphasis on how to read and interpret phylogenetic trees. Topic: DNA & RNA More…
Resources for Genomics: Webinar	Webtools; Metagenomics	This 25 minute webinar from Dr Laura Emery provides you with an introduction to EMBL-EBI and the data resources available (recorded on 25th February 2015). The webinar focuses in particular on three core resources - Ensembl, ENA and the Metagenomics portal. Topic: DNA & RNA More...
Rfam: Quick Tour	Functional Analysis; Databases	This quick tour provides a brief introduction to Rfam, the EBI's database of RNA families. Topic: DNA & RNA More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
The European Nucleotide Archive (ENA) - An Introduction: Webinar	Databases	In this webinar, Marc Rossello gives an introduction the European Nucleotide Archive (ENA). This webinar took place on 8 April 2015. Topic: DNA & RNA More...
The European Nucleotide Archive: Quick Tour	Databases	This quick tour provides a brief introduction to the European Nucleotide Archive, the EBI's repository for nucleotide sequence data. Topic: DNA & RNA More...
An Introduction to Metabolomics		This course provides a basic introduction into the rapidly emerging field of metabolomics and its importance and applications. Topic: Systems, Chemical biology More...
Biomodels Database: Quick Tour	Systems Biology	This quick tour provides a brief introduction to BioModels Database, EMBL-EBI's repository of mathematical models of biological interest. Topic: Systems More...
IMPC: Using the Mouse Phenotyping Portal	Functional Analysis; Databases; Systems Biology	The International Mouse Phenotyping Consortium (IMPC) portal allows you to search for phenotypes, disease models and knockout mouse strains for your gene of interest. This course will show you how to use the IMPC portal and what data is available. Topic: Systems, Ontologies More...
IntAct: Molecular Interactions at the EBI	Proteomics; Systems Biology	This course will show you what kind of information you can find in IntAct (one of the EBI's molecular interactions databases), how to access it, the different tools that can be used to access data and some practical examples on how to search and use the database. Topic: Systems More...
IntAct: Quick Tour	Proteomics; Systems Biology	This quick tour provides a brief introduction to the EBI's molecular interactions database, IntAct. Topic: Systems, Proteins More…
MetaboLights: Quick Tour	Metabolomics; Functional Analysis	This quick tour provides a brief introduction to the EBI's metabolomics resource: MetaboLights. Topic: Systems, Chemical biology More...
Protein Interactions and Their Importance	Proteomics	This course will provide an introduction to molecular interactions, their importance and the methodologies use to generate and capture interaction data. Topic: Systems, Proteins More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Reactome - Exploring Biological Pathways: Webinar	Metabolomics; Functional Analysis; Systems Biology	This two-part webinar from Steve Jupe provides you with an introduction to Reactome and how you can use it to explore biological pathways (recorded on 6th May 2015). Part 1 gives an overview of what Reactome is and why it is important. Part 2 provides a demo of the Reactome interface. Find out about upcoming webinars. Topic: Systems More...
Reactome: Exploring and Analysing Biological Pathways	Metabolomics; Functional Analysis; Systems Biology	This course provides an overview to the Reactome pathway database web interface and the database content. For a short introduction to Reactome, please visit the Reactome quick tour. Topic: Systems More...
Reactome: Quick Tour	Metabolomics; Functional Analysis; Systems Biology	This quick tour provides a brief introduction to Reactome, the biological pathway database. Topic: Systems More...
GO: Quick Tour	Systems Biology; Functional Analysis	This quick tour provides a brief introduction to the EBI's Gene Ontology resource. For information about gene ontology annotation, see the UniProt-GOA quick tour. More...
Uniprot-GOA: Quick Tour	Databases; Systems Biology	This quick tour provides a brief introduction to UniProt-GOA, the Gene Ontology Annotation resource. For information about the Gene Ontology, see the GO quick tour. Topic: Ontologies More...
Biomacromolecular Structures: An Introduction to the EBI Resources	Proteomics	Introduction to structural biology and an introduction to resources at EBI related to this field Topic: Proteins More...
Enzyme Portal: Quick Tour	Proteomics	This quick tour provides a brief introduction to the Enzyme Portal - a data resource that provides access to information from several enzyme-related databases, both at EMBL-EBI and the Swiss Institute of Bioinformatics (SIB). Topic: Proteins, Chemical biology More...
InterPro: Functional and Structural Analysis of Protein Sequences	Proteomics; Systems Biology	InterPro is a classification database that provides predictive information about protein sequences. This course will show you what kind of information is available in InterPro, how to access it, and how to search the database. More...
InterPro: Quick Tour	Proteomics; Systems Biology	This quick tour provides a brief introduction to InterPro, the EBI's database of protein families, domains and functional sites. A full course will be here soon. Topic: Proteins More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Introduction to Protein Classification at the EBI	Proteomics	This course will provide an introduction to protein classification and basic concepts, such as proteins families, domains and sequence features. Topic: Proteins More...
PDBe: Quick Tour	Proteomics; Functional Analysis	This quick tour provides a brief introduction to the Protein Data Bank in Europe (PDBe), EMBL-EBI's resource for the collection, organisation and dissemination of data on biological macromolecular structures. Topic: Proteins, Structures More...
PDBeChem: Searching for Small Molecules and Small Molecule Fragments	Metabolomics; Functional Analysis	PDBeChem allows you to search for chemical components (ligands, small molecules and monomers) that appear in PDB entries, and discover which protein structures bind a particular ligand. This course will show you how to use PDBeChem and what you can do with it. Topic: Proteins, Chemical biology, Structures More...
PDBeFold: Searching for Structural Homologues of a Protein	Proteomics	PDBeFold can be used to identify structural homologues in the PDB. PDBe's Secondary Structure Matching service (SSM) allows you to interactively compare, align and superimpose protein structures in 3D. This course will show you how to use PDBeFold and what you can do with it. Topic: Proteins, Structures More...
PDPePISA: Identifying and Interpreting the Likely Biological Assemblies of a Protein Structure	Proteomics; Functional Analysis	PDBePISA allows you to explore macromolecular (protein, DNA/RNA and ligand) interfaces and predict the quaternary stucture of your protein. This course will show you how to use PDBePISA and what you can do with it. Topic: Proteins, Structures More...
PRIDE: Quick Tour	Proteomics	This quick tour provides a brief introduction to the EMBL-EBI's PRoteomics IDEntifications database, PRIDE. Topic: Proteins More...
ProteomeXchange Submissions Via PRIDE	Proteomics	How to submit MS/MS data to ProteomeXchange via PRIDE. This course is aimed at proteomics researchers with data that they want to make available through public-domain databases of proteomics experiments. Topic: Proteins More...
Proteomics: An Introduction to the EBI Resources	Proteomics	This course will provide an overview of proteomics. We will then introduce resources provided by the EBI related to proteomics. Topic: Proteins More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
UniProt: Exploring Protein Sequence and Functional Information	Proteomics; Databases	This course is a guide to the UniProt resource, including what kinds of information it provides and how to access the data using the UniProt website. Topic: Proteins More...
UniProt: Exploring Protein Sequence and Functional Information - Webinar	Proteomics; Databases	In this webinar, Sangya Pundir shows us how we can use UniProt (www.uniprot.org) to explore protein sequence and functional information. Topic: Proteins More…
UniProt: Quick Tour	Proteomics; Databases	This quick tour provides a brief introduction to the Universal Protein Resource (UniProt). A full tutorial of UniProt can be found here. Topic: Proteins More...
ChEBI: Quick Tour	Metabolomics; Databases	This quick tour provides a brief introduction to ChEBI, the EBI's Chemical Entities of Biological Interest database, which focuses on 'small' chemical compounds. Topic: Chemical biology More...
ChEMBL: Quick Tour	Metabolomics; Databases	This quick tour provides a brief introduction to ChEMBL, the EBI's chemogenomics resource. Topic: Chemical biology More...
SureChEMBL - Accessing Chemical Patent Data: Webinar	Metabolomics	This two-part webinar from George Papadatos provides you with an introduction to the chemical patent database SureChEMBL (recorded on 11th March 2015). Part 1 gives an overview of what SureChEMBL is and why it is important. Part 2 provides a demo of the SureChEMBL interface. Topic: Chemical biology More...
Penn State University Online Graduate Certificate in Bioinformatics	Graduate Certificate Program; Statistics; Comparative Genomics	With ongoing public attention on the Human Genome Project, understanding, analyzing, and interpreting genomic data continue to be a focus across many disciplines. By merging biology, computer science, and information technology, bioinformatics allows us to combine mathematics and computers to gain a better understanding of biological processes. Professionals in this field will be required to use technologies to gather, store, analyze, and integrate biological and genetic information, which can then be applied to gene-based drug discovery and development. To help you learn about the latest techniques, Penn State World Campus has partnered with Penn State's Eberly College of Science to offer the online Graduate Certificate in Applied Bioinformatics. More...
Genomics	Statistics; Comparative Genomics	Structure and function of genomes including use of some current web-based tools and resources for studies and research in genomics. This is one of four courses required for the Penn State University Online Graduate Certificate in Bioinformatics. More...
Foundations in Data Driven Life Sciences	Statistics; Comparative Genomics	Expanded overview of current developments and technique in computational biology and genomics. This is one of four courses required for the Penn State University Online Graduate Certificate in Bioinformatics. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Applied Bioinformatics	Statistics; Comparative Genomics	This course provides a foundation for students with biology backgrounds in the computational analysis and interpretation of biological data. This is one of four courses required for the Penn State University Online Graduate Certificate in Bioinformatics. More...
Statistical Analysis of Genomics Data	Statistics; Comparative Genomics	Statistical analysis of high throughput biology experiments. This is one of four courses required for the Penn State University Online Graduate Certificate in Bioinformatics. More...
Johns Hopkins Online Bioinformatics MS	Comparative Genomics; DNA Sequencing Technology; Expression Analysis; Systems Biology; Variant Analysis; HPC/Cloud; Metagenomics; Computer Science	Core Courses (5 total) • 410.602 Molecular Biology • 410.610 Gene Organization and Expression • 605.421 Foundations of Algorithms OR 605.420 Algorithms for Bioinformatics • 605.441 Principles of Database Systems OR 410.634 Practical Computer Concepts for Bioinformatics • 410.633 Introduction to Bioinformatics OR 605.452 Biological Databases and Database Tools More...
Algorithms for Bioinformatics	Computer Science	This follow-on course to data structures (e.g., 605.202) provides a survey of computer algorithms, examines fundamental techniques in algorithm design and analysis, and develops problem-solving skills required in all programs of study involving computer science. Topics include advanced data structures (red-black and 2-3-4 trees, union-find), algorithm analysis and computational complexity (recurrence relations, big-O notation, introduction to NP completeness), sorting and searching, design paradigms (divide and conquer, greedy heuristic, dynamic programming), and graph algorithms (depth-first and breadth-first search, minimum spanning trees,). More...
Principles of Database Systems	Databases	This course examines the underlying concepts and theory of database management systems. Topics include database system architectures, data models, query languages, conceptual and logical database design, physical organization, and transaction management. The entity-relationship model and relational model are investigated in detail, object-oriented databases are introduced, and legacy systems based on the network and hierarchical models are briefly described. More...
Practical Computer Concepts for Bioinformatics	General Computing; Languages; Databases	This course introduces students with a background in the life sciences to the basic computing concepts of the UNIX operating system, relational databases, structured programming, object-oriented programming, and the Internet. Included is an introduction to SQL and the Perl scripting language. The course emphasizes relevance to molecular biology and bioinformatics. More...
Introduction to Bioinformatics	Databases	Retrieval and analysis of electronic information are essential in today's research environment. This course explores the theory and practice of biological database searching and analysis. In particular, students are introduced to integrated systems where a variety of data sources are connected through World Wide Web access. Information retrieval and interpretation are discussed, and many practical examples in a computer laboratory setting enable students to improve their data mining skills. More...
Biological Databases and Database Tools	Databases; Webtools	The sequencing of the human genome and intense interest in proteomics and molecular structure have resulted in an explosive need for biological databases. This course surveys a wide range of biological databases and their access tools and enables students to develop proficiency in their use. Databases introduced include genome and sequence databases such as GenBank and Ensemble, as well as protein databases such as PDB and SWISS-PROT. Tools for accessing and manipulating sequence databases such as BLAST, multiple alignment, Perl, and gene finding tools are covered. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Bioinformatics: Tools for Genome Analysis	Functional Analysis; Comparative Genomics	Several large-scale DNA sequencing efforts have resulted in megabase amounts of DNA sequences being deposited in public databases. As such, the sequences are of less use than those sequences that are fully annotated. Assigning annotations such as exon boundaries, repeat regions, and other biologically relevant information accurately in the feature tables of these sequences requires a significant amount of human intervention. This course instructs students on computer analytical methods for gene identification, promoter analysis, and introductory gene expression analysis using software methods. Additionally, students are introduced to comparative genomics and proteomic analysis methods. Students will become proficient in annotating large genomic DNA sequences. More...
Protein Bioinformatics	Proteomics	Because the gap between the number of protein sequences and the number of protein crystal structures continues to expand, protein structural predictions are increasingly important. This course provides a working knowledge of various computer-based tools available for predicting the structure and function of proteins. Topics include protein database searching, protein physicochemical properties, secondary structure prediction, and statistical verification. Also covered are graphic visualization of the different types of three-dimensional folds and predicting 3-D structures by homology. More...
Molecular Phylogenetic Techniques	Phylogenomics	This course will provide a practical, hands-on introduction to the study of phylogenetics and comparative genomics. Theoretical background on molecular evolution will be provided only as needed to inform the comparative analysis of genomic data. The emphasis of the course will be placed squarely on the understanding and use of a variety of computational tools designed to extract meaningful biological information from molecular sequences. More...
Methods in Proteomics	Proteomics	This course covers the analytical methods used to separate and characterize pharmaceutical compounds (predominantly proteins) derived through biotechnology. While emphasis is placed on the general principles and applicability of the methods, current protocols are discussed, and problem sets representing realistic developmental challenges are assigned. Topics include chromatography (HPLC, SEC, IEC), electrophoretic techniques (2-D gel electrophoresis), spectroscopic methods (UV/Vis, fluorescence, CD), analytical ultracentrifugation, microarrays, mass spectroscopy, amino acid analysis, sequencing, and methods to measure protein-protein interactions. More...
Next Generation DNA Sequencing and Analysis	DNA Sequencing Technology; Comparative Genomics	The recent revolution in DNA sequencing technologies has transformed biology within a few short years, dropping the cost and ease of sequencing dramatically to the point where the "$1,000 Human Genome" is in sight. Armed with complete genome sequences, biologists need to identify the genes encoded within and the variation in these genes between individuals, assign functions to the genes, and to put these into functional and metabolic pathways. This course will provide an overview of next generation sequencing technologies in the historical context of DNA sequencing, the pros and cons of each technology, and the bioinformatics techniques used with this sequence information, beginning with quality control assessment, genome assembly and annotation. More...
Microarrays and Analysis	Expression Analysis; Statistics	This course will focus on the analysis and visualization of microarray data. The general aim is to introduce students to the various techniques and issues involved with analyzing multivariate expression data. Additionally, students will visualize the results in modern statistical scripting software. Topics include detecting and attributing sources of data variability, determining differentially expressed genes with relevant statistical tests, and controlling for false positive discovery (multiple test corrections, permutations, etc.). An introduction to linear and non-linear dimension reduction methods (PCA, PLS, isometric feature mapping, etc.) and an introduction to common pattern recognition (clustering), classification, and discrimination techniques will be included. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Advanced Practical Computer Concepts for Bioinformatics	Computer Science; Languages	This intermediate-to-advanced-level course, intended as a follow-on to 410.634 Practical Computer Concepts for Bioinformatics (a prerequisite for this new class), will integrate and expand on the concepts from that introductory class to allow students to create working, Web-based bioinformatics applications in a project-based course format. After a review of the concepts covered in 410.634, students will learn how to create functional Web applications on a UNIX system, using Perl and CGI to create forms that can be acted upon, and using the Perl DBI module to interface with MySQL relational databases that they will create and populate to retrieve and present information. More...
Advanced Genomics and Genetic Analysis	Variant Analysis; Comparative Genomics	The next generation of array and sequencing technologies provides the ability to investigate large quantities of genomics information with higher sensitivity, greater throughput, and lower costs. This also introduces new challenges in data management, novel algorithmic approaches, and general interpretation. This course builds on the topics in 410.671 Microarrays and Analysis to address analysis of both genetic variation and genomics content using technologies measuring splice variants, single nucleotide polymorphisms (SNPs), copy number variation (CNV), and transcription factor binding sites. More...
Practical Introduction to Metagenomics	Metagenomics	The emerging field of metagenomics allows for the study of entire communities of microorganisms at once, with far-reaching applications in a wide array of fields such as medicine, agriculture and bioremediation. Students will learn the principles of metagenomics through exploration of published project data and guided readings of recent literature. Using data from the Human Microbiome Project, students will explore practical analysis tasks including sequence assembly, gene prediction and annotation, metabolic reconstruction, taxonomic community profiling and more. More...
Genomic and Personalized Medicine	Variant Analysis; Comparative Genomics; Functional Analysis	This integrative course will be of interest to a wide variety of students in different concentration areas. Applying knowledge from their core courses and introductory bioinformatics, students will examine the current applications of whole genome sequencing and genome wide association studies in clinical medicine, and explore evolving applications and their impact on future medical diagnoses and treatments. Students will review both established and emerging sequencing platforms in detail. This course will closely examine whole genome sequencing applications in inherited and heritable diseases and cancer, amongst others. Class discussions will include ethical, legal, regulatory, and economic implications of genomic medicine. More...
Principles of Computational Biology	Computer Science; Comparative Genomics	This course is an interdisciplinary introduction to computational methods used to solve important problems in DNA and protein sequence analysis. The course focuses on algorithms but includes material to provide the necessary biological background for science and engineering students. More...
Computational Drug Discovery and Development	Systems Biology; Functional Analysis	Recent advances in bioinformatics and drug discovery platforms have brought us significantly closer to the realization of rational drug design and development. Across the pharmaceutical industry, considerable effort is being invested in developing experimental and translational medicine, and it is starting to make a significant impact on the drug discovery process itself. This course examines the major steps of the evolving modern drug discovery platforms, the computational techniques and tools used during each step of rational drug discovery, and how these techniques facilitate the integration of experimental and translational medicine with the discovery/development platforms. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Modeling and Simulation of Complex Systems	Systems Biology; Functional Analysis	This course focuses on the application of modeling and simulation principles to complex systems. A complex system is a large-scale nonlinear system consisting of interconnected or interwoven parts (such as a biological cell, the economy, or an ecological system). The course begins with an overview of complex systems, followed by modeling and simulation techniques based on nonlinear differential equations, networks, stochastic models, cellular automata, and swarm-like systems. More...
Computational Aspects of Molecular Structure	Proteomics; Functional Analysis	This course focuses on computational methods for studying protein and RNA structure, protein-protein interactions, and biological networks. Algorithms for prediction of RNA secondary structure, protein-protein interactions, and annotation of protein secondary/tertiary structure and function are studied in depth. More...
Computational Genomics	Statistics; Comparative Genomics	This course focuses on current problems of computational genomics. Students will explore bioinformatics software, discuss bioinformatics research, and learn the principles underlying a variety of bioinformatics algorithms. The emphasis is on algorithms that use probabilistic and statistical approaches. Topics include analyzing eukaryotic, bacterial, and viral genes and genomes, genome sequencing and assembling, finding genes in genomes and identifying their biological functions, predicting regulatory sites, and assessing gene and genome evolution. More...
Analysis of Gene Expression and High-Content Biological Data	Expression Analysis	The development of microarray technology, rapid sequencing, protein chips, and metabolic data has led to an explosion in the collection of “high-content” biological data. This course explores the analysis and mining of gene expression data and high-content biological data. A survey of gene and protein arrays, laboratory information management systems, data normalization, and available tools is followed by a more in-depth treatment of differential gene expression detection, clustering techniques, pathway extraction, network model building, biomarker evaluation, and model identification. More...
Systems Biology	Systems Biology	During the last decade, systems biology has emerged as an effective tool for investigation of complex biological problems, placing emphasis on the analysis of large-scale data sets and quantitative treatment of experimental results. In this course, students will explore recent advances in systems biology analysis of intracellular processes. Examples of modeling and experimental studies of metabolic, genetic, signal transduction, and cell cycle regulation networks will be studied in detail. More...
Machine Learning	Statistics	How can machines improve with experience? How can they discover new knowledge from a variety of data sources? What computational issues must be addressed to succeed? These are questions that are addressed in this course. Topics range from determining appropriate data representation and models for learning, understanding different algorithms for knowledge and model discovery, and using sound theoretical and experimental techniques in assessing performance. More...
Stanford Distance Education Master of Science in Biomedical Informatics Professional/Honors Cooperative Program	Online Graduate Program	Core Curriculum in Biomedical Informatics 1. Core Biomedical Informatics (17 units) 2. Computer Science, Statistics, Mathematics & Engineering (18 units) 3. Social and Ethical Issues (4 units) 4. Unrestricted Electives (6 units) More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Stanford Online Bioinformatics Graduate Certificate	Online Graduate Certificate; Comparative Genomics; DNA Sequencing Technology; Expression Analysis; Systems Biology; Variant Analysis; HPC/Cloud; Metagenomics; Computer Science; Statistics	The Bioinformatics Graduate Certificate focuses on developing an understanding of techniques for analyzing the vast amount of biological data from recent genomic research to new applications relevant to basic biology. • Understand the use of different techniques to analyze biological data from high throughput approaches • Learn how the techniques are used in new applications in biomedicine • Acquire an understanding of how molecular biology is used to address topics ranging from sequence, structure and function analysis in the context of algorithms, databases and visualization More...
Introduction to Biomedical Informatics Research Methodology	Online MS Program	Hands-on software building. Student teams conceive, design, specify, implement, evaluate, and report on a software project in the domain of biomedicine. Creating written proposals, peer review, providing status reports, and preparing final reports. More...
Representations and Algorithms for Computational Molecular Biology	Online Graduate Certificate; Online MS Program; Comparative Genomics; Statistics; Computer Science	This course provides an introduction to computing with DNA, RNA, proteins and small molecules. Learn how to program both basic and advanced algorithms for sequence analysis, 3D structure analysis and high-throughput functional data analysis. Receive hands-on experience with the algorithms used in the field. More...
Translational Bioinformatics	Online Graduate Certificate; Online MS Program; Expression Analysis; Databases; Variant Analysis	Focused on the convergence of molecular bioinformatics, biostatistics, statistical genetics, bioinformatics optimizes translational medicine through the transformation of data into diagnostics and therapeutics. Analyze genetic, genomic, and biological data to become skilled at identifying different types of genome-scale measurements in molecular biology and genomic medicine. More...
Modeling Biomedical Systems: Ontology, Terminology, Problem Solving	Online Graduate Certificate; Online MS Program; Systems Biology; Functional Analysis	This course provides an introduction to semantic technology in biomedicine, providing a platform for understanding how computers are being used to communicate knowledge and integrate data in the health care and life sciences fields. More...
Data Driven Medicine	Online Graduate Certificate; Online MS Program;	With the spread of electronic health records and increasingly low cost assays for patient molecular data, powerful data repositories with tremendous potential for biomedical research, clinical care and personalized medicine are being built. But these databases are large and difficult for any one specialist to analyze. To find the hidden associations within the full set of data, we introduce methods for data-mining at the internet scale, the handling of large-scale electronic medical records data for machine learning, methods in natural language processing and text-mining applied to medical records, methods for using ontologies for the annotation and indexing of unstructured content as well as semantic web technologies. More...
Computational Methods for Biomedical Image Analysis and Interpretation	Online Graduate Certificate; Online MS Program; General Computing	The latest biological and medical imaging modalities and their applications in research and medicine. Focus is on computational analytic and interpretive approaches to optimize extraction and use of biological and clinical imaging data for diagnostic and therapeutic translational medical applications. Case studies include linking image data to genomic, phenotypic and clinical data, developing representations of image phenotypes for use in medical decision support and research applications and the role that biomedical imaging informatics plays in new questions in biomedical science. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Introduction to Decision Analysis	Online Graduate Certificate; Online MS Program; Statistics	Apply a methodical approach to making important personal and professional decisions in a complex, dynamic and uncertain world. Examine uncertainties and tradeoffs and use a structured conversation based on actional thought to obtain clarity of action in a wide variety of domains. Directly apply course concepts and distinctions to your professional and personal experiences using insight from a professional guest speaker currently practicing as a decision analyst. Topics Include • Probabilities • Value of information and experimentation • Relevance and decision diagrams • Risk attitude More...
Genomics, Bioinformatics and Medicine	Online Graduate Certificate; Online MS Program; Databases; Functional Analysis	The explosion of information available from human genome mapping provides many opportunities for preventative medicine. Explore the potential of personal genomics, pharmacogenomics and clinical genomics and their role in the future of preventive medicine. Examine the ethical, social and legal issues facing current health care policy and treatment. More...
Principles of Pharmacogenomics	Online Graduate Certificate	Introduction to the relevant pharmacology, genomics, experimental methods for high-throughput measurements (sequencing, expression, genotyping), analysis methods for GWAS, chemoinformatics, and natural language processing. Review of key gene classes (cytochromes, transporters, GPCRs), key drugs for which genetics is critical (warfarin, clopidogrel, statins, NSAIDs, neuropsychiatric drugs and cancer drugs). More...
Introductory Unix for Bioinformatics	Languages	The basic 101 level course teaches the applications of Unix tools and utilities to perform routine sequence analysis tasks. This is an introductory course for those who want to obtain a basic understanding of the Unix OS and can be completed in 2-3 months. All commands are customized for the Tcsh shell. More...
Advanced Unix for Bioinformatics	Languages	Unix is the platform of choice for large-scale Bioinformatics operations. Among other things, 201 describes work-flow operations in a typical high-throughput sequencing center - a fundamental aspect of large-scale sequencing that controls how sequence data is stored, distributed and processed in these centers - and, the biology of the sequencing process itself. More...
Introductory Perl Programming for Bioinformatics	Languages	Perl for Bioinformatics 101 The basic 101 level course teaches the fundamentals of Bioinformatics and the use of Perl scripting for automating sequence analysis. This is an introductory course for those who want to obtain a basic understanding of Bioinformatics and can be completed in 2-3 months. More...
Advanced Perl Programming for Bioinformatics	Languages	Perl for Bioinformatics 201 201 is an advanced level course and the 7 modules together describe the tools and techniques that are currently used in the industry for such diverse tasks as genome annotation, comparative genomics, new target identification and so on. During the course students will be required to read and analyze scientific papers on Bioinformatics and Genomics and complete assignments in Genomics and programming. Perl 201 covers the basic aspects of Molecular Biology, Bioinformatics and Genomics and students will therefore get ample opportunity to understand the biology behind Bioinformatics during the course of the training. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Introductory Java for Bioinformatics	Languages	101. Introductory Java for Bioinformatics The basic Java 101 level course teaches the fundamentals of Bioinformatics and the use of Java 2 Standard Edition (J2SE) technologies for building robust enterprise application for Bioinformatics applications. This is an introductory course for those who want to obtain a basic understanding of J2SE and Bioinformatics and can be completed in 2-3 months. More...
Advanced Java for Bioinformatics	Languages	201. Advanced Java for Bioinformatics Java 201 is an advanced level course and the 5 modules together describe the tools and techniques that are currently used in the industry for building Java 2 Enterprise Edition (J2EE) applications for genomics and bioinformatics analyses. More...
Foundation Course in Biotechnology	Functional Analysis	Basics of Biotechnology This foundation course is for individuals who do not have prior (formal or informal) training in molecular biology and modern day recombinant DNA technologies. These are typically students with non-biology backgrounds such as IT or computer science professionals, engineers, attorneys, and others who are seeking to acquire a basic but firm understanding of the science of biotechnology that they can apply immediately at work (without needing to acquire a University-level degree). Coursework is based on the research method where students are trained to read and critique original research articles and supporting materials with the objective of giving them a first-hand experience of the process of scientific inquiry - formulating the hypothesis, experimental design and conduct, and the reporting of findings supported by veriafiable, reproducible experimental data. More...
Foundation Course in Bioinformatics	Languages; Comparative Genomics	Basics of Bioinformatics What truly differentiates a bioinformaticist from a biologist is the ability to perform data extraction, organization, mining, analysis and interpretation in a high-throughput manner as against in a manual, piecemeal fashion, which is both extremely tedious and time intensive. This training helps students achieve tremendous productivity by giving them the ability to automate routine and highly data intensive bioinformatics tasks. The focus of the foundation course in Bioinformatics is on using Perl's powerful regular expression and pattern searching libraries for analyzing any kind of biological data, viz., DNA and protein sequences, gene expression data, etc. and using its in-built modules and libraries to build"wrappers" around essential genomics tools such as homology searching, sequence alignment, gene prediction, etc., to create automated routines for web-based sequence analysis. More...
Mathematical Modeling in Bioscience Online Graduate Certificate	Graduate Certificate Program; Statistics; Systems Biology; Computer Science; Microbiology	The online graduate certificate in Mathematical Modeling in Bioscience will provide those with a traditional background in science, mathematics, or technology the skills and content knowledge needed for work in the high-demand, highly-relevant area of mathematical and computational bioscience. Five online courses are required for the completion of the certificate, which will cover the fundamentals of predictive modeling, data mining and visualization, mathematical modeling in biomedicine and the study of computational complexity that is required for data science. More...
Analytics and Predictive Modeling	Statistics	This is a course in predictive modeling, machine learning, and basic informatics with applications to business analytics and biomedical data mining. Emphasis is on algorithms implementing precision-recall analysis, the receiver operating characteristic, logistic regression, neural networks, the quantification of uncertainty, and systems modeling. Emphasis is on the mathematics necessary for the use and interpretation of important algorithms used in data mining, analytics, and machine learning. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Complex Networks and Systems	Systems Biology	This course introduces the student to the study of complex networks through the lens of graph theory. Concepts of the mathematical properties of networks such as distance, connectivity, expansibility and clusters or hubs (centrality) are studied. Computational tools and data visualization techniques are also studied. Applications with emphasis on recent work regarding properties of biological networks are covered. More...
Mathematical Modeling Using Graph Theory	Computer Science	This course introduces the student to applied graph theory. Graph theoretical concepts will be approached as models for practical, real-world problems. The course will provide an introduction to graph modeling, integrated with applications based on emerging methods and needs. The emphasis is both on graphs as models – communication networks, for example – and on the algorithms used for obtaining information from those models. More...
Modeling of Infectious Diseases and Social Networks	Microbiology; Systems Biology; Computer Science	This course integrates mathematical model formulation, qualitative model analysis, computer simulation, and data analysis. All these areas are explored in the context of infectious diseases of human populations. More precisely, this course reviews topics of current interest in the following fields: theoretical ecology (e.g., predator-prey interactions); mathematical epidemiology (e.g., basic reproductive number); theoretical immunology (e.g., antigenic variation); evolutionary game theory (e.g., Nash equilibria); and social networks (e.g., sexual-partner networks). More...
Stochastic Modeling	Statistics	This is a course in stochastic modeling with an emphasis on applications and computation. Topics covered include stochastic modeling and simulation using discrete-time Markov chains, continuous-time Markov chains, and stochastic differential equations. More...
Bioinformatics Approaches to Identify Causative Sequence Variants in Farm Animals	Comparative Genomics; DNA Sequencing Technology; Expression Analysis; Systems Biology; Variant Analysis;	The training is mainly intended for researchers that want or already use techniques like genome-wide SNP genotyping, candidate gene sequencing, transcriptome sequencing and other bioinformatics tools in their work to elucidate the specific contributions of genetic and other factors in shaping the phenotypic variability in farm animals. More...
STAO 2014 Understanding a Genetic Disease Thanks to Bioinformatics	Comparative Genomics	This workshop covers several bioinformatics tools and databases (genome browser, alignment tool, BLAST, dbSNP, UniProtKB, PDB) in the context of the discovery of a rare variant leading to the production of a non-functional insulin in a Norwegian family. More...
Metagenome Data Analysis Workshop, May 21-23, 2014	Metagenomics	This is a SciLifelab and AllBio workshop on the analysis and interpretation of metagenomics data. In this workshop we will combine talks by experts in the field with practical tutorials guiding the participants in the analysis of representative datasets. More...
UPGMA Worked Example	Phylogenomics	A walkthrough of clustering 7 biological sequences (A-G) using the Unweighted Pair-Group Method with Arithmetic mean (UPGMA) method. Note that UPGMA is actually a generic method and thus the walkthrough could apply to any objects A-G for which pairwise distances can be calculated. A small CGI site for generating a UPGMA tree from a distance matrix can be found here. More...
QuickGuides	Languages	A range of Quick Guides to commonly used bioinformatics tools and resources. More…
Basic Bioinformatics and HOPE	Comparative Genomics	Many bioinformatics tools have been developed over the last decennium, most of which were meant to be used in the lab of the life scientist. Unfortunately, only a few made it, because the tools are often too non-intuitive and too much a black box to the life scientist. Therefore Hanka Venselaar developed HOPEto at least make the explanation of the phenotypic effect of mutations in (human) proteins intuitive for the non-bioinformatics expert. We developed this course to explain the basics of this program, and the underlying theory. More...
Perl 1 Training Course - for Programming Beginners	Languages	A set of slides from The Sainsbury Laboratory Perl course for absolute beginners. More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
RNA-Seq Analysis 2014 Module 4 - Isoform Discovery and Alternative Expression	Expression Analysis	Explore use of Cufflinks in reference annotation based transcript (RABT) assembly mode and 'de novo' assembly mode. Both modes require a reference genome sequence. More...
RNA-Seq Analysis 2014 Module 3 - Expression and Differential Expression	Expression Analysis	• Get FPKM style expression estimates using Cufflinks • Perform differential expression analysis with Cuffdiff • Perform summary analysis with CummeRbund • Downstream interpretation of expression analysis (multiple testing, clustering, heatmaps, classification, pathway analysis, etc.) More...
RNA-Seq Analysis 2014 Module 2 - Alignment and Visualization	Expression Analysis	• Use of Bowtie/TopHat • 'Regular mode' vs. 'Fusion mode' • Introduction to the BAM format • Basic manipulation of BAMs with samtools, etc. • Visualization of RNA-seq alignments - IGV • BAM read counting and determination of variant allele expression status More...
RNA-Seq Analysis 2014 Module 1 - Introduction to RNA-Seq Analysis	Expression Analysis	• Basic introduction to biology of RNA-seq • Experimental design considerations • Commonly asked questions • Data visualization using IGV More…
Bioinformatics Introductory Module	Comparative Genomics	This Bioinformatics Introductory Module for self-study was designed for future students of the Molecular Mechanisms of Disease (MMD) master's program at Radboud University Medical Centre. To level out the starting differences in bioinformatics knowledge between this incoming heterogeneous group of students as much as possible, we have designed an introductory course module that should allow them – via self study and hands-on exercises – to acquire sufficient basic bioinformatics knowledge. More...
Pathway and Network Analysis 2014 Module 6 - Gene Function Prediction	Metabolomics; Functional Analysis; Systems Biology	• Functional association networks and gene function prediction • Homology based prediction • Guilt-by-association: GeneMANIA More…
Pathway and Network Analysis 2014 Module 5 - Network Visualization	Systems Biology	• Introduction to network visualization • Visualizing omics data on a network or pathway • Active modules in Cytoscape More…
Pathway and Network Analysis 2014 Module 4 - Pathway and Network Analysis	Systems Biology	• Introduction to pathway and network analysis • Basic network concepts • Types of pathway and network information • Pathway Databases: Reactome, KEGG, etc. • Pathway analysis of large scale genomics data sets, including cancer genomics More…
Pathway and Network Analysis 2014 Module 3 - Gene Regulation Analysis	Systems Biology	• Overview of transcription • Data sources for regulatory data - Chromatin IP, DNA hypersensitivity, other chip data • Basics of processing data • Pattern discovery More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Pathway and Network Analysis 2014 Module 2 - Finding Over-Represented Pathways	Systems Biology; Functional Analysis	• Over-representation analysis (ORA) • Statistics for detecting over-representation e.g. hypergeometric test, GSEA • Multiple testing correction: Bonferroni, Benjamini-Hochberg FDR • Filtering Gene Ontology e.g. using evidence codes More…
Pathway and Network Analysis 2014 Module 1 - Introduction to Gene Lists	Systems Biology	• Gene list analysis overview: Workflow of concepts and tools from gene list to pathway analysis • Where do gene lists come from? • Working with gene function information More…
BLAST and Multiple Sequence Alignment (MSA) Programs	Comparative Genomics	The rapid identification of pathogens infecting livestock is essential to appropriately respond to the threat. The number and the variety of pathogen sequenced genomes have been growing more dramatically these recent years, because of the new sequencing technologies. This wealth of new data is very useful to the research field through the development of bioinformatics tools and databases that deal with large amount of sequences. Among them, BLAST (Basic Local Alignment Search Tool) and MSA () programs are very efficient for protein or nucleotide sequence similarity search. The present course introduces the main biological databases, alignment tool BLAST and Multiple sequence alignments (MSA) programs, and interpretation of results. More...
Phylogenetics of Animal Viral Pathogens	Phylogenomics	The vast diversity of the pathogens affecting livestock demands a very specific diagnostic procedure in identification and characterization of each pathogen. In this context, the enormous amount of sequence and genotype data is being generated on animal pathogens, which is further useful in understanding their pathogenicity and molecular epidemiology. The usage of this data in developing efficient molecular diagnostic tools needs basic understanding of the phylogenetic analysis. Phylogenetic classification, construction of trees, interpretation unveils the geographical distribution and migration of pathogens which helps in better management of animal diseases. The present course is designed with introduction to phylogenetics, tools, building and interpreting trees and finally its application to veterinary diagnostics. Though the course is driven in veterinary aspects, the same implicates to the human and plant pathogen study. More...
Working with Affymetrix CEL Files in R	Languages; Expression Analysis	This tutorial shows how to download some public Affymetrix microarray data, load the data into R, calculate expression values and do some very simple plotting. More…
Simple Plotting in R	Languages	This quick and simple tutorial demonstrates some of the easy plotting tools in the R core software. More…
Unix Fundamentals	General Computing	This self-learning tutorial aims to present the UNIX environment and to provide the most basic commands to users with no or very little UNIX knowledge. More...
Introduction to Multiple Sequence Alignments (MSAs) and Phylogenies	Comparative Genomics	Slides used for teaching an introduction to phylogenies and MSAs in the context of phylogenies for the first day of a two-day course on MSAs at Cambridge University, in the UK, in December 2013. More…
Clinical Bioinformatics I - Tutor Notes	Variant Analysis; Comparative Genomics; Functional Analysis	Clinical Bioinformatics I is a 10 credit module of the new MSc in Clinical Bioinformatics, delivered by Nowgen/NGRL and the University of Manchester in the UK. More…
Sequence Comparison - Undergraduate Lab	Comparative Genomics	This lab makes use of EMBOSS programs, prss in the FASTA package, as well as the NCBI BLAST website. More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Introduction to Biopython	Languages	This is a module from the "Python for Biologists" course. The module presents an introduction to Biopython. It shows how to deal with sequences and sequence records, how to download records from NCBI databases, how to run Blast and how to parse XML Blast outputs. More...
Using R with Python	Languages	This is a module from the "Python for Biologists" course. It describes the Python module interfacing the R package for statistics. The module shows how to calculate mean, standard deviation, z-score and p-value of a set of numbers, and how to generate plots. Input files for the scripts presented are also provided. More...
Searching Data Using Python	Languages	This is a module from the "Python for Biologists" course. It describes how to use Python dictionary and set data structures to search your data. In particular, how to use a dictionary to represent the genetic code table and use it to translate a nucleotide sequence into a protein sequence, and how to use sets to find unique records in two datasets and remove redundancy. More...
Pattern Matching	Languages; Computer Science	This is a module from the "Python for Biologists" course. It teaches how to do pattern matching in Python, i.e. how to find a substring (or a set of substrings) in a string. To this aim, it introduces the regular expression syntax, and the tools needed to search regular expressions in biological sequences and in regular text, such as PubMed abstracts. Exercises and suggested solutions are presented in a separate file. More...
Writing Functions in Python Programming	Languages	This is a module from the "Python for Biologists" course. It deals with functions and how to write and use them. It also introduces namespaces and the tuple data structure. The module contains several exercises and suggested solutions. The text of exercises is also provided in a separate file. More...
Python Programs	Languages	This is a module from the "Python for Biologists" course. It deals with Python programs, how to write and run them, and how to provide input and generate output. The module also contains exercises and suggested solutions. More…
Bioinformatics for Mass Spectrometry Analysis	Functional Analysis	This tutorial on Bioinformatics for Mass Spectrometry Analysis introduces the basic ideas behind mass spectrometry and bioinformatics for protein identification from mass spectrometry data. More…
Introduction to Bioinformatics	Comparative Genomics; Databases	An introduction to bioinformatics for bench biologists delivered as part of the EMBL Australia Masterclass on Protein Sequence Analysis. Focuses on using UniProt to explore different reasons why information inferred by "direct assay" and "prediction" could be wrong, and what we can do to spot it. More...
Interpreting Phylogenies	Phylogenomics	Uses examples taken from several published papers to explore some of the assumptions and concepts we use when presenting and interpreting phylogenetic trees. Includes exercises on visulaising and manipulating trees using Dendroscope and NJplot to reinforce some of these ideas, while also providing a very basic overview of steps involved in a generic phylogenetic analysis. More...
An Introduction to Unix, Perl and Python	Languages	This course provides an introduction to Unix, Perl, and Python. More…
Bioinformatics for Mass Spectrometry Analysis	Functional Analysis	The purpose of this course is to teach students the fundamental concepts underlying the analysis of proteins using mass spectrometry. More…
Parsing Data Records Using Python Programming	Languages	This is a module from the "Python for Biologists" course. One typical problem in bioinformatics is parsing data files. This module explains how to parse FASTA files and GenBank records. It also introduces the if/elif/else construct to make choice in programming and the list data structure. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Introduction to Unix	General Computing; Languages; Databases	• Introductory lecture to the Unix/Linux command-line • Description of the computer shell and the command-line interface • Differences between graphical and command-line interfaces • The most common Unix/Linux commands are provided More…
RNA-Seq Analysis	Expression Analysis	An overview of the analysis of gene expression in plants using RNA-seq data. This course provides a foundation on the tuxedo software suite: TopHat, Cufflinks, CummeRbund. More…
Georgia Tech Bioinformatics Phd Degree	Comparative Genomics; DNA Sequencing Technology; Expression Analysis; Systems Biology; Variant Analysis	Georgia Tech Bioinformatics PhD Degree Courses are offered on-site at Georgia Tech. A. 9 credit hours of Bioinformatics and Computational Bioscience (e.g. BIOL 7023 and BMED 6780, BMED 7027) B. 9 credit hours in Biology, Biochemistry or Biomedical Engineering (e.g. BIOL 6608, BIOL 7668, CHEM 6572) C. 9 credit hours of Mathematics and Computer Science (e.g. MATH 6266, MATH 6267, CS 6411) D. 9 credit hours of courses in an approved minor E. 24 research credit hours More...
Georgia Tech Professional MS Bioinformatics Degree	Comparative Genomics; DNA Sequencing Technology; Expression Analysis; Systems Biology; Variant Analysis; HPC/Cloud; Metagenomics; Computer Science; Statistics	Georgia Tech Professional MS Bioinformatics Degree Courses are offered on-site at Georgia Tech. CORE CURRICULUM Offered fall semesters: CS 4710 Introduction to Computing Concepts in Bioinformatics Biol 4150/6150 Genomics and Applied Bioinformatics Biol 8803 Programming for Bioinformatics Math 6705 Modeling and Dynamics Offered spring semesters: Biol 7210 Computational Genomics Offered every semester (and summer terms): CS 4400 Introduction to Database Systems Math 3215 Introduction to Probability and Statistics More...
Introduction to Computing Concepts in Bioinformatics	General Computing	This course is part of the Georgia Tech Professional MS Bioinformatics Degree. Introduction to programming concepts and computing tools such as formal models and algorithms with applications from conceptual biology. More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Genomics and Applied Bioinformatics	Comparative Genomics	This course is part of the Georgia Tech Professional MS Bioinformatics Degree 1. DNA Sequencing 2. DNA sequence annotation 3. NCBI Resources and other on-line databases 4. Pairwise sequence alignment 5. BLAST and advanced BLAST 6. Multiple sequence alignment 7. Evolutionary trees and molecular phylogenetic inference 8. Gene expression 9. Affymetrix microarray gene expression data 10. RNA-Seq 11. Clustering and pathways 12. Protein structure 13. Homology modeling 14. Genome variation and phenotype 15. Genomics and personalized medicine More...
Programming for Bioinformatics	Computer Science; Languages	This course is part of the Georgia Tech Professional MS Bioinformatics Degree New graduate lecture courses in areas of current interest. More…
Modeling and Dynamics	Systems Biology	This course is part of the Georgia Tech Professional MS Bioinformatics Degree Mathematical methods for solving problems in the life sciences. Models-based course on basic facts from the theory of ordinary differential equations and numerical methods of their solution. Introduction to the control theory, diffusion theory, maximization, minimization and curve fitting. More...
Computational Genomics	Computer Science; Languages; Webtools; Comparative Genomics	This course is part of the Georgia Tech Professional MS Bioinformatics Degree The science of genomics involves the intersection of experimentation and computation. Computers are quite obviously required to handle the massive amount of data produced by genome sequencing projects. More importantly however, genome sequencing efforts yield 'information' alone, which can only be converted into 'knowledge' through the use of computers. In this class, the students will convert raw genomic information (i.e. sequence reads) into knowledge through the use of computational genomics tools and applications. The class will be provided with unassembled genome sequence data from the Centers for Disease Control and Prevention (CDC) and will proceed through five distinct stages of analysis and interpretation of that data. More...
Introduction to Database Systems	Databases	This course is part of the Georgia Tech Professional MS Bioinformatics Degree • Basic concepts • Conceptual database design - Entity-Relationship Model • DBMS Design Methodology • Relational Data Model - introduction, relational algebra, relational calculus • Mapping from ER Model to Relational Model • SQL Query Language • Relational database design - normal forms, functional dependencies • Physical database design - storage structures More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Introduction to Probability and Statistics	Statistics	This course is part of the Georgia Tech Professional MS Bioinformatics Degree This course is a problem oriented introduction to the basic concepts of probability and statistics, providing a foundation for applications and further study. More...
Microbial Genomics	Microbiology	This course is part of the Georgia Tech Professional MS Bioinformatics Degree New graduate lecture courses in areas of current interest. More…
Mathematical Biology	Systems Biology; Functional Analysis; Computer Science	This course is part of the Georgia Tech Professional MS Bioinformatics Degree. An introduction to practical applications of mathematical models to help unravel the underlying mechanisms involved in biological processes. More…
Case Study: RNA-seq Data Analysis. Basic Workflow for Analyzing RNA-seq Datasets	Expression Analysis; Languages	This course is presented by Harvard University on edX. You'll learn how to analyze RNA-seq data with step-by-step instructions in order to investigate relevant biological questions. More…
Advanced Statistics for the Life Sciences	Statistics; Languages	This course is presented by Harvard University on edX. You'll learn: • Intermediate R programming in the context of analyzing life science data • Application of statistical techniques commonly used in the analysis of high throughput data More…
Introduction to Linear Models and Matrix Algebra. The Basics of Linear Models You Need to Know for Data Analysis in the Life Sciences	Statistics	This course is presented by Harvard University on edX. You'll learn: • Linear algebra, including matrix notation and matrix operations • How to fit linear models in R to test hypotheses and analyze data More…
Introduction to Bioconductor	Languages	This course is presented by Harvard University on edX. You'll learn: • How to use the Bioconductor project software packages • Methods to analyze data from next generation sequencing and microarray technologies More…
Case Study: Variant Discovery and Genotyping. Basic Workflow for Performing Genetic Variant Discovery and Genotyping	Languages	This course is presented by Harvard University on edX. You'll learn how to find genetic variants in DNA re-sequencing datasets with step-by-step instructions in order to investigate relevant biological questions. More…
Case Study: ChIP-seq Data Analysis. Basic Workflow for Analyzing ChIP-seq Datasets.	Expression Analysis; Languages	This course is presented by Harvard University on edX. You'll learn how to analyze ChIP-seq datasets with step-by-step instructions in order to investigate relevant biological questions. More...
Case Study: DNA Methylation Data Analysis. Basic Workflow for Analyzing DNA Methylation Data	Expression Analysis; Languages	This course is presented by Harvard University on edX. • You'll learn how to analyze DNA methylation data with step-by-step instructions in order to investigate relevant biological questions. More…
Useful Links to Genomics Tools	Comparative Genomics	Links to these webtools (contains no annotation): Tools and Databases for Genome Annotation and Comparative Analyses Tools and Databases for SSU rRNA Gene Analyses Tools for Phylogenetic Analyses Other Bioinformatics Tools More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Microbial Genomics and Infectious Diseases	Microbiology	Microbial Genomics and Infectious Diseases by David A. Relman, M.D. - discusses how advances in genomic technologies have permitted a better understanding of the biology of microbes, pathogenic or benign, and the effects of genomic information on our understanding of and response to microbial infections. More...
New England Journal of Medicine Series on Genomic Medicine	Comparative Genomics	The publication of the draft sequence of the human genome in 2000 heralded the promise of incorporating genomic knowledge into patient care. Ten years later, a new series of articles, beginning with the August 26, 2010 issue of the New England Journal of Medicine, is taking a comprehensive look at what has been accomplished in the quest to screen, prevent and treat disease in the new world of genomic medicine. More...
What's Bugging You? The Intersection of Genomics and Infectious Disease	Microbiology	Genomics has revolutionized the tools used by clinicians to detect and treat infectious diseases. By sequencing the human microbiome, researchers have identified scores of previously unidentified species, which coexist with their human host, and exploration has begun to understand how disease states alter the host microbial flora. Genomic-based diagnostic testing is more rapid and accurate than traditional cultures, and dramatically changed the clinician and public health approach to sexually transmitted and hospital-acquired infections. More...
Case Studies in Reproducible Research in Bioinformatics and Other Disciplines	Reproducible Research	This web page was created to provide convenient links to resources on reproducible research in bioinformatics. More....
Forum: Reproducible Research in High-Throughput Biology: Case Studies in Forensic Bioinformatics	Reproducible Research	A well delivered, highly entertaining lecture on the importance of reproducible research in high-throughput biology. Keith Baggerly walks us through an exercise in 'forensic bioinformatics.' More…
Rosalind Python Village	Languages	Rosalind is a platform for learning bioinformatics and programming through problem solving. Python Village: If you are completely new to programming, try these initial problems to learn a few basics about the Python programming language. You'll get familiar with the operations needed to start solving bioinformatics challenges in the Stronghold. More...
Rosalind Bioinformatics Stronghold		Rosalind is a platform for learning bioinformatics and programming through problem solving. Bioinformatics Stronghold Discover the algorithms underlying a variety of bioinformatics topics: computational mass spectrometry, alignment, dynamic programming, genome assembly, genome rearrangements, phylogeny, probability, string algorithms and others. More...
Rosalind Bioinformatics Armory		Rosalind is a platform for learning bioinformatics and programming through problem solving. Bioinformatics Armory: Ready-to-use software tools abound for bioinformatics analysis. Whereas in the Stronghold you implement algorithms on your own, in the Armory you solve similar problems by using existing tools. More...
Rosalind Bioinformatics Textbook Track		Rosalind is a platform for learning bioinformatics and programming through problem solving. Bioinformatics Textbook Track: A collection of exercises to accompany Bioinformatics Algorithms: An Active-Learning Approach by Phillip Compeau & Pavel Pevzner. A full version of this text is hosted on stepic.org. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Rosalind Algorithmic Heights	Computer Science	Rosalind is a platform for learning bioinformatics and programming through problem solving. Algorithmic Heights: A collection of exercises in introductory algorithms to accompany "Algorithms", the popular textbook by Dasgupta, Papadimitriou, and Vazirani. More...
Emacs + org-mode + Python in Reproducible Research; SciPy 2013 Presentation	Reproducible Research	The author presents his solution to tracking big data projects. More…
Reproducible Research	Statistics; Languages; Reproducible Research	This Johns Hopkins course is offered through Coursera. Course 5 in Data Science Specialization Certificate: Reproducible Research In this course you will learn to write a document using R markdown, integrate live R code into a literate statistical program, compile R markdown documents using knitr and related tools, and organize a data analysis so that it is reproducible and accessible to others. More...
JGI Microbial Genomics & Metagenomics Workshop	Microbiology	The U.S. Department of Energy Joint Genome Institute (DOE JGI) will be offering two five-day workshops on Microbial Genomics and Metagenomics during 2015. Each workshop will have a similar agenda and content, and will include seminars and extensive hands-on tutorials on how to use the IMG family of systems for comparative analysis of isolate genomes and metagenomes. More...
An Introduction to Metagenomics Data Analysis	Metagenomics	Vall d'Hebron Institut de Recerca's (VHIR) Metagenomics Training. Session 1. 2013/08/26. An Introduction to Metagenomics Data Analysis. More…
Introduction to Metagenomics. Applications, Approaches and Tools (Bioinformatics for Biological Researchers Course - CSIC, Blanes)	Metagenomics	Vall d'Hebron Institut de Recerca (VHIR) 05/28/2014 More...
Tools for Metagenomics with 16S/ITS and Whole Genome Shotgun Sequences	Metagenomics	Presented at Cornell Symbiosis symposium. Workflow for processing amplicon based 16S/ITS sequences as well as whole genome shotgun sequences are described. More...
Single-Cell Genomics		16 collected videos on single-cell genomics, single-cell mRNA sequencing, single-cell gene expression, and other scientific applications performed on the Fluidigm C1 Single-Cell Auto Prep System. More…
Single Cell Research: An Overview of Recent Single Cell Research Publications Featuring Illumnia Technology		This report was compiled by Illumina to market their technology, but it does contain some interesting information. Contents Applications Sample Preparation Data Analysis DNA Applications Epigenetics RNA Applications More…
UNIX Tutorial for Beginners	Languages	Introduction to the UNIX Operating System. More…
Bioconductor Courses and Conferences	Languages	This is a list of courses and conference presentations on Bioconductor. Many of the links lead to course materials such as slides. More…

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Google Developers ' R Programming Video Lectures	Statistics; Languages	These videos provide a solid foundation for programming tools, data manipulation, and functions in the R language and software. The series of short videos is organized into four subsections: intro to R, loading data and more data formats, data processing and writing functions. More...
De Novo Genome Assembly	Comparative Genomics	Lex Nederbragt at the Norwegian Sequencing Center put together this course on de novo genome assembly and released all the course materials on Github under Creative Commons/Public Domain. More…
Bioinformatics for Cancer Genomics (BiCG) (2014)		Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. The CBW has developed a 5-day workshop covering the key bioinformatics concepts and tools required to analyze cancer genomic data sets. More...
Exploratory Analysis of Biological Data Using R (2014)	Statistics; Languages	Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. Before we can begin to apply rigorous statistical tools to research data, we often need to approach our data intuitively, and look for meaningful associations, surprising patterns, or irregularities, to formulate hypotheses. This is commonly referred to as Exploratory Data Analysis–EDA. This workshop introduces the essential tools and strategies that are available through the free statistical workbench R. More...
Informatics on High-Throughput Sequencing Data (2014)		Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. With the introduction of high-throughput sequencing platforms from Illumina, Roche and ABI, it is becoming feasible to consider sequencing approaches to address many research projects. However, knowing how to manage and interpret the large volume of sequence data resulting from such technologies is less clear. The CBW has developed a 2-day course covering the bioinformatics tools available for managing and interpreting high-throughput sequencing data. More...
Informatics and Statistics for Metabolomics (2014)	Metabolomics; Statistics	Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. The workshop will cover many topics ranging from understanding metabolomics technologies, data collection and analysis, using pathway databases, performing pathway analysis, conducting univariate and multivariate statistics, working with metabolomic databases and exploring chemical databases. Participants will be given various data sets and short assignments to assist with the learning process. More...
High-Throughput Biology: From Sequence to Networks (2015)		Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. The Canadian Bioinformatics Workshops, in collaboration withCold Spring Harbor and New York Genome Center, has developed a comprehensive 7-day course covering the key bioinformatics concepts and tools required to analyze DNA- and RNA-sequence reads using a reference genome. More...

Brief View of Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Course Description
Introduction to R (2015)	Languages	Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. R is rapidly becoming the most important scripting language for both experimental- and computational biologists. It is well designed, efficient, widely adopted and has a very large base of contributors who add new functionality for all modern aspects of data analysis and visualization. Moreover it is free and open source. However, R's great power and expressivity can at first be difficult to approach without guidance, especially for those who are new to programming. This workshop introduces the essential ideas and tools of R. More...
Microarray Expression Analysis (2015)	Expression Analysis	Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. Microarrays remain the most popular, most affordable, and best-established technique for functional genomics. Hundreds of thousands of datasets have been generated to address diverse aspects of biology. This workshop provides an overview of the analysis of microarray data ranging in size from one to two samples to hundreds of samples. The goal of this workshop is to provide procedures and analysis workflows for the analysis of microarray datasets. More...

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Avaliable	Notes
Introduction to Clinical Genomics	Variant Analysis; Databases	Clinical Genomics	This class describes how to access information about genes and their variants associated with diseases and the impact of variants on drug response and dosing guidelines. The class also provides an introduction to determination of the impact of the variants on function, pathogenicity or deleteriousness. Several publicly available resources will be covered. Topics to be covered: Types of mutations; Nomenclature for the description of sequence variants by the Human Genome Variation Society (HGVS); Introduction to resources, such as ClinVar, Clinical Genomic Database (CGD), dbSNP, Online Mendelian Inheritance in Man (OMIM), Exome Variant Server (EVS), Genetic Testing Registry (GTR), Phenotype-Genotype Integrator (PheGenI) and 1000 Genomes, to access information about genes and their variants associated with diseases; Introduction to resources, such as Clinical Pharmacogenetics Implementation Consortium (CPIC) and Pharmacogenomics Knowledgebase (PharmGKB), to obtain information about the impact of variants on drug response and dosing guidelines; Introduction to resources, such as Combined Annotation Dependent Depletion (CADD), Variant Effect Predictor, Variant Reporter, wANNOVAR and Site Directed Mutator (SDM), for functional, pathogenicity or deleteriousness annotation of variants	Bioinformatician, Epidemiologist	Introductory	http://nihlibrary.nih.gov/Services/Bioinformatics/Pages/bioclasstrain.aspx	Lecture	4/15/2015	NIH Library Training Room, Bethesda, MD	1:30pm-4:00pm EST	free to NIH and HHS staff	Travel	NIH Library (training is managed by CIT)			301.594.6248	CITTraining@mail.nih.gov		Bethesda	MD					
Ingenuity Pathway Analysis	Metabolomics	Ingenuity; Pathway Analysis	N/A	Bioinformatician	Introductory	http://nihlibrary.nih.gov/Services/Bioinformatics/Pages/bioclasstrain.aspx	Lecture	4/16/2015	NIH Library Training Room, Bethesda, MD	10:00am-4:00pm EST	free to NIH and HHS staff	Travel	NIH Library (training is managed by CIT)			301.594.6248	CITTraining@mail.nih.gov		Bethesda	MD					
Gene Resources: From Transcription Factor Binding Sites to Function	Databases; Functional Analysis	Gene Transcription Factor Binding Sites; Gene Function	This course describes how to obtain information about a human gene at all levels of the central dogma of life, genome, transcript and protein, and prediction of transcription factors regulating its expression. It also covers information about single nucleotide polymorphisms (SNPs) in the gene and which ones are known to be associated with disease	Bioinformatician	Introductory	http://nihlibrary.nih.gov/Services/Bioinformatics/Pages/bioclasstrain.aspx	Lecture	5/5/2015	NIH Library Training Room, Bethesda, MD	1:30pm-4:00pm EST	free to NIH and HHS staff	Travel	NIH Library (training is managed by CIT)			301.594.6248	CITTraining@mail.nih.gov		Bethesda	MD					
Expression Data Analysis on Microarray and NGS in Partek	Expression Analysis	Expression Data Analysis; Microarrays; NGS; Partek	N/A	Bioinformatician	Introductory	http://nihlibrary.nih.gov/Services/Bioinformatics/Pages/bioclasstrain.aspx	Lecture	5/14/15-5/15/2015	NIH Library Training Room, Bethesda, MD	9:00am-4pm (2 days)	free to NIH and HHS staff	Travel	NIH Library (training is managed by CIT)			301.594.6248	CITTraining@mail.nih.gov		Bethesda	MD					
Pathway Studio	Metabolomics; Functional Analysis	Pathway Studio; Pathway Analysis	N/A	Bioinformatician	Introductory	http://nihlibrary.nih.gov/Services/Bioinformatics/Pages/bioclasstrain.aspx	Lecture	5/20/2015	NIH Library Training Room, Bethesda, MD	1:00pm-3:00pm	free to NIH and HHS staff	Travel	NIH Library (training is managed by CIT)			301.594.6248	CITTraining@mail.nih.gov		Bethesda	MD					
CS101A Perl for Biologists, Level 1	Languages	Perl	Taught in the context of biological research, this course teaches biologists how to use the scripting language Perl to automate certain tasks. Armed with some knowledge and hands-on experience with a programming or scripting language, scientists taking a CS101 course at the Bioinformatics Organization will be able to perform basic software development tasks and phrase research questions in the context of the language. As a result, they will be able to appreciate and use computers better in their organization and communicate better with their IT group. No experience is required, although prior experience with any other programming language will be helpful. Math skills will also be useful. Session 1. Installing and running simple Perl programs Session 2. Variables (scalars, arrays), printing, variable interpolation, string operations Session 3. Mathematical, conditional and logical operators, file input/output, loops (if-then-else, for, while) Session 4. List operations, regular expressions, functions, introduction to BioPerl. Students will be assigned a project. This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00	Bioinformatician; Laboratorian	Introductory	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	$300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			Level 2 and 3 are also available.
CS101A Perl for Biologists, Level 2	Languages	Perl; BLAST; Microarrays	Taught in the context of biological research, this course shows biologists how to use the scripting language Perl to automate certain tasks. It is a continuation of CS101A Perl for Biologists, Level 1 and covers advanced topics and projects. Session 1. Perl basics (a quick review) • How to use Perl commands in scripts and functions • Good programming practices • Specials notes, shortcuts, basic commands you may have forgotten • Case study: Automating BLAST o Downloading sequences and formatting them for querying using the "formatdb.exe" program o Creating FASTA file with sequences on which to use BLAST o Writing a program to call "blastall.exe", finding the best hits • Case study: Gene expression analysis o Reading ~20000 gene scores in a text file corresponding to 8 samples, and a gene information file o Performing thresholding and normalization for this data o Calculating fold change, difference, t-statistics, p-value, confidence intervals, etc. o Outputting the filtered results, sorted by lower confidence interval, and removing Affymetrix control genes Session 2. Creating and using modules, namespaces, packages. References and object-oriented programming Session 3. The Perl DBI and DBD for the MySQL DBMS. Using BioPerl for sequence analysis Session 4. Project: Microarray database with sequence information • Use SantaLucia rules to calculate the delta-G value of all 25-mer Perfect Match (PM) probe sequences. • Create tables in a database using Perl to accommodate the data. This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00	Bioinformatician	Intermediate	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	$300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			Level 1 and 3 are also available.
CS103A Perl for Biologists, Level 3	Languages	Perl	Taught in the context of biological research, this course shows biologists how to use the scripting language Perl to automate certain tasks. It is a continuation of CS102A Perl for Biologists, Level 2 and covers advanced topics in regular expressions, objects, modules will be covered, along with tips and tricks to fine-tune programs and resolve bugs. Perl for Biologists, Level 1 & 2 or equivalent training is required. The course is divided into 4 sessions. The 5th session is reserved for project discussion and any other issues the students may want to discuss. Session 1. All topics of the Level 1 and 2 courses, with some new case studies to understand the best use of modules for developing solutions in bioinformatics. Session 2. Regular Expressions in much detail, using them in case studies involving gene annotation and literature mining. Session 3. Object oriented programming once again, and some new case studies will be covered, depicting solutions to real life situations. Session 4. Exception handling and debugging. Software development project using BioPerl will be done. This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00	Bioinformatician	Advanced	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			Level 1 and 2 are also available.
CS101B R for Biologists, Level 1	Languages	R	Taught in the context of biological research, this course helps biologists learn how to use the statistical scripting language R for data analysis. Unlike Bioinformatics Organization course MA101A Distributions, Tests and Graphics, this course focuses on the syntax and functionality of the language R and may be used in preparation for MA101A. Armed with some knowledge and hands-on experience with a programming or scripting language, scientists taking a CS101 course at Bioinformatics.Org will be able to perform basic software development tasks and phrase research questions in the context of the language. As a result, they will be able to appreciate and use computers better in their organization and communicate better with their IT group. Session 1. Installing and running R; understanding the R interactive environment Session 2. Creating, storing and manipulating R data objects; reading data from files Session 3. Applying built-in functions on data; for-loops; if-then-else statements Session 4. Scripts, functions, packages; introduction to Bioconductor. Students will be assigned a project. This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00	Bioinformatician; Laboratorian	Introductory	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			
CS101B R for Biologists, Level 2	Languages	R	Taught in the context of biological research, this course helps biologists understand the data analysis and visualization language R. It is a continuation of CS101B R for Biologists, Level 1 and covers advanced topics and projects. Session 1. Review of basic R commands for loading, manipulating and visualizing data • How to create, manage and visualize data in R objects -- vectors, matrices, data frames, lists • Good programming practices • Specials notes, shortcuts, and basic commands that you may have forgotten • Project: Create a function that will compute the t-statistic, fold change, difference and p-value for all genes, and filter the data to keep the up- or down-regulated genes. Session 2. Case studies in linear regression, t-test, anova Session 3. Advanced graphics with par() Session 4. Bioconductor objects and algorithms; getting differentially regulated genes from Affymetrix CEL files • More case studies • Project: Use limmaGUI or affylmGUI datasets to perform an analysis. This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00	Bioinformatician	Intermediate	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			
CS101C MySQL for Biologists, Level 1	Languages; Databases	MySQL	Taught in the context of biological research, this course teaches biologists how to use the database management system MySQL to store, manage and query biological information. Armed with some knowledge and hands-on experience with a database system, scientists taking a CS101 course at the Bioinformatics Organization will be able to perform basic data storage tasks and phrase research questions in the context of the database. As a result, they will be able to appreciate and use computers better in their organization and communicate better with their IT group. No experience is required, although prior experience with any database system (Microsoft Access) will be helpful. Session 1. Fundamentals of databases and deciding what to store, and how to install a database Session 2. Creating and designing a database; populating the database with sample data Session 3. Data retrieval and manipulation concepts using SQL queries (Select, Update, Delete, Insert) Session 4. Additional topics such as interfacing the database with the Microsoft Access front end and mining the data using Perl database interface; project discussion This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00	Bioinformatician; Laboratorian	Introductory	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			
CS101D MATLAB for Biologists, Level 1	Languages	MATLAB	Taught in the context of biological research, this course helps biologists learn how to use the technical computing language MATLAB to automate certain tasks. Armed with some knowledge and hands-on experience with a programming or scripting language, scientists taking a CS101 course at the Bioinformatics Organization will be able to perform basic software development tasks and phrase research questions in the context of the language. As a result, they will be able to appreciate and use computers better in their organization and communicate better with their IT group. No experience is required, although prior experience with any other programming language will be helpful. Math skills will also be useful. Session 1. Installing and running simple MATLAB programs Session 2. Variables (scalars, arrays), printing, variable interpolation, string operations Session 3. Mathematical, conditional and logical operators, file input/output, loops (if-then-else, for, while) Session 4. List operations, regular expressions, functions, introduction to the Bioinformatics toolbox. Students will be assigned a project. This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00	Bioinformatician; Laboratorian	Introductory	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			
CS101E Python for Biologists, Level 1	Languages	Python	This course teaches biologists how to use Python as a programming language to automate routine data management tasks in biological research and solve difficult data-related computational problems. Data could be DNA or amino acid sequence, microarray data, images, mass spectrometry data, LIMS data, or any other kind of biological information. Session 1. Installation issues and simple exercises that illustrate how to create and execute simple Python programs using variables and the print statement. The Python interpreter and editor will be introduced. Session 2. Fundamentals of programming with Python, such as operators (mathematical, conditional, logical), file input/output, loops (if-then-else, for, while), etc. Session 3. Functions, hashes and object oriented programming Session 4. Installation of Python packages such as iPython, NumPy (Numeric Python), and Biopython. Some basic tasks in these packages will be covered. Project discussion. This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00	Bioinformatician	Introductory	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			
CS112A Image Processing for Biologists, Level 1	General Computing; Computer Science; Statistics	Gene Expression Analysis	This course teaches biologists how to analyze and manipulate biological images, and extract meaningful information from them, using a variety of tools. For large quantities of images that need to be analyzed with the same algorithm, the course teaches how to automate these routine tasks and generate reports in a high throughput fashion. Session 1. The different types of image file formats, and how the image data is stored in them. Tools to perform simple operations such as zoom, pan, rotate, crop, cut, paste, stretch/skew, etc. will be introduced. File format conversion and compression issues will be discussed. Session 2. Fundamentals of image processing, such as contrast and brightness adjustment, sampling, transformation Session 3. More fundamentals like filtering, registration, morphological operations. These techniques will be used to demonstrate noise removal, image deblurring, image conversion, edge detection, etc. Session 4. The automation of tasks in analyzing a single image, and then using the algorithm to analyze multiple images. GUI tool development for point-n-click users will be shown. Project discussion.F14 This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00	Bioinformatician; Laboratorian	Introductory	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			
BI231 NGS Data Analysis	Functional Analysis; Comparative Genomics; Variant Analysis; DNA Sequencing Technology	Distributions; Tests; Graphics; NGS	This course teaches biologists how to analyze data from Next Generation Sequencing (NGS) platforms. Topics to be covered include the description of sequencing strategies and platforms, experiment types, data formats, and command line tools for various workflows, such as quantification of transcripts, alternative splice forms, copy number variants, single nucleotide polymorphisms, etc. Session 1. • What is Next Generation Sequencing, and how is it different from traditional sequencing? • Various NGS technologies/platforms, experiment types and applications • Workflows for various NGS experiments Session 2. • Steps involved in implementing various NGS workflows (variant discovery, expression profiling, etc.) - working with reads, alignments, quality scores, etc. • Algorithms and tools for NGS read alignment, SNP calling, etc. • Various file formats such as SAM, VCF, BED, WIG, PILEUP, etc. Session 3. • Four different workflows for mutation discovery (CrossBow, Bowtie, BWA, MAQ) • Variant effect prediction on genes • Functional consequence of gene product variation (GO, SIFT, POLYPHEN) Session 4. • TopHat and Cufflinks for RNA-seq • Finding novel transcripts • Expression of splice variants This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00	Bioinformatician	Intermediate	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description
BI201 Gene Expression Analysis	Expression Analysis	Gene Expression Analysis; MATLAB; R; Biocinductor	This course helps to demystify Affymetrix analysis so that any researcher can take the basic steps to go from a chip image to a list of genes that are up- or down-regulated in an experiment. Various tools will be covered, e.g. Affymetrix Expression Console (replacing GCOS), Microsoft Excel, MathWorks MATLAB, and free tools like R/Bioconductor and dChip. It is geared towards researchers who conduct microarray experiments to study genome-wide expression changes and understand the underlying mechanisms of gene regulation in samples of interest. Most scientists are not able to analyze the resulting data themselves, and they are not able to get desired results using traditional tools like Microsoft Word and Excel or with advanced software provided by commercial vendors. The freeware solutions come either with a steep learning curve or as black-box interfaces that provide limited functionality with little or no technical support. In the midst of all this is the fundamental lack of understanding among scientists on how the technology works and what the fundamental parts of the analysis are. No experience is required, although prior experience with any other programming language will be helpful. Math skills will also be useful. Sessions 1 & 2. Introduction to Expression Console -- the environment, creating and saving experiments, importing and exporting data, normalization settings, from DAT->CEL->CHP->RPT files and their significance, importing and exporting data Sessions 3 & 4. dChip software: importing expression data and annotation information into dChip, normalization, gene filtering, clustering, visualization along chromosome, gene ranking by confidence intervals and pvalues for group studies, exporting to Excel Sessions 5 & 6. R/Bioconductor: installing and configuring bioconductor for gene expression analysis, obtaining normalized gene expression scores, performing statistics to obtaining differentially regulated genes in time series or group studies Sessions 7 & 8. MATLAB: importing expression data in MATLAB, thresholding, normalization, gene filtering, clustering, classification, statistical gene ranking for time series and group studies, exporting to excel, building custom user interfaces for advanced applications. This course is taught by Shailender Nagpal, M.S. Create an online account to see course schedule and to register. http://www.bioinformatics.org/edu/login/signup.php
BI202 SNP Genotyping	Variant Analysis	SNP Genotyping; GCOS; GTYPE; BRLMM; CNAT; Excel; MATLAB; dChip	This course helps to demystify Affymetrix analysis so that any researcher can take the basic steps to go from a chip image to genotypes, for each SNP, and to the copy number or linkage associated with the SNPs in given samples. Various tools will be covered, such as GCOS, GTYPE, BRLMM, CNAT, Excel, MATLAB, and free tools like dChip. It is geared towards researchers who conduct microarray-based SNP genotyping experiments to study genome-wide polymorphisms and then use the information for genotyping and linkage analysis. Most scientists are not able to analyze resulting microarray data themselves and are not able to get desired results using traditional tools like Microsoft Word and Excel, or the advanced software provided by commercial vendors. The free solutions come either with a steep learning curve or as black-box interfaces that provide limited functionality, with little or no technical support. In the midst of all this is the fundamental lack of understanding among scientists on how the technology works and what the fundamental parts of the analysis are. No experience is required, although prior experience with any other programming language will be helpful. Math skills will also be useful. Sessions 1 & 2. Introduction to GCOS -- the environment, creating and saving experiments, importing and exporting data, normalization settings, from DAT->CEL->CHP files and their significance, importing and exporting data, SNP chip layout and algorithms for generating genotypes Sessions 3 & 4. GTYPE, BRLMM for generating genotypes, sample mismatch report, gender calls, pedigree check, creating virtual sets, and copy number analysis Sessions 5 & 6. dChip software: importing SNP data and annotation information into dChip, LOH analysis, copy number analysis, linkage disequilibrium analysis, allele sharing analysis, and exporting to Excel Sessions 7 & 8. MATLAB: importing SNP data in MATLAB, manipulating and filtering SNP genotypes, automating tasks using API to Affymetrix SDK, building custom user interfaces for advanced applications, and exporting to Excel This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00
BI203 dChip for Gene Expression and SNP Microarray Data Analysis	Expression Analysis; Variant Analysis	dChip; Gene Expression Analysis; SNP Microarray Data Analysis	This course will teach the workings of the dChip application and cover topics such as importing arrays, performing normalization, model based expression calculations, gene and SNP filtering, clustering, linkage, LOH and copy number analysis. Session 1. Gene Expression Analysis: Preparing to import CEL and CHP exported txt files, with basic actions such as normalization and model-based expression index calculations. Re-importing saved "DCP" files and importing expression indices from saved text files. Use of array list file, sample information file, dChip data file list. Session 2. Gene Expression Analysis: Case studies with comparison of two groups, gene filtering and clustering Session 3. Gene Expression Analysis: Case studies with ANOVA, correlation, enrichment and classification Session 4. Gene Expression Analysis: Resampling, manipulating trees, gene function enrichment, pathways, FDR, combine comparisons Session 5. SNP Array Analysis: Preparing to import CEL and CHP exported txt files, with basic actions such as normalization and model-based expression index calculations for copy number analysis; re-importing saved "DCP" files and importing genotypes and SNP signals from saved text files; use of array list file and sample information file Session 6. SNP Array Analysis: LOH and copy number analysis with sample data; export Session 7. SNP Array Analysis: Intricacies of copy number and LOH analysis, parameters used Session 8. SNP Array Analysis: Allele sharing analysis, linkage analysis; automation in dChip This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00
MA101A Distributions, Tests and Graphics	Statistics	Distributions; Tests; Graphics	The various statistical distributions covered will help you know when assumptions can be made about a normal distribution and how to test whether or not these assumptions are true. Essential descriptive statistics are reviewed and then used in various situations to calculate background, noise, normalization and thresholding. Additionally, hypothesis testing is introduced so that you can assess groups of observations for a particular parameter and calculate whether or not the difference between groups is significant. Data visualization using various graphs will also be reviewed. Armed with these techniques, you will be able to better deal with the challenges of data analysis. Plus, you'll be able to understand and interpret data at a more fundamental level and draw the correct conclusions about them. The entire course will be conducted in R, a free and open-source package for statistical computing that has become an essential part of the biostatistician's toolbox. Unlike Bioinformatics.Org course CS101B R for Biologists, Level 1, this course focuses on the mathematical principles of statistical analysis and not on the syntax and functionality of R. No experience is required, although prior experience with a programming language will be helpful. Math skills will also be useful. Session 1. Probability distributions and how to work with them Session 2. Descriptive statistics for summarizing vector and matrix data Session 3. Student t-tests, Wilcoxon tests for analyzing one and two sample data Session 4. Use of the techniques covered in the previous sessions to do a biological data analysis project This course is taught by Shailender Nagpal, M.S. Online on-demand courses are $300 each, or perpetual access to the on-demand "course bundle" is $3,000.00
Introduction to Computational Microbial Genomics	Microbiology; Comparative Genomics; Functional Analysis	Microbial Genomics	o DNA sequence and molecular structure o Principles of gene/operon architecture o Principles of genome organization o Methods for genome sequencing and characterization o Basics of genome sequence analysis o Genome sequence features o Applications/uses of microbial genome sequences The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.
Next-Generation Sequencing	DNA Sequencing Technology	Illumina; PacBio	o DNA sequence and molecular structure o Principles of DNA sequencing o Sanger sequencing o Advantages of next-generation sequencing o Example: Illumina sequencing o Example: PacBio sequencing o Applications and uses of next-generation sequencing The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.
Computational Sequence Analysis	Comparative Genomics	Computational Sequence Analysis	o DNA sequence file formats o DNA sequence file access and download o Sequence search applications o Multiple sequence alignment o Phylogenetic analysis o Three-dimensional protein sequence/structure analysis The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.
Introduction to Bioinformatic Databases	Databases; Webtools	Bioinformatic Databases	o Principles of biological databases o Database search utilities o Examples of bioinformatics databases o Health and disease related databases o Genome browser examples o Microbial genome sequence databases and tools o Metagenomic sequence databases and tools o Custom database design and implementation The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.
Introduction to Computational Genomics	Comparative Genomics; Variant Analysis	Computational Genomics; SNP; Alignment	o Genome sequence data and file formats o Sequence read quality control and trimming o Genome assembly: ab initio and reference o Read-to-genome mapping o SNP calling and validation o Gene and feature prediction The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.

Title	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Avaliable	Notes
BI201 Gene Expression Analysis	Bioinformatician	Intermediate	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			
BI202 SNP Genotyping	Bioinformatician	Intermediate	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			
BI203 dChip for Gene Expression and SNP Microarray Data Analysis	Bioinformatician	Introductory	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			
MA101A Distributions, Tests and Graphics	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://www.bioinformatics.org/education/	Videos, slides, datasets, examples	On-demand	Online	Self-paced	300		Bioinformatics Organization, Inc.				edu@bioinformatics.org					Continuing Science Education units within the Bioinformatics Organization, Inc.			
Introduction to Computational Microbial Genomics	Bioinformatician	Intermediate	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	4 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Next-Generation Sequencing	Bioinformatician; Laboratorian	Advanced	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	4 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Computational Sequence Analysis	Bioinformatician	Intermediate	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	4 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Introduction to Bioinformatic Databases	Bioinformatician	Intermediate	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	4 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Introduction to Computational Genomics	Bioinformatician	Advanced	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	4 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Available	Notes
Comparative Genomics	Comparative Genomics; Variant Analysis	Alignment	Module 5: Comparative Genomics o Principles of sequence homology and similarity o Sequence similarity and search algorithms o Local and global sequence alignment o Whole genome sequence comparison and alignment o Genome sequence and alignment visualization o Sequence clustering and orthologous group comparison o Core genome and accessory genome analysis o Applications of comparative genomics to molecular epidemiology The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Intermediate	http://abi.ihrc.org/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	4 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	marketing@ihrc.com		Atlanta	GA					
Genomic Approaches to Molecular Epidemiology and Typing	Comparative Genomics; Variant Analysis	Molecular Epidemiology; Typing; PFGE	o Principles of molecular epidemiology and typing o Pulse field gel electrophoresis and PulseNet o Multi-locus sequence typing o Ribosomal-gene sequence typing o Whole genome sequence comparison o SNP based genome typing and characterization o Rationale genome-based design of novel typing methods ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Epidemiologist	Intermediate	http://abi.ihrc.org/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	4 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	marketing@ihrc.com		Atlanta	GA					
Clinical Metagenomics	Metagenomics	Clinical Metagenomics	o Introduction to genomics and metagenomics o Review of next-generation sequencing methods o Principles of clinical metagenomics o Methods for sequence similarity searching o Sequence comparison methods o K-mer based methods o Supervised and unsupervised sequence characterization o Applications for sterile versus non-sterile sites o Clinical metagenomic case studies The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician; Epidemiologist; Laboratorian	Intermediate	http://abi.ihrc.org/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	4 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	marketing@ihrc.com		Atlanta	GA					
Introduction to Scientific Computing	General Computing	Unix; Linux	o Introduction to the Unix/Linux compute environment o System administration and program installation o Command line operations o Shell scripting o Version control and code sharing o Computing in the cluster environment The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician; Epidemiologist; Laboratorian	Intermediate	http://abi.ihrc.org/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	4 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	marketing@ihrc.com		Atlanta	GA					
High-Performance and Cluster Computing	HPC/Cloud	High Performance Computing	o Cluster environment and architecture o Cloud computing environment o Review of command line environment o Remote access to servers and cluster o Queuing systems and file management o Principles of threading and parallelization o Examples of parallel sequence analysis applications o Assembly o Sequence similarity searches The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact Michael Astwood at IHRC (marketing@ihrc.com) to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Advanced	http://abi.ihrc.org/workforce.html	Lecture, computer exercises	July 7, 2015 – July 10, 2015	CDC	4 days (8 hours/day)	Free through OAMD offering		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Melissa Olsen Rasmussen	Public Health Advisor	(404) 639-4836	mar2@cdc.gov		Atlanta	GA					
Introduction to Sequence Data Manipulation	Comparative Genomics	DNA; Proteins; Sequence Data Manipulation	o DNA file formats o Protein file formats o Alignment based formats o Miscellaneous commonly used formats o Conversion between formats: available tools and languages The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact Michael Astwood at IHRC (marketing@ihrc.com) to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://abi.ihrc.org/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	marketing@ihrc.com		Atlanta	GA					
Sequence Alignments	Comparative Genomics	Alignment	o Small sequences: Pairwise & Multiple o Genome alignment o Alignment viewing o Editing alignments o Verifying goodness of alignments The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Introductory	http://abi.ihrc.org/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	marketing@ihrc.com		Atlanta	GA					
Computational Phylogenetics	Phylogenomics	Computational Phylogenetics	o Molecular evolution vs Phylogenetics o Genes phylogeny vs Species phylogeny o Tree representation: rooted vs unrooted o Distance-based methods (UPGMA, NJ) o Character-based methods (ML, MP) o Tree evaluation o Tree viewing and editing The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician; Epidemiologist	Introductory	http://abi.ihrc.org/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	marketing@ihrc.com		Atlanta	GA					
MLST Based Molecular Epidemiology	Phylogenomics; Databases; Microbiology	MLST	o MLST basics o MLST databases and resources o Few examples o Other MLST based techniques: ribosomal MLST, gMLST o Principles of creating your own MLST The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician; Epidemiologist; Laboratorian	Intermediate	http://abi.ihrc.org/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	marketing@ihrc.com		Atlanta	GA					
Gene Prediction	Comparative Genomics; Functional Analysis	Gene Prediction	o Prediction basics: biology, underlying models o Prokaryotic gene prediction o Eukaryotic gene prediction (they have fungal division) o Promoter and regulatory elementary predictions The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Advanced	http://abi.ihrc.org/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	marketing@ihrc.com		Atlanta	GA					
Introduction to NCBI	Databases; Webtools	Genbank; RefSeq; NCBI; Genome Workbench; BLAST	o NCBI structure – site tour o Genbank; RefSeq o BLAST o Taxonomy o Genomes o SRA o Sequence submission The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician; Epidemiologist; Laboratorian	Intermediate	http://abi.ihrc.org/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	4 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	marketing@ihrc.com		Atlanta	GA					

Back to Brief View

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Protein Functional Annotation	**Functional Analysis; Proteomics**	Proteins	o Functional annotation basics o Sequence homology and similarity o Sequence clustering based tools o Gene ontology based tools o Automated annotation pipelines o Pathway analysis The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Intermediate	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Structural Bioinformatics	**Functional Analysis; Proteomics**	Structural Biology	o Structure basics: hierarchy, determination of protein structure o Protein structure database o Visualization o Comparison o Classification Prediction techniques basics: Secondary structure prediction, tertiary structure prediction The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact Michael Astwood at IHRC (mastwood@ihrc.com) to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Introductory	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Bioinformatics Programming Basics	**General Computing; Languages**	Unix; Linux	o Introduction of *nix based environment o Command line navigation o Introduction to program installations o Environment setting o Basic error debugging in installations o Redirection, shell scripting and pipelining The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact Michael Astwood at IHRC (mastwood@ihrc.com) to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	June 23, 2015 – June 24, 2015	CDC	2 days (8 hours/day)	Free through OAMD offering		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Melissa Olsen Rasmussen	Public Health Advisor	(404) 639-4836	mxr2@cdc.gov		Atlanta	GA					
Genome Assembly	**Comparative Genomics; Metagenomics**	Genome Assembly; DNA	o DNA sequencing and its generations o Assembly problem o De novo assembly o Reference based assembly o Read to genome mapping o Metagenomic assembly The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact Michael Astwood at IHRC (mastwood@ihrc.com) to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Advanced	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	July 21, 2015 – July 22, 2015	Georgia Tech (tentative)	2 days (8 hours/day)	Free through OAMD offering		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Melissa Olsen Rasmussen	Public Health Advisor	(404) 639-4836	mxr2@cdc.gov		Atlanta	GA					
Genome Assembly I	**Comparative Genomics**	Genome Assembly; NGS; FastQC; PRINSEQ; Velvet; SOAPdenovo2: QUAST; CISA; Sequencing Basics; Illumina Paired End Sequencing	Sub-module 14: Genome Assembly I This advanced level bioinformatics sub-module provides participants with the opportunity to gain hands on experience in handling and assembly of next-generation sequencing (NGS) data. Course material includes bioinformatics aspects of sequencing basics, Illumina paired end sequencing, and de novo genome assembly. The module will involve a mix of graphical user interface (GUI) and command line tools such as FastQC, PRINSEQ, Velvet, SOAPdenovo2, QUAST and CISA among others. The participants will receive instruction in command line Linux and gain experience working at the command line to perform bioinformatics analysis of NGS data. The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Advanced	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Genome Assembly II	**Comparative Genomics**	Genome Assembly; NGS; FastQC; PRINSEQ; BWA; SAMtools; BCFtools; IGV; Sequencing Basics; Genome Mapping; Variant Calling	Sub-module 15: Genome Assembly II This advanced level bioinformatics sub-module provides participants with the opportunity to gain hands on experience in the handling and analysis of next-generation sequencing (NGS) data. Course material includes bioinformatics aspects of sequencing basics, genome mapping and variant calling. Bioinformatics programs for which instruction will be provided include a mix of graphical user interface (GUI) and command line tools such as FastQC, PRINSEQ, BWA, SAMtools, BCFtools and IGV among others. The participants will receive instruction in command line Linux and gain experience working at the command line to perform bioinformatics analysis of NGS data. The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Advanced	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Perl for Bioinformatics Programming	**Languages**	Perl	Module 9: Perl for Bioinformatics Programming This intermediate level bioinformatics module provides participants with the opportunity to gain hands on experience working with the Perl programming language, a commonly used tool in the analysis of biological data. Course material includes the basics of programming concepts and Perl, file access, handling and manipulation, searching and regular expressions and CPAN. By the end of the course, participants will have sufficient knowledge to develop their own working Perl scripts and pipelines that can be applied to their work and research. The whole course will be geared towards application of Perl in bioinformatics. The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Intermediate	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	4 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Introduction to Sequence Storage Formats		Linux; FastQC, Mauve, IGV, Plink, BWA, SAMtools, Jmol, Cytoscape, MEGA, NCBI and EBI	This basic level bioinformatics sub-module provides participants with the opportunity to gain hands on experience working with numerous sequence storage formats and their inter-conversions. The participants will receive instruction in basic command line Linux and gain experience working at the command line to perform the required tasks. Course material includes discussions and exercises on sequence read formats, mapping formats, variant formats, nucleotide and protein formats and alignment and tree formats. The discussions will focus on the description of the format, type of data stored, common software that can read the format and conversion of one format into other equivalent formats. Bioinformatics programs for which instruction is provided include graphical user interfaces (GUIs), webservers and command line tools such as FastQC, Mauve, IGV, Plink, BWA, SAMtools, Jmol, Cytoscape, MEGA, NCBI and EBI among others. The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Introductory	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Intermediate Bioinformatics Programming	**Languages**	Perl	Sub-module 9: Intermediate Bioinformatics Programming This intermediate level bioinformatics sub-module provides participants with the opportunity to gain hands on experience working with the Perl programming language, a commonly used tool in the analysis of biological data. Course material includes the basics of programming concepts and Perl, file access, file handling and manipulation, loops, subroutines and modules. By the end of the course, participants will have sufficient knowledge to develop their own working Perl scripts and pipelines that can be applied to their research. The whole course will be geared towards application of Perl in bioinformatics. The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Intermediate	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Sequence Visualization		MEGA; Mauve; CGView Comparison Tool (CCT); BWA; SAMtools; Cytoscape	Sub-module 10: Sequence Visualization This intermediate level bioinformatics sub-module provides participants with the opportunity to gain hands on experience with sequence visualization. Course material includes discussions and exercises on the visualization of different types of sequences and analyses such as multiple sequence alignments, trees, read to genome mapping, genome alignments, circular genome visualization and network visualization. The participants will receive instruction in basic command line Linux and gain experience working at the command line to perform bioinformatics analysis. Bioinformatics programs for which instruction is provided include graphical user interface (GUI) and command line tools such as MEGA, Mauve, CGView Comparison Tool (CCT), BWA, SAMtools and Cytoscape among others. The IHRC faculty are at Georgia Tech and can teach at courses to CDC staff at CDC or Georgia Tech. Course content can be customized. The courses involve lectures and hands-on computer exercises that take the participants through theory as well as the applications of different bioinformatics workflows. The courses are supplemented with booklets that detail the theory, software, and the workflows discussed during the course. All of the software programs covered in these trainings are open-source or free to use. ***If this course is not currently scheduled to be offered at CDC or Georgia Tech, please contact IHRC to inquire about course offerings. IHRC will schedule a course for 10-15 students for a negotiated cost. All courses can be customized in terms of content and duration.	Bioinformatician	Intermediate	http://abil.ihrc.com/workforce.html	Lecture, computer exercises	Can be scheduled at CDC Atlanta campus for a group of 10-15.	Can be scheduled at CDC Atlanta campus for a group of 10-15.	2 days (8 hours/day)	Contact Michael Astwood at IHRC for cost		This Workforce Development Training is provided by IHRC, Inc., and the Georgia Institute of Technology.	Michael Astwood	Chief Science Officer	(678) 615-3220	mastwood@ihrc.com		Atlanta	GA					
Writing Functions in Python Programming	**Languages**	Python	This is a module from the "Python for Biologists" course. It deals with functions and how to write and use them. It also introduces namespaces and the tuple data structure. The module contains several exercises and suggested solutions. The text of exercises is also provided in a separate file. These materials are provided on the Goblet Training Materials page. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Intermediate	http://www.mygoblet.org/training-portal/materials/writing-functions-python-programming	Slides, PDF	On-demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Avaliable	Notes
Pathway and Network Analysis of -Omics Data (2014)	Metabolomics; Functional Analysis	Pathway Analysis; Networks	Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. Many research programs often slow or stall after generating a gene list. The Canadian Bioinformatics Workshops at Bioinformatics.ca has developed a 3-day course covering the bioinformatics concepts and tools available for annotating and determining functional enrichment of a gene list and analyzing networks. The workshop is focused on the principles and concepts required for analyzing and conducting pathway analysis on a gene list from any organism, although focus will be on human and model Eukaryotic organisms. Specifically, we will focus on 1) getting more information about a gene list, 2) finding out how a set of genes is connected, 3) discovering what's enriched in a gene list (and using it for hypothesis generation), and 4) extending or refining a gene list. An analysis flow chart will be developed throughout the course. Target Audience This workshop is intended for biologists working with 'Omics data' (e.g. gene expression, protein expression, molecular interactions, large-scale genetic screens and other omics data) from human and model eukaryotic organisms who are interested in interpreting large gene lists resulting from their experiments. Concepts will be applicable to omics data from non-eukaryotic organisms, but software and demonstrations will not cover them.	Bioinformatician	Intermediate	http://bioinformatics.ca/workshops/2014	Slides, PDF, MP4	On-demand	Online	Self-paced	Free		Bioinformatics.ca												
Informatics for RNA-Seq Analysis (2014)	Expression Analysis	RNA-Seq	available under a Creative Commons license, are placed on their website. High-throughput sequencing of RNA libraries (RNA-seq) has become increasingly common and largely supplanted gene microarrays for transcriptome profiling. When processed appropriately, RNA-seq data has the potential to provide a considerably more detailed view of the transcriptome. The CBW has developed a 2-day course providing an introduction to RNA-seq data analysis followed by integrated tutorials demonstrating the use of popular RNA-seq analysis packages. The tutorials are designed as self-contained units that include example data (Illumina paired-end RNA-seq data) and detailed instructions for installation of all required bioinformatics tools (TopHat, Cufflinks, etc.). Participants will gain practical experience and skills to be able to: 1) Align RNA-seq data to a reference genome 2) Estimate known gene and transcript expression 3) Perform differential expression analysis 4) Discover novel isoforms 5) Visualize and summarize the output of RNA-seq analyses Target Audience Graduates, postgraduates and PIs working with or about to embark on an analysis of RNA-seq data. Attendees may be familiar with some aspect of RNA-seq analysis (e.g. gene expression analysis) or have no direct experience. A reference genome is required. Prerequisites for attendance: Basic familiarity with Linux environment and S, R, or Matlab. Must be able to complete and understand the following simple Linux and R tutorials (up to and including "Descriptive Statistics")before attending: • UNIX Tutorial (up to and including Tutorial Four) • Quick & Dirty Guide to R	Bioinformatician	Intermediate	http://bioinformatics.ca/workshops/2014	Slides, PDF, MP4	On-demand	Online	Self-paced	Free		Bioinformatics.ca												
Introduction to Biopython	Languages	Python; Biopython	Understand what Biopython is and what it can do. Learn how to get Biopython running. Learn how to retrieve data records from NCBI. Learn how to read and write sequence files. Learn how to run BLAST from Python and read the results. Learn how to read and write phylogenetic tree files. Learn how to read and write 3D structure files. Learn how to use the Biopython documentation, examples, and where to find help. Understand what alternatives to Biopython exist and what they can do.	Bioinformatician	Intermediate	https://www.bits.vib.be/index.php/training/111-bits/training/previous-trainings/176-biopython	Notes, slides, exercises	On-demand	Online	Self-paced	Free		BITSvib												
Multiple Sequence Alignment and Phylogenetics	Phylogenomics	Multiple Sequence Alignments; Phylogenetics	The overall course aim is to provide an introduction to the computation of quality Multiple Sequence Alignments (MSAs), primarily for phylogenetic analysis. More specifically, we aim to discuss (i) What alignments are useful for - why we align sequences; (ii) What's in a sequence; what's in an alignment; (iii) What alignments mean - introducing metaphor; (iv) Visualising alignments; (v) Alternative interpretations (evolutionary and structural) of sequence alignments; (vi) Building automatic and manual multiple sequence alignments (MSAs) with JalView; (vii) MSAs and short protein linear motifs (viii) MSAs and phylogenetics. Course objectives are primarily to enable participants to better (i) Understand the range of contexts in which alignments are used & are useful; (ii) Understand the importance of sequence similarities & differences, & what they tell us; (iii) Understand the meaning of alignments; (iv) Understand the use of metaphor & its role in interpreting alignments. These materials are provided on the Goblet Course pages. This site aims to provide a centralized repository of open-source course pages, to help bioinformatics trainers to prepare, manage and disseminate their course information and contents. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices.	Bioinformatician	Intermediate	http://www.mygoblet.org/training-portal/courses/multiple-sequence-alignment-and-phylogenetics	PDF	On-demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Flow Cytometry Data Analysis Using R (2013)	Laboratory; Metabolomics; Functional Analysis	R; Flow Cytometry	With the underlying technology rapidly increasing in complexity, Flow Cytometry (FCM) data analysis is becoming more crucial for biological experiments. This workshop aims to provide participants some familiarity with the open source software environment R as an analysis tool for FCM data as they explore the fundamental concepts of taking their data to diagnosis and discovery. Participants will be able to open their FCS files within R, explore their data using various visualizations, perform simple automated pre-processing tasks, quickly generate quality assurance reports to identify potential technical issues with the data, and automate simple gating strategies. As well, some basic clustering techniques will be explained and demonstrated, and new advanced analysis options presented (e.g., flowType, flowDensity, flowMeans, RchyOptimyx, flowClust3.0, SPADE, flowFP/flowBin, SamSPECTRAL). Workshop participants will come away with a better understanding of bioinformatics approaches to FCM analysis, be able to write their own analysis scripts in R to explore their FCM data, as well automate a gating strategy and record statistics of interest (e.g., proportions of cells in specific populations of interest). These materials are provided on the Goblet Course pages. This site aims to provide a centralized repository of open-source course pages, to help bioinformatics trainers to prepare, manage and disseminate their course information and contents. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices.	Bioinformatician; Laboratorian	Intermediate	http://www.mygoblet.org/training-portal/courses/flow-cytometry-data-analysis-using-r-2013	PDF	On-demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Statistics and R for the Life Sciences	Statistics	Math; R	We will learn the basics of statistical inference in order to understand and compute p-values and confidence intervals. We will provide examples by programming in R in a way that will help make the connection between concepts and implementation. Problems sets requiring R programming will be used to test understanding and ability to implement basic data analyses. We will use visualization techniques to explore new data sets and determine the most appropriate approach. We will describe robust statistical techniques as alternative when data do not fit assumptions required by the standard approaches. We will also introduce the basics of using R scripts to conduct reproducible research. Topics: •Distributions •Exploratory Data Analysis •Inference •Non-parametric statistics	Bioinformatician; Epidemiologist; Laboratorian	Introductory	https://www.edx.org/course/statistics-r-life-sciences-harvardx-ph525-1x	edX course	See website for schedule	Online	Self-paced	Free		Harvard University through edX												
UCSC Genome Browser	Webtools	UCSC Genome Browser	Bioinformatics Tutorials Series (BITS) Short video tutorials from a collaboration of MIT Engineering and Science Libraries and Harvard's Countway Library. BIT 1.1: UCSC Genome Browser: Getting DNA Sequence (3:57) BIT 1.2: UCSC Genome Browser: Using Annotation Tracks (5:47) BIT 1.3: UCSC Genome Browser: Locating Intron-Exon Boundaries (4:56) BIT 1.4: UCSC Genome Browser: Searching with BLAT (6:14)	Bioinformatician	Introductory	https://legacy.countway.harvard.edu/menuNavigation/libraryServices/classes/videoTutorials.html	Video	On-demand	Online	Self-paced	Free		MIT and Harvard University												
NCBI BLAST	Functional Analysis; Comparative Genomics	BLAST	Bioinformatics Tutorials Series (BITS) Short video tutorials from a collaboration of MIT Engineering and Science Libraries and Harvard's Countway Library. BIT 2.1: BLAST Link (7:24) BIT 2.2: Do I Need BLAST? The Use of the Related Sequences Tool (6:53) BIT 2.3: Nucleotide BLAST (5:46) BIT 2.4: Nucleotide BLAST: Algorithm Comparison (6:14)	Bioinformatician; Laboratorian	Introductory	https://legacy.countway.harvard.edu/menuNavigation/libraryServices/classes/videoTutorials.html	Video	On-demand	Online	Self-paced	Free		MIT and Harvard University												
OMIM and OMIA	Databases; Webtools	OMIM and OMIA	Bioinformatics Tutorials Series (BITS) Short video tutorials from a collaboration of MIT Engineering and Science Libraries and Harvard's Countway Library. BIT 3.1: OMIM and OMIA (6:34)	Bioinformatician	Introductory	https://legacy.countway.harvard.edu/menuNavigation/libraryServices/classes/videoTutorials.html	Video	On-demand	Online	Self-paced	Free		MIT and Harvard University												
Entrez Gene	Databases; Webtools	Entrez Gene	Bioinformatics Tutorials Series (BITS) Short video tutorials from a collaboration of MIT Engineering and Science Libraries and Harvard's Countway Library. BIT 3.2: Entrez Gene (5:35)	Bioinformatician	Introductory	https://legacy.countway.harvard.edu/menuNavigation/libraryServices/classes/videoTutorials.html	Video	On-demand	Online	Self-paced	Free		MIT and Harvard University												
Coffee Break: Tutorials for NCBI Tools	Databases; Webtools	Entrez Gene; BLAST; dbSNAP; NCBI	Coffee Break is a resource at NCBI that combines reports on recent biomedical discoveries with use of NCBI tools. The result is an interactive tutorial that tells a biological story. Each report is based on a discovery reported in one or more articles from the recently published peer-reviewed literature. After a brief introduction that sets the work described into a broader context, the report focuses on how a molecular understanding can provide explanations of observed biology and lead to therapies for diseases. Each vignette also highlights the NCBI tools and resources used in the research process. These tools include PubMed, PubMed Central, Entrez Gene, and MapViewer. Coffee Break articles should be fun and informative reading for molecular biologists, clinicians, and students, and may serve as teaching aids for college and graduate students. Tutorial list organized by NCBI bioinformatics resource featured in tutorial that accompanies the story: http://www.ncbi.nlm.nih.gov/books/NBK2310/	Bioinformatician; Laboratorian	Introductory	http://www.ncbi.nlm.nih.gov/books/NBK2345/	HTML and video	On-demand	Online	Self-paced	Free		National Center for Biotechnology Information												
Entrez Gene Tutorial	Databases; Webtools	Entrez Gene	This resource is a brief animated tour of a Entrez Gene record, from NIH.	Bioinformatician; Laboratorian	Introductory	http://nihlibrary.ors.nih.gov/bioinfo/online_tutorial_gene/online_gene.html	Video	On-demand	Online	6 min 10 sec	Free		National Institutes of Health Library												
NCBI YouTube	Databases; Webtools	Introductory	This resource contains videos about NCBI tools.	Bioinformatician; Laboratorian	Introductory	https://www.youtube.com/user/NCBINLM/videos	Video	On-demand	Online	Self-paced	Free		National Center for Biotechnology Information												
Online Lectures on Bioinformatics	Comparative Genomics; Functional Analysis	Proteins; Alignment	A link to this resource appears on the NIH Online Bioinformatics Tutorials webpage, http://nihlibrary.nih.gov/Services/Bioinformatics/Pages/Biotutorials.aspx. Lecture outline: 1. Biological preliminaries o Introduction o References o Exercises -- Answers 2. Analysis of individual sequences o Introduction o Helical wheels, amphipatic helices and coiled-coils o References o Exercises 3. Pairwise sequence comparison o Introduction o Dot plots o Sequence Alignment o References o Exercises -- Answers 4. Algorithms for the comparison of two sequences o Introduction: Type I and type II alignments o Type I alignment o Type II alignment o General gap functions for type II alignments o Minimum distance alignments o Minimum distance alignment score as a metric on sequences	Bioinformatician	Introductory	http://lectures.molgen.mpg.de/online_lectures.html	HTML	On-demand	Online	Self-paced	Free		Hannes Luz												

Back to Brief View

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UCSC Genome Browser Workshop and Training Materials	**Webtools**	UCSC Genome Browser	This webpage contains links to training materials (including a YouTube channel) on the UCSC Genome Browser, and a list of workshop locations/times. The workshop can be scheduled at your institution. Online Training and Tutorials: NEW ! Videos ! YouTube Channel • Finding a list of genes in a region. • Finding exon numbers. • Finding SNPs in a gene. • Finding SNPs upstream from a gene. • Find which tables belong to a data track. • Identifying codon numbers in a gene. Produced at UCSC • Nature: Guide to the UCSC Genome Browser • Fishing for genes in the UCSC Browser (pdf) • The UCSC genome browser and associated tools • UCSC genome browser tutorial • Step-by-step tutorial presented at ASHG 2009 annual meeting - basic browser navigation and functionality in the context of interpreting clinical genetics reports. • Step-by-step tutorial presented at ABRF 2010 annual meeting - how to convert files and display high-throughput sequencing results. • Step-by-step tutorial presented at ASHG 2014 annual meeting - includes Custom Tracks and Table Browser queries with and without filters. External • Open Helix tutorial and training materials • Teaching bioinformatics and neuroinformatics by using free web-based tools - student-level tutorial that demonstrates the combined use of several major bioinformatics tools (including the UCSC Genome Browser) in answering a series of related research questions User's Guides for Tools in the Genome Browser Workshops:	Bioinformatician	Introductory	https://genome.ucsc.edu/training/index.html	Video	On-demand	Online	Self-paced	Free		University of California, Santa Cruz												
CLC Genomics	**Comparative Genomics**	CLC Genomics	Tutorials	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://www.clcbio.com/support/tutorials/	PDF	On-demand	Online	Self-paced	Free		CLCbio												
DNAStar	**Comparative Genomics**	DNAStar	Tutorials	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://www.dnastar.com/t-support-tutorials.aspx	Online Tutorial	On-demand	Online	Self-paced	Free		DNASTAR												
DNAStar SeqManNGen	**Comparative Genomics; DNA Sequencing Technology**	DNAStar SeqManNGen	Tutorials	Bioinformatician	Introductory	http://www.dnastar.com/t-tutorials-seqman-ngen.aspx	Online Tutorial	On-demand	Online	Self-paced	Free		DNASTAR												
Genomatix	**Comparative Genomics; DNA Sequencing Technology**	Genomatix	Help pages	Bioinformatician	Introductory	http://www.genomatix.de/online_help/help/online_help.html	HTML	On-demand	Online	Self-paced	Free		Genomatix												
GeneSpring	**Expression Analysis**	GeneSpring; Microarrays	GeneSpring Support Portal	Bioinformatician	Introductory	http://genespring-support.com/	HTML, recorded and live Webinars	On-demand	Online	Self-paced	Free		Agilent Technologies												
Golden Helix SVS	**Variant Analysis**	Golden Helix SVS	Tutorials	Bioinformatician	Introductory	http://goldenhelix.com/SNP_Variation/tutorials/index.html	HTML, PDF	On-demand	Online	Self-paced	Free		Golden Helix												
Golden Helix VarSeq	**Variant Analysis**	Golden Helix VarSeq	Tutorials	Bioinformatician	Intermediate	http://doc.goldenhelix.com/VarSeq/tutorials/cancer_gene_panel/index.html	HTML, PDF	On-demand	Online	Self-paced	Free		Golden Helix												
BIOBASE Archived Webinars	**Variant Analysis; Databases**	Genome Trax	Webinars Webinar: Sourcing Multiple Databases for NGS Variant Discovery? March 19, 2015 Webinar: Integrating Morphology and Genetics in Clinical Diagnostics No date given When Silent Mutations Scream: Revisiting Annotation of Regulatory Elements August 2014 Using disease mutations and PGx variants to personalize patient diagnosis and treatment June 2014 Got Diagnosed, Now What? Leveraging PGx for Truly Personalized Medicine March 2014 Leveraging Pharmacogenomics for Truly Personalized Medicine October 2013 Filtering Genetic Variants from NGS Data October 2013 Request Recording Enriching protein interaction networks with transcription factor-gene interactions using TRANSFAC September 2013 Webinar: A Traveler's Guide to Next Generation Sequencing: Navigating the Sea of Genetic Variants June 2013 GEN WebBrief: Personal Exomes: 5 Insights for Interpretation and Diagnosis No date given Whole genome variant analysis for diagnostics and medical research April 2013 Upstream analysis of gene expression data February 2013 ANNOVAR: How to annotate genetic variants	Bioinformatician	Introductory	http://www.biobase-international.com/archive/webinars	Archived webinars	On-demand	Online	Self-paced	Free		BIOBASE												
Ingenuity Pathway Analysis (2)	**Metabolomics; Functional Analysis**	Ingenuity; Pathway Analysis	Online training and webinars	Bioinformatician	Introductory	http://www.ingenuity.com/products/ipa#/?tab=training	Video, archived webinars	On-demand	Online	Self-paced	Free		Ingenuity												
Metacore	**Variant Analysis; Functional Analysis**	Metacore; Pathway Analysis	This is a list of tips and archived webinars compiled by NIH.	Bioinformatician	Introductory	http://nihlibrary.nih.gov/Services/Bioinformatics/Pages/MetaCore.aspx	Archived WebEx	On-demand	Online	Self-paced	Free		National Institutes of Health Library												
Partek Genomics	**Comparative Genomics; DNA Sequencing Technology**	Partek; Genomics	Tutorials	Bioinformatician	Introductory	http://www.partek.com/partek-resources1	HTML, PDF	On-demand	Online	Self-paced	Free		Partek												
Protein Lounge	**Proteomics**	Protein Lounge	Databases Tutorials • Pathways - Visual Guide • A Better Way To Know Kinase-Phosphatase • Exploit GPCR Database In A Better Way • How To Use - Transcription Factor • A Short Tour To Peptide Antigen Database • Guide To Best Use Protein Interaction Database • Video Tour Of siRNA Database • Guide To Use Biochemical Compound • How To Use - Protein Database Tools Tutorials • Explore Pathway Builder • Protein Hydroplotter • Clone Easy - Guide To Use • Peptide-Antigen Finder For Antibodies and Drugs • Easy siRNA - The Easiest Way TO Predict siRNA • Protein Vision - Unique 3D Interactive Protein Structure	Bioinformatician	Introductory	http://www.proteinlounge.com/VideoTutorials.aspx	Video	On-demand	Online	Self-paced	Free		Protein Lounge												
NCBI Training and Tutorials	**Comparative Genomics; Webtools; Databases**	NCBI tools (all); BLAST; Entrez	This resource consists of training and tutorials for all NCBI tools. Databases NCBI C++ Toolkit Manual A comprehensive manual on the NCBI C++ toolkit, including its design and development framework, a C++ library reference, software examples and demos, FAQs and release notes. The manual is searchable online and can be downloaded as a series of PDF documents. NCBI Education Page Provides links to tutorials and training materials, including PowerPoint slides and print handouts. NCBI Glossary Part of the NCBI Handbook, this glossary contains descriptions of NCBI tools and acronyms, bioinformatics terms and data representation formats. NCBI Handbook An extensive collection of articles about NCBI databases and software. Designed for a novice user, each article presents a general overview of the resource and its design, along with tips for searching and using available analysis tools. All articles can be searched online and downloaded in PDF format; the handbook can be accessed through the NCBI Bookshelf. NCBI Help Manual Accessed through the NCBI Bookshelf, the Help Manual contains documentation for many NCBI resources, including PubMed, PubMed Central, the Entrez system, Gene, SNP and LinkOut. All chapters can be downloaded in PDF format. NCBI Website Search A database of static NCBI web pages, documentation, and online tools. These pages include such content as specialized online sequence analysis tools, back issues of newsletters, legacy resource description pages, sample code, and other miscellaneous	Bioinformatician; Laboratorian	Introductory	http://www.ncbi.nlm.nih.gov/guide/training-tutorials/	HTML, pdf	On-demand	Online	Self-paced	Free		National Center for Biotechnology Information												
NLM Georgia Biomedical Informatics Course	**General Computing**	Imaging; Maths	The National Library of Medicine (NLM) has awarded Robert B. Greenblatt, M.D. Library, Georgia Regents University a multi-year, $1.7 million contract to host the NLM Georgia Biomedical Informatics Course. Applications for the NLM Georgia Biomedical Informatics Course 2015 are closed. They will reopen for the 2016 course later in 2015. See webpage for application and 2016 date of training. This week-long survey course is designed to familiarize individuals with the application of computer technologies and information science in biomedicine and health science. Through a combination of lectures and hands-on computer exercises, participants will be introduced to the fundamental concepts and application areas of biomedical informatics. The conceptual components will include principles of controlled terminology, standards, mathematical modeling, bioinformatics, natural language processing, clinical information systems architectures, and methods for assessing and influencing institutional adoption of information technology. Application areas will include: use of the Internet for biomedical applications, current and emerging wide area network technologies, use of literature and molecular sequence databases, telemedicine, public health, patient-centered care, clinical research, and disaster response. Evening workshops will include hands-on projects to give students the opportunity to bring their own expertise to bear and apply the lessons learned in class to a relevant informatics application. Taught by a nationally known faculty, the course will prepare the student to become actively involved in making informed decisions about computer-based tools in his/her organizational environment, and improve the student's own computer skills. This is a National Library of Medicine fellowship program directed at medical educators, medical librarians, medical administrators, clinical practitioners, and faculty who are not currently knowledgeable but can become agents of change in their institutions. Limited to 30 fellows per session. Costs of attending this course, including travel, housing, and meals at the Brasstown Valley, are fully supported by the National Library of Medicine, NIH. The application is open to U.S. citizens and U.S. permanent residents.	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://gru.edu/library/greenblatt/informaticscourse/index.php	Lecture	2016	Brasstown Valley, GA	1 Week	Free		Georgia Regents University, National Library of Medicine	Kathy Davies	Associate Professor; Chair, Research and Education Services	706-721-9911	kadavies@gru.edu		Augusta	GA		CME, CNE, CDE, allied health CEU, MLA CE			2016 application will open later in 2015. See webpage.

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters/PhD Program	Non-Degree Option Avaliable	Notes
Data Analysis	Statistics	Data Analysis; R;	This resource includes Jeff Leek's (Johns Hopkins) lectures on data analysis for a 2013 Coursera course. Coursera course description: You have probably heard that this is the era of "Big Data". Stories about companies or scientists using data to recommend movies, discover who is pregnant based on credit card receipts, or confirm the existence of the Higgs Boson regularly appear in Forbes, the Economist, the Wall Street Journal, and The New York Times. But how does one turn data into this type of insight? The answer is data analysis and applied statistics. Data analysis is the process of finding the right data to answer your question, understanding the processes underlying the data, discovering the important patterns in the data, and then communicating your results to have the biggest possible impact. There is a critical shortage of people with these skills in the workforce, which is why Hal Varian (Chief Economist at Google) says that being a statistician will be the sexy job for the next 10 years. This course is an applied statistics course focusing on data analysis. The course will begin with an overview of how to organize, perform, and write-up data analyses. Then we will cover some of the most popular and widely used statistical methods like linear regression, principal components analysis, cross-validation, and p-values. Instead of focusing on mathematical details, the lectures will be designed to help you apply these techniques to real data using the R statistical programming language, interpret the results, and diagnose potential problems in your analysis. You will also have the opportunity to critique and assist your fellow classmates with their data analyses. Recommended Background Some familiarity with the R statistical programming language (http://www.r-project.org/) and proficiency in writing in English will be useful. At Johns Hopkins, this course is taken by first-year graduate students in Biostatistics.	Bioinformatician; Epidemiologist	Introductory	https://www.youtube.com/user/jtleek2007/videos?flow=grid&tag_id=UC8xNPQ-3a5t9uMU7Vah-jWA.3.coursera&view=46	Video	On-demand	Online	Self-paced	Free		Johns Hopkins on Coursera												
Genomic Data Science Certificate	Online Certificate Program; Comparative Genomics; DNA Sequencing Technology	Genomic Data Science	This Johns Hopkins specialization certificate is offered through Coursera. Content: • Basic computational, biological, and statistical skills for analyzing big genomic data • Foundational tools for successfully engaging in this rapidly changing field • How to go from unprocessed next generation sequencing data to meaningful biological results Recommended background: • Some programming experience (in any language) • Working knowledge of mathematics up to algebra (neither calculus or linear algebra are required) and basic biological principles Specialization Certificate: • To obtain the specialization certificate, you must complete 7 courses ($49 each). The cost to complete the 7 courses for the certificate is $392. The courses are offered multiple times a year. • You may also take the courses for free, or take less than the 7 courses, but you will not earn the specialization certificate. • It is recommended, but not necessary, to take the courses in order. • Completion of a Genomic Data Science Capstone project is required to earn the specialization certificate. Course 1. Introduction to Genomic Technologies Duration: 4 weeks Estimated Workload: 3-5 hours/week 1. The Central Dogma of Molecular Biology 2. How next generation sequencing works 3. Applications of next generation sequencing to measure o DNA o RNA o Epigenetics (e.g. DNA methylation) 4. Basic concepts in computing on next generation sequencing data o What is an algorithm?	Bioinformatician; Epidemiologist; Laboratorian	Introductory	https://www.coursera.org/specialization/genomics/41/overview	Coursera course	See schedule on website	Online	Less than one year	Free or can pay for certificate, $49 per course or $392 for 7 course certificate		Johns Hopkins on Coursera									Coursera certificate			
Introduction to Genomic Technologies	DNA Sequencing Technology	NGS	This Johns Hopkins course is offered through Coursera. Recommended background: • Some programming experience (in any language) • Working knowledge of mathematics up to algebra (neither calculus or linear algebra are required) and basic biological principles Specialization Certificate: • This course may be taken as a free stand-alone course, or as part of the Genomic Data Science specialization certificate (https://www.coursera.org/specialization/genomics/41/overview). • It is recommended, but not necessary, to take the courses in order. • To obtain the specialization certificate, you must complete 7 courses ($49 each). The cost to complete the 7 courses for the certificate is $392. The courses are offered multiple times a year.. • Completion of a Genomic Data Science Capstone project is required to earn the specialization certificate. Course 1 in Genomic Data Science Certificate: Introduction to Genomic Technologies Duration: 4 weeks Estimated Workload: 3-5 hours/week 1. The Central Dogma of Molecular Biology 2. How next generation sequencing works 3. Applications of next generation sequencing to measure o DNA o RNA o Epigenetics (e.g. DNA methylation) 4. Basic concepts in computing on next generation sequencing data o What is an algorithm? o What is a data structure? o How to share data? 5. Basic concepts in statistics for next generation sequencing	Bioinformatician; Epidemiologist	Introductory	https://www.coursera.org/course/genintro	Coursera course	June 1 to June 27, 2015; see schedule on website	Online	4 weeks, 3-5 hours/week	Free or can pay for certificate, $49 per course or $392 for 7 course certificate		Johns Hopkins on Coursera									Coursera certificate			
Genomic Data Science with Galaxy	Webtools	Galaxy	This Johns Hopkins course is offered through Coursera. Recommended background: • Some programming experience (in any language) • Working knowledge of mathematics up to algebra (neither calculus or linear algebra are required) and basic biological principles Specialization Certificate: • This course may be taken as a free stand-alone course, or as part of the Genomic Data Science specialization certificate (https://www.coursera.org/specialization/genomics/41/overview). • It is recommended, but not necessary, to take the courses in order. • To obtain the specialization certificate, you must complete 7 courses ($49 each). The cost to complete the 7 courses for the certificate is $392. The courses are offered multiple times a year.. • Completion of a Genomic Data Science Capstone project is required to earn the specialization certificate. Course 2 in Genomic Data Science Certificate: Genomic Data Science with Galaxy Duration: 4 weeks Estimated Workload: 3-5 hours/week 1. The challenge of reproducibility 2. Introduction to the Galaxy platform 3. Working with genomic Intervals 4. Galaxy Workflows 5. Annotation, Sharing, Publishing 6. Sequence Data Quality Control 7. ChIP-seq analysis with MACS 8. RNA-seq mapping and assembly 9. Galaxy on the cloud 10. Installing your own Galaxy	Bioinformatician	Introductory	https://www.coursera.org/course/gengalaxy	Coursera course	July 6 to August 1, 2015; see schedule on website	Online	4 weeks, 3-5 hours/week	Free or can pay for certificate, $49 per course or $392 for 7 course certificate		Johns Hopkins on Coursera									Coursera certificate			
Command Line Tools for Genomic Data Science	General Computing; Languages	Unix; Linux	This Johns Hopkins course is offered through Coursera. Recommended background: • Some programming experience (in any language) • Working knowledge of mathematics up to algebra (neither calculus or linear algebra are required) and basic biological principles Specialization Certificate: • This course may be taken as a free stand-alone course, or as part of the Genomic Data Science specialization certificate (https://www.coursera.org/specialization/genomics/41/overview). • It is recommended, but not necessary, to take the courses in order. • To obtain the specialization certificate, you must complete 7 courses ($49 each). The cost to complete the 7 courses for the certificate is $392. The courses are offered multiple times a year.. • Completion of a Genomic Data Science Capstone project is required to earn the specialization certificate. Course 3 in Genomic Data Science Certificate: Command Line Tools for Genomic Data Science Duration: 4 weeks Estimated Workload: 3-5 hours/week 1. Unix commands o Basic commands o Pipes 2. Sequences and genomic features o Formats: Fastq, BED, GTF, SAM o Tools: Samtools, Bedtools 3. Alignment and sequence variation o Bowtie, BWA o Samtools, Bcftools o Application: variant calling 4. Transcriptomics	Bioinformatician; Epidemiologist; Laboratorian	Introductory	https://www.coursera.org/course/gencommand	Coursera course	July 6 to August 1, 2015; see schedule on website	Online	4 weeks, 3-5 hours/week	Free or can pay for certificate, $49 per course or $392 for 7 course certificate		Johns Hopkins on Coursera									Coursera certificate			
Python for Genomic Data Science	Languages	Python	This Johns Hopkins course is offered through Coursera. Recommended background: • Some programming experience (in any language) • Working knowledge of mathematics up to algebra (neither calculus or linear algebra are required) and basic biological principles Specialization Certificate: • This course may be taken as a free stand-alone course, or as part of the Genomic Data Science specialization certificate (https://www.coursera.org/specialization/genomics/41/overview). • It is recommended, but not necessary, to take the courses in order. • To obtain the specialization certificate, you must complete 7 courses ($49 each). The cost to complete the 7 courses for the certificate is $392. The courses are offered multiple times a year.. • Completion of a Genomic Data Science Capstone project is required to earn the specialization certificate. Course 4 in Genomic Data Science Certificate: Python for Genomic Data Science Duration: 4 weeks Estimated Workload: 3-5 hours/week 1. Introduction to Programming o Numbers and Strings o Variable types o String Functions o Data input and output 2. Data structures o Lists o Tuples o Sets o Dictionaries 3. Controls and Repetitions	Bioinformatician; Epidemiologist	Introductory	https://www.coursera.org/course/genpython	Coursera course	July 6 to August 1, 2015; see schedule on website	Online	4 weeks, 3-5 hours/week	Free or can pay for certificate, $49 per course or $392 for 7 course certificate		Johns Hopkins on Coursera									Coursera certificate			
Algorithms for DNA Sequencing			This Johns Hopkins course is offered through Coursera. Recommended background: • Some programming experience (in any language) • Working knowledge of mathematics up to algebra (neither calculus or linear algebra are required) and basic biological principles Specialization Certificate: • This course may be taken as a free stand-alone course, or as part of the Genomic Data Science specialization certificate (https://www.coursera.org/specialization/genomics/41/overview). • It is recommended, but not necessary, to take the courses in order. • To obtain the specialization certificate, you must complete 7 courses ($49 each). The cost to complete the 7 courses for the	Bioinformatician	Introductory	https://www.coursera.org/course/ads1	Coursera course	July 6 to August 1, 2015; see schedule on website	Online	4 weeks, 4-6 hours/week	Free or can pay for certificate, $49 per course or $392 for 7 course certificate		Johns Hopkins on Coursera									Coursera certificate			

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Avaliable	Notes
Bioconductor for Genomic Data Science	Languages	Bioconductor; R	This Johns Hopkins course is offered through Coursera. Recommended background: • Some programming experience (in any language) • Working knowledge of mathematics up to algebra (neither calculus or linear algebra are required) and basic biological principles Specialization Certificate: • This course may be taken as a free stand-alone course, or as part of the Genomic Data Science specialization certificate (https://www.coursera.org/specialization/genomics/41/overview). • It is recommended, but not necessary, to take the courses in order. • To obtain the specialization certificate, you must complete 7 courses ($49 each). The cost to complete the 7 courses for the certificate is $392. The courses are offered multiple times a year.. • Completion of a Genomic Data Science Capstone project is required to earn the specialization certificate. Course 6 in Genomic Data Science Certificate: Bioconductor for Genomic Data Science Duration: 4 weeks Estimated Workload: 3-5 hours/week 1. Introduction to Bioconductor 2. Introduction to common data structures 3. Getting data into Bioconductor 4. Data analysis using Bioconductor 5. Annotate your results using Bioconductor 6. Visualize your data using Bioconductor	Bioinformatician	Introductory	https://www.coursera.org/course/genbioconductor	Coursera course	August 3 to August 29, 2015; see schedule on website	Online	4 weeks, 3-5 hours/week	Free or can pay for certificate, $49 per course or $392 for 7 course certificate		Johns Hopkins on Coursera									Coursera certificate			
Statistics for Genomic Data Science	Statistics	Genomics	This Johns Hopkins course is offered through Coursera. Recommended background: • Some programming experience (in any language) • Working knowledge of mathematics up to algebra (neither calculus or linear algebra are required) and basic biological principles Specialization Certificate: • This course may be taken as a free stand-alone course, or as part of the Genomic Data Science specialization certificate (https://www.coursera.org/specialization/genomics/41/overview). • It is recommended, but not necessary, to take the courses in order. • To obtain the specialization certificate, you must complete 7 courses ($49 each). The cost to complete the 7 courses for the certificate is $392. The courses are offered multiple times a year.. • Completion of a Genomic Data Science Capstone project is required to earn the specialization certificate. Course 7 in Genomic Data Science Certificate: Statistics for Genomic Data Science Duration: 4 weeks Estimated Workload: 5-7 hours/week 1. Experimental desgin • Types of data • Populations and samples • Bias and variance • Sample sizes 2. Exploratory analysis/data processing • Plots (scatter, box, MA, funnel, loess) • Plots to avoid • Tables 3. Statistical inference • Normalization	Bioinformatician; Epidemiologist	Introductory	https://www.coursera.org/course/genstats	Coursera course	August 3 to August 29, 2015; see schedule on website	Online	4 weeks, 5-7 hours/week	Free or can pay for certificate, $49 per course or $392 for 7 course certificate		Johns Hopkins on Coursera									Coursera certificate			
Bioinformatic Methods I	Comparative Genomics; Functional Analysis	BLAST; Multiple Sequence Alignments; Phylogenetics; Selection Analysis; Metagenomics	This University of Toronto course is offered on Coursera. This course may be taken for free, or you may pay for a certificate can be shared on LinkedIn. This course is offered on-demand. Description: Large-scale biology projects such as the sequencing of the human genome and gene expression surveys using RNA-seq, microarrays and other technologies have created a wealth of data for biologists. However, the challenge facing scientists is analyzing and even accessing these data to extract useful information pertaining to the system being studied. This course focuses on employing existing bioinformatic resources – mainly web-based programs and databases – to access the wealth of data to answer questions relevant to the average biologist, and is highly hands-on. Topics covered include multiple sequence alignments, phylogenetics, gene expression data analysis, and protein interaction networks, in two separate parts. Bioinformatic Methods I deals with databases, BLAST, multiple sequence alignments, phylogenetics, selection analysis and metagenomics. Bioinformatic Methods II covers motif searching, protein-protein interactions, structural bioinformatics, gene expression data analysis, and cis-element predictions. This pair of courses is useful to any student considering graduate school in the biological sciences, as well as students considering molecular medicine.	Bioinformatician	Introductory	https://www.coursera.org/learn/bioinformatics-methods-1	Coursera course	On-demand	Online	12-18 hours of videos and labs	Free or can pay $49 for certificate		University of Toronto on Coursera									Coursera certificate			
Bioinformatic Methods II	Comparative Genomics; Functional Analysis	Motif Searching; Proteins; Structures; Gene Expression Analysis: Cis-element Predictions	This University of Toronto course is offered on Coursera. This course may be taken for free, or you may pay for a certificate can be shared on LinkedIn. This course is offered on-demand. Description: Large-scale biology projects such as the sequencing of the human genome and gene expression surveys using RNA-seq, microarrays and other technologies have created a wealth of data for biologists. However, the challenge facing scientists is analyzing and even accessing these data to extract useful information pertaining to the system being studied. This course focuses on employing existing bioinformatic resources – mainly web-based programs and databases – to access the wealth of data to answer questions relevant to the average biologist, and is highly hands-on. Topics covered include multiple sequence alignments, phylogenetics, gene expression data analysis, and protein interaction networks, in two separate parts. Bioinformatic Methods I deals with databases, BLAST, multiple sequence alignments, phylogenetics, selection analysis and metagenomics. Bioinformatic Methods II covers motif searching, protein-protein interactions, structural bioinformatics, gene expression data analysis, and cis-element predictions. This pair of courses is useful to any student considering graduate school in the biological sciences, as well as students considering molecular medicine.	Bioinformatician	Intermediate	https://www.coursera.org/learn/bioinformatics-methods-2	Coursera course	On-demand	Online	12-18 hours of videos and labs	Free or can pay $49 for certificate		University of Toronto on Coursera									Coursera certificate			
Clustering Biological Data (Bioinformatics V)		Algorithms; Saccharomyces Yeast	This UC San Diego course is offered on Coursera. This course may be taken for free, or you may pay for a certificate can be shared on LinkedIn. This course will be offered Sept. 28, 2015 to Oct. 25, 2015. About the Course One of the first organisms to be domesticated by humans was yeast. Saccharomyces yeast is remarkable because it can not only convert the glucose in grapes into ethanol (which we then consume as wine), but it can also invert its own metabolism, consuming the ethanol it just produced in a process called the diauxic shift. To find genes implicated in the diauxic shift, we will learn about clustering algorithms that will divide yeast genes into distinct groups based on their patterns of regulatory behavior. A similar method can be applied to distinguish normal and tumor cells, an approach that led to diagnostic tests like MammaPrint for predicting the return of cancer after chemotherapy. We can also apply clustering algorithms to identify the genetic foundation of human population structure and discover which populations have contributed to your own genome. To do so, we will need to power up the clustering algorithms we encounter using a powerful computational approach called principal component analysis. Course Syllabus How Did Yeast Become a Wine Maker? (Clustering Algorithms) • An Evolutionary History of Wine Making • Identifying Genes Responsible for the Diauxic Shift • Introduction to Clustering • k-Means Clustering • The Lloyd Algorithm • Clustering Genes Implicated in the Diauxic Shift • Limitations of k-Means Clustering • From Coin Flipping to k-Means Clustering		Introductory	https://www.coursera.org/course/clustering	Coursera course	September 28 to October 25, 2015; see schedule on website	Online	4 weeks, 8-10 hours per week	Free or can pay $49 for certificate		University of California San Diego on Coursera									Coursera certificate			
Deciphering Molecular Evolution (Bioinformatics IV)	Phylogenomics	SARS; Dinosaur Proteins	This UC San Diego course is offered on Coursera. This course may be taken for free, or you may pay for a certificate can be shared on LinkedIn. This course will be offered Aug. 17, 2015 to Sept. 20, 2015. About the Course Two landmark bioinformatics-related discoveries made headlines in 2003. First, the deadly Severe Acute Respiratory Syndrome (SARS) virus caused panic as it swept around the globe in a few weeks. But where did SARS come from? By constructing an evolutionary tree of the unknown virus as well as viruses taken from other species, we can not only understand which animal gave us SARS, but also reconstruct its path around the globe. This is just one of many problems in modern biology related to constructing evolutionary trees. Second, a team of biologists announced that some proteins had miraculously survived within a 68 million year old dinosaur fossil. Moreover, they concluded that the amino acid sequences of these dinosaur proteins were nearly identical to sequences in modern-day chickensl. Based on this discovery, famed paleontologist Jack Horner (who partly inspired the character of Dr. Grant from Jurassic Park) hopes to resurrect dinosaurs by genetically re-engineering a chicken. But did these peptides really come from T. rex, or do they represent statistical artifacts or contamination? To answer this question, we will need to explore the field of computational proteomics. Course Syllabus Which Animal Gave Us SARS? (Evolutionary Tree Reconstruction) • The Fastest Outbreak • Transforming Distance Matrices into Evolutionary Trees • Toward An Algorithm for Distance-Based Phylogeny Construction • Additive Phylogeny • Using Least Squares to Construct Approximate Distance-Based Phylogenies • Ultrametric Evolutionary Trees	Bioinformatician; Epidemiologist	Introductory	https://www.coursera.org/course/molecularevolution	Coursera course	August 17 to September 20, 2015; see schedule on website	Online	5 weeks, 8-10 hours/week	Free or can pay $49 for certificate		University of California San Diego on Coursera									Coursera certificate			
Finding Hidden Messages in DNA (Bioinformatics I)	Phylogenomics	DNA; Algorithms	This UC San Diego course is offered on Coursera. This course may be taken for free, or you may pay for a certificate can be shared on LinkedIn. This course will be offered May 25, 2015 to June 28, 2015. About the Course A genome may look like an incomprehensible string of the letters A, C, G, and T. Yet hidden in the three billion nucleotides of your genome is a secret language. This course offers an introduction to how we can start to understand this language by using algorithms to find hidden messages in DNA. What do these hidden messages say? In the first chapter of the course, hidden DNA messages indicate where a bacterium starts replicating its genome, a problem with applications in bioengineering and beyond. In the second chapter, hidden DNA messages tell us how organisms know whether it is day or night as well as how the bacterium causing tuberculosis is able to hide from antibiotics. We will see how randomized algorithms, which toss coins and roll dice, can be used to find these messages. Each of the two central topics in the course builds the algorithmic knowledge required to address this challenge. Along the way, coding challenges and exercises, many of which ask you to apply your skills to real genetic data, will be directly integrated into the text at the exact moment they are needed. Course Syllabus Where in the Genome Does Replication Begin? (Algorithmic Warmup): • Introduction to DNA replication • Hidden messages in the replication origin • Some hidden messages are more surprising than others • An explosion of hidden messages • The simplest way to replicate DNA • Asymmetry of replication • Peculiar statistics of the forward and reverse half-strands • Some hidden messages are more elusive than others • A final attempt at finding DnaA boxes in E. coli	Bioinformatician	Introductory	https://www.coursera.org/course/hiddenmessages	Coursera course	June 7 to July 12, 2015; see schedule on website	Online	4 weeks, 8-10 hours/week	Free or can pay $49 for certificate		University of California San Diego on Coursera									Coursera certificate			

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

	Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Avaliable	Notes
93	Assembling Genomes and Sequencing Antibiotics (Bioinformatics II)	Comparative Genomics	DNA; Antibiotics; Sequencing Genomes; Assembly	This UC San Diego course is offered on Coursera. This course may be taken for free, or you may pay for a certificate can be shared on LinkedIn. This course will be offered May 25, 2015 to June 28, 2015. About the Course In "Finding Hidden Messages in DNA", we discussed how to separate some of the signal from the apparent noise of DNA sequences. But how do we know what the DNA sequence making up a genome is in the first place? After all, DNA nucleotides are far too small to view with a normal microscope, and biologists still do not possess technology that would read all the nucleotides of your genome from beginning to end. In the first chapter of this course, we will see that entire genomes are assembled from millions of short overlapping pieces of DNA. The scale of this problem (the human genome is 3 billion nucleotides long!) implies that computers must be involved. Yet the problem is even more complex than it may appear ... to solve it, we will need to travel back in time to meet three famous mathematicians, and learn about algorithms based on graph theory. In the second chapter of the course, we will consider antibiotics, which are mini-proteins engineered by bacteria to fight each other. Determining the sequence of amino acids making up an antibiotic is an important problem for medical research, but the practical barriers to sequencing an antibiotic containing just 10 amino acids are often more substantial than the limitations when assembling a genome with 10 million nucleotides! To decode the amino acid sequence of an antibiotic, biologist must blast many copies of this antibiotic into pieces and use an expensive molecular scale to weigh the resulting fragments. It may not seem possible that we can determine an antibiotic just from the masses of these fragments, but we will see that brute force algorithms will often succeed. Course Syllabus How Do We Assemble Genomes? (Graph Algorithms) • Exploding Newspapers • The String Reconstruction Problem • String reconstruction as a walk in the overlap graph	Bioinformatician	Introductory	https://www.coursera.org/course/assembly	Coursera course	June 7 to July 12, 2015; see schedule on website	Online	4 weeks, 8-12 hours/week	Free or can pay $49 for certificate		University of California San Diego on Coursera									Coursera certificate			
94	Comparing Genes, Proteins, and Genomes (Bioinformatics III)	Comparative Genomics	DNA; Proteins; Genomes	This UC San Diego course is offered on Coursera. This course may be taken for free, or you may pay for a certificate can be shared on LinkedIn. This course will be offered July 7, 2015 to August9, 2015. About the Course DNA mutations can broadly be divided into two categories. Point mutations, in which a single nucleotide (A, C, G, T) is altered, inserted, or deleted, are comparable to erosion slowly changing the shape of a boulder. Much of human differentiation is attributable to the accumulation of point mutations. The other type of mutation is extremely rare and can cause dramatic effects on the scale of species evolution. In genome rearrangements, huge blocks of DNA are heaved around, often from one chromosome to another. These mutations are comparable to earthquakes, which hoist up mountains and wrench apart continents. When we compare two relatively short pieces of DNA that have not been affected by genome rearrangements (say, two genes taken from individuals from the same species), our goal is to identify a "path of least resistance" connecting these two genes via point mutations. We can find such a path using a powerful algorithmic paradigm called dynamic programming. On the other hand, when we zoom out to the compare entire genomes taken from different species that diverged millions of years ago (such as humans and mice), the effects of genome rearrangements become more pronounced. To determine how far diverged these genomes are, we will need completely different combinatorial algorithms that will help us answer questions about the patterns of genome rearrangements. For example, in order to move around large blocks of DNA, a genome rearrangement must "break" the genome in at least two places. We know that there are fault lines on the earth's surface where earthquakes are more likely; are there analogous "fragile regions" in the human genome where breakage has been more likely to occur during a genome rearrangement? Course Syllabus How Do We Compare Biological Sequences? (Dynamic Programming) • Cracking the non-ribosomal code	Bioinformatician	Introductory	https://www.coursera.org/course/comparinggenomes	Coursera course	July 21 to August 23, 2015; see schedule on website	Online	4 weeks, 8-12 hours/week	Free or can pay $49 for certificate		University of California San Diego on Coursera									Coursera certificate			
95	Finding Mutations in DNA and Proteins (Bioinformatics VI)	Variant Analysis	DNA; Proteins; Genomes	This UC San Diego course is offered on Coursera. This course may be taken for free, or you may pay for a certificate can be shared on LinkedIn. This course will be offered November 2, 2015 to December 6, 2015. About the Course Although biologists assembled a reference human genome in 2001, your own genome differs from this reference genome by millions of mutations. In this chapter, we will learn combinatorial pattern matching algorithms for finding these mutations, something that future doctors will be able to do within minutes in order to find disease genes. We will then examine the problem of detecting subtle similarities that evade the traditional sequence comparison algorithms that we studied in "Comparing Genes, Genomes, and Proteins". Having efficient algorithms for comparing highly diverged sequences is important, since a single misaligned nucleotide can misclassify a protein and prevent biologists from inferring its function. We will consider a popular approach to sequence comparison based on an abstract machine called a Hidden Markov Model. Course Syllabus How Do We Locate Disease-Causing Mutations? (Combinatorial Pattern Matching) • What Causes Ohdo Syndrome? • Introduction to Multiple Pattern Matching • Herding Patterns into a Trie • Preprocessing the Genome Instead • Suffix Trees • Suffix Arrays • The Burrows-Wheeler Transform • Inverting the Burrows-Wheeler Transform • Pattern Matching with the Burrows-Wheeler Transform • Speeding Up Burrows-Wheeler Pattern Matching • Where are the Matched Patterns?	Bioinformatician	Introductory	https://www.coursera.org/course/mutations	Coursera course	November 2 to December 6, 2015; see schedule on website	Online	5 weeks, 6-10 hours/week	Free or can pay $49 for certificate		University of California San Diego on Coursera									Coursera certificate			
96	Algorithms, Biology, and Programming for Beginners	Statistics	Algorithms; Genomes; Math	This UC San Diego course is offered on Coursera. This course may be taken for free, or you may pay for a certificate can be shared on LinkedIn. This course will be offered May 18, 2015 to July 26, 2015. About the Course The sequencing of the human genome fueled a computational revolution in biology. As a result, modern biology produces as many new algorithms as any other fundamental realm of science. Genome sequencing is just one of hundreds of biological problems that have become inextricable from the computational methods required to solve them. In this course, we will uncover some of the algorithmic ideas that are fundamental to an understanding of modern biology. Computational concepts like dynamic programming and graph theory will help us explore algorithms applied to a wide range of biological topics, from finding regulatory motifs to determining whether the human genome has "fragile" regions. Throughout the process, we will apply bioinformatics algorithms to real genetic data. Each chapter in the course textbook covers a single biological question and slowly builds the algorithmic knowledge required to address this challenge. Along the way, coding challenges and exercises will be integrated into the text at the exact moment they are needed. Course Syllabus The course will be based around the following biological questions, with the algorithmic ideas that we will use to solve them in parentheses: • Where Does DNA Replication Begin? (Algorithmic Warm-up) • How Do We Sequence Antibiotics? (Brute Force Algorithms) • Which DNA Patterns Act As Cellular Clocks? (Greedy and Randomized Algorithms) • How Do We Assemble Genomes? (Graph Algorithms) • How Do We Compare Biological Sequences? (Dynamic Programming Algorithms) • Are There Fragile Regions in the Human Genome? (Combinatorial Algorithms) • Which Animal Gave Us SARS? (Evolutionary Trees) • How Do We Locate Disease-Causing Mutations? (Combinatorial Pattern Matching)	Bioinformatician; Epidemiologist	Introductory	https://www.coursera.org/course/algobioprogramming	Coursera course	August 17 to October 25, 2015; see schedule on website	Online	8 weeks, 6-10 hours/week	Free or can pay $49 for certificate		University of California San Diego on Coursera									Coursera certificate			
97	20th Summer Institute in Statistical Genetics (SISG 2015)	Statistics; Variant Analysis; Expression Analysis; Phylogenomics; Metagenomics	Statistical Genomics	The 20th Summer Institute in Statistical Genetics (SISG 2015) will be held at the University of Washington in Seattle, Washington during July 6-24, 2015. The Institute consists of a series of two-and-a-half day workshops designed to introduce geneticists to modern methods of statistical analysis and to introduce statisticians to the statistical challenges posed by modern genetic data. Prerequisites are minimal, and the modular nature of the Institute enables participants to design a program best suited to their backgrounds and interests. Most participants take two or three modules. Individuals attending the Institute will receive certificates of course completion in recognition of their participation. Registration is now open for SISG 2015. Modules listed together in each session are concurrent. Therefore, only one (1) module may be taken for each 2.5-day session. This also applies if you are registering for more than one Summer Institute. Please review the schedules carefully. Course descriptions are here: http://www.biostat.washington.edu/suminst/sisg/modules. WEEK 1, SESSION 1 (July 6-8) Mod 1: Probability and Statistical Inference* Mod 2: Molecular Genetics and Genomics Mod 3: Introduction to R* Mod 4: (SISBID 1) Accessing Biomedical Big Data WEEK 1, SESSION 2 (July 8-10) Mod 5: Regression and Analysis of Variance Mod 6: Gene Expression Profiling Mod 7: Elements of R for Genetics and Bioinformatics Mod 8: (SISBID 2) Visualization of Biomedical Big Data WEEK 2, SESSION 3 (July 13-July 15) Mod 9: Population Genetic Data Analysis Mod 10: Quantitative Genetics Mod 11: Genetic Epidemiology Mod 12: (SISBID 3) Supervised Methods for Statistical Machine Learning WEEK 2, SESSION 4 (July 15-July 17) Mod 13: Association Mapping: GWAS and Sequencing Data Mod 14: QTL Mapping	Bioinformatician; Epidemiologist	Intermediate	http://www.biostat.washington.edu/suminst/sisg/general	Lecture	July 6-24, 2015	University of Washington, Seattle, Washington	Up to 21 days depending on courses selected	Free tuition and course materials, meals, travel and lodging are not covered)		University of Washington			(206) 543-1044; option 5	sisg@uw.edu	SISG 2015 c/o UW BIOSTATISTICS UW Tower, 15T-420 4333 Brooklyn Avenue NE Campus Box 359461	Seattle	WA	98195-9461	Certificate of completion			
98	Pacbio SMRT Portal Bootcamp	DNA Sequencing Technology	Pacbio; SMRT	These training materials are from a course presented by the University of California, Davis. • Introduction to Amazon Web Services EC2 • SMRT-Sequencing, Assembly - lecture • SMRT-Portal Assembly, Alignment - exercises • Finishing circular assemblies - lecture	Bioinformatician; Laboratorian	Introductory	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	0nline	Self-paced	Free		University of California, Davis												
99	RNA-Seq and ChIP-Seq Analysis with Galaxy	Webtools; Expression Analysis	Galaxy; RNA-Seq; ChiP-Seq	These training materials are from a course presented by the University of California, Davis. Monday • General Comments - lecture • Sequencing Technologies - lecture • Introduction to Amazon Web Services EC2 • Intro to Galaxy, and Illumina Read Grooming - lecture and exercises Tuesday • Using FTP with Galaxy - exercise • Read Alignment - lecture and exercise • Introduction to ChIP-Seq - lecture • ChIP-Seq Data Analysis - lecture • ChIP-Seq Analysis - exercise • Visualizing ChIP-Seq data on the UCSC Genome Browser - exercise Wednesday • RNA-Seq Concepts, Terminology, and Work Flows - lecture • Aligning SE RNA-Seq Reads to a Reference Genome - exercises • Aligning PE RNA-Seq Reads to a Genome - exercises • RNA-Seq Guest Lecture - lecture • The Tuxedo Suite and Other RNA-Seq Topics - lecture • Alignment to a Reference Transcriptome - exercises • Differential Expression Analysis with edgeR from Genome Alignments - exercises • Some Helpful Links Thursday • I've Done My Analysis, Now What? - discussion	Bioinformatician	Intermediate	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	0nline	Self-paced	Free		University of California, Davis												

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters/PhD Program	Non-Degree Option Available	Notes
Using the Linux Command Line for Analysis of High Throughput Sequencing Data	General Computing; Language; Expression Analysis; HPC/Cloud; Comparative Genomics	Linux; UNIX; RNA-seq; AWS; Illumina	These training materials are from a course presented by the University of California, Davis. Monday • Workshop Welcome - lecture • Course, Bioinformatics Overview - lecture • High Throughput Sequencing Fundamentals - lecture • Introduction to Amazon Web Services EC2 - lecture • Read Quality Assessment & Improvement - lecture • Illumina Read Quality Assessment & Improvement - exercises Tuesday • Alignment & Variant Discovery - lecture • Next Generation Sequence Alignment - exercises • GATK Best Practices for Variant Discovery - lecture • Variant Discovery using GATK3 - exercises • Effect Prediction and the UCSC Genome Browser - exercises • Useful links for GATK3 variant analysis and snpEff • AWS Simple Storage Service Basics Wednesday • Genome Assembly - lecture • Genome Assembly - exercises • Genome Assembly: then and now - guest lecture Thursday • RNA-Seq Concepts, Terminology, and Work Flows - lecture • Aligning SE RNA-Seq Reads to a Reference Genome - exercises • Aligning PE RNA-Seq Reads to a Genome - exercises	Bioinformatician	Intermediate	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	Online	Self-paced	Free		University of California, Davis													
Using Galaxy for Analysis of High Throughput Sequence Data	Webtools; Expression Analysis; Expression Analysis	Galaxy; RNA-seq	These training materials are from a course presented by the University of California, Davis. Monday • Course, Bioinformatics Overview - lecture • High Throughput Sequencing Fundamentals - lecture • Introduction to Amazon Web Services EC2 • Read Quality Assessment & Improvement - lecture • Illumina Read Quality Assessment & Improvement - exercises Tuesday • Alignment & Variant Discovery - lecture • Next Generation Sequence Alignment - exercises • GATK Best Practices for Variant Discovery - lecture • Variant Discovery using GATK2 • Effect Prediction and the UCSC Genome Browser • Useful links for GATK2 variant analysis and snpEff Wednesday • Genome Assembly - lecture • Genome Assembly: then and now - guest lecture • Genome Assembly - exercises Thursday • RNA-Seq Concepts, Terminology, and Work Flows - lecture • Aligning SE RNA-Seq Reads to a Reference Genome - exercises • Aligning PE RNA-Seq Reads to a Genome - exercises • Differential Expression Analysis with edgeR from Genome Alignments - exercises • Gene Construction - lecture and exercises	Bioinformatician	Intermediate	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	Online	Self-paced	Free		University of California, Davis													
Bootcamp: Introduction to the Amazon Cloud for Galaxy and the Command-Line	HPC/Cloud; General Computing	Galaxy; Amazon Cloud/AWS;Linux	These training materials are from a course presented by the University of California, Davis. Contents: • Amazon Cloud Computing o Introduction to Services o Launching into the Cloud o Anatomy of a Cloud Computer o Saving, Sharing, and Public Data Sets o Mounting Drives • Linux Command Line bootcamp o Connecting to your Terminal o Connecting via Java o Connecting via Windows without Java o Connecting via Mac/Linux o The Terminal and Linux o Linux file system o Cleaning up o Clearing the air o Moving around o Spaces are delimiters o Moving on Up o It's all relative o Going Home o Man, this is complicated o Making directories o Removing directories o Tab completion and arrows o Touch	Bioinformatician	Intermediate	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	Online	Self-paced	Free		University of California, Davis													
Bootcamp: Genome Assembly Using Next Generation Sequence Data	Comparative Genomics	NGS	These training materials are from a course presented by the University of California, Davis. • Genome Assembly - lecture • Genome Assembly - exercises • Assembly Assessment, and the Assemblathon Competitions - lecture	Bioinformatician	Intermediate	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	Online	Self-paced	Free		University of California, Davis													
Bootcamp: Next Generation Sequence Alignment and Variant Discovery	DNA Sequencing Technology; Variant Analysis	NGS; GATK	These training materials are from a course presented by the University of California, Davis. • Alignment & Variant Discovery - lecture • Next Generation Sequence Alignment - exercises • GATK Best Practices for Variant Discovery - lecture • Variant Discovery exercise • Useful links for GATK variant analysis and snpEff • Effect Prediction and the UCSC Genome Browser	Bioinformatician	Intermediate	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	Online	Self-paced	Free		University of California, Davis													
Bootcamp: Introduction to Next Generation Sequence Analysis with Galaxy	Webtools	Galaxy; NGS	These training materials are from a course presented by the University of California, Davis. • Next Generation Sequencing Fundamentals - lecture • Read Quality Assessment & Improvement - lecture • Introduction to Galaxy and Sequence Quality Assessment & Improvement - exercises • Creating Galaxy Workflows from scratch - exercises • Running Galaxy Workflows - exercises	Bioinformatician	Introductory	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	Online	Self-paced	Free		University of California, Davis													
Bioinformatics Short Course 2013	Comparative Genomics; Expression Analysis	Introduction to Bioinformatics; NGS; Galaxy; GATK; UCSC Genome Browser; Genome Assembly; RNA-Seq; Amazon Cloud; Unix	These training materials are from a course presented by the University of California, Davis. Monday • 2013 Bioinformatics Short Course - Welcome Lecture • Next Generation Sequencing Fundamentals - lecture • Read Quality Assessment & Improvement - lecture • Introduction to Galaxy and Sequence Quality Assessment & Improvement - exercises • Running Workflows - exercises • Creating Workflows from scratch - exercises Tuesday • Next Generation Sequence Alignment - lecture • Next Generation Sequence Alignment - exercises • GATK Best Practices for Variant Discovery - lecture • Variant Discovery exercise • Effect Prediction and the UCSC Genome Browser • Useful links for GATK variant analysis and snpEff Wednesday • Genome Assembly - lecture • Genome Assembly - exercises • Assembly Assessment, and the Assemblathon Competitions - lecture Thursday • RNA-Seq Concepts, Terminology, and Work Flows - lecture • Aligning SE RNA-Seq Reads to a Reference Genome - exercises • RNA-Seq Statistics - lecture • Aligning PE RNA-Seq Reads to a Genome - exercises	Bioinformatician	Introductory	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	Online	Self-paced	Free		University of California, Davis													
RNA-Seq Workshop: From Plants to P-Value!	Laboratory; Expression Analysis	RNA-Seq	These training materials are from a course presented by the University of California, Davis. Monday • Monday Sept. 9, 2013 AM Lectures • Monday Sept. 9, 2013 PM Computer Track: Unix Command Line bootcamp • Monday Sept. 9, 2013 PM Bench Track Tuesday • Tuesday Sept. 10, 2013 AM Computer Track: Command Line RNA-Seq • Tuesday Sept. 10, 2013 PM: Introduction to Galaxy and Sequence Quality Assessment & Improvement • Tuesday Sept. 10, 2013 PM: Alignment of RNA-Seq Reads to a Reference Transcriptome • Tuesday Sept. 10, 2013 PM: Alignment of RNA-Seq Reads to a Reference Genome Wednesday • Wednesday Sept. 11, 2013 Additional Resources • Gene Construction • Some Helpful Links	Bioinformatician; Laboratorian	Introductory	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	Online	Self-paced	Free		University of California, Davis													
Bootcamp: Cloud Computing for Bioinformatics	HPC/Cloud; General Computing	Cloud Computing	These training materials are from a course presented by the University of California, Davis. • Introduction to Services.pdf • Launching into the Cloud.pdf • Anatomy of a Cloud Computer.pdf • Saving, Sharing, & Public Data Sets.pdf • Mounting Drives.pdf	Bioinformatician	Introductory	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	Online	Self-paced	Free		University of California, Davis													

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Avaliable	Notes
Bootcamp: Introduction to RNA-Seq	Expression Analysis	RNA-seq	These training materials are from a course presented by the University of California, Davis. • RNA-Seq Concepts, Terminology, and Work Flows • Next Generation Sequence Quality Assessment & Improvement o Note On UCD Bioinformatics Core Tools o Experimental Files o Importing the Example Reads o Quality Assurance and Improvement • Alignment of RNA-Seq Reads to a Reference Transcriptome o Aligning Sequences with BWA o Calculating Library Insert Size o Generate a Table of Raw Counts by Sample o Running DESeq • RNA-Seq: Experimental Design & Statistics for Differential Expression - Blythe Durbin-Johnson, Ph. D. • Alignment of RNA-Seq Reads to a Reference Genome o Alignment Workflow and Files o RNA-Seq Read Alignment with TopHat o Running Cuffdiff to Identify Differentially Expressed Genes • Gene Construction o Overview of Concepts o Finding novel transcripts/genes with TopHat and Cufflinks • Some Helpful Links	Bioinformatician	Intermediate	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	0nline	Self-paced	Free		University of California, Davis												
Bootcamp: Introduction to Galaxy	Webtools; Functional Analysis	Galaxy; CHiP-seq	These training materials are from a course presented by the University of California, Davis. • Introduction to Galaxy o UCSC Genome Browser and IGV o Workflows o UCSC Genome Browser o IGV • Next Generation Sequence Quality Assessment & Improvement o Note On UCD Bioinformatics Core Tools o Read QA&I Walkthrough o Read QA&I Exercise • Unreplicated DE analysis using DESeq • Visualization with Trackster • Genome Assembly With Velvet in Galaxy o Data Needs o Uploading Data to Galaxy o Single End Velvet Assembly o Reviewing Assembly Output o Paired End Velvet Assembly o Comparing the Single and Paired End Assemblies • ChIP-Seq Analysis using Sissrs on Galaxy o Roadmap • Galaxy Workflows • Galaxy Toolshed • Directed Exercise / Challenge o Challenge Analysis Workflow Diagrams	Bioinformatician	Intermediate	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	0nline	Self-paced	Free		University of California, Davis												
Data Analysis & Visualization	Statistics; Expression Analysis	R; Bioconductor; Gene Expression Analysis; Visualization	These training materials are from a course presented by the University of California, Davis. Day 1 Course Overview R/Bioconductor Installation and Configuration Introduction to the R Language - Vince Buffalo Working with Data in R - Vince Buffalo Basics Graphics in R - Vince Buffalo Bioconductor Basics - Vince Buffalo Genome & Function Annotation - Vince Buffalo Rsamtools & Genomic Ranges - Vince Buffalo Day 2 GRanges, GenomicFeatures, and BSGenome - Vince Buffalo Short Read Contamination and Quality Issues (PDF slides) - Joe Fass Working with Short Reads in R: qrqc and RNA-Seq - Vince Buffalo Gene Expression Analysis (PDF slides) - Jie Peng Gene Expression Data Visualization - Dawei Lin Network Biology and Visualization (PDF slides) - Dawei Lin Gene Module Discovery Based on Large Data Sets - Dawei Lin	Bioinformatician	Intermediate	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	0nline	Self-paced	Free		University of California, Davis												
Using the Linux Command Line for Analysis of High Throughput Sequence Data (2)	General Computing; Languages; Variant Analysis; DNA Sequencing Technology; HPC/Cloud	Linux; Sequencing; Ilumina HiSeq/MiSeq; PacBio RS; SNP; RNA-Seq; Cloud Computing	This course is presented by the University of California, Davis. This workshop covers modern high throughput sequencing technologies, applications, and ancillary topics, including: • Illumina HiSeq / MiSeq, and PacBio RS technologies • Read Quality Assessment & Improvement • Genome assembly • SNP and indel discovery • RNA-Seq differential expression analysis • Experimental design • Hardware and software considerations • Cloud Computing	Bioinformatician	Intermediate	http://training.bioinformatics.ucdavis.edu/documentation/	Slides, PDF, exercises	On-demand	0nline	Self-paced	Free		University of California, Davis												
Using Galaxy for Analysis of High Throughput Sequence Data (2)	Webtools; Variant Analysis; DNA Sequencing Technology; HPC/Cloud	Galaxy; Sequencing; Ilumina HiSeq/MiSeq; PacBio RS; SNP; RNA-Seq; Cloud Computing	This course is presented by the University of California, Davis. This workshop covers modern high throughput sequencing technologies, applications, and ancillary topics, including: • Illumina HiSeq / MiSeq, and PacBio RS technologies • Read Quality Assessment & Improvement • Genome assembly • SNP and indel discovery • RNA-Seq differential expression analysis • Experimental design • Hardware and software considerations • Cloud Computing	Bioinformatician	Intermediate	http://training.bioinformatics.ucdavis.edu/events/	Lecture, slides, PDF, exercises	September 14-18, 2015 (training materials will be posted online after the course)	Davis, California	5 days	1500 (does not include meals, travel, and lodging) (training materials will be posted online for free after the course)		University of California, Davis												
Analyzing Next-Generation Sequencing Data	DNA Sequencing Technology; Variant Analysis; HPC/Cloud; Languages	NGS; AWS; Python	Michigan State University NGS Summer Course 2015 Analyzing Next-Generation Sequencing Data Registration closed on April 17, 2015, for the August 10 to August 21, 2015 Summer Course. Sign up for the announcements mailing list for future course announcements, http://lists.idyll.org/listinfo/ngs-course-announce. This course is sponsored by NIH. This intensive two week summer course will introduce attendees with a strong biology background to the practice of analyzing short-read sequencing data from Illumina and other next-gen platforms. The first week will introduce students to computational thinking and large-scale data analysis on UNIX platforms. The second week will focus on mapping, assembly, and analysis of short-read data for resequencing, ChIP-seq, and RNAseq. No prior programming experience is required, although familiarity with some programming concepts is helpful, and bravery in the face of the unknown is necessary. 2 years or more of graduate school in a biological science is strongly suggested. Faculty, postdocs, and research staff are more than welcome! Students will gain practical experience in: • Python and bash shell scripting • cloud computing/Amazon EC2 • basic software installation on UNIX • installing and running bowtie, Trinity, Velvet, SPAdes and other bioinformatics tools. • querying mappings and evaluating assemblies Materials from previous courses are available at http://angus.readthedocs.org/ under a Creative Commons/full use+reuse license.	Bioinformatician	Intermediate	http://bioinformatics.msu.edu/ngs-summer-course-2015	Lecture, exercises	August 10-21, 2015 (training materials will be posted online after the course)	Kellogg Biological Station, Michigan State University	12 days	900 (training materials will be posted online for free after the course)		Michigan State University												
Next-Gen Sequence Analysis Workshop	DNA Sequencing Technology; Variant Analysis; HPC/Cloud; Languages	NGS; Python; Amazon Cloud	Michigan State University NGS Summer Course 2014 Analyzing Next-Generation Sequencing Data This resource contains materials from the 2014 NGS Summer Course, under a Creative Commons/full use+reuse license. Sign up for the announcements mailing list for future course announcements, http://lists.idyll.org/listinfo/ngs-course-announce. This course is sponsored by NIH. Course Description This intensive two week summer course will introduce attendees with a strong biology background to the practice of analyzing short-read sequencing data from Illumina and other next-gen platforms. The first week will introduce students to computational thinking and large-scale data analysis on UNIX platforms. The second week will focus on mapping, assembly, and analysis of short-read data for resequencing, ChIP-seq, and RNAseq. No prior programming experience is required, although familiarity with some programming concepts is helpful, and bravery in the face of the unknown is necessary. 2 years or more of graduate school in a biological science is strongly suggested. Faculty, postdocs, and research staff are more than welcome! Students will gain practical experience in: • Python and bash shell scripting • cloud computing/Amazon EC2 • basic software installation on UNIX • installing and running maq, bowtie, and velvet • querying mappings and evaluating assemblies Day Schedule Monday 8/4 • 1:30pm lecture: Welcome! (Titus) • Tutorial: Day 1 - Getting started with Amazon • 7pm: research presentations Tuesday 8/5 • Day 2 – Running BLAST and other things at the command line	Bioinformatician	Introductory	http://angus.readthedocs.org/en/2014/	HTML, exercises	On-demand	0nline	Self-paced	Free		Michigan State University												
2013 CEMI Workshop at Caltech (Microbial Bioinformatics)		BLAST; Amazon Cloud; Microbial Bioinformatics	This 2013 Caltech workshop was sponsored by CEMI, the Caltech Environmental Microbial Initiative. Titus Brown taught the course. Below is the outline to training materials. • 1:15pm: Igor Antoschechkin on local sequencing core • 2pm Lecture: Cloud computing etc. • Afternoon lab 1: Getting started with Amazon EC2 • 3:30pm lecture: BLAST • Afternoon lab 2: Basic EC2, command line, and BLAST • Final lecture: A belated welcome! Wednesday 9/18 • 9am: lecture, Short read mapping • morning lab: Understanding Read Formats and Quality Controlling Data • morning lab 2: Mapping with bwa • 1:15pm: assembly exercise • 2pm: lecture, Assembly Thursday 9/19 • lab: Basic (single-genome) assembly and BLASTing your assembled data • ~10am: lecture: metagenome assembly • late morning lab: Annotating a bacterial genome with Prokka • afternoon lab: Some exercises to try • afternoon lecture: pipelines and automation • tutorial: the shell Friday 9/20 • Arms building first floor (Buwalda Room 151A) • 9am: lecture: metagenome assembly • morning: open lab time to work through pipelines (see especially Kalamazoo Metagenome Assembly and Some exercises to try • More resources for help • Assembly Assembly Scavenger Hunt			http://2013-caltech-workshop.readthedocs.org/en/latest/	Slides, PDF, exercises	On-demand	0nline	Self-paced	Free		Caltech												

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Available	Notes
Computational Science for Biologists	General Computing; Comparative Genomics	BLAST; Python	This 2013 Michigan State University (MSU) workshop was co-sponsored by BEACON (a National Science Foundation center at MSU) and ICER (Institute for Cyber-Enabled Research). Below is the outline to training materials. 2013 MSU Zero-Entry Workshop: Computational Science for Biologists Sep 23 and 25, 2013. Michigan State University. Lecturers: Titus Brown; Tracy Teal; Jory Schossau. Monday 9/23 - 1pm: Getting started: logging in • Basic EC2; command line, and BLAST • Sequence analysis work (lecture) • 2:30pm: break • 3pm: ICER/HPC; shell introduction • 3:45pm: pipelines and automation (lecture) • 4:15pm: Using the IPython Notebook for graphing and data processing • 5pm: end Wednesday 9/25 • 1pm: Monte Carlo simulations • 3pm: Presentation on background, bioinformatics, etc. • 5pm: end. Also see More resources for help	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://2013-msu-zero-entry.readthedocs.org/en/latest/	HTML, exercises	On-demand	Online	Self-paced	Free		Michigan State University												
The Unix Shell	General Computing; Languages	Programming; Unix	These training materials are from a Software Carpentry course. The Software Carpentry Foundation is a non-profit volunteer organization whose members teach researchers basic software skills. All materials for Software Carpentry lessons are freely available under the Creative Commons - Attribution License. Software Carpentry can also teach workshops at your work site by request, http://software-carpentry.org/workshops/request.html The Unix shell The Unix shell has been around longer than most of its users have been alive. It has survived so long because it's a power tool that allows people to do complex things with just a few keystrokes. More importantly, it helps them combine existing programs in new ways and automate repetitive tasks so that they don't have to type the same things over and over again. Use of the shell is fundamental to using a wide range of other powerful tools and computing resources (including "high-performance computing" supercomputers). These lessons will start you on a path towards using these resources effectively. Prerequisites This lesson guides you through the basics of filesystems and the shell. If you have stored files on a computer at all and recognize the word "file" and either "directory" or "folder" (two common words for the same thing), you're ready for this lesson. If you're already comfortable manipulating files and directories, searching for files with grep and find, and writing simple loops and scripts, you probably won't learn much from this lesson. Topics 1. Introducing the Shell 2. Files and Directories 3. Creating Things 4. Pipes and Filters 5. Loops 6. Shell Scripts 7. Finding Things	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://software-carpentry.org/lessons.html	HTML, exercises	On-demand	Online	Self-paced	Free		Software Carpentry												
Version Control with Git	Reproducible Research; General Computing	Programming; Git	These training materials are from a Software Carpentry course. The Software Carpentry Foundation is a non-profit volunteer organization whose members teach researchers basic software skills. All materials for Software Carpentry lessons are freely available under the Creative Commons - Attribution License. Software Carpentry can also teach workshops at your work site by request, http://software-carpentry.org/workshops/request.html Version Control with Git Wolfman and Dracula have been hired by Universal Missions (a space services spinoff from Euphoric State University) to investigate if it is possible to send their next planetary lander to Mars. They want to be able to work on the plans at the same time, but they have run into problems doing this in the past: they take turns, each one will spend a week or more waiting for the other to finish, but if they work on their own copies and email changes back and forth things will be lost, and they'll waste a lot of time. A colleague suggests using version control to manage their work. Version control is better than mailing files back and forth: • Nothing that is committed to version control is ever lost. Since all old versions of files are saved, it's always possible to go back in time to see exactly who wrote what on a particular day, or what version of a program was used to generate a particular set of results. • As we have this record of who made what changes when, we know who to ask if we have questions later on, and, if needed it, revert to a previous version, much like the "undo" feature in an editor. • When several people collaborate in the same project, it's possible to accidentally overlook or overwrite someone's changes: the version control system automatically notifies users whenever there's a conflict between one person's work and another's. • Teams are not the only ones to benefit from version control: lone researchers can benefit immensely. Keeping a record of what was changed, when, and why is extremely useful for all researchers if they ever need to come back to the project later on (e.g., a year later, when memory has faded). Version control is the lab notebook of the digital world: it's what professionals use to keep track of what they've done and to collaborate with other people. Every large software development project relies on it, and most programmers use it for their small jobs as well. And it isn't just for software: books, papers, small data sets, and anything that changes over time or needs to be shared can and should be stored in a version control system.	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://software-carpentry.org/lessons.html	HTML, exercises	On-demand	Online	Self-paced	Free		Software Carpentry												
Using Databases and SQL	Databases	Programming; SQL	These training materials are from a Software Carpentry course. The Software Carpentry Foundation is a non-profit volunteer organization whose members teach researchers basic software skills. All materials for Software Carpentry lessons are freely available under the Creative Commons - Attribution License. Software Carpentry can also teach workshops at your work site by request, http://software-carpentry.org/workshops/request.html Databases and SQL In the late 1920s and early 1930s, William Dyer, Frank Pabodie, and Valentina Roerich led expeditions to the Pole of Inaccessibility in the South Pacific, and then onward to Antarctica. Two years ago, their expeditions were found in a storage locker at Minkatonic University. We have scanned and OCR'd the data they contain, and we now want to store that information in a way that will make search and analysis easy. Three common options for storage are text files, spreadsheets, and databases. Text files are easiest to create, and work well with version control, but then we would have to build search and analysis tools ourselves. Spreadsheets are good for doing simple analyses, but they don't handle large or complex data sets well. Databases, however, include powerful tools for search and analysis, and can handle large, complex data sets. These lessons will show how to use a database to explore the expeditions' data. Prerequisites If SQLite is being used from the shell, learners will need to be able to navigate directories and run simple commands from the command line. If a GUI such as the Firefox SQLite plugin is being used, learners will need to know how to install browser plugins (and have permission to do so). Topics 1. Setting up 2. Selecting Data 3. Sorting and Removing Duplicates 4. Filtering 5. Calculating New Values 6. Missing Data 7. Aggregation	Bioinformatician	Introductory	http://software-carpentry.org/lessons.html	HTML, exercises	On-demand	Online	Self-paced	Free		Software Carpentry												
Version Control with Mercurial	Reproducible Research; General Computing	Programming; Mercurial	Not included from Software Carpentry, as per Tim Read	Bioinformatician	Introductory	http://software-carpentry.org/lessons.html	HTML, exercises	On-demand	Online	Self-paced	Free		Software Carpentry												
Programming with Python	Languages	Programming; Python	These training materials are from a Software Carpentry course. The Software Carpentry Foundation is a non-profit volunteer organization whose members teach researchers basic software skills. All materials for Software Carpentry lessons are freely available under the Creative Commons - Attribution License. Software Carpentry can also teach workshops at your work site by request, http://software-carpentry.org/workshops/request.html Programming with Python The best way to learn how to program is to do something useful, so this introduction to Python is built around a common scientific task: data analysis. Our real goal isn't to teach you Python, but to teach you the basic concepts that all programming depends on. We use Python in our lessons because: 1. we have to use something for examples; 2. it's free, well-documented, and runs almost everywhere; 3. it has a large (and growing) user base among scientists; and 4. experience shows that it's easier for novices to pick up than most other languages. But the two most important things are to use whatever language your colleagues are using, so that you can share your work with them easily, and to use that language well. We are studying inflammation in patients who have been given a new treatment for arthritis, and need to analyze the first dozen data sets of their daily inflammation. The data sets are stored in comma-separated values (CSV) format: each row holds information for a single patient, and the columns represent successive days. We want to: • load that data into memory, • calculate the average inflammation per day across all patients, and • plot the result.	Bioinformatician	Introductory	http://software-carpentry.org/lessons.html	HTML, exercises	On-demand	Online	Self-paced	Free		Software Carpentry												
Programming with R	Languages	Programming; R	These training materials are from a Software Carpentry course. The Software Carpentry Foundation is a non-profit volunteer organization whose members teach researchers basic software skills. All materials for Software Carpentry lessons are freely available under the Creative Commons - Attribution License. Software Carpentry can also teach workshops at your work site by request, http://software-carpentry.org/workshops/request.html Programming with R The best way to learn how to program is to do something useful, so this introduction to R is built around a common scientific task: data analysis. Our real goal isn't to teach you R, but to teach you the basic concepts that all programming depends on. We use R in our lessons because: 1. we have to use something for examples; 2. it's free, well-documented, and runs almost everywhere; 3. it has a large (and growing) user base among scientists; and 4. it has a large library of external packages available for performing diverse tasks. But the two most important things are to use whatever language your colleagues are using, so that you can share you work with them easily, and to use that language well. Topics 1. Analyzing Patient Data 2. Creating Functions 3. Analyzing Multiple Data Sets 4. Making Choices 5. Command-Line Programs Supplemental Lessons	Bioinformatician; Epidemiologist	Introductory	http://software-carpentry.org/lessons.html	HTML, exercises	On-demand	Online	Self-paced	Free		Software Carpentry												

Back to Brief View

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Programming with MATLAB	Languages	Programming: MATLAB	These training materials are from a Software Carpentry course. The Software Carpentry Foundation is a non-profit volunteer organization whose members teach researchers basic software skills. All materials for Software Carpentry lessons are freely available under the Creative Commons - Attribution License. Software Carpentry can also teach workshops at your work site by request, http://software-carpentry.org/workshops/request.html. Programming with MATLAB The best way to learn how to program is to do something useful, so this introduction to MATLAB is built around a common scientific task: data analysis. Our real goal isn't to teach you MATLAB, but to teach you the basic concepts that all programming depends on. We use MATLAB in our lessons because: 1. we have to use something for examples; 2. it's well-documented; 3. it has a large (and growing) user base among scientists in academia and the industry; and 4. it has a large library of packages available for performing diverse tasks. But the two most important things are to use whatever language your colleagues are using, so that you can share you work with them easily, and to use that language well. Topics 1. Analyzing Patient Data 2. Writing MATLAB Scripts 3. Repeating With Loops 4. Creating Functions 5. Making Choices 6. Defensive Programming	Bioinformatician; Epidemiologist	Introductory	http://software-carpentry.org/lessons.html	HTML, exercises	On-demand	Online	Self-paced	Free		Software Carpentry												
ArrayExpress: Exploring Functional Genomics Data with ArrayExpress	Expression Analysis; Functional Analysis	Gene Expression Analysis; ArrayExpress; Microarray	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: ArrayExpress: Exploring functional genomics data with ArrayExpress Gabry Rustici This course will show you how to search, retrieve and interpret data from ArrayExpress, a repository of data from functional genomics experiments. ArrayExpress allows you to search and download this data. NB: The ArrayExpress course on submitting data using MAGE-tab has been removed as ArrayExpress are retiring the MAGE-tab submission tool. Future updates to this course will be available in due course. Topic: Gene Expression Level: Beginner Duration: 1 hour	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/13	HTML, exercises	On-demand	Online	1 hr	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
ArrayExpress: Quick Tour	Expression Analysis; Functional Analysis	Gene Expression Analysis; ArrayExpress	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: ArrayExpress: Quick tour Gabry Rustici This quick tour provides a brief introduction to the EBI's functional genomics resource: ArrayExpress. To learn more, see the full courses on the Expression Atlas and ArrayExpress. NB: The ArrayExpress course on submitting data using MAGE-tab has been removed as ArrayExpress are retiring the MAGE-tab submission tool. Future updates to this course will be available in due course. Topic: Gene Expression Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/13	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
diXa Data Warehouse: Exploring Data From Toxicogenomics Studies	Databases; Metabolomics	Gene Expression Analysis; Ontologies; Chemical Biology; diXa; Toxicogenomics	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: diXa data warehouse: Exploring data from toxicogenomics studies Vera Matser The diXa data warehouse is a curated collection of toxicogenomics experiments, accessible through the diXa website. This course will show you how to use the diXa warehouse and what data is available. Topic: Gene Expression, Ontologies, Chemical biology Level: Beginner Duration: 1 hour	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/13	HTML	On-demand	Online	1 hr	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
EBI: Next Generation Sequencing Practical Course	DNA Sequencing Technology	DNA & RNA; Gene Expression Analysis; NGS	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: EBI: Next Generation Sequencing Practical Course Emily Perry Here you will find a collection of video lectures from the 'Hands on training in Next-Generation Sequencing' course that took place at EMBL-EBI on 12-14 March 2012, available for you to watch in your own time. The workshop provides an introduction to Next Generation Sequencing (NGS) and addresses how to interpret the data and how the analysis is applied in Genomics. Note: the videos in this course will only run on Google Chrome, Internet Explorer and Safari. Topic: DNA & RNA, Gene Expression Level: Beginner Duration: 15 hours	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/subjects/13	Video, slides, PDF, exercises	On-demand	Online	15 hrs	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
EMBO Practical Course on Analysis of High-Throughput Sequencing Data	Expression Analysis	Gene Expression Analysis	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: EMBO Practical Course on Analysis of High-Throughput Sequencing Data Gabry Rustici Here you will find a collection of materials including videos of lectures from the 'EMBO Practical Course on Analysis of High-Throughput Sequencing Data' that took place at EMBL-EBI on 23-29 October 2011. This course was aimed at advanced PhD students and post-doctoral researchers who are applying or planning to apply high throughput sequencing technologies and bioinformatics methods in their research. The aim of this course was to familiarize the participants with advanced data analysis methodologies and provide hands-on training on the latest analytical approaches. Topic: Gene Expression Level: Intermediate Duration: 5 hours	Bioinformatician	Intermediate	http://www.ebi.ac.uk/training/online/subjects/13	Video	On-demand	Online	5 hrs	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Expression Atlas: Quick Tour	Expression Analysis; Databases	Gene Expression Analysis; Expression Atlas	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Expression Atlas: Quick tour Maria Keays This extended quick tour provides a brief introduction to the Expression Atlas ("Atlas"). An undergraduate-level understanding of biology is an advantage. This course was updated in January 2015. Topic: Gene Expression Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/13	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Functional Genomics: An Introduction to EMBL-EBI Resources	Functional Analysis; Databases	Gene Expression Analysis	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Functional genomics: An introduction to EMBL-EBI resources Amy Tang This course will introduce the field of functional genomics and provide an overview of the major resources for this field at EMBL-EBI. Updated in August 2014. Topic: Gene Expression Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/13	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Introduction to EMBL-EBI Resources: Bioinformatics Forum 2012	Webtools; Databases	Gene Expression Analysis; DNA & RNA; Ontologies; Proteins; Chemical Biology	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Introduction to EMBL-EBI resources: Bioinformatics Forum 2012 Katrina Costa This course is a collection of videos and slides from the EMBL-EBI's SME Bioinformatics Forum, which took place in Barcelona on 8-9 October 2012. The event was aimed at researchers working in small and medium-sized enterprises (SMEs) and will be of interest to anyone who would like to learn more about the core data resources available from EMBL-EBI. For an overview of the event, there is a summary on EMBL-EBI's SME Forum web pages and a full list of talks. Topic: DNA & RNA, Gene Expression, Ontologies, Proteins, Chemical biology Level: Beginner Duration: 5 hours	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/subjects/13	Video, slides, PDF	On-demand	Online	5 hrs	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
DGVa: Quick Tour	Databases	DNA & RNA; DGVa	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: DGVa: Quick tour Lisa Skipper This quick tour provides a brief introduction to the DGVa, the EBI's Database of Genomic Variants archive. Topic: DNA & RNA Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												

Back to Brief View

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134	EBI Metagenomics Resource: Quick Tour	Metagenomics; Databases	DNA & RNA; EBI Metagenomics resource	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: EBI Metagenomics resource: Quick tour Hubert Denise This quick tour provides a brief introduction to the EBI Metagenomics resource, for archiving, analysing and integrating metagenomics data. Topic: DNA & RNA Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML	On-demand	0nline	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
135	EGA: Quick Tour	Functional Analysis; Databases	DNA & RNA; EGA	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: EGA: Quick tour Gary Saunders This Quick tour provides a brief introduction to the European Genome-phenome archive (EGA). Topic: DNA & RNA Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML	On-demand	0nline	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
136	Ensembl Genomes (Non-Chordates): Quick Tour	Databases	DNA & RNA; Ensembl Genomes (Non-Chordate)	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Ensembl Genomes (non-chordates): Quick tour Paul Kersey This quick tour provides a brief introduction to Ensembl Genomes, the non-chordate genome browser. Topic: DNA & RNA Level: Beginner Duration: 0.5 hours	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML	On-demand	0nline	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
137	Ensembl Tools: Webinar	Comparative Genomics	DNA & RNA; Variant Effect Predictor (VEP); BLAST/BLAT	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Ensembl tools: webinar Emily Perry Emily Perry from the Ensembl Outreach Team presents this webinar on Ensembl tools, including the ever-popular Variant Effect Predictor (VEP), BLAST/BLAT and BioMart. This webinar took place on 22nd April 2015. NB: This video works best using Google Chrome and when viewed in full screen. Find out about upcoming webinars. Topic: DNA & RNA Level: Beginner Duration: 30 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	Video	On-demand	0nline	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
138	Ensembl: Browsing Chordate Genomes	Webtools	DNA & RNA; Ensembl Chordate	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Ensembl: Browsing chordate genomes Giulietta M. Spudich This course focuses on chordate (mostly vertebrate) genomes on the Ensembl website at www.ensembl.org. It provides a quick beginner's guide to the overall structure of the Ensembl genome browser. Topic: DNA & RNA Level: Beginner Duration: 3 hours	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML, exercises	On-demand	0nline	3 hrs	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
139	Ensembl: Filmed API Workshop	Databases	DNA & RNA; Ensembl API	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Ensembl: Filmed API Workshop Emily Perry Ensembl runs API workshops worldwide, and for the first time we make one available online. Here you will find a collection of video lectures from the 'Ensembl API workshop' that took place at EMBL-EBI 22nd-24th May 2013, using Ensembl version 71. The exercises associated with the workshop are included to carry out at your leisure. Note: the videos in this course will only run on Google Chrome, Internet Explorer and Safari. Topic: DNA & RNA Level: Beginner Duration: 18 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML, video, slides, PDF, exercises	On-demand	0nline	18 hrs	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
140	Ensembl: Filmed Browser Workshop	Webtools	DNA & RNA; Ensembl Browser	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Ensembl: Filmed browser workshop Emily Perry Ensembl runs on the order of 100 browser workshops a year worldwide, and for the first time we make one available online. Here you will find a collection of video lectures from the 'Ensembl Browser workshop' that took place at EMBL-EBI on 31st January 2013, using Ensembl version 70. The exercises associated with the workshop are included to carry out at your leisure. This workshop provides an introduction to Ensembl, what kind of data Ensembl has, and how to browse and export the data. We'll also be holding live web-chats to discuss the exercises, or any other Ensembl issues. Have a look at the webchat page to find out when we'll next be online to take your questions … live! Topic: DNA & RNA Level: Beginner Duration: 8 hours	Bioinformatician; EpidemioBlogist; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML, video, slides, PDF, exercises	On-demand	0nline	8 hrs	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
141	Ensembl: Quick Tour	Webtools	DNA & RNA; Ensembl Website	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Ensembl: Quick tour Emily Perry This course provides a very short introduction to the Ensembl website for browsing chordate genomes. This is a quick overview to the browser, designed to give you an idea of what is possible, and will not give you a full tutorial on how to do specific tasks. Links are provided throughout to other tutorials and videos that may help you. Topic: DNA & RNA Level: Beginner Duration: 0.5 hours	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML	On-demand	0nline	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
142	European Nucleotide Archive: Using the Primary Nucleotide Sequence Resource	Databases	DNA & RNA; European Nucleotide Archive	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: European Nucleotide Archive: Using the primary nucleotide sequence resource Clara Amid This course will show you how to search and retrieve nucleotide sequence data from the European Nucleotide Archive (ENA). The ENA provides sequence assembly details and biological annotation, and uses versioning to track sequence changes. Topic: DNA & RNA Level: Intermediate Duration: 3 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML, exercises	On-demand	0nline	3 hrs	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
143	Genomics: An Introduction to the EBI Resources	Databases	DNA & RNA; EBI resources	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Genomics: An introduction to the EBI resources Giulietta M. Spudich This course will introduce the field of genomics and provide an overview of the different resources at the EBI which are related to this field. The course is aimed at graduates in the life sciences or related subjects, with an interest in using bioinformatics resources to solve problems related to genome biology. Topic: DNA & RNA Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML	On-demand	0nline	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Available	Notes
Introduction to Phylogenetics	Phylogenomics	DNA & RNA; Phylogenetics	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Introduction to phylogenetics Laura Emery This course provides a basic introduction to the field of phylogenetics, with an emphasis on how to read and interpret phylogenetic trees. An undergraduate-level understanding of biology would be an advantage. Topic: DNA & RNA Level: Beginner Duration: 1.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML	On-demand	Online	1 hr 30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Resources for Genomics: Webinar	Webtools; Metagenomics	DNA & RNA; Ensembl; European Nucleotide Archive	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Resources for Genomics: webinar This 25 minute webinar from Dr Laura Emery provides you with an introduction to EMBL-EBI and the data resources available (recorded on 25th February 2015). The webinar focuses in particular on three core resources - Ensembl, ENA and the Metagenomics portal. NB: This video works best using Google Chrome and when viewed in full screen. Find out about upcoming webinars. Topic: DNA & RNA Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	Video	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Rfam: Quick Tour	Functional Analysis; Databases	DNA & RNA; Rfam	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Rfam: Quick tour Sarah Burge This quick tour provides a brief introduction to Rfam, the EBI's database of RNA families. Topic: DNA & RNA Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
The European Nucleotide Archive (ENA) – An Introduction: Webinar	Databases	DNA & RNA; European Nucleotide Archive	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: The European Nucleotide Archive (ENA) – an introduction: webinar Marc Rosello In this webinar, Marc Rosello gives an introduction the European Nucleotide Archive (ENA). This webinar took place on 8 April 2015. NB: This video works best using Google Chrome and when viewed in full screen. Find out about upcoming webinars. Topic: DNA & RNA Level: Beginner Duration: 0.5 hours	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	Video	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
The European Nucleotide Archive: Quick Tour	Databases	DNA & RNA; European Nucleotide Archive	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: The European Nucleotide Archive: Quick tour Clara Amid This quick tour provides a brief introduction to the European Nucleotide Archive, the EBI's repository for nucleotide sequence data. Topic: DNA & RNA Level: Beginner Duration: 0.5 hours	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/subjects/11	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
An Introduction to Metabolomics		Chemical Biology; Systems; Metabolomics	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: An introduction to metabolomics Author: Reza Salek This course provides a basic introduction into the rapidly emerging field of metabolomics and its importance and applications. Topic: Systems, Chemical biology Level: Beginner Duration: 1 hour Type: Introductory		Introductory	http://www.ebi.ac.uk/training/online/subjects/479	HTML	On-demand	Online	1 hr	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
BioModels Database: Quick Tour	Systems Biology	Systems; BioModels Database; Pathway Analysis; Ontologies	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: BioModels Database: Quick tour Author: Camille Laibe This quick tour provides a brief introduction to BioModels Database, EMBL-EBI's repository of mathematical models of biological pathways. Topic: Systems Level: Beginner Duration: 0.5 hour Type: Quick tour	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/479	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
IMPC: Using the Mouse Phenotyping Portal	Functional Analysis; Databases; Systems Biology	Systems; Ontologies; Mouse Phenotyping Portal	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: IMPC: Using the mouse phenotyping portal Author: Terry Meehan The International Mouse Phenotyping Consortium (IMPC) portal allows you to search for phenotypes, disease models and knockout mouse strains for your gene of interest. This course will show you how to use the IMPC portal and what data is available. Topic: Systems, Ontologies Level: Beginner Duration: 1 hour Type: Tutorial	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/479	HTML	On-demand	Online	1 hr	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
IntAct: Molecular Interactions at the EBI	Proteomics; Systems Biology	Systems; IntAct	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: IntAct: Molecular Interactions at the EBI Author: Pablo Porras Millan This course will show you what kind of information you can find in IntAct (one of the EBI's molecular interactions databases), how to access it, the different tools that can be used to access data and some practical examples on how to search and use the database. Topic: Systems Level: Beginner Duration: 2 hours Type: Tutorial	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/479	HTML	On-demand	Online	2 hrs	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
IntAct: Quick Tour	Proteomics; Systems Biology	Systems; IntAct	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: IntAct: Quick tour Author: Sandra Orchard This quick tour provides a brief introduction to the EBI's molecular interactions database, IntAct. Topic: Systems, Proteins Level: Beginner Type: Quick tour	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/479	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
MetaboLights: Quick Tour	Metabolomics; Functional Analysis	Chemical Biology; Systems; Metabolights	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: MetaboLights: Quick tour Author: Kenneth Haug This quick tour provides a brief introduction to the EBI's metabolomics resource: MetaboLights. Topic: Systems, Chemical biology Level: Beginner Duration: 0.5 hour Type: Quick tour	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/subjects/479	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Available	Notes
Protein Interactions and Their Importance	Proteomics	Proteins; Systems	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Protein interactions and their importance Author: Pablo Porras Millan This course will provide an introduction to molecular interactions, their importance and the methodologies use to generate and capture interaction data. Topic: Systems, Proteins Level: Beginner Type: Introductory	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/courses/478	HTML	On-demand	Online	1 hr	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Reactome - Exploring Biological Pathways: Webinar	Metabolomics; Functional Analysis; Systems Biology	Systems; Reactome	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Reactome - exploring biological pathways: webinar Author: Steve Jupe This two-part webinar from Steve Jupe provides you with an introduction to Reactome and how you can use it to explore biological pathways (recorded on 6th May 2010). Part 1 gives an overview of what Reactome is and why it is important. Part 2 provides a demo of the Reactome interface. NB: These videos works best using Google Chrome and when viewed in full screen. Find out about upcoming webinars. Topic: Systems Level: Beginner Duration: 1 hour Type: Webinar	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/courses/479	Video	On-demand	Online	1 hr	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Reactome: Exploring and Analysing Biological Pathways	Metabolomics; Functional Analysis; Systems Biology	Systems; Reactome	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Reactome: exploring and analysing biological pathways Author: Steve Jupe This course provides an overview to the Reactome pathway database web interface and the database content. For a short introduction to Reactome, please visit the Reactome quick tour. Topic: Systems Level: Intermediate Duration: 3 hours Type: Tutorial	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/courses/476	HTML, exercises	On-demand	Online	3 hrs	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Reactome: Quick Tour	Metabolomics; Functional Analysis; Systems Biology	Systems; Reactome	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Reactome: Quick tour Author: Steve Jupe This quick tour provides a brief introduction to Reactome, the biological pathway database. Topic: Systems Level: Beginner Duration: 0.5 hour Type: Quick tour	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/courses/478	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
GO: Quick Tour	Systems Biology; Functional Analysis	Ontologies; GO; Pathway Analysis	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: GO: Quick tour Rebecca Foulger This quick tour provides a brief introduction to the EBI's Gene Ontology resource. For information about gene ontology annotation, see the UniProt-GOA quick tour. Topic: Ontologies Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/courses/432	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Uniprot-GOA: Quick Tour	Databases; Systems Biology	Ontologies; UniProt-GOA	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: UniProt-GOA: Quick tour Rachael Huntley This quick tour provides a brief introduction to UniProt-GOA, the Gene Ontology Annotation resource. For information about the Gene Ontology, see the GO quick tour. Topic: Ontologies Level: Beginner Duration: 0.5 hours	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/courses/432	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Biomacromolecular Structures: An Introduction to the EBI Resources	Proteomics	Proteins; EBI Resources; Biomacromolecular Structures	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Biomacromolecular structures: an introduction to the EBI resources Joanna Argasinska Introduction to structural biology and an introduction to resources at EBI related to this field Topic: Proteins Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/courses/34	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Enzyme Portal: Quick Tour	Proteomics	Proteins; Chemical Biology; Enzyme Portal	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Enzyme Portal: Quick tour Rafael Alcántara This quick tour provides a brief introduction to the Enzyme Portal - a data resource that provides access to information from several enzyme-related databases, both at EMBL-EBI and the Swiss Institute of Bioinformatics (SIB). Topic: Proteins, Chemical biology Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/courses/34	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
InterPro: Functional and Structural Analysis of Protein Sequences	Proteomics; Systems Biology	Proteins; InterPro	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: InterPro: functional and structural analysis of protein sequences Alex Mitchell InterPro is a classification database that provides predictive information about protein sequences. This course will show you what kind of information is available in InterPro, how to access it, and how to search the database. Topic: Proteins Level: Beginner Duration: 1 hour	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/courses/34	HTML, exercises	On-demand	Online		Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
InterPro: Quick Tour	Proteomics; Systems Biology	Proteins; InterPro	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: InterPro: Quick tour Alex Mitchell This quick tour provides a brief introduction to InterPro, the EBI's database of protein families, domains and functional sites. A full course will be here soon. Topic: Proteins Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/courses/34	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Introduction to Protein Classification at the EBI	Proteomics	Proteins; EBI	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Introduction to protein classification at the EBI Amela Sangvalor This course will provide an introduction to protein classification and basic concepts, such as proteins families, domains and sequence features. Topic: Proteins Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/courses/34	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Available	Notes
PDBe: Quick Tour	Proteomics; Functional Analysis	Proteins; Structures; PDBe	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: PDBe: Quick tour Sameer Velankar This quick tour provides a brief introduction to the Protein Data Bank in Europe (PDBe), EMBL-EBI's resource for the collection, organisation and dissemination of data on biological macromolecular structures. Topic: Proteins, Structures Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/14	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
PDBeChem: Searching for Small Molecules and Small Molecule Fragments	Metabolomics; Functional Analysis	Proteins; Chemical Biology; Structures; PDBeChem	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: PDBeChem: Searching for small molecules and small molecule fragments Gary Battle PDBeChem allows you to search for chemical components (ligands, small molecules and monomers) that appear in PDB entries, and discover which protein structures bind a particular ligand. This course will show you how to use PDBeChem and what you can do with it. An undergraduate degree in a life science subject would be an advantage. You may wish to look at the PDBe quick tour and Biomacromolecular structures course as an introduction to this tutorial. Topic: Proteins, Chemical biology, Structures Level: Beginner Duration: 1 hour	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/14	HTML	On-demand	Online	Not available	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
PDBeFold: Searching for Structural Homologues of a Protein	Proteomics	Proteins; Structures; PDBeFold	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: PDBeFold: Searching for structural homologues of a protein Gary Battle PDBeFold can be used to identify structural homologues in the PDB. PDBe's Secondary Structure Matching service (SSM) allows you to interactively compare, align and superimpose protein structures in 3D. This course will show you how to use PDBeFold and what you can do with it. An undergraduate degree in a life science subject would be an advantage. You may wish to look at the PDBe quick tour and Biomacromolecular structures course as an introduction to this tutorial. Topic: Proteins, Structures Level: Beginner	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/14	HTML	On-demand	Online	Not available	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
PDBePISA: Identifying and Interpreting the Likely Biological Assemblies of a Protein Structure	Proteomics; Functional Analysis	Proteins; Structures; PDBePISA	PDBePISA: Identifying and interpreting the likely biological assemblies of a protein structure Gary Battle PDBePISA allows you to explore macromolecular (protein, DNA/RNA and ligand) interfaces and predict the quaternary stucture of your protein. This course will show you how to use PDBePISA and what you can do with it. An undergraduate degree in a life science subject and some background knowledge in protein structure would be an advantage. You may wish to look at the PDBe quick tour and Biomacromolecular structures course as an introduction to this tutorial. Topic: Proteins, Structures Level: Beginner Duration: 1 hour	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/14	HTML	On-demand	Online	1 hr	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
PRIDE: Quick Tour	Proteomics	Proteins; PRIDE	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: PRIDE: Quick tour Juan Antonio Vizcaino This quick tour provides a brief introduction to the EMBL-EBI's PRoteomics IDEntifications database, PRIDE. Topic: Proteins Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/14	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
ProteomeXchange Submissions Via PRIDE	Proteomics	Proteins; ProteomeXchange Submissions; PRIDE	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: ProteomeXchange submissions via PRIDE Juan Antonio Vizcaino How to submit MIAPE data to ProteomeXchange via PRIDE. This course is aimed at proteomics researchers with data that they want to make available through public-domain databases of proteomics experiments. Topic: Proteins Level: Beginner Duration: 1.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/14	HTML	On-demand	Online	1 hr 30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Proteomics: An Introduction to the EBI Resources	Proteomics	Proteins; Proteomics; EBI Resources	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: Proteomics: an introduction to the EBI resources Sandra Orchard This course will provide an overview of proteomics. We will then introduce resources provided by the EBI related to proteomics. Topic: Proteins Level: Beginner Duration: 0.5 hours	Bioinformatician; Laboratorian	Introductory	http://www.ebi.ac.uk/training/online/subjects/14	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
UniProt: Exploring Protein Sequence and Functional Information	Proteomics; Databases	Proteins; UniProt	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: UniProt: Exploring protein sequence and functional information Michele Magrane This course is a guide to the UniProt resource, including what kinds of information it provides and how to access the data using the UniProt website. Some knowledge of biology and proteins is required. Some bioinformatics knowledge is useful but not essential. Topic: Proteins Level: Beginner	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/14	HTML	On-demand	Online	Not available	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
UniProt: Exploring Protein Sequence and Functional Information - Webinar	Proteomics; Databases	Proteins; UniProt	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: UniProt: Exploring protein sequence and functional information - webinar Sangya Pundir In this webinar, Sangya Pundir shows us how we can use UniProt (www.uniprot.org) to explore protein sequence and functional information. Topic: Proteins Level: Beginner Duration: 1 hour	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/14	Video	On-demand	Online	1 hr	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
UniProt: Quick Tour	Proteomics; Databases	Proteins; UniProt	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: UniProt: Quick tour Michele Magrane This quick tour provides a brief introduction to the Universal Protein Resource (UniProt). A full tutorial of UniProt can be found here. Topic: Proteins Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/14	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
ChEBI: Quick Tour	Metabolomics; Databases	Chemical Biology; ChEBI	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: ChEBI: Quick tour Gareth Owen This quick tour provides a brief introduction to ChEBI, the EBI's Chemical Entities of Biological Interest database, which focuses on 'small' chemical compounds. Updated in March 2015. Topic: Chemical biology Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/283	HTML	On-demand	Online	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters/PhD Program	Non-Degree Option Avaliable	Notes
ChEMBL: Quick Tour	Metabolomics; Databases	Chemical Biology; ChEBI	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: ChEMBL: Quick tour Louisa Bellis This quick tour provides a brief introduction to ChEMBL, the EBI's chemogenomics resource. Topic: Chemical biology Level: Beginner Duration: 0.5 hours	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/363	HTML	On-demand	0nline	30 min	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
SureChEMBL - Accessing Chemical Patent Data: Webinar	Metabolomics	Chemical Biology; SureChEMBL	Train online provides free courses on Europe's most widely used data resources, created by experts at EMBL-EBI and collaborating institutes. You do not need to have any previous experience of bioinformatics to benefit from this training. We want to help you to be a highly competent user of our data resources; we are not trying to train you to become a bioinformatician. You can use Train online to learn in your own time and at your own pace. You can repeat the courses as many times as you like, or just complete part of a course if you want to brush up on how to perform a specific task. Description: SureChEMBL - accessing chemical patent data: webinar This two-part webinar from George Papadatos provides you with an introduction to the chemical patent database SureChEMBL (recorded on 11th March 2015). Part 1 gives an overview of what SureChEMBL is and why it is important. Part 2 provides a demo of the SureChEMBL interface. NB: These videos works best using Google Chrome and when viewed in full screen. Find out about upcoming webinars. Topic: Chemical biology Level: Beginner Duration: 1 hour	Bioinformatician	Introductory	http://www.ebi.ac.uk/training/online/subjects/363	Video	On-demand	0nline	1 hr	Free		European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI)												
Penn State University Online Graduate Certificate in Bioinformatics	Graduate Program; Statistics; Comparative Genomics	Genomics; Bioinformatics; Online Graduate Certificate Program	To take a course, students must enroll in the graduate school for a certificate or degree program. Courses are offered on a schedule (http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/course-schedule). Credits Required for Certificate: 11 (4 courses, taken in any order) Tuition per credit: $930.00 Prerequisites To apply to the program, you must have a baccalaureate degree from an accredited institution. A background in biology, computer science, or statistics is highly encouraged. Course List (http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/courses) • Genomics: Structure and function of genomes including use of some current web-based tools and resources for studies and research in genomics. 3 credits. • Foundations in Data Driven Life Sciences: Expanded overview of current developments and technique in computational biology and genomics. 3 credits. • Applied Bioinformatics: This course provides a foundation for students with biology backgrounds in the computational analysis and interpretation of biological data. 2 credits. • Statistical Analysis of Genomics Data: Statistical analysis of high throughput biology experiments. 3 credits. Lead the Application of Genomic Information With ongoing public attention on the Human Genome Project, understanding, analyzing, and interpreting genomic data continue to be a focus across many disciplines. By merging biology, computer science, and information technology, bioinformatics allows us to combine mathematics and computers to gain a better understanding of biological processes.	Bioinformatician	Intermediate	http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/courses	Online Graduate Certificate Program	Schedule: http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/course-schedule	Online	Semester	$930/credit, annual $131 technology fee		Penn State University	Istvan Albert	Associate Professor, Bioinformatics		bioinformatics@psu.edu						Online Graduate Certificate Program		
Genomics	Statistics; Comparative Genomics	Genomics; Bioinformatics	To take a course, students must enroll in the graduate school for a certificate or a degree program. Courses are offered on a schedule (http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/course-schedule). Credits Required for Certificate: 11 (4 courses, taken in any order) Tuition per credit: $930.00 Prerequisites To apply to the program, you must have a baccalaureate degree from an accredited institution. A background in biology, computer science, or statistics is highly encouraged. Course Description Genomics Structure and function of genomes including use of some current web-based tools and resources for studies and research in genomics. Certificate Course List (http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/courses) This is one of four courses re+E181quired for the Penn State University Online Graduate Certificate in Bioinformatics. • Genomics: Structure and function of genomes including use of some current web-based tools and resources for studies and research in genomics. 3 credits. • Foundations in Data Driven Life Sciences: Expanded overview of current developments and technique in computational biology and genomics. 3 credits. • Applied Bioinformatics: This course provides a foundation for students with biology backgrounds in the computational analysis and interpretation of biological data. 2 credits. • Statistical Analysis of Genomics Data: Statistical analysis of high throughput biology experiments. 3 credits.	Bioinformatician	Intermediate	http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/courses	Online Graduate Program Course, Skype, Blackboard Collaborate, email, discussion forums	Spring 2016; see schedule on website	Online	Semester	$930/credit, annual $131 technology fee		Penn State University										Online Graduate Program Course		
Foundations in Data Driven Life Sciences	Statistics; Comparative Genomics	Genomics; Bioinformatics	To take a course, students must enroll in the graduate school for a certificate or a degree program. Courses are offered on a schedule (http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/course-schedule). Credits Required for Certificate: 11 (4 courses, taken in any order) Tuition per credit: $930.00 Prerequisites To apply to the program, you must have a baccalaureate degree from an accredited institution. A background in biology, computer science, or statistics is highly encouraged. Course Description Foundations in Data Driven Life Sciences Expanded overview of current developments and technique in computational biology and genomics. Certificate Course List (http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/courses) This is one of four courses required for the Penn State University Online Graduate Certificate in Bioinformatics. • Genomics: Structure and function of genomes including use of some current web-based tools and resources for studies and research in genomics. 3 credits. • Foundations in Data Driven Life Sciences: Expanded overview of current developments and technique in computational biology and genomics. 3 credits. • Applied Bioinformatics: This course provides a foundation for students with biology backgrounds in the computational analysis and interpretation of biological data. 2 credits. • Statistical Analysis of Genomics Data: Statistical analysis of high throughput biology experiments. 3 credits.	Bioinformatician	Intermediate	http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/courses	Online Graduate Program Course, Skype, Blackboard Collaborate, email, discussion forums	8/24/2015 - 12/11/2015; see schedule on website	Online	Semester	$930/credit, annual $131 technology fee		Penn State University	Istvan Albert	Associate Professor, Bioinformatics		bioinformatics@psu.edu						Online Graduate Program Course		
Applied Bioinformatics	Statistics; Comparative Genomics	Genomics; Bioinformatics	To take a course, students must enroll in the graduate school for a certificate or a degree program. Courses are offered on a schedule (http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/course-schedule). Credits Required for Certificate: 11 (4 courses, taken in any order) Tuition per credit: $930.00 Prerequisites To apply to the program, you must have a baccalaureate degree from an accredited institution. A background in biology, computer science, or statistics is highly encouraged. Course Description Applied Bioinformatics This course provides a foundation for students with biology backgrounds in the computational analysis and interpretation of biological data. Certificate Course List (http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/courses) This is one of four courses required for the Penn State University Online Graduate Certificate in Bioinformatics. • Genomics: Structure and function of genomes including use of some current web-based tools and resources for studies and research in genomics. 3 credits. • Foundations in Data Driven Life Sciences: Expanded overview of current developments and technique in computational biology and genomics. 3 credits. • Applied Bioinformatics: This course provides a foundation for students with biology backgrounds in the computational analysis and interpretation of biological data. 2 credits. • Statistical Analysis of Genomics Data: Statistical analysis of high throughput biology experiments. 3 credits.	Bioinformatician	Intermediate	http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/courses	Online Graduate Program Course, Skype, Blackboard Collaborate, email, discussion forums	5/18/2015 - 8/12/2015; see schedule on website	Online	Semester	$930/credit, annual $131 technology fee		Penn State University	Istvan Albert	Associate Professor, Bioinformatics		bioinformatics@psu.edu						Online Graduate Program Course		
Statistical Analysis of Genomics Data	Statistics; Comparative Genomics	Genomics; Bioinformatics	To take a course, students must enroll in the graduate school for a certificate or a degree program. Courses are offered on a schedule (http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/course-schedule). Credits Required for Certificate: 11 (4 courses, taken in any order) Tuition per credit: $930.00 Prerequisites To apply to the program, you must have a baccalaureate degree from an accredited institution. A background in biology, computer science, or statistics is highly encouraged. Course Description Statistical Analysis of Genomics Data Statistical analysis of high throughput biology experiments. Certificate Course List (http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/courses) This is one of four courses required for the Penn State University Online Graduate Certificate in Bioinformatics. • Genomics: Structure and function of genomes including use of some current web-based tools and resources for studies and research in genomics. 3 credits. • Foundations in Data Driven Life Sciences: Expanded overview of current developments and technique in computational biology and genomics. 3 credits. • Applied Bioinformatics: This course provides a foundation for students with biology backgrounds in the computational analysis and interpretation of biological data. 2 credits. • Statistical Analysis of Genomics Data: Statistical analysis of high throughput biology experiments. 3 credits.	Bioinformatician	Intermediate	http://www.worldcampus.psu.edu/degrees-and-certificates/applied-bioinformatics-certificate/courses	Online Graduate Program Course, Skype, Blackboard Collaborate, email, discussion forums	8/24/2015 - 12/11/2015; see schedule on website	Online	Semester	$930/credit, annual $131 technology fee		Penn State University	Istvan Albert	Associate Professor, Bioinformatics		bioinformatics@psu.edu						Graduate Certificate Program		

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters/PhD Program	Non-Degree Option Avaliable	Notes
Johns Hopkins Online Bioinformatics MS	Graduate Program; Comparative Genomics; DNA Sequencing Technology; Expression Analysis; Systems Biology; Variant Analysis; HPC/Cloud; Metagenomics; Computer Science	Online Master's Program	Johns Hopkins Online Bioinformatics MS To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses are offered on a schedule (http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/). Courses Required for MS: 11 courses; thesis option available Tuition per course: $3,955.00 Prerequisites • Bachelor's degree from an accredited college or university in the biological sciences or in engineering. Programs require a minimum GPA of 3.0 on a 4.0 scale. Meeting the minimum GPA requirement does not guarantee admission. All the prerequisites listed below can be taken from the existing Master of Science in Computer Science or in the Master of Science in Biotechnology program. Students who have not completed all the prerequisites may be admitted provisionally to complete the admission requirements. • Two semesters of Organic Chemistry (or 410.302 Bio-Organic Chemistry) • One semester of Biochemistry (or 410.601 Biochemistry) • Introduction to Programming Using Java, C++, or C (or 605.201 Introduction to Programming Using Java) • Data Structures (or 605.202 Data Structures) • One course in Probability and Statistics (or 410.645 Biostatistics) and • Calculus Degree Requirements This program is a blended program offering courses from the School of Arts and Sciences and the School of Engineering. The courses that are linked below are offered through the School of Arts and Sciences and all have the same first three numbers 410. The courses that start with 605 are the courses that are offered through the School of Engineering. All the 605 course descriptions are available on the School of Engineering's website. Core Courses (5 total) • 410.602 Molecular Biology	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Master's Program	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Master's Program	Yes	
Algorithms for Bioinformatics	Computer Science	Algorithms; Computer Science; Math	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 605.420 Algorithms for Bioinformatics This follow-on course to data structures (e.g., 605.202) provides a survey of computer algorithms, examines fundamental techniques in algorithm design and analysis, and develops problem-solving skills required in all programs of study involving computer science. Topics include advanced data structures (red-black and 2-3-4 trees, union-find), algorithm analysis and computational complexity (recurrence relations, big-O notation, introduction to NP completeness), sorting and searching, design paradigms (divide and conquer, greedy heuristic, dynamic programming), and graph algorithms (depth-first and breadth-first search, minimum spanning trees,). Advanced topics are selected from among the following: multithreaded algorithms, matrix operations, linear programming, string matching, computational geometry, and approximation algorithms. The course will draw on applications from Bioinformatics. This course does not satisfy the foundation course requirement for Computer Science or Cybersecurity. Students cannot earn credit for both 605.420 and 605.421. Prerequisites: 605.202 Data Structures or equivalent. 605.203 Discrete Mathematics or equivalent is recommended.	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Principles of Database Systems	Databases	SQL; QBE; Database Management Systems	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 605.441 Principles of Database Systems This course examines the underlying concepts and theory of database management systems. Topics include database system architectures, data models, query languages, conceptual and logical database design, physical organization, and transaction management. The entity-relationship model and relational model are investigated in detail, object-oriented databases are introduced, and legacy systems based on the network and hierarchical models are briefly described. Mappings from the conceptual level to the logical level, integrity constraints, dependencies, and normalization are studied as a basis for formal design. Theoretical languages such as the relational algebra and the relational calculus are described, and high-level languages such as SQL and QBE are discussed. An overview of file organization and access methods is provided as a basis for discussion of heuristic query optimization techniques. Finally, transaction-processing techniques are presented with a specific emphasis on concurrency control and database recovery.	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Practical Computer Concepts for Bioinformatics	General Computing; Languages; Databases	UNIX; SQL; Perl	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.634 Practical Computer Concepts for Bioinformatics This course introduces students with a background in the life sciences to the basic computing concepts of the UNIX operating system, relational databases, structured programming, object-oriented programming, and the Internet. Included is an introduction to SQL and the Perl scripting language. The course emphasizes relevance to molecular biology and bioinformatics. It is intended for students with no computer programming background but with a solid knowledge of molecular biology. Prerequisites: 410.601 Biochemistry; 410.602 Molecular Biology	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Introduction to Bioinformatics	Databases	Database Searching and Analysis; Data Mining	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.633 Introduction to Bioinformatics Retrieval and analysis of electronic information are essential in today's research environment. This course explores the theory and practice of biological database searching and analysis. In particular, students are introduced to integrated systems where a variety of data sources are connected through World Wide Web access. Information retrieval and interpretation are discussed, and many practical examples in a computer laboratory setting enable students to improve their data mining skills. Methods included in the course are searching the biomedical literature, sequence homology searching and multiple alignment, protein sequence motif analysis, and several genome analytical methods. Classes are held in a computer laboratory. Acquaintance with computers is required. Prerequisites: 410.601 Biochemistry; 410.602 Molecular Biology	Bioinformatician	Introductory	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Biological Databases and Database Tools	Databases; Webtools	GenBank; Ensemble; PDB; SWISS-PROT; BLAST; Perl; Kegg; HapMap; Biological Databases	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 605.452 Biological Databases and Database Tools The sequencing of the human genome and intense interest in proteomics and molecular structure have resulted in an explosive need for biological databases. This course surveys a wide range of biological databases and their access tools and enables students to develop proficiency in their use. Databases introduced include genome and sequence databases such as GenBank and Ensemble, as well as protein databases such as PDB and SWISS-PROT. Tools for accessing and manipulating sequence databases such as BLAST, multiple alignment, Perl, and gene finding tools are covered. Specialized databases such as KEGG and HapMap are surveyed for their design and use. The course also focuses on the design of biological databases and examines issues related to heterogeneity, interoperability, complex data structures, object orientation, and tool integration. Students will create their own small database as a course project and will complete homework assignments using biological databases and database tools. Prerequisites: 605.205 Molecular Biology for Computer Scientists or equivalent. 605.441 Principles of Database Systems or 410.634 Practical Computer Concepts for Bioinformatics recommended.	Bioinformatician	Introductory	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Bioinformatics: Tools for Genome Analysis	Functional Analysis; Comparative Genomics	Genome Analysis	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.635 Bioinformatics: Tools for Genome Analysis Several large-scale DNA sequencing efforts have resulted in megabase amounts of DNA sequences being deposited in public databases. As such, the sequences are of less use than those sequences that are fully annotated. Assigning annotations such as exon boundaries, repeat regions, and other biologically relevant information accurately in the feature tables of these sequences requires a significant amount of human intervention. This course instructs students on computer analytical methods for gene identification, promoter analysis, and introductory gene expression analysis using software methods. Additionally, students are introduced to comparative genomics and proteomic analysis methods. Students will become proficient in annotating large genomic DNA sequences. Students complete two large sequence analysis projects during the course. Prerequisites: 410.601 Biochemistry; 410.602 Molecular Biology; 410.633 Introduction to Bioinformatics; or all Bioinformatics core courses	Bioinformatician	Introductory	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Protein Bioinformatics	Proteomics	Proteins	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.639 Protein Bioinformatics Because the gap between the number of protein sequences and the number of protein crystal structures continues to expand, protein structural predictions are increasingly important. This course provides a working knowledge of various computer-based tools available for predicting the structure and function of proteins. Topics include protein database searching, protein physicochemical properties, secondary structure prediction, and statistical verification. Also covered are graphic visualization of the different types of three-dimensional folds and predicting 3-D structures by homology. Computer laboratories complement material presented in lectures. Prerequisites: 410.601 Biochemistry, 410.602 Molecular Biology, 410.633 Introduction to Bioinformatics	Bioinformatician	Introductory	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Molecular Phylogenetic Techniques	Phylogenomics	Phylogenetics; Comparative Genomics	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.640 Molecular Phylogenetic Techniques This course will provide a practical, hands-on introduction to the study of phylogenetics and comparative genomics. Theoretical background on molecular evolution will be provided only as needed to inform the comparative analysis of genomic data. The emphasis of the course will be placed squarely on the understanding and use of a variety of computational tools designed to extract meaningful biological information from molecular sequences. Lectures will provide information on the conceptual essence of the algorithms that underlie various sequence analysis tools and the rationale behind their use. Only programs that are freely available, as either downloadable executables or as Web servers, will be used in this course. Students will be encouraged to use the programs and approaches introduced in the course to address questions relevant to their own work. Prerequisites: 410.601 Biochemistry; 410.602 Molecular Biology; 410.633 Introduction to Bioinformatics	Bioinformatician	Introductory	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Methods in Proteomics	Proteomics	Proteomics	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.661 Methods in Proteomics This course covers the analytical methods used to separate and characterize pharmaceutical compounds (predominantly proteins) derived through biotechnology. While emphasis is placed on the general principles and applicability of the methods, current protocols are discussed, and problem sets representing realistic developmental challenges are assigned. Topics include chromatography (HPLC, SEC, IEC), electrophoretic techniques (2-D gel electrophoresis), spectroscopic methods (UV/Vis, fluorescence, CD), analytical ultracentrifugation, microarrays, mass spectroscopy, amino acid analysis, sequencing, and methods to measure protein-protein interactions. Prerequisites: 410.601 Biochemistry; 410.602 Molecular Biology	Bioinformatician	Introductory	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Next Generation DNA Sequencing and Analysis	DNA Sequencing Technology; Comparative Genomics	Next Generation Sequencing	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.666 Next Generation DNA Sequencing and Analysis The recent revolution in DNA sequencing technologies has transformed biology within a few short years, dropping the cost and ease of sequencing dramatically to the point where the "$1,000 Human Genome" is in sight. Armed with complete genome sequences, biologists need to identify the genes encoded within and the variation in these genes between individuals, assign functions to the genes, and to put these into functional and metabolic pathways. This course will provide an overview of next generation sequencing technologies in the historical context of DNA sequencing, the pros and cons of each technology, and the bioinformatics techniques used with this sequence information, beginning with quality control assessment, genome assembly and annotation. Prerequisites: 410.602 Molecular Biology; 410.633 Introduction to Bioinformatics; 410.634 Practical Computer Concepts for Bioinformatics	Bioinformatician	Introductory	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	

Back to Brief View

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Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor or Zip Code	Continuing Education Credit	Graduate Certificate/Masters/PhD Program	Non-Degree Option Avaliable	Notes
Microarrays and Analysis	Expression Analysis; Statistics	Microarray Analysis; S-plus; R; SAS	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.671 Microarrays and Analysis This course will focus on the analysis and visualization of microarray data. The general aim is to introduce students to the various techniques and issues involved with analyzing multivariate expression data. Additionally, students will visualize the results in modern statistical scripting software. Topics include detecting and attributing sources of data variability, determining differentially expressed genes with relevant statistical tests, and controlling for false positive discovery (multiple test corrections, permutations, etc.). An introduction to linear and non-linear dimension reduction methods (PCA, PLS, isometric feature mapping, etc.) and an introduction to common pattern recognition (clustering), classification, and discrimination techniques will be included. Assignments and concepts will make use of publicly available Affymetrix and cDNA microarray data sets. Examples will mostly be demonstrated in S-plus and R (publicly available) code, with some in SAS. Free demo software tools such as Minitab, Spotfire, TreeView, Expression Profiler, and web UIs will also be utilized. Prerequisites: 410.601 Biochemistry; 410.602 Molecular Biology; 410.645 Biostatistics; 410.634 Practical Computer Concepts for Bioinformatics or an undergraduate computer programming course	Bioinformatician	Introductory	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Advanced Practical Computer Concepts for Bioinformatics	Computer Science; Languages	Web Applications; UNIX; Perl; CGI; SQL	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.712 Advanced Practical Computer Concepts for Bioinformatics This intermediate-to-advanced-level course, intended as a follow-on to 410.634 Practical Computer Concepts for Bioinformatics (a prerequisite for this new class), will integrate and expand on the concepts from that introductory class to allow students to create working, Web-based bioinformatics applications in a project-based course format. After a review of the concepts covered in 410.634, students will learn how to create functional Web applications on a UNIX system, using Perl and CGI to create forms that can be acted upon, and using the Perl DBI module to interface with MySQL relational databases that they will create and populate to retrieve and present information. This will be demonstrated by building an in-class, instructor led project. More advanced SQL concepts and database modeling will also be covered, as well as introductions to HTML5, CSS3 and Javascript. Class time in the latter weeks of the class will be devoted to individual assistance on student projects as well as to short lectures on advanced topics. Once again, whenever possible, this course will emphasize relevance to solving problems in molecular biology and bioinformatics. Pre-requisites: 410.601 Biochemistry, 410.602 Molecular Biology, 410.634 Practical Computer Concepts	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Advanced Genomics and Genetic Analysis	Variant Analysis; Comparative Genomics	Genomics; Genetic Analysis; Microarray Analysis	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.713 Advanced Genomics and Genetic Analysis The next generation of array and sequencing technologies provides the ability to investigate large quantities of genomics information with higher sensitivity, greater throughput, and lower costs. This also introduces new challenges in data management, novel algorithmic approaches, and general interpretation. This course builds on the topics in 410.671 Microarrays and Analysis to address analysis of both genetic variation and genomics content using technologies measuring splice variants, single nucleotide polymorphisms (SNPs), copy number variation (CNV), and transcription factor binding sites. Analysis methods for deep sequencing technologies are also introduced including: quantitative mRNA content (RNA-Seq) and whole genome assembly methods with de novo and reference-based approaches. Prereqisites: Molecular Biology, Introduction to Bioinformatics, Microarrays	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Practical Introduction to Metagenomics	Metagenomics	Metagenomics	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.734 Practical Introduction to Metagenomics The emerging field of metagenomics allows for the study of entire communities of microorganisms at once, with far-reaching applications in a wide array of fields such as medicine, agriculture and bioremediation. Students will learn the principles of metagenomics through exploration of published project data and guided readings of recent literature. Using data from the Human Microbiome Project, students will explore practical analysis tasks including sequence assembly, gene prediction and annotation, metabolic reconstruction, taxonomic community profiling and more. Pre-requisites: 410.601 Biochemistry, 410.602 Molecular Biology; 410.634 Practical Computer Concepts for Bioinformatics	Bioinformatician	Introductory	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Genomic and Personalized Medicine	Variant Analysis; Comparative Genomics; Functional Analysis	Genomics; Personalized Medicine	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 410.736 Genomic and Personalized Medicine This integrative course will be of interest to a wide variety of students in different concentration areas. Applying knowledge from their core courses and introductory bioinformatics, students will examine the current applications of whole genome sequencing and genome wide association studies in clinical medicine, and explore evolving applications and their impact on future medical diagnoses and treatments. Students will review both established and emerging sequencing platforms in detail. This course will closely examine whole genome sequencing applications in inherited and heritable diseases and cancer, amongst others. Class discussions will include ethical, legal, regulatory, and economic implications of genomic medicine. Students and faculty will regularly report on new developments in the field as they emerge throughout the course. Prerequisites: 410.601 Biochemistry; 410.602 Molecular Biology; 410.633 Introduction to Bioinformatics	Bioinformatician	Introductory	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Principles of Computational Biology	Computer Science; Comparative Genomics	Algorithms; Smith-Waterman; FASTA; BLAST	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 605.451 Principles of Computational Biology This course is an interdisciplinary introduction to computational methods used to solve important problems in DNA and protein sequence analysis. The course focuses on algorithms but includes material to provide the necessary biological background for science and engineering students. Algorithms to be covered include dynamic programming for sequence alignment, such as Smith-Waterman, FASTA, and BLAST; hidden Markov models, such as the forward, Viterbi, and expectation maximization algorithms; a range of gene-finding algorithms; phylogenic tree construction; and clustering algorithms. Prerequisites: Familiarity with probability and statistics; working knowledge of Java, C++, or C; 605.205 Molecular Biology for Computer Scientists or a course in molecular biology; and either a course in cell biology or biochemistry.	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Computational Drug Discovery and Development	Systems Biology; Functional Analysis	Pharmacogenomics	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 605.456 Computational Drug Discovery and Development Recent advances in bioinformatics and drug discovery platforms have brought us significantly closer to the realization of rational drug design and development. Across the pharmaceutical industry, considerable effort is being invested in developing experimental and translational medicine, and it is starting to make a significant impact on the drug discovery process itself. This course examines the major steps of the evolving modern drug discovery platforms, the computational techniques and tools used during each step of rational drug discovery, and how these techniques facilitate the integration of experimental and translational medicine with the discovery/development platforms. The course will build on concepts from a number of areas including bioinformatics, computational genomic/ proteomics, in silico system biology, computational medicinal chemistry, and pharmaceutical biotechnology. Topics covered in the course include comparative pharmacogenomics, protein/ antibody modeling, interaction and regulatory networks, QSAR/ pharmacophores, ADME/toxicology, and clinical biomarkers. Relevant mathematical concepts are developed as needed in the course. Prerequisites: 605.205 Molecular Biology for Computer Scientists or equivalent.	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Modeling and Simulation of Complex Systems	Systems Biology; Functional Analysis	E-Cell; COPASI; BioSpice; Modeling; Pathway Analysis	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 605.716 Modeling and Simulation of Complex Systems This course focuses on the application of modeling and simulation principles to complex systems. A complex system is a large-scale nonlinear system consisting of interconnected or interwoven parts (such as a biological cell, the economy, or an ecological system). The course begins with an overview of complex systems, followed by modeling and simulation techniques based on nonlinear differential equations, networks, stochastic models, cellular automata, and swarm-like systems. Existing software systems will be used to illustrate systems and provide practical experience. During the semester, each student will complete a modeling project of a complex system. While this course is intended for computer science or engineering students interested in modeling any complex system, it may also be taken by bioinformatics students interested in modeling complex biological systems. Students interested in bioinformatics will study a parallel track exposing them to existing whole-cell modeling tools such as E-Cell, COPASI, and BioSpice. Prerequisites: Knowledge of elementary probability and statistics and previous exposure to differential equations. Students applying this course to the MS in Bioinformatics should also have completed at least one Bioinformatics course prior to enrollment.	Bioinformatician	Advanced	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Computational Aspects of Molecular Structure	Proteomics; Functional Analysis	Algorithms; Proteins; RNA	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 605.751 Computational Aspects of Molecular Structure This course focuses on computational methods for studying protein and RNA structure, protein-protein interactions, and biological networks. Algorithms for prediction of RNA secondary structure, protein-protein interactions, and annotation of protein secondary/tertiary structure and function are studied in depth. Students will apply various computer programs and structure-visualization software to secondary and tertiary protein structure prediction, structure-structure comparison, protein domain classification, annotation of functionally important sites, and protein design. Interesting aspects of protein interaction and metabolic networks are also discussed. Prerequisites: 605.205 Molecular Biology for Computer Scientists or equivalent. 605.451 Principles of Computational Biology is recommended.	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Computational Genomics	Statistics; Comparative Genomics	Genomics	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 605.453 Computational Genomics This course focuses on current problems of computational genomics. Students will explore bioinformatics software, discuss bioinformatics research, and learn the principles underlying a variety of bioinformatics algorithms. The emphasis is on algorithms that use probabilistic and statistical approaches. Topics include analyzing eukaryotic, bacterial, and viral genes and genomes, genome sequencing and assembling, finding genes in genomes and identifying their biological functions, predicting regulatory sites, and assessing gene and genome evolution. Prerequisites: 605.205 Molecular Biology for Computer Scientists or equivalent and familiarity with probability and statistics.	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Analysis of Gene Expression and High-Content Biological Data	Expression Analysis	Microarrays; RNA-seq	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 605.754 Analysis of Gene Expression and High-Content Biological Data The development of microarray technology, rapid sequencing, protein chips, and metabolic data has led to an explosion in the collection of "high-content" biological data. This course explores the analysis and mining of gene expression data and high-content biological data. A survey of gene and protein arrays, laboratory information management systems, data normalization, and available tools is followed by a more in-depth treatment of differential gene expression detection, clustering techniques, pathway extraction, network model building, biomarker evaluation, and model identification. Both clinical and research data will be considered. The student will develop skills in statistical analysis and data mining, including statistical detection theory, nonlinear and multiple regression, entropy measurement, detection of hidden patterns in data, heuristic search, and learning algorithms. Applied mathematical concepts and biological principles will be introduced, and students will focus on algorithm design and software application for designing and implementing novel ways of analyzing gene, protein, and metabolic expression data. Students will complete data analysis assignments individually and in small teams. Prerequisites: 605.205 or equivalent or a prior course in bioinformatics, a course in probability and statistics, and ability to program in a high-level language.	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Systems Biology	Systems Biology	Systems Biology	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 605.755 Systems Biology During the last decade, systems biology has emerged as an effective tool for investigation of complex biological problems, placing emphasis on the analysis of large-scale data sets and quantitative treatment of experimental results. In this course, students will explore recent advances in systems biology analysis of intracellular processes. Examples of modeling and experimental studies of metabolic, genetic, signal transduction, and cell cycle regulation networks will be studied in detail. The classes will alternate between consideration of network-driven and network element (gene, metabolite, or protein)- driven approaches. Students will learn to use Boolean, differential equations, and stochastic methods of analysis and will become acquainted with several powerful experimental techniques, including basics of microfabrication and microfluidics. For their course projects, students will develop models of a signal transduction or metabolic pathway. Prerequisites: Courses in molecular biology (605.205 Molecular Biology for Computer Scientists or 410.602 Molecular Biology) and differential equations.	Bioinformatician	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters/PhD Program	Non-Degree Option Avaliable	Notes
Machine Learning	Statistics	Statistics; Data Mining	This course is offered as part of the Johns Hopkins Online Bioinformatics MS program (see entry in this database). To take a course, students must enroll in Advanced Academic Programs for the Bioinformatics MS. Courses Required for MS: 11 courses; thesis option available 605.746 Machine Learning How can machines improve with experience? How can they discover new knowledge from a variety of data sources? What computational issues must be addressed to succeed? These are questions that are addressed in this course. Topics range from determining appropriate data representation and models for learning, understanding different algorithms for knowledge and model discovery, and using sound theoretical and experimental techniques in assessing performance. Specific approaches covered include statistical techniques (e.g., k- nearest neighbor and Bayesian learning), logical techniques (e.g., decision tree and rule induction), function approximation (e.g., neural networks and kernel methods), and reinforcement learning. The topics are discussed in the context of current machine learning and data mining research. Students will participate in seminar discussions and will complete and present the results of an individual project. Prerequisites: 605.445 Artificial Intelligence is recommended but not required.	Bioinformatician; Epidemiologist	Intermediate	http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/	Online Graduate Program Course	Fall, Spring, or Summer Semester; schedule: http://advanced.jhu.edu/academics/graduate-degree-programs/bioinformatics/course-schedule/	Online	Semester	$3,955/course, $150 online course fee		Johns Hopkins University	Kristina Odom	Director, Center for Biotechnology Education; Program Director, Bioinformatics and Biotechnology	(301 294-7159	kobom@jhu.edu						Online Graduate Program Course	Yes	
Stanford Distance Education Master of Science in Biomedical Informatics Professional/Honors Cooperative Program	Graduate Program	Online Master's Program	Stanford Distance Education Master of Science in Biomedical Informatics Professional/Honors Cooperative Program This degree is designed primarily for the working professional who already has advanced training in one discipline and wishes to acquire interdisciplinary skills. All classes necessary for the degree are available online. The professional M.S. is offered in conjunction with Stanford Center for Professional Development (SCPD), which establishes the rates of tuition and fees. The program uses the honors cooperative program (HCP) model, which assumes that the student is working in a corporate setting and is enrolled in the M.S. on a part-time basis. The student has up to five years to complete the program. Research projects are optional and the student must make arrangements with program faculty. Graduates of this program are prepared to contribute creatively to basic or applied projects in biomedical informatics. Core Curriculum in Biomedical Informatics Students are expected to participate regularly in BIOMEDIN 201 Biomedical Informatics Student Seminar and a research colloquium. In addition, all students are expected to fulfill requirements in the following five categories: 1. Core Biomedical Informatics (17 units) Students are expected to complete the core offerings in biomedical informatics: a. BIOMEDIN 212 Introduction to Biomedical Informatics Research Methodology b. and 4 of the following: BIOMEDIN 210 Modeling Biomedical Systems: Ontology, Terminology, Problem Solving BIOMEDIN 214 Representations and Algorithms for Computational Molecular Biology BIOMEDIN 215 Data Driven Medicine BIOMEDIN 217 Translational Bioinformatics BIOMEDIN 260 Computational Methods for Biomedical Image Analysis and Interpretation c. Any remaining units must be graduate level courses listed under BIOMEDIN. d. Note that BIOMEDIN 211 is no longer offered, however that course may be used by students who completed it to fulfill a core BMI requirement. 2. Computer Science, Statistics, Mathematics & Engineering (18 units) Students are expected to create a program of study with a mixture of graduate-level courses in computer science, statistics or other	Bioinformatician	Intermediate	http://exploredegrees.stanford.edu/schoolofmedicine/biomedicalinformatics/#masterstext	Online Master's Program	See schedule on website http://explorecourses.stanford.edu/	Online	Up to 5 years	$45,375 (45 units) to complete the masters; $3,025/course for graduate/certificate credit; $1,295/course for non-degree enrollment		Stanford University	Mary Jeanne Oliva	Student Services Administrator, Biomedical Informatics	(650) 723-1398	mjoliva@stanford.edu		Stanford	CA			Online Master's Program	Yes	
Stanford Online Bioinformatics Graduate Certificate	Graduate Program; Comparative Genomics; DNA Sequencing Technology; Expression Analysis; Systems Biology; Variant Analysis; HPC/Cloud; Metagenomics; Computer Science; Statistics		Stanford Online Bioinformatics Graduate Certificate Students may take a course without being formally admitted to a degree program by enrolling under the Non-Degree Option. The Bioinformatics Graduate Certificate focuses on developing an understanding of techniques for analyzing the vast amount of biological data from recent genomic research to new applications relevant to basic biology. • Understand the use of different techniques to analyze biological data from high throughput approaches • Learn how the techniques are used in new applications in biomedicine • Acquire an understanding of how molecular biology is used to address topics ranging from sequence, structure and function analysis in the context of algorithms, databases and visualization 3 Courses Required Required Courses: • BIOMEDIN214 Representations and Algorithms for Computational Molecular Biology • BIOMEDIN217 Translational Bioinformatics Electives (Choose One) • BIOMEDIN210 Modeling Biomedical Systems: Ontology, Terminology, Problem Solving • BIOMEDIN215 Data Driven Medicine • BIOMEDIN260 Computational Methods for Biomedical Image Analysis and Interpretation • MS&E152 Introduction to Decision Analysis • BIOMEDIN258 Genomics, Bioinformatics and Medicine Earning the Certificate • Tailor the certificate to your interests and career goals • Begin your certificate any academic quarter that an applicable course is offered, subject to prerequisites • Take courses for graduate credit and a grade	Bioinformatician	Introductory	http://scpd.stanford.edu/public/category/courseCategoryCertificateProfile.do?method=load&certificateId=1226682	Online Graduate Certificate Program	See schedule on website http://explorecourses.stanford.edu/	Online	Up to 3 years	$12,320 - $15,840 (11 - 12 units) to complete the certificate; $3,025/course for graduate/certificate credit; $1,295/course for non-degree enrollment		Stanford University	Mary Jeanne Oliva	Student Services Administrator, Biomedical Informatics	(650) 723-1398	mjoliva@stanford.edu						Online Graduate Certificate Program	Yes	
Introduction to Biomedical Informatics Research Methodology	General Computing	Research Methodology; Software	This course is a core required course for the Stanford Distance Education Master of Science in Biomedical Informatics Professional/Honors Cooperative Program (see entry in this database). Students may take a course without being formally admitted to a degree program by enrolling under the Non-Degree Option. BIOMEDIN212 - Introduction to Biomedical Informatics Research Methodology Hands-on software building. Student teams conceive, design, specify, implement, evaluate, and report on a software project in the domain of biomedicine. Creating written proposals, peer review, providing status reports, and preparing final reports. Guest lectures from professional biomedical informatics systems builders on issues related to the process of project management. Software engineering basics. Because the team projects start in the first week of class, attendance that week is strongly recommended. Prerequisites: BIOMEDIN 210, 211, 214, 217 or consent of instructor. Same as: BIOE 212, CS 272, GENE 212.			Master's Program: http://exploredegrees.stanford.edu/schoolofmedicine/biomedicalinformatics/#masterstext Certificate Program: http://scpd.stanford.edu/public/category/courseCategoryCertificateProfile.do?method=load&certificateId=1226682 Course Catalog: http://explorecourses.stanford.edu/	Online Graduate Program Course	See schedule on website http://explorecourses.stanford.edu/	Online	Semester	$3,025/course for graduate/certificate credit; $1,295/course for non-degree enrollment		Stanford University	Mary Jeanne Oliva	Student Services Administrator, Biomedical Informatics	(650) 723-1398	mjoliva@stanford.edu						Online Graduate Program Course	Yes	
Representations and Algorithms for Computational Molecular Biology	Comparative Genomics; Statistics; Computer Science	Algorithms; DNA; RNA; Proteins; Small Molecules	This course is required for the Stanford Online Bioinformatics Graduate Certificate (see entry in this database). 3 courses are required for the certificate. This course may be taken as a core required course for the Stanford Distance Education Master of Science in Biomedical Informatics Professional/Honors Cooperative Program (see entry in this database). Students may take a course without being formally admitted to a degree program by enrolling under the Non-Degree Option. BIOMEDIN214 - Representations and Algorithms for Computational Molecular Biology Overview The explosion of molecular data continues to fuel academic and industry interest in biomedical informatics. This is an exciting time in bioinformatics, and there is great potential for harnessing information produced by genome sequencing projects for medical diagnostic and therapeutic uses. This course provides an introduction to computing with DNA, RNA, proteins and small molecules. Learn how to program both basic and advanced algorithms for sequence analysis, 3D structure analysis and high-throughput functional data analysis. Receive hands-on experience with the algorithms used in the field. You Will Learn • DNA and protein sequence alignment • RNA expression analysis • 3D protein structure modeling and prediction • Dynamic programming algorithms for alignment • Machine learning for 3D structure • Clustering and classification algorithms • Introductions to biological natural language processing, human genomics, and chemoinformatics	Bioinformatician	Introductory	Master's Program: http://exploredegrees.stanford.edu/schoolofmedicine/biomedicalinformatics/#masterstext Certificate Program: http://scpd.stanford.edu/public/category/courseCategoryCertificateProfile.do?method=load&certificateId=1226682 Course Catalog: http://explorecourses.stanford.edu/	Online Graduate Program Course	See schedule on website http://explorecourses.stanford.edu/	Online	Semester	$3,025/course for graduate/certificate credit; $1,295/course for non-degree enrollment		Stanford University	Mary Jeanne Oliva	Student Services Administrator, Biomedical Informatics	(650) 723-1398	mjoliva@stanford.edu						Online Graduate Program Course	Yes	
Translational Bioinformatics	Expression Analysis; Databases; Variant Analysis	Translational Bioinformatics	This course is required for the Stanford Online Bioinformatics Graduate Certificate (see entry in this database). 3 courses are required for the certificate. This course may be taken as a core required course for the Stanford Distance Education Master of Science in Biomedical Informatics Professional/Honors Cooperative Program (see entry in this database). Students may take a course without being formally admitted to a degree program by enrolling under the Non-Degree Option. BIOMEDIN217 - Translational Bioinformatics Overview Focused on the convergence of molecular bioinformatics, biostatistics, statistical genetics, bioinformatics optimizes translational medicine through the transformation of data into diagnostics and therapeutics. Analyze genetic, genomic, and biological data to become skilled at identifying different types of genome-scale measurements in molecular biology and genomic medicine. Case studies will enforce your understanding of course material and address new questions in the biomedical industry. Topics Include • Access and utility of publicly available data sources • Analysis of microarray data • Analysis of polymorphisms, proteomics, and protein interactions • Linking genome-scale data to clinical data and phenotypes	Bioinformatician	Introductory	Master's Program: http://exploredegrees.stanford.edu/schoolofmedicine/biomedicalinformatics/#masterstext Certificate Program: http://scpd.stanford.edu/public/category/courseCategoryCertificateProfile.do?method=load&certificateId=1226682 Course Catalog: http://explorecourses.stanford.edu/	Online Graduate Program Course	See schedule on website http://explorecourses.stanford.edu/	Online	Semester	$3,025/course for graduate/certificate credit; $1,295/course for non-degree enrollment		Stanford University	Mary Jeanne Oliva	Student Services Administrator, Biomedical Informatics	(650) 723-1398	mjoliva@stanford.edu						Online Graduate Program Course	Yes	
Modeling Biomedical Systems: Ontology, Terminology, Problem Solving	Systems Biology; Functional Analysis	Semantic Technology	This course is an elective for the Stanford Online Bioinformatics Graduate Certificate (see entry in this database). 3 courses are required for the certificate. This course may be taken as a core required course for the Stanford Distance Education Master of Science in Biomedical Informatics Professional/Honors Cooperative Program (see entry in this database). Students may take a course without being formally admitted to a degree program by enrolling under the Non-Degree Option. BIOMEDIN210 - Modeling Biomedical Systems: Ontology, Terminology, Problem Solving Overview The abundance of data in the life sciences and the widespread adoption of electronic health records have spawned a rapidly growing industry that works towards the proper management and intelligent use of biomedical data. This course provides an introduction to semantic technology in biomedicine, providing a platform for understanding how computers are being used to communicate knowledge and integrate data in the health care and life sciences fields. Students will connect with practitioners in the field who will discuss practical applications of semantic technology in biomedicine and provide their unparalleled frst-hand experience. Topics Include • Knowledge representation • Controlled terminologies • Ontologies • Reusable problem solvers • Knowledge acquisition	Bioinformatician	Introductory	Master's Program: http://exploredegrees.stanford.edu/schoolofmedicine/biomedicalinformatics/#masterstext Certificate Program: http://scpd.stanford.edu/public/category/courseCategoryCertificateProfile.do?method=load&certificateId=1226682 Course Catalog: http://explorecourses.stanford.edu/	Online Graduate Program Course	See schedule on website http://explorecourses.stanford.edu/	Online	Semester	$3,025/course for graduate/certificate credit; $1,295/course for non-degree enrollment		Stanford University	Mary Jeanne Oliva	Student Services Administrator, Biomedical Informatics	(650) 723-1398	mjoliva@stanford.edu						Online Graduate Program Course	Yes	

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters/PhD Program	Non-Degree Option Avaliable	Notes
Data Driven Medicine	**Databases; General Computing**	Electronic Medical Records	This course is an elective for the Stanford Online Bioinformatics Graduate Certificate (see entry in this database). 3 courses are required for the certificate. This course may be taken as a core required course for the Stanford Distance Education Master of Science in Biomedical Informatics Professional/Honors Cooperative Program (see entry in this database). Students may take a course without being formally admitted to a degree program by enrolling under the Non-Degree Option. BIOMEDIN 215. Data Driven Medicine. 3 Units. With the spread of electronic health records and increasingly low cost assays for patient molecular data, powerful data repositories with tremendous potential for biomedical research, clinical care and personalized medicine are being built. But these databases are large and difficult for any one specialist to analyze. To find the hidden associations within the full set of data, we introduce methods for data-mining at the internet scale, the handling of large-scale electronic medical records data for machine learning, methods in natural language processing and text-mining applied to medical records, methods for using ontologies for the annotation and indexing of unstructured content as well as semantic web technologies. Prerequisites: CS 106A; familiarity with statistics (STATS 202) and biology. Recommended: one of CS 246 (previously CS 345A), STATS 305, or CS 229.	Bioinformatician	Introductory	Master's Program: http://exploredegrees.stanford.edu/schoolofmedicine/biomedicalinformatics/#masterstext Certificate Program: http://scpd.stanford.edu/public/category/courseCategoryCertificateProfile.do?method=load&certificateId=1226682 Course Catalog: http://explorecourses.stanford.edu/	Online Graduate Program Course	See schedule on website http://explorecourses.stanford.edu/	Online		$3,025/course for graduate/certificate credit; $1,295/course for non-degree enrollment		Stanford University	Mary Jeanne Oliva	Student Services Administrator, Biomedical Informatics	(650) 723-1398	mjoliva@stanford.edu						Online Graduate Program Course	Yes	
Computational Methods for Biomedical Image Analysis and Interpretation	**General Computing**	Image Analysis and Interpretation	This course is an elective for the Stanford Online Bioinformatics Graduate Certificate (see entry in this database). 3 courses are required for the certificate. This course may be taken as a core required course for the Stanford Distance Education Master of Science in Biomedical Informatics Professional/Honors Cooperative Program (see entry in this database). Students may take a course without being formally admitted to a degree program by enrolling under the Non-Degree Option. BIOMEDIN260 - Computational Methods for Biomedical Image Analysis and Interpretation Overview The latest biological and medical imaging modalities and their applications in research and medicine. Focus is on computational analytic and interpretive approaches to optimize extraction and use of biological and clinical imaging data for diagnostic and therapeutic translational medical applications. Case studies include linking image data to genomic, phenotypic and clinical data, developing representations of image phenotypes for use in medical decision support and research applications and the role that biomedical imaging informatics plays in new questions in biomedical science. Includes a project. Enrollment for 3 units with reduced project requirements requires instructor consent. Topics Include • Major image databases • Fundamental methods in image processing • Quantitative extraction of image features • Structured recording of image information including semantic features and ontologies • Indexing, search and content-based image retrieval	Bioinformatician	Introductory	Master's Program: http://exploredegrees.stanford.edu/schoolofmedicine/biomedicalinformatics/#masterstext Certificate Program: http://scpd.stanford.edu/public/category/courseCategoryCertificateProfile.do?method=load&certificateId=1226682 Course Catalog: http://explorecourses.stanford.edu/	Online Graduate Program Course	See schedule on website http://explorecourses.stanford.edu/	Online	Semester	$3,025/course for graduate/certificate credit; $1,295/course for non-degree enrollment		Stanford University	Mary Jeanne Oliva	Student Services Administrator, Biomedical Informatics	(650) 723-1398	mjoliva@stanford.edu						Online Graduate Program Course	Yes	
Introduction to Decision Analysis	**Statistics**	Decision Analysis	This course is an elective for the Stanford Online Bioinformatics Graduate Certificate (see entry in this database). 3 courses are required for the certificate. Students may take a course without being formally admitted to a degree program by enrolling under the Non-Degree Option. MS&E 152. Introduction to Decision Analysis Overview Apply a methodical approach to making important personal and professional decisions in a complex, dynamic and uncertain world. Examine uncertainties and tradeoffs and use a structured conversation based on actional thought to obtain clarity of action in a wide variety of domains. Directly apply course concepts and distinctions to your professional and personal experiences using insight from a professional guest speaker currently practicing as a decision analyst. Topics Include • Probabilities • Value of information and experimentation • Relevance and decision diagrams • Risk attitude	Bioinformatician	Introductory	Master's Program: http://exploredegrees.stanford.edu/schoolofmedicine/biomedicalinformatics/#masterstext Certificate Program: http://scpd.stanford.edu/public/category/courseCategoryCertificateProfile.do?method=load&certificateId=1226682 Course Catalog: http://explorecourses.stanford.edu/	Online Graduate Program Course	See schedule on website http://explorecourses.stanford.edu/	Online	Semester	$3,025/course for graduate/certificate credit; $1,295/course for non-degree enrollment		Stanford University	Mary Jeanne Oliva	Student Services Administrator, Biomedical Informatics	(650) 723-1398	mjoliva@stanford.edu						Online Graduate Program Course	Yes	
Genomics, Bioinformatics and Medicine	**Databases; Functional Analysis**	Genomics; Pharmacogenomics	This course is an elective for the Stanford Online Bioinformatics Graduate Certificate (see entry in this database). 3 courses are required for the certificate. Students may take a course without being formally admitted to a degree program by enrolling under the Non-Degree Option. BIOMEDIN258 - Genomics, Bioinformatics and Medicine Overview The explosion of information available from human genome mapping provides many opportunities for preventative medicine. Explore the potential of personal genomics, pharmacogenomics and clinical genomics and their role in the future of preventive medicine. Examine the ethical, social and legal issues facing current health care policy and treatment. This course is cross listed with BIOC258. Topics Include • Disease and genome databases • Sequencing the human genome • Bioinformatics, personal and functional genomics • Stem cells and stem cell therapies • Pharmacogenomics	Bioinformatician	Introductory	Master's Program: http://exploredegrees.stanford.edu/schoolofmedicine/biomedicalinformatics/#masterstext Certificate Program: http://scpd.stanford.edu/public/category/courseCategoryCertificateProfile.do?method=load&certificateId=1226682 Course Catalog: http://explorecourses.stanford.edu/	Online Graduate Program Course	See schedule on website http://explorecourses.stanford.edu/	Online	Semester	$3,025/course for graduate/certificate credit; $1,295/course for non-degree enrollment		Stanford University	Mary Jeanne Oliva	Student Services Administrator, Biomedical Informatics	(650) 723-1398	mjoliva@stanford.edu						Online Graduate Program Course	Yes	
Introductory Unix for Bioinformatics	**Languages**	Unix; Perl	PerlSource provides cross-functional training to professionals from a wide variety of backgrounds such as healthcare, pharma, biotechnology and IT, to name a few. In order to make such advanced training accessible to everyone in a convenient form, we have designed web-based courses that can be taken at your convenience and completed as per individual schedules in a self-paced manner. Our courses are built gradually from the ground up and therefore can be done by professionals from diverse backgrounds. We currently have students from US, Europe and Asia who are biologists, physicians and software engineers with a BS, MS, MBA, MBBS, MD or Ph.D. To request course details and to register for our courses, please send us the completed Application Form on our website via email to courses@perlsource.net specifying which courses you wish to take. We will be in touch with you shortly to counsel on the appropriate courses to take, taking your prior experience and future goals in mind. 101. Introductory Unix for Bioinformatics The basic 101 level course teaches the applications of Unix tools and utilities to perform routine sequence analysis tasks. This is an introductory course for those who want to obtain a basic understanding of the Unix OS and can be completed in 2-3 months. All commands are customized for the Tcsh shell. Unix for Bioinformatics 101 covers the following topics: § The Bioinformatics working environment § Navigating the Unix file system § Creating and manipulating sequence files § Downloading and manipulating sequences from Entrez § Unix commands and utilities (piping, redirection) § Editing files in Unix with the Emacs editor	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://www.perlsource.net/courses.html	Online	Schedule with vendor	Online	Unknown	Contact vendor		PerlSource Informatics				courses@perlsource.net								
Advanced Unix for Bioinformatics	**Languages**	Unix	PerlSource provides cross-functional training to professionals from a wide variety of backgrounds such as healthcare, pharma, biotechnology and IT, to name a few. In order to make such advanced training accessible to everyone in a convenient form, we have designed web-based courses that can be taken at your convenience and completed as per individual schedules in a self-paced manner. Our courses are built gradually from the ground up and therefore can be done by professionals from diverse backgrounds. We currently have students from US, Europe and Asia who are biologists, physicians and software engineers with a BS, MS, MBA, MBBS, MD or Ph.D. To request course details and to register for our courses, please send us the completed Application Form on our website via email to courses@perlsource.net specifying which courses you wish to take. We will be in touch with you shortly to counsel on the appropriate courses to take, taking your prior experience and future goals in mind. 201. Advanced Unix for Bioinformatics Unix is the platform of choice for large-scale Bioinformatics operations. Among other things, 201 describes work-flow operations in a typical high-throughput sequencing center - a fundamental aspect of large-scale sequencing that controls how sequence data is stored, distributed and processed in these centers - and, the biology of the sequencing process itself. Unix 201 can be taken in combination with Perl 201. Unix for Bioinformatics 201 covers the following topics: § Editing and manipulating sequence files with the vi editor § FTP and downloading databases from NCBI § Unix commands and utilities for sequence analysis § Using wild cards with commands § File compression and uncompression § Process control	Bioinformatician	Advanced	http://www.perlsource.net/courses.html	Online	Schedule with vendor	Online	Unknown	Contact vendor		PerlSource Informatics				courses@perlsource.net								
Introductory Perl Programming for Bioinformatics	**Languages**	Perl	PerlSource provides cross-functional training to professionals from a wide variety of backgrounds such as healthcare, pharma, biotechnology and IT, to name a few. In order to make such advanced training accessible to everyone in a convenient form, we have designed web-based courses that can be taken at your convenience and completed as per individual schedules in a self-paced manner. Our courses are built gradually from the ground up and therefore can be done by professionals from diverse backgrounds. We currently have students from US, Europe and Asia who are biologists, physicians and software engineers with a BS, MS, MBA, MBBS, MD or Ph.D. To request course details and to register for our courses, please send us the completed Application Form on our website via email to courses@perlsource.net specifying which courses you wish to take. We will be in touch with you shortly to counsel on the appropriate courses to take, taking your prior experience and future goals in mind. Perl for Bioinformatics 101 The basic 101 level course teaches the fundamentals of Bioinformatics and the use of Perl scripting for automating sequence analysis. This is an introductory course for those who want to obtain a basic understanding of Bioinformatics and can be completed in 2-3 months. 101. Introductory Perl for Bioinformatics covers the following topics: § Introduction to Perl: Scalars § Introduction to Perl: Arrays § Using standard Perl modules § Perl regular expressions § Perl control structures § Bioinformatics project	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://www.perlsource.net/courses.html	Online	Schedule with vendor	Online	Unknown	Contact vendor		PerlSource Informatics				courses@perlsource.net								

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Available	Notes
Advanced Perl Programming for Bioinformatics	**Languages**	Perl	PerlSource provides cross-functional training to professionals from a wide variety of backgrounds such as healthcare, pharma, biotechnology and IT, to name a few. In order to make such advanced training accessible to everyone in a convenient form, we have designed web-based courses that can be taken at your convenience and completed as per individual schedules in a self-paced manner. Our courses are built gradually from the ground up and therefore can be done by professionals from diverse backgrounds. We currently have students from US, Europe and Asia who are biologists, physicians and software engineers with a BS, MS, MBA, MBBS, MD or Ph.D. To request course details and to register for our courses, please send us the completed Application Form on our website via email to courses@perlsource.net specifying which courses you wish to take. We will be in touch with you shortly to counsel on the appropriate courses to take, taking your prior experience and future goals in mind. Perl for Bioinformatics 201 201 is an advanced level course and the 7 modules together describe the tools and techniques that are currently used in the industry for such diverse tasks as genome annotation, comparative genomics, new target identification and so on. During the course students will be required to read and analyze scientific papers on Bioinformatics and Genomics and complete assignments in Genomics and programming. Perl 201 covers the basic aspects of Molecular Biology, Bioinformatics and Genomics and students will therefore get ample opportunity to understand the biology behind Bioinformatics during the course of the training. Students can choose to take modules based on their background and current skills and drop those that they already have prior experience or training in. The entire course can be completed in a self-paced manner in 6-8 months. 201. Advanced Perl for Bioinformatics covers the following topics: § Module 1: Elements of Perl programming § Module 2: Sequence analysis with web-based tools § Module 3: Perl/BioPerl programming for sequence analysis § Module 4: Perl/BioPerl for database access (Ensembl, ACEDB, Flybase, ...) § Module 5: MySQL/Oracle database design and development with Perl Perl 201 readies students to apply the powerful in-built libraries and regular expression capabilities of Perl to perform a wide variety of tasks encountered during Bioinformatics research such as mining differential gene expression data from genome wide platforms (viz, Affymetrix Genechip, Massively Parallel Signature Sequencing - MPSS, etc.); for preparation of data for analysis with Spotfire (viz.	Bioinformatician	Advanced	http://www.perlsource.net/courses.html	Online	Schedule with vendor	Online	Unknown	Contact vendor		PerlSource Informatics				courses@perlsource.net								
Introductory Java for Bioinformatics	**Languages**	Java	PerlSource provides cross-functional training to professionals from a wide variety of backgrounds such as healthcare, pharma, biotechnology and IT, to name a few. In order to make such advanced training accessible to everyone in a convenient form, we have designed web-based courses that can be taken at your convenience and completed as per individual schedules in a self-paced manner. Our courses are built gradually from the ground up and therefore can be done by professionals from diverse backgrounds. We currently have students from US, Europe and Asia who are biologists, physicians and software engineers with a BS, MS, MBA, MBBS, MD or Ph.D. To request course details and to register for our courses, please send us the completed Application Form on our website via email to courses@perlsource.net specifying which courses you wish to take. We will be in touch with you shortly to counsel on the appropriate courses to take, taking your prior experience and future goals in mind. 101. Introductory Java for Bioinformatics The basic Java 101 level course teaches the fundamentals of Bioinformatics and the use of Java 2 Standard Edition (J2SE) technologies for building robust enterprise application for Bioinformatics applications. This is an introductory course for those who want to obtain a basic understanding of J2SE and Bioinformatics and can be completed in 2-3 months. Java for Bioinformatics 101 covers the following topics: § Introduction to Java § Java Language Fundamentals § Java Input and Output (I/O) § Creating a Graphical User Interface (GUI) with Java Swing Libraries § Bioinformatics Project	Bioinformatician	Introductory	http://www.perlsource.net/courses.html	Online	Schedule with vendor	Online	Unknown	Contact vendor		PerlSource Informatics				courses@perlsource.net								
Advanced Java for Bioinformatics	**Languages**	Java	PerlSource provides cross-functional training to professionals from a wide variety of backgrounds such as healthcare, pharma, biotechnology and IT, to name a few. In order to make such advanced training accessible to everyone in a convenient form, we have designed web-based courses that can be taken at your convenience and completed as per individual schedules in a self-paced manner. Our courses are built gradually from the ground up and therefore can be done by professionals from diverse backgrounds. We currently have students from US, Europe and Asia who are biologists, physicians and software engineers with a BS, MS, MBA, MBBS, MD or Ph.D. To request course details and to register for our courses, please send us the completed Application Form on our website via email to courses@perlsource.net specifying which courses you wish to take. We will be in touch with you shortly to counsel on the appropriate courses to take, taking your prior experience and future goals in mind. 201. Advanced Java for Bioinformatics Java 201 is an advanced level course and the 5 modules together describe the tools and techniques that are currently used in the industry for building Java 2 Enterprise Edition (J2EE) applications for genomics and bioinformatics analyses. During the course students will be required to read and analyze scientific papers on Bioinformatics and Genomics and complete assignments in Genomics and programming. Java 201 covers the basic aspects of Molecular Biology, Bioinformatics and Genomics and students will therefore get ample opportunity to understand the biology behind Bioinformatics during the course of the training. Students can choose to take modules based on their background and current skills and drop those that they already have prior experience or training in. The entire course can be completed in a self-paced manner in 6-8 months. Java for Bioinformatics 201 covers the following topics: § Module 1: Elements of Java programming § Module 2: Developing advanced GUI applications with Swing (Blast/Genscan) § Module 3: Building web applications with JSP/Servlets technology (PubMed) § Module 4: Java Database programming with MySQL/Oracle	Bioinformatician	Advanced	http://www.perlsource.net/courses.html	Online	Schedule with vendor	Online	Unknown	Contact vendor		PerlSource Informatics				courses@perlsource.net								
Foundation Course in Biotechnology	**Functional Analysis**	Molecular Biology; Recombinant DNA Technologies; Scientific Inquiry	PerlSource provides cross-functional training to professionals from a wide variety of backgrounds such as healthcare, pharma, biotechnology and IT, to name a few. In order to make such advanced training accessible to everyone in a convenient form, we have designed web-based courses that can be taken at your convenience and completed as per individual schedules in a self-paced manner. Our courses are built gradually from the ground up and therefore can be done by professionals from diverse backgrounds. We currently have students from US, Europe and Asia who are biologists, physicians and software engineers with a BS, MS, MBA, MBBS, MD or Ph.D. To request course details and to register for our courses, please send us the completed Application Form on our website via email to courses@perlsource.net specifying which courses you wish to take. We will be in touch with you shortly to counsel on the appropriate courses to take, taking your prior experience and future goals in mind. Basics of Biotechnology This foundation course is for individuals who do not have prior (formal or informal) training in molecular biology and modern day recombinant DNA technologies. These are typically students with non-biology backgrounds such as IT or computer science professionals, engineers, attorneys, and others who are seeking to acquire a basic but firm understanding of the science of biotechnology that they can apply immediately at work (without needing to acquire a University-level degree). Coursework is based on the research method where students are trained to read and critique original research articles and supporting materials with the objective of giving them a first-hand experience of the process of scientific inquiry - formulating the hypothesis, experimental design and conduct, and the reporting of findings supported by veriafiable, reproducible experimental data. Basics of Biotechnology covers the following topics: § Module 1: Essentials of Molecular Biology § Module 2: Essentials of Genomics The course covers essential topics such as structure and function of biomolecules (nucleic acid and proteins), fundamental life processes such as DNA replication, transcription, translation, RNA editing, and use of genomics and high-throughput technologies such as microarrays and DNA chips to conduct whole genome studies and finally, the effect of dysregulation of these processes on health and disease (molecular basis of disease).	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://www.perlsource.net/courses.html	Online	Schedule with vendor	Online	Unknown	Contact vendor		PerlSource Informatics				courses@perlsource.net								
Foundation Course in Bioinformatics	**Languages; Comparative Genomics**	Perl	PerlSource provides cross-functional training to professionals from a wide variety of backgrounds such as healthcare, pharma, biotechnology and IT, to name a few. In order to make such advanced training accessible to everyone in a convenient form, we have designed web-based courses that can be taken at your convenience and completed as per individual schedules in a self-paced manner. Our courses are built gradually from the ground up and therefore can be done by professionals from diverse backgrounds. We currently have students from US, Europe and Asia who are biologists, physicians and software engineers with a BS, MS, MBA, MBBS, MD or Ph.D. To request course details and to register for our courses, please send us the completed Application Form on our website via email to courses@perlsource.net specifying which courses you wish to take. We will be in touch with you shortly to counsel on the appropriate courses to take, taking your prior experience and future goals in mind. Basics of Bioinformatics What truly differentiates a bioinformaticist from a biologist is the ability to perform data extraction, organization, mining, analysis and interpretation in a high-throughput manner as against in a manual, piecemeal fashion, which is both extremely tedious and time intensive. This training helps students achieve tremendous productivity by giving them the ability to automate routine and highly data intensive bioinformatics tasks. The focus of the foundation course in Bioinformatics is on using Perl's powerful regular expression and pattern searching libraries for analyzing any kind of biological data, viz., DNA and protein sequences, gene expression data, etc. and using its in-built modules and libraries to build"wrappers" around essential genomics tools such as homology searching, sequence alignment, gene prediction, etc., to create automated routines for web-based sequence analysis. Basics of Bioinformatics covers the following topics: § Module 1: Elements of Perl programming § Module 2: Sequence analysis with web-based tools § Module 3: Perl/BioPerl programming for sequence analysis	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://www.perlsource.net/courses.html	Online	Schedule with vendor	Online	Unknown	Contact vendor		PerlSource Informatics				courses@perlsource.net								
Mathematical Modeling in Bioscience Online Graduate Certificate	**Graduate Program; Statistics; Systems Biology; Computer Science; Microbiology**	Math/Statistics; Online Graduate Certificate Program	East Tennessee State University online graduate certificate in Mathematical Modeling in Bioscience Students may take at least 1 course as a non-degree student. The online graduate certificate in Mathematical Modeling in Bioscience will provide those with a traditional background in science, mathematics, or technology the skills and content knowledge needed for work in the high-demand, highly-relevant area of mathematical and computational bioscience. Five online courses are required for the completion of the certificate, which will cover the fundamentals of predictive modeling, data mining and visualization, mathematical modeling in biomedicine and the study of computational complexity that is required for data science. A student can use the certificate as a stand-alone achievement or to enhance a graduate degree in a related field. This online Graduate Certificate program was designed with working professionals in mind, offering the flexibility and convenience of online coursework. Please contact us for more detailed information about this program. This certificate is offered as an online degree and consists of 5 courses: • Math 5830- Analytics and Predictive Modeling (3 credits) • Math 5840- Complex Networks and Systems (3 credits) • Math 5870- Mathematical Modeling using Graph Theory (3 credits) • Math 5880- Modeling of Infectious Diseases and Social Networks (3 credits) • Math 5890- Stochastic Modeling (3 credits) Schedule Courses are scheduled, and not available on demand. Math 5830 will be offered each summer. Math 5840 and Math 5890 will be offered each fall and Math 5870 and Math 5880 will be offered each spring. Thus the certificate will be attainable in one calendar year. Tuition $688 per semester hour or $2,064 for out-of-state students, plus other fees Program requirements: The certificate consists of 5 three-hour courses and can be completed in one academic year. Students need	Bioinformatician	Intermediate	http://www.etsu.edu/online/Mathematical_Modeling BioSciCert.aspx	Online Graduate Certificate Program	See schedule on website	Online		$10,320 ($2,064 per course, including fees)		East Tennessee State University	Debra Knisley			knisleyd@etsu.edu						Online Graduate Certificate Program	May take at least one course as non-degree student	

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Row	Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters/PhD Program	Non-Degree Option Available	Notes
227	Analytics and Predictive Modeling	Statistics	Alogorithms	Bioscience (see entry in this database). Students may take at least 1 course as a non-degree student. Schedule Courses are scheduled, and not available on demand. Math 5830 will be offered each summer. Math 5840 and Math 5890 will be offered each fall and Math 5870 and Math 5880 will be offered each spring. Thus the certificate will be attainable in one calendar year. Tuition $688 per semester hour or $2,064 for out-of-state students, plus other fees MATH 5830 - Analytics and Predictive Modeling (3 credits) Prerequisites: MATH 1910 and 1920. Beginning Spring 2013, the prerequisite will be: Admission to the math graduate program or permission. This is a course in predictive modeling, machine learning, and basic informatics with applications to business analytics and biomedical data mining. Emphasis is on algorithms implementing precision-recall analysis, the receiver operating characteristic, logistic regression, neural networks, the quantification of uncertainty, and systems modeling. Emphasis is on the mathematics necessary for the use and interpretation of important algorithms used in data mining, analytics, and machine learning. All mathematics beyond basic calculus is developed within the course and no previous computer skills are required. Program requirements: The certificate consists of 5 three-hour courses and can be completed in one academic year. Students need to be admitted to the school of graduate studies to enroll in a course. To be awarded the certificate, students must be admitted to the certificate program. Both applications can be found at the ETSU School of Graduate Studies website. Students who have taken non-degree coursework at ETSU (including the certificate courses) or other universities may petition to transfer up to six hours to the graduate certificate requirements. However, at least 9 hours of the certificate coursework must be at ETSU in order to complete the	Bioinformatician; Epidemiologist	Introductory	http://www.etsu.edu/online/Mathematical_ModelingBioSciCert.aspx	Online Graduate Program Course	Summer	Online	Semester	$2,064 (including fees)		East Tennessee State University	Debra Knisley			knisleyd@etsu.edu						Online Graduate Program Course	May take at least one course as non-degree student	
228	Complex Networks and Systems	Systems Biology	Pathway Analysis; Networks	This course is offered as part of the East Tennessee State University online graduate certificate in Mathematical Modeling in Bioscience (see entry in this database). Students may take at least 1 course as a non-degree student. Schedule Courses are scheduled, and not available on demand. Math 5830 will be offered each summer. Math 5840 and Math 5890 will be offered each fall and Math 5870 and Math 5880 will be offered each spring. Thus the certificate will be attainable in one calendar year. Tuition $688 per semester hour or $2,064 for out-of-state students, plus other fees MATH 5840 - Complex Networks and Systems (3 credits) Prerequisites: MATH 5830 This course introduces the student to the study of complex networks through the lens of graph theory. Concepts of the mathematical properties of networks such as distance, connectivity, expansibility and clusters or hubs (centrality) are studied. Computational tools and data visualization techniques are also studied. Applications with emphasis on recent work regarding properties of biological networks are covered. Program requirements: The certificate consists of 5 three-hour courses and can be completed in one academic year. Students need to be admitted to the school of graduate studies to enroll in a course. To be awarded the certificate, students must be admitted to the certificate program. Both applications can be found at the ETSU School of Graduate Studies website. Students who have taken non-degree coursework at ETSU (including the certificate courses) or other universities may petition to transfer up to six hours to the graduate certificate requirements. However, at least 9 hours of the certificate coursework must be at ETSU in order to complete the requirements. Thus, a student can take at most 2 of the 5 courses as a non-degree student before applying to the certificate program and then request the credit be transferred to the program.	Bioinformatician	Introductory	http://www.etsu.edu/online/Mathematical_ModelingBioSciCert.aspx	Online Graduate Program Course	Fall	Online	Semester	$2,064 (including fees)		East Tennessee State University	Debra Knisley			knisleyd@etsu.edu						Online Graduate Program Course	May take at least one course as non-degree student	
229	Mathematical Modeling Using Graph Theory	Computer Science	Graph Theory	This course is offered as part of the East Tennessee State University online graduate certificate in Mathematical Modeling in Bioscience (see entry in this database). Students may take at least 1 course as a non-degree student. Schedule Courses are scheduled, and not available on demand. Math 5830 will be offered each summer. Math 5840 and Math 5890 will be offered each fall and Math 5870 and Math 5880 will be offered each spring. Thus the certificate will be attainable in one calendar year. Tuition $688 per semester hour or $2,064 for out-of-state students, plus other fees MATH 5870 - Mathematical Modeling Using Graph Theory (3 credits) This course introduces the student to applied graph theory. Graph theoretical concepts will be approached as models for practical, real-world problems. The course will provide an introduction to graph modeling, integrated with applications based on emerging methods and needs. The emphasis is both on graphs as models – communication networks, for example – and on the algorithms used for obtaining information from those models. Program requirements: The certificate consists of 5 three-hour courses and can be completed in one academic year. Students need to be admitted to the school of graduate studies to enroll in a course. To be awarded the certificate, students must be admitted to the certificate program. Both applications can be found at the ETSU School of Graduate Studies website. Students who have taken non-degree coursework at ETSU (including the certificate courses) or other universities may petition to transfer up to six hours to the graduate certificate requirements. However, at least 9 hours of the certificate coursework must be at ETSU in order to complete the requirements. Thus, a student can take at most 2 of the 5 courses as a non-degree student before applying to the certificate program and then request the credit be transferred to the program	Bioinformatician; Epidemiologist	Introductory	http://www.etsu.edu/online/Mathematical_ModelingBioSciCert.aspx	Online Graduate Program Course	Spring	Online	Semester	$2,064 (including fees)		East Tennessee State University	Debra Knisley			knisleyd@etsu.edu						Online Graduate Program Course	May take at least one course as non-degree student	
230	Modeling of Infectious Diseases and Social Networks	Microbiology; Systems Biology; Computer Science	Epidemiology; Math	Bioscience (see entry in this database). Students may take at least 1 course as a non-degree student. Schedule Courses are scheduled, and not available on demand. Math 5830 will be offered each summer. Math 5840 and Math 5890 will be offered each fall and Math 5870 and Math 5880 will be offered each spring. Thus the certificate will be attainable in one calendar year. Tuition $688 per semester hour or $2,064 for out-of-state students, plus other fees MATH 5880 - Modeling of Infectious Diseases and Social Networks (3 credits) Prerequisites: Linear Algebra, Mulivariate Calculus, Differential Equations or equivalent. Corequisites: Permission of the instructor. This course integrates mathematical model formulation, qualitative model analysis, computer simulation, and data analysis. All these areas are explored in the context of infectious diseases of human populations. More precisely, this course reviews topics of current interest in the following fields: theoretical ecology (e.g., predator-prey interactions); mathematical epidemiology (e.g., basic reproductive number); theoretical immunology (e.g., antigenic variation); evolutionary game theory (e.g., Nash equilibria); and social networks (e.g., sexual-partner networks). Program requirements: The certificate consists of 5 three-hour courses and can be completed in one academic year. Students need to be admitted to the school of graduate studies to enroll in a course. To be awarded the certificate, students must be admitted to the certificate program. Both applications can be found at the ETSU School of Graduate Studies website. Students who have taken non-degree coursework at ETSU (including the certificate courses) or other universities may petition to transfer up to six hours to the graduate certificate requirements. However, at least 9 hours of the certificate coursework must be at ETSU in order to complete the requirements. Thus, a student can take at most 2 of the 5 courses as a non-degree student before applying to the certificate program and then request the credit be transferred to the program	Bioinformatician; Epidemiologist	Introductory	http://www.etsu.edu/online/Mathematical_ModelingBioSciCert.aspx	Online Graduate Program Course	Spring	Online	Semester	$2,064 (including fees)		East Tennessee State University	Debra Knisley			knisleyd@etsu.edu						Online Graduate Program Course	May take at least one course as non-degree student	
231	Stochastic Modeling	Statistics	Stochastic Modeling; Markov Chains	This course is offered as part of the East Tennessee State University online graduate certificate in Mathematical Modeling in Bioscience (see entry in this database). Students may take at least 1 course as a non-degree student. Schedule Courses are scheduled, and not available on demand. Math 5830 will be offered each summer. Math 5840 and Math 5890 will be offered each fall and Math 5870 and Math 5880 will be offered each spring. Thus the certificate will be attainable in one calendar year. Tuition $688 per semester hour or $2,064 for out-of-state students, plus other fees MATH 5890 - Stochastic Modeling (3 credits) Prerequisites: Course in Linear Algebra or equivalent. This is a course in stochastic modeling with an emphasis on applications and computation. Topics covered include stochastic modeling and simulation using discrete-time Markov chains, continuous-time Markov chains, and stochastic differential equations. Program requirements: The certificate consists of 5 three-hour courses and can be completed in one academic year. Students need to be admitted to the school of graduate studies to enroll in a course. To be awarded the certificate, students must be admitted to the certificate program. Both applications can be found at the ETSU School of Graduate Studies website. Students who have taken non-degree coursework at ETSU (including the certificate courses) or other universities may petition to transfer up to six hours to the graduate certificate requirements. However, at least 9 hours of the certificate coursework must be at ETSU in order to complete the requirements. Thus, a student can take at most 2 of the 5 courses as a non-degree student before applying to the certificate program and then request the credit be transferred to the program.	Bioinformatician; Epidemiologist	Intermediate	http://www.etsu.edu/online/Mathematical_ModelingBioSciCert.aspx	Online Graduate Program Course	Fall	Online	Semester	$2,064 (including fees)		East Tennessee State University	Debra Knisley			knisleyd@etsu.edu						Online Graduate Program Course	May take at least one course as non-degree student	
232	Bioinformatics Approaches to Identify Causative Sequence Variants in Farm Animals	Comparative Genomics; DNA Sequencing Technology; Expression Analysis; Systems Biology; Variant Analysis;	AllBio; RNASeq; QTL; Farm Animals; Transcription factors	ALLBIO and DEANN Training course: 12-16 May 2014, SLU, Uppsala, Sweden The training is mainly intended for researchers that want or already use techniques like genome-wide SNP genotyping, candidate gene sequencing, transcriptome sequencing and other bioinformatics tools in their work to elucidate the specific contributions of genetic and other factors in shaping the phenotypic variability in farm animals. These materials are provided on the Goblet Training Materials page. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Intermediate	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	On-demand	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
233	STAO 2014 Understanding a Genetic Disease Thanks to Bioinformatics	Comparative Genomics	Genome Browsing; BLAST; Protein Structure Visualisation; Variant Detection	This workshop covers several bioinformatics tools and databases (genome browser, alignment tool, BLAST, dbSNP, UniProtKB, PDB) in the context of the discovery of a rare variant leading to the production of a non-functional insulin in a Norwegian family. Additional documents are available: http://education.expasy.org/cours/Toronto. Audience: high school These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
234	Metagenome Data Analysis Workshop, May 21-23, 2014	Metagenomics	AllBio; Data Analysis; Assembly; Binning	This is a SciLifelab and AllBio workshop on the analysis and interpretation of metagenomics data. In this workshop we will combine talks by experts in the field with practical tutorials guiding the participants in the analysis of representative datasets. These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												

Back to Brief View

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UPGMA Worked Example	Phylogenomics	Molecular Phylogeny; Phylogenetics; UPGMA	A walkthrough of clustering 7 biological sequences (A-G) using the Unweighted Pair-Group Method with Arithmetic mean (UPGMA) method. Note that UPGMA is actually a generic method and thus the walkthrough could apply to any objects A-G for which pairwise distances can be calculated. A small CGI site for generating a UPGMA tree from a distance matrix can be found here. The source data for this worked example is a subset of Cytochrome C distances from Table 3 of one of the seminal phylogenetic papers: Fitch WM & Margoliash E (1967). Construction of phylogenetic trees. Science 155:279-84. PowerPoint timings are set up to be consistent with autoloping the presentation. Audience: Beginners These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
QuickGuides	Languages	UnixLinux; Perl; BLAST; Phylip; Velvet; EMBOSS; mySQL	A range of Quick Guides to commonly used bioinformatics tools and resources. Audience: Beginners These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Basic Bioinformatics and HOPE	Comparative Genomics	Disease Causing Mutation; Predicting Effect of Mutation on Structure; Predicting Effect of Mutation on Protein Funcion	Many bioinformatics tools have been developed over the last decennium, most of which were meant to be used in the lab of the life scientist. Unfortunately, only a few made it, because the tools are often too non-intuitive and too much a black box to the life scientist. Therefore Hanka Venselaar developed HOPEto at least make the explanation of the phenotypic effect of mutations in (human) proteins intuitive for the non-bioinformatics expert. We developed this course to explain the basics of this program, and the underlying theory. These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Perl 1 Training Course - for Programming-Beginners	Languages	Programming; Perl	A set of slides from The Sainsbury Laboratory Perl course for absolute beginners Audience: Beginners Bench Biologists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician; Epidemiologist; Laboratorian	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
RNA-Seq Analysis 2014 Module 4 - Isoform Discovery and Alternative Expression	Expression Analysis	Transcript Isoforms; Alternative Expression; RNA	Explore use of Cufflinks in reference annotation based transcript (RABT) assembly mode and 'de novo' assembly mode. Both modes require a reference genome sequence. Audience: Graduate Students Post-Doctoral Fellows Researchers Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Intermediate	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
RNA-Seq Analysis 2014 Module 3 - Expression and Differential Expression	Expression Analysis	Transcript Expression; Differential Expression; RNA	• Get FPKM style expression estimates using Cufflinks • Perform differential expression analysis with Cuffdiff • Perform summary analysis with CummeRbund • Downstream interpretation of expression analysis (multiple testing, clustering, heatmaps, classification, pathway analysis, etc.) Audience: Graduate Students Post-Doctoral Fellows Researchers Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Intermediate	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
RNA-Seq Analysis 2014 Module 2 - Alignment and Visualization	Expression Analysis	RNA-seq Alignment; Data Visualization; RNA	• Use of BowtieTophat • 'Regular mode' vs. 'Fusion mode' • Introduction to the BAM format • Basic manipulation of BAMs with samtools, etc. • Visualization of RNA-seq alignments - IGV • BAM read counting and determination of variant allele expression status Audience: Graduate Students Post-Doctoral Fellows Researchers Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Intermediate	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
RNA-Seq Analysis 2014 Module 1 - Introduction to RNA-Seq Analysis	Expression Analysis	Introduction to RNA-Seq Analysis; IGV; Experimental Design for RNA-seq; RNA	• Basic introduction to biology of RNA-seq • Experimental design considerations • Commonly asked questions • Data visualization using IGV Audience: Graduate Students Post-Doctoral Fellows Researchers Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Intermediate	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Bioinformatics Introductory Module	Comparative Genomics	Genome Browsing; Protein Structure; Genomics	This Bioinformatics Introductory Module for self-study was designed for future students of the Molecular Mechanisms of Disease (MMD) master's program at Radboud University Medical Centre. To level out the starting differences in bioinformatics knowledge between this incoming heterogeneous group of students as much as possible, we have designed an introductory course module that should allow them – via self study and hands-on exercises – to acquire sufficient basic bioinformatics knowledge. Anticipated time needed to complete the module: 40 hours. Answers for all the exercises are available on request. Of course you do need internet connection to perform the hands-on exercises. There is no need, however, to install programs onto your computer and also low-speed data transfer should be sufficient. All literature that is cited and used throughout the module was taken from open access sources. Audience: Master students Life Science Researchers These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced; 40 hours	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Pathway and Network Analysis 2014 - Module 6 - Gene Function Prediction	Metabolomics; Functional Analysis; Systems Biology	Functional Association Networks; Gene Function Prediction; GeneMANIA	• Functional association networks and gene function prediction • Homology based prediction • Guilt-by-association: GeneMANIA Audience: Graduate Students Post-Doctoral Fellows Researchers Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Intermediate	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Pathway and Network Analysis 2014 - Module 5 - Network Visualization	Systems Biology	Network Visualization; Cytoscape	• Introduction to network visualization • Visualizing omics data on a network or pathway • Active modules in Cytoscape Audience: Graduate Students Post-Doctoral Fellows Researchers Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												

Back to Brief View

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Pathway and Network Analysis 2014, Module 4 - Pathway and Network Analysis	Systems Biology	Pathway Analysis; Biological Networks; Reactome; KEGG	• Introduction to pathway and network analysis • Basic network concepts • Types of pathway and network information • Pathway Databases: Reactome, KEGG, etc. • Pathway analysis of large scale genomics data sets, including cancer genomics Audience: Graduate Students Post-Doctoral Fellows Researchers Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Pathway and Network Analysis 2014, Module 3 - Gene Regulation Analysis	Systems Biology	Transcriptional Regulation; Pattern Discovery	• Overview of transcription • Data sources for regulatory data - Chromatin IP, DNA hypersensitivity, other chip data • Basics of processing data • Pattern discovery Audience: Graduate Students Post-Doctoral Fellows Researchers Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Intermediate	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Pathway and Network Analysis 2014, Module 2 - Finding Over-Represented Pathways	Systems Biology; Functional Analysis	Over-Representation Analysis; GSEA	• Over-representation analysis (ORA) • Statistics for detecting over-representation e.g. hypergeometric test, GSEA • Multiple testing correction: Bonferroni, Benjamini-Hochberg FDR • Filtering Gene Ontology e.g. using evidence codes Audience: Graduate Students Post-Doctoral Fellows Researchers Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Pathway and Network Analysis 2014, Module 1 - Introduction to Gene Lists	Systems Biology	Gene Lists; Gene Ontology	• Gene list analysis overview: Workflow of concepts and tools from gene list to pathway analysis • Where do gene lists come from? • Working with gene function information Audience: Graduate Students Post-Doctoral Fellows Researchers Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
BLAST and Multiple Sequence Alignment (MSA) Programs	Comparative Genomics	BLAST; Multiple Sequence Alignment; E-Learning	The rapid identification of pathogens infecting livestock is essential to appropriately respond to the threat. The number and the variety of pathogen sequenced genomes have been growing more dramatically these recent years, because of the new sequencing technologies. This wealth of new data is very useful to the research field through the development of bioinformatics tools and databases that deal with large amount of sequences. Among them, BLAST (Basic Local Alignment Search Tool) and MSA () programs are very efficient for protein or nucleotide sequence similarity search. The present course introduces the main biological databases, alignment tool BLAST and Multiple sequence alignments (MSA) programs, and interpretation of results. Goal The ultimate aim is the better management of animal diseases by preparing laboratory technicians, veterinarians and molecular epidemiologists from diagnostic and research laboratories of developing FAO and IAEA member states, to be self-sufficient in the data analysis by interpreting the phylogenetic trees and their relationships. Audience Researchers, Laboratory technicians, veterinarians, epidemiologists from diagnostic and research laboratories of member states of IAEA and FAO. The concepts are explained in generalized way to help all academicians, researchers, students from all countries working in the field of molecular genetics and epidemiology. Authors Viral-zone, Swiss-Prot group at the SIB Swiss Institute of Bioinformatics These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Phylogenetics of Animal Viral Pathogens	Phylogenomics	Phylogenetics; Animal Pathogens; E-Learning	[illegible] characterization of each pathogen. In this context, the enormous amount of sequence and genotype data is being generated on animal pathogens, which is further useful in understanding their pathogenicity and molecular epidemiology. The usage of this data in developing efficient molecular diagnostic tools needs basic understanding of the phylogenetic analysis. Phylogenetic classification, construction of trees, interpretation unveils the geographical distribution and migration of pathogens which helps in better management of animal diseases. The present course is designed with introduction to phylogenetics, tools, building and interpreting trees and finally its application to veterinary diagnostics. Though the course is driven in veterinary aspects, the same implicates to the human and plant pathogen study. Goal The ultimate aim is the better management of animal diseases by preparing laboratory technicians, veterinarians and molecular epidemiologists from diagnostic and research laboratories of developing FAO and IAEA member states, to be self-sufficient in the data analysis by interpreting the phylogenetic trees and their relationships. Audience Researchers, Laboratory technicians, veterinarians, epidemiologists from diagnostic and research laboratories of member states of IAEA and FAO. The concepts are explained in generalized way to help all academicians, researchers, students from all countries working in the field of molecular genetics and epidemiology. Authors Viral-Zone, Swiss-Prot Group at SIB Swiss Institute of Bioinformatics Audience: Researchers Laboratory technicians Veterinarians Biologists Bench biologists	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Working with Affymetrix CEL Files in R	Languages; Expression Analysis	Affymetrix; Microarrays; R	This tutorial shows how to download some public Affymetrix microarray data, load the data into R, calculate expression values and do some very simple plotting. Links: http://www.ark-genomics.org/events-online-training/working-affymetrix-cel-files Audience: PhD students Researchers Beginners These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Simple Plotting in R	Languages	Visualisation; Microarray Data Analysis; Plotting Data; R	This quick and simple tutorial demonstrates some of the easy plotting tools in the R core software. The data are in the "data" directory and come from an old two-colour microarray experiment where spots on the array were printed with different buffers, in different concentrations and with different pins. Also, both channels Cy5 and Cy3 were spotted identically, and so the fold ratio for all spots should be 1 - this helps us see bias in the data. Audience: Beginners Scientists Researchers PhD students These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Unix Fundamentals	General Computing	Unix; Problem Based Learning; Programming	[illegible] UNIX knowledge. The examples are taken from various Biological fields but have been chosen carefully to be easily accessible to a wide audience. At the end of the course, participants are expected to be able to • Have some understanding on UNIX systems • Navigate through the UNIX filesystem • Execute and understand some UNIX process commands • Correctly set file permissions • Perform basic file management Participants are encouraged to follow the tutorial sections sequentially. The tutorial content is sometimes an oversimplification of the Truth - yes, we know! Due to the diversity of computer systems, we will just assume that participants do have access to a terminal. For help, please contact your IT support - or a good friend! Authors are affiliated to the SIB Swiss Institute of Bioinformatics: Vassilios Ioannidis With some content provided by Frédéric Schütz, Volker Flegel and Heinz Stockinger Content integration by Grégoire Rossier and Vassilios Ioannidis Audience: beginner bioinformaticians Bench biologists biocurators Graduate Students Clinical Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												

Back to Brief View

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Introduction to Multiple Sequence Alignments (MSAs) and Phylogenies	Comparative Genomics	Sequence Alignment; Multiple Sequence Alignment; Protein Sequence Analysis; Phylogenetics; Molecular Evolution	Slides used for teaching an introduction to phylogenies and MSAs in the context of phylogenies for the first day of a two-day course on MSAs at Cambridge University, in the UK, in December 2013. Course taught together with Holger Dinkel and Terri Attwood. Audience: Postgraduate students Post-Doctoral Fellows principle investigators Bench biologists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Clinical Bioinformatics I - Tutor Notes	Variant Analysis; Comparative Genomics; Functional Analysis	Clinical Bioinformatics; Genomics	Clinical Bioinformatics I is a 10 credit module of the new MSc in Clinical Bioinformatics, delivered by Nosgen/NGRL and the University of Manchester in the UK. Clinical Bioinformatics is one of the streams of the NHS Scientific Training Programme (STP). The programme is a mixture of work placement based training interspersed with academic teaching. The tutor notes describe the content taught on each day of the 5-day course, and the approach used to teach the materials. Each day is divided into two parts, a series of lectures in the morning to introduce the topics, then the afternoon sessions present a series of case studies for the students to work through in a 'problem based learning (PBL) approach to reinforce the lecture content. Audience: postgrad Life Science Researchers healthcare professionals These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Intermediate	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Sequence Comparison - Undergraduate Lab	Comparative Genomics	Dotmatrix Plots; Sequence Alignment; Scoring Matrices	This is lab 2 in a series of labs developed as part of a "bioinformatics for biology undergraduates" course and targeted at 2nd and 3rd year undergraduates. It is meant to be easily assessible. The lab includes some instructions that are specific to our computer lab environment but the content of the lab should be easy to adapt to other environments. This lab makes use of EMBOSS programs, pros in the FASTA package, as well as the NCBI BLAST website. I usually deliver this lab after a series of lectures discussing dotmatrix plots and sequence alignment. Students enter their answers to the questions into a quiz set up within moodle which allows for easier marking. Audience: Undergraduate students These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Introduction to Biopython	Languages	Programming; Python for Biologists; Python; BioPython	This is a module from the "Python for Biologists" course. The module presents an introduction to Biopython. It shows how to deal with sequences and sequence records, how to download records from NCBI databases, how to run Blast and how to parse XML Blast outputs. Audience: Biologists bioinformaticians Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Using R with Python	Languages	Programming; Python for Biologists; Python	This is a module from the "Python for Biologists" course. It describes the Python module interfacing the R package for statistics. The module shows how to calculate mean, standard deviation, z-score and p-value of a set of numbers, and how to generate plots. Input files for the scripts presented are also provided. Audience: Biologists bioinformaticians beginner bioinformaticians Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Searching Data Using Python	Languages	Programming; Python for Biologists; Python	This is a module from the "Python for Biologists" course. It describes how to use Python dictionary and set data structures to search your data. In particular, how to use a dictionary to represent the genetic code table and use it to translate a nucleotide sequence into a protein sequence, and how to use sets to find unique records in two datasets and remove redundancy. Audience: beginner bioinformaticians Biologists Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Pattern Matching	Language; Computer Science	Python; Python for Biologists; Programming; Pattern Matching	This is a module from the "Python for Biologists" course. It teaches how to do pattern matching in Python, i.e. how to find a substring (or a set of substrings) in a string. To this aim, it introduces the regular expression syntax, and the tools needed to search regular expressions in biological sequences and in regular text, such as PubMed abstracts. Exercises and suggested solutions are presented in a separate file. Audience: Biologists beginner bioinformaticians Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Writing Functions in Python Programming	Languages	Programming; Python for Biologists; Python	This is a module from the "Python for Biologists" course. It deals with functions and how to write and use them. It also introduces namespaces and the tuple data structure. The module contains several exercises and suggested solutions. The text of exercises is also provided in a separate file. Audience: Biologists beginner bioinformaticians Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Python Programs	Languages	Programming; Python for Biologists; Python	This is a module from the "Python for Biologists" course. It deals with Python programs, how to write and run them, and how to provide input and generate output. The module also contains exercises and suggested solutions. Audience: Biologists beginner bioinformaticians Biologists, Genomicists, Computer Scientists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Bioinformatics for Mass Spectrometry Analysis	Functional Analysis	Protein Identification; Mass Spectrometry	This tutorial on Bioinformatics for Mass Spectrometry Analysis was part of a full series of tutorials that I organised in 2009 while sitting in the Educational Committee of the European Proteomics Association (EuPA). Some information on bioinformatics tools would need to be verified, but the core of slides is still up to date. It introduces the basic ideas behind mass spectrometry and bioinformatics for protein identification from mass spectrometry data. Audience: master PhD students Post-Doctoral Fellows Technicians Bench biologists bioinformaticians These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Introduction to Bioinformatics	Comparative Genomics; Databases	Introduction to Bioinformatics	An introduction to bioinformatics for bench biologists delivered as part of the EMBL Australia Masterclass on Protein Sequence Analysis http://sz-masterclass.wikispaces.com/ . Focuses on using UniProt to explore different reasons why information inferred by "direct assay" and "prediction" could be wrong, and what we can do to spot it. Audience: Bench biologists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician; Laboratorian	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters/PhD Program	Non-Degree Option Available	Notes
Interpreting Phylogenies	Phylogenomics	Phylogenetics; Molecular Evolution	Content for a one-day course delivered in April 2013 at the University of Cambridge, together with Sarah Parks, Cilia Antoniou, and Adrian Friday. Uses examples taken from several published papers to explore some of the assumptions and concepts we use when presenting and interpreting phylogenetic trees. Includes exercises on visualising and manipulating trees using Dendroscope and NJplot to reinforce some of these ideas, while also providing a very basic overview of steps involved in a generic phylogenetic analysis. Audience: experimental biologist researchers field biologist researchers These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
An Introduction to Unix, Perl and Python	Languages	Unix; Perl; Python	This course provides an introduction to Unix, Perl, and Python. In addition to lecture material (in the form of slides), there are exercises, answers to the exercises and pointers to addition resources. Audience: Bench biologists These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Bioinformatics for Mass Spectrometry Analysis	Functional Analysis	Identification; Mass Spectrometry; Proteins	The purpose of this course is to teach students the fundamental concepts underlying the analysis of proteins using mass spectrometry. These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Parsing Data Records Using Python Programming	Languages	Programming; Record Parsing; Python; Python for Biologists	This is a module from the "Python for Biologists" course. One typical problem in bioinformatics is parsing data files. This module explains how to parse FASTA files and GenBank records. It also introduces the iWriteWise construct to make choice in programming and the list data structure. The text of exercises is provided in a separate file. Audience: bioinformaticians Biologists programmers beginner bioinformaticians These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Introduction to Unix	General Computing; Languages; Databases	Programming; UnixLinux	• Introductory lecture to the UnixLinux command-line • Description of the computer shell and the command-line interface • Differences between graphical and command-line interfaces • The most common UnixLinux commands are provided Audience: Anyone who wants to start using the UnixLinux OS These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
RNA-Seq Analysis	Expression Analysis	RNA-seq; Tuxedo; TopHat; Cufflinks; CummeRbund	An overview of the analysis of gene expression in plants using RNA-seq data. This course provides a foundation on the tuxedo software suite: TopHat, Cufflinks, CummeRbund. These materials are provided on the Goblet Training Materials webpage. This site aims to provide a centralized repository of open-source training materials, to help bioinformatics trainers to share, adapt, develop and make available a wide range of resources to the community. Here, trainers can also liaise with, and get help from, other trainers, and readily share ideas and best practices. Downloadable content in this section is licensed under a Creative Commons Attribution-ShareAlike 2.5 Generic License.	Bioinformatician	Introductory	http://www.mygoblet.org/training-portal/materials	Online	On-Demand	Online	Self-paced	Free		Global Organisation for Bioinformatics Learning, Education & Training (GOBLET)												
Georgia Tech Bioinformatics Phd Degree	Comparative Genomics; DNA Sequencing Technology; Expression Analysis; Systems Biology; Variant Analysis	Residential PhD Program	Courses are offered on-site at Georgia Tech. Students must enroll in the PhD program. PhD students are fully supported with tuition waiver and monthly stipend. The requirements for each student in the PhD program in Bioinformatics include the successful completion of a set of core courses in Biology, Biochemistry, Mathematics, and Computer Science, while the main emphasis of the program is on the successful completion of an original and independent research project. Each student must also complete a minor program of studies in accordance with Institute policies. Admission to candidacy requires passing written and oral comprehensive examinations administered by the Bioinformatics PhD Graduate Committee (see the Qualifying Exams section below). The PhD dissertation written on results of the individual research project should provide evidence that the PhD candidate is ready to start an independent research career. The PhD thesis should be defended publicly and approved by the thesis committee. Credit hours requirements (Each student regardless of his home unit is required to complete the following course work): A. 9 credit hours of Bioinformatics and Computational Bioscience (e.g. BIOL 7023 and BMED 6780, BMED 7027) B. 9 credit hours in Biology, Biochemistry or Biomedical Engineering (e.g. BIOL 6658, BIOL 7658, CHEM 6572) C. 9 credit hours of Mathematics and Computer Science (e.g. MATH 6265, MATH 6267, CS 6413) D. 3 credit hours of courses in an approved minor E. 24 research credit hours Credit hours for courses in categories A, B, and C could be completed by previous graduate studies (such as study in the Georgia Tech Master's Degree in Bioinformatics program). Approval of transfer of credits from courses taken elsewhere is done by the Bioinformatics graduate committee. Typically, 2/3 of credit hours in each category A, B, C, D should be at 6000 or higher level. Students can get appropriate credits for 4000 level courses from the list of recommended courses (see separate tab), if the student's thesis committee approves them and includes into a program of studies. A student must maintain a GPA of 3.2 in his/her course work.	Bioinformatician	Advanced	http://bioinformatics.gatech.edu/phd-curriculum	Residential PhD Program	See schedule on website	Atlanta, GA	5 years	$0 (full-time PhD students are fully supported with tuition waiver and monthly stipend.)	Georgia Institute of Technology		Lisa Redding	404-385-1720	lisa.redding@biology.gatech.edu		Atlanta	GA	30332		Residential PhD Program	Yes	
Georgia Tech Professional Master's Bioinformatics Degree	Comparative Genomics; DNA Sequencing Technology; Expression Analysis; Systems Biology; Variant Analysis; HPC/Cloud; Metagenomics; Computer Science; Statistics	Residential Master's Program	Courses are offered on-site at Georgia Tech. Students can take courses as "non-degree" seeking students on a space-available basis. Non-degree registration information: http://www.registrar.gatech.edu/students/formlanding/transcripts/special.php Students may also enroll in the MS program. In-state tuition is $663 per hour for 1-11 credit hours, and $7,953 for 12 or more credit hours. MS students are eligible to apply for Computational Biology Faculty GRA awards after their first semester of study. These are awarded competitively and include a tuition waiver and stipend. Although the program has no thesis requirement, virtually all students perform research with faculty at Georgia Tech, as well as professional internships and co-op work experiences. CORE CURRICULUM Offered fall semesters: CS 4710 Introduction to Computing Concepts in Bioinformatics Biol 4150/6150 Genomics and Applied Bioinformatics Biol 8803 Programming for Bioinformatics Math 6705 Modeling and Dynamics Offered spring semesters: Biol 7210 Computational Genomics Offered every semester (and summer terms): CS 4400 Introduction to Database Systems Math 3215 Introduction to Probability and Statistics RECOMMENDED ELECTIVES Suggested Elective Courses for students interested in	Bioinformatician	Advanced	http://bioinformatics.gatech.edu/ms-degree-curriculum	Residential Master's Program	See website for schedule	Atlanta, GA	2 years for MS; non-degree, each course = 1 semester	In-state tuition is $663 per hour for 1-11 credit hours, and $7,953 for 12 or more credit hours.	Georgia Institute of Technology		Lisa Redding	404-385-1720	lisa.redding@biology.gatech.edu		Atlanta	GA	30332		Residential Master's Program	Yes	
Introduction to Computing Concepts in Bioinformatics	General Computing	Computing	This course is part of the Georgia Tech Professional MS Bioinformatics Degree Courses are offered on-site at Georgia Tech. Students can take courses as "non-degree" seeking students on a space-available basis. Non-degree registration information: http://www.registrar.gatech.edu/students/formlanding/transcripts/special.php Students may also enroll in the MS program. CS 4710 Introduction to Computing Concepts in Bioinformatics Introduction to programming concepts and computing tools such as formal models and algorithms with applications from conceptual biology.	Bioinformatician	Introductory	http://bioinformatics.gatech.edu/ms-degree-curriculum	Residential Graduate Program Course	Fall Semester	Atlanta, GA	2 years for MS; non-degree, each course = 1 semester	In-state tuition is $663 per hour for 1-11 credit hours, and $7,953 for 12 or more credit hours.	Georgia Institute of Technology		Lisa Redding	404-385-1720	lisa.redding@biology.gatech.edu		Atlanta	GA	30332		Residential Graduate Program Course	Yes	
Genomics and Applied Bioinformatics	Comparative Genomics		This course is part of the Georgia Tech Professional MS Bioinformatics Degree Courses are offered on-site at Georgia Tech. Students can take courses as "non-degree" seeking students on a space-available basis. Non-degree registration information: http://www.registrar.gatech.edu/students/formlanding/transcripts/special.php Students may also enroll in the MS program. BIOL 4150/6150 Genomics and Applied Bioinformatics 1. DNA Sequencing 2. DNA sequence annotation 3. NCBI Resources and other on-line databases 4. Pairwise sequence alignment 5. BLAST and advanced BLAST 6. Multiple sequence alignment 7. Evolutionary trees and molecular phylogenetic inference 8. Gene expression 9. Affymetrix microarray gene expression data 10. RNA-Seq 11. Clustering and pathways 12. Protein structure 13. Homology modeling 14. Genome variation and phenotype 15. Genomics and personalized medicine	Bioinformatician	Intermediate	http://bioinformatics.gatech.edu/ms-degree-curriculum	Residential Graduate Program Course	Fall Semester	Atlanta, GA	2 years for MS; non-degree, each course = 1 semester	In-state tuition is $663 per hour for 1-11 credit hours, and $7,953 for 12 or more credit hours.	Georgia Institute of Technology		Lisa Redding	404-385-1720	lisa.redding@biology.gatech.edu		Atlanta	GA	30332		Residential Graduate Program Course	Yes	
Programming for Bioinformatics	Computer Science; Languages	Programming	This course is part of the Georgia Tech Professional MS Bioinformatics Degree Courses are offered on-site at Georgia Tech. Students can take courses as "non-degree" seeking students on a space-available basis. Non-degree registration information: http://www.registrar.gatech.edu/students/formlanding/transcripts/special.php Students may also enroll in the MS program. BIOL 8803 Programming for Bioinformatics New graduate lecture courses in areas of current interest.	Bioinformatician	Intermediate	http://bioinformatics.gatech.edu/ms-degree-curriculum	Residential Graduate Program Course	Fall Semester	Atlanta, GA	2 years for MS; non-degree, each course = 1 semester	In-state tuition is $663 per hour for 1-11 credit hours, and $7,953 for 12 or more credit hours.	Georgia Institute of Technology		Lisa Redding	404-385-1720	lisa.redding@biology.gatech.edu		Atlanta	GA	30332		Residential Graduate Program Course	Yes	

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Available	Notes
Modeling and Dynamics	Systems Biology	Modeling	This course is part of the Georgia Tech Professional MS Bioinformatics Degree Courses are offered on-site at Georgia Tech. Students can take courses as "non-degree" seeking students on a space-available basis. Non-degree registration information: http://www.registrar.gatech.edu/students/formlanding/transspec/special.php Students may also enroll in the MS program. Math 6705 Modeling and Dynamics Mathematical methods for solving problems in the life sciences. Models-based course on basic facts from the theory of ordinary differential equations and numerical methods of their solution. Introduction to the control theory, diffusion theory, maximization, minimization and curve fitting. Prerequisites: RESTRICTED to biology, bioinformatics, biomedical engineering, bioengineering, and chemistry students. Graduate students in other majors cannot take this course. Math majors may not use this course toward any degree in the School of Mathematics. Topic Outline • Discrete Dynamics • Stationary and Periodic States • Their Stability • Compartment Models • Ordinary Differential Equations • Diffusion • Circular Reactions • Oscillations and Regulation • Random Walk • Numerical Methods • Curve Fitting • Method of Least Squares • Partial Differential Equations	Bioinformatician	Intermediate	https://bioinformatics.gatech.edu/ms-degree-curriculum	Residential Graduate Program Course	Fall Semester	Atlanta, GA	2 years for MS; non-degree, each course = 1 semester	In-state tuition is $663 per hour for 1-11 credit hours, and $7,953 for 12 or more credit hours.		Georgia Institute of Technology		Lisa Redding	404-385-1720	lisa.redding@biology.gatech.edu		Atlanta	GA	30332		Residential Graduate Program Course	Yes	
Computational Genomics	Computer Science; Languages; Webtools; Comparative Genomics	Genomics; Genome Browser	This course is part of the Georgia Tech Professional MS Bioinformatics Degree Courses are offered on-site at Georgia Tech. Students can take courses as "non-degree" seeking students on a space-available basis. Non-degree registration information: http://www.registrar.gatech.edu/students/formlanding/transspec/special.php Students may also enroll in the MS program. BIOL 7230 Computational Genomics The science of genomics involves the intersection of experimentation and computation. Computers are quite obviously required to handle the massive amount of data produced by genome sequencing projects. More importantly however, genome sequencing efforts yield "information" alone, which can only be converted into "knowledge" through the use of computers. In this class, the students will convert raw genomic information (i.e. sequence reads) into knowledge through the use of computational genomics tools and applications. The class will be provided with unassembled genome sequence data from the Centers for Disease Control and Prevention (CDC) and will proceed through the distinct stages of analysis and interpretation of that data: 1 - genome assembly 2 - gene prediction 3 - functional annotation 4 - comparative genomics 5 - production of a genome browser. This course will be entirely practical in nature. Students will learn to do the actual work of computational genomics. Expert guest lectures will be brought in to provide information on state-of-the-art computational genomics tools. Based on this information, other class lectures and their own research, students will be solely responsible for choosing which tools (e.g. programs and/or databases) to use, how to implement them and for producing and thoroughly documenting their final results. All results will be integrated into a publicly available genome browser.	Bioinformatician	Intermediate	https://bioinformatics.gatech.edu/ms-degree-curriculum	Residential Graduate Program Course	Spring Semester	Atlanta, GA	2 years for MS; non-degree, each course = 1 semester	In-state tuition is $663 per hour for 1-11 credit hours, and $7,953 for 12 or more credit hours.		Georgia Institute of Technology		Lisa Redding	404-385-1720	lisa.redding@biology.gatech.edu		Atlanta	GA	30332		Residential Graduate Program Course	Yes	
Introduction to Database Systems	Databases	SQL; DBMS	This course is part of the Georgia Tech Professional MS Bioinformatics Degree Courses are offered on-site at Georgia Tech. Students can take courses as "non-degree" seeking students on a space-available basis. Non-degree registration information: http://www.registrar.gatech.edu/students/formlanding/transspec/special.php Students may also enroll in the MS program. CS 4400 Introduction to Database Systems • Basic concepts • Conceptual database design - Entity-Relationship Model • DBMS Design Methodology • Relational Data Model - introduction, relational algebra, relational calculus • Mapping from ER Model to Relational Model • SQL Query Language • Relational database design - normal forms, functional dependencies • Physical database design - storage structures	Bioinformatician	Introductory	https://bioinformatics.gatech.edu/ms-degree-curriculum	Residential Graduate Program Course	Every Semester	Atlanta, GA	2 years for MS; non-degree, each course = 1 semester	In-state tuition is $663 per hour for 1-11 credit hours, and $7,953 for 12 or more credit hours.		Georgia Institute of Technology		Lisa Redding	404-385-1720	lisa.redding@biology.gatech.edu		Atlanta	GA	30332		Residential Graduate Program Course	Yes	
Introduction to Probability and Statistics	Statistics	Probability	Courses are offered on-site at Georgia Tech. Students can take courses as "non-degree" seeking students on a space-available basis. Non-degree registration information: http://www.registrar.gatech.edu/students/formlanding/transspec/special.php Students may also enroll in the MS program. MATH 3215 Introduction to Probability and Statistics This course is a problem oriented introduction to the basic concepts of probability and statistics, providing a foundation for applications and further study. Basic Principles Covered: • Multiplication principle, combinations, permutations • Inclusion-exclusion • Expected value, variance, standard deviation • Conditional probability; Bayes rule, partitions • Random variable, p.d.f., c.d.f., m.g.f. • Independence • Joint distributions, marginals, conditional expectations • Covariance, correlation • Transformations of a random variable • Central limit theorem, approximations • Basic distributions: uniform, binomial, multinomial, normal, exponential, Poisson, geometric, Gamma, Chi-squared, Student t, use of tables Topics: Probability • Experiments, events, sets, probabilities, and random variables • Equally likely outcomes, counting techniques	Bioinformatician	Introductory	https://bioinformatics.gatech.edu/ms-degree-curriculum	Residential Graduate Program Course	Every Semester	Atlanta, GA	2 years for MS; non-degree, each course = 1 semester	In-state tuition is $663 per hour for 1-11 credit hours, and $7,953 for 12 or more credit hours.		Georgia Institute of Technology		Lisa Redding	404-385-1720	lisa.redding@biology.gatech.edu		Atlanta	GA	30332		Residential Graduate Program Course	Yes	
Microbial Genomics	Microbiology	Microbial Genomics	This course is part of the Georgia Tech Professional MS Bioinformatics Degree Courses are offered on-site at Georgia Tech. Students can take courses as "non-degree" seeking students on a space-available basis. Non-degree registration information: http://www.registrar.gatech.edu/students/formlanding/transspec/special.php Students may also enroll in the MS program. BIOL 8802 Microbial Genomics New graduate lecture courses in areas of current interest.	Bioinformatician	Introductory	http://bioinformatics.gatech.edu/ms-degree-curriculum	Residential Graduate Program Course	Check schedule on website	Atlanta, GA	2 years for MS; non-degree, each course = 1 semester	In-state tuition is $663 per hour for 1-11 credit hours, and $7,953 for 12 or more credit hours.		Georgia Institute of Technology		Lisa Redding	404-385-1720	lisa.redding@biology.gatech.edu		Atlanta	GA	30332		Residential Graduate Program Course	Yes	
Mathematical Biology	Systems Biology; Functional Analysis; Computer Science	Modeling																							
Case Study: RNA-seq Data Analysis, Basic Workflow for Analyzing RNA-seq Datasets	Expression Analysis; Languages	R; Bioconductor; RNA-seq data analysis	This course is presented by Harvard University on edX. You'll learn how to analyze RNA-seq data with step-by-step instructions in order to investigate relevant biological questions. ***This is a pastarchived course on edX. At this time, you can only explore this course in a self-paced fashion. Certain features of this course may not be active, but many people enjoy watching the videos and working with the materials. Make sure to check for reruns of this course. In the case studies, we will explore the data analysis of an experimental protocol in depth, using various open source software, including R and Bioconductor. We will explain how to start with raw data, and perform the standard processing and normalization steps to get to the point where one can investigate relevant biological questions. Throughout the case studies, we will make use of exploratory plots to get a general overview of the shape of the data and the result of the experiment. We will learn the basic steps for analyzing an RNA-seq dataset for an organism with a well-defined genome and curated gene annotation. This will include read alignment, inferring presence of isoforms, counting reads in genes, exploring sample distances, differential expression analysis, and creating visual summaries. This course is part of a larger set of 8 total courses: PH525.1x: Statistics and R for the Life Sciences PH525.2x: Introduction to Linear Models and Matrix Algebra PH525.3x: Advanced Statistics for the Life Sciences PH525.4x: Introduction to Bioconductor PH525.5x: Case study: RNA-seq data analysis PH525.6x: Case study: Variant Discovery and Genotyping PH525.7x: Case study: ChIP-seq data analysis PH525.8x: Case study: DNA methylation data analysis	Bioinformatician	Intermediate	https://www.edx.org/course/case-study-rna-seq-data-analysis-harvardx-ph525.5x#!	edX, video	On-demand	Online	Self-paced	Free		Harvard University through edX											
Advanced Statistics for the Life Sciences	Statistics; Languages	R; Statistical modeling; Multiple testing; Distance and clustering; Prediction; Factor analysis (batch effects); Empirical Bayes (hierarchical modeling)	This course is presented by Harvard University on edX. You'll learn: • Intermediate R programming in the context of analyzing life science data • Application of statistical techniques commonly used in the analysis of high throughput data *** This is a pastarchived course on edX. At this time, you can only explore this course in a self-paced fashion. Certain features of this course may not be active, but many people enjoy watching the videos and working with the materials. Make sure to check for reruns of this course. Here we will cover the advanced techniques being used by data analysis experts in the life sciences. These methods are required to analyze some of the more complex datasets, such as those found in genomics. We will cover several topics including statistical modeling, multiple test correction, clustering, prediction methods, factor analysis and empirical Bayes methods. We will also elaborate on the use of R markdown to conduct reproducible research. Topics: • Statistical modeling • Multiple testing • Distance and clustering • Prediction • Factor analysis (batch effects) • Empirical Bayes (hierarchical modeling) This course is part of a larger set of 8 total courses: PH525.1x: Statistics and R for the Life Sciences PH525.2x: Introduction to Linear Models and Matrix Algebra PH525.3x: Advanced Statistics for the Life Sciences PH525.4x: Introduction to Bioconductor	Bioinformatician	Intermediate	https://www.edx.org/course/advanced-statistics-life-sciences-harvardx-ph525.3x#!	edX, video	On-demand	Online	Self-paced	Free		Harvard University through edX											

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Available	Notes
Introduction to Linear Models and Matrix Algebra. The Basics of Linear Models You Need to Know for Data Analysis in the Life Sciences	Statistics	Linear algebra; linear models	This course is presented by Harvard University on edX. You'll learn: • Linear algebra, including matrix notation and matrix operations • How to fit linear models in R to test hypotheses and analyze data *** This is a past/archived course on edX. At this time, you can only explore this course in a self-paced fashion. Certain features of this course may not be active, but many people enjoy watching the videos and working with the materials. Make sure to check for reruns of this course. We will teach a review of linear algebra, including matrix notation, which underlies many of the current tools for analyzing large-dimensional data. We will then use linear models to represent differences between experimental units and perform statistical inference on these differences. Topics: ☐ Linear algebra: matrix notation, matrix operations ☐ Linear models: comparing groups of samples, multiple variables, contrasts, and interaction terms. This course is part of a larger set of 8 total courses: PH525.1x: Statistics and R for the Life Sciences PH525.2x: Introduction to Linear Models and Matrix Algebra PH525.3x: Advanced Statistics for the Life Sciences PH525.4x: Introduction to Bioconductor PH525.5x: Case study: RNA-seq data analysis PH525.6x: Case study: Variant Discovery and Genotyping PH525.7x: Case study: ChIP-seq data analysis PH525.8x: Case study: DNA methylation data analysis	Bioinformatician	Introductory	https://www.edx.org/course/introduction-linear-models-matrix-harvardx-ph525-2x#!	edX, video	On-demand	Online	Self-paced	Free		Harvard University through edX												
Introduction to Bioconductor	Languages	Bioconductor; NGS; Microarrays	This course is presented by Harvard University on edX. You'll learn: • How to use the Bioconductor project software packages • Methods to analyze data from next generation sequencing and microarray technologies *** This is a past/archived course on edX. At this time, you can only explore this course in a self-paced fashion. Certain features of this course may not be active, but many people enjoy watching the videos and working with the materials. Make sure to check for reruns of this course. We will cover some common uses of the software packages within the Bioconductor project. You will get to decide if you learn methods for next generation sequencing, microarrays or both. We will cover a number of normalization, batch correction, and testing methods for high throughput data. Topics: • Intro to Biology • Next Generation Sequencing o GRanges, Rsamtools o Statistical modeling of counts o Differential expression of counts • Microarrays o eSets o Background correction o Differential expression of arrays • Normalization • Advanced differential expression • Batch effects • Gene set testing This course is part of a larger set of 8 total courses:	Bioinformatician	Intermediate	https://www.edx.org/course/introduction-bioconductor-harvardx-ph525-4x#!	edX, video	On-demand	Online	Self-paced	Free		Harvard University through edX												
Case Study: Variant Discovery and Genotyping. Basic Workflow for Performing Genetic Variant Discovery and Genotyping	Languages	R; Bioconductor; Variant Discovery	This course is presented by Harvard University on edX. You'll learn how to find genetic variants in DNA re-sequencing datasets with step-by-step instructions in order to investigate relevant biological questions. *** This is a past/archived course on edX. At this time, you can only explore this course in a self-paced fashion. Certain features of this course may not be active, but many people enjoy watching the videos and working with the materials. Make sure to check for reruns of this course. In the PH525 case studies, we will explore the data analysis of an experimental protocol in depth, using various open source software, including R and Bioconductor. We will explain how to start with raw data, and perform the standard processing and normalization steps to get to the point where one can investigate relevant biological questions. Throughout the case studies, we will make use of exploratory plots to get a general overview of the shape of the data and the result of the experiment. We will learn the basic steps involved in finding genetic variants in DNA re-sequencing datasets, from read alignment to calling and aggregating variant data across many samples. This course is part of a larger set of 8 total courses: PH525.1x: Statistics and R for the Life Sciences PH525.2x: Introduction to Linear Models and Matrix Algebra PH525.3x: Advanced Statistics for the Life Sciences PH525.4x: Introduction to Bioconductor PH525.5x: Case study: RNA-seq data analysis PH525.6x: Case study: Variant Discovery and Genotyping PH525.7x: Case study: ChIP-seq data analysis PH525.8x: Case study: DNA methylation data analysis	Bioinformatician	Intermediate	https://www.edx.org/course/case-study-variant-discovery-genotyping-harvardx-ph525-6x	edX, video	On-demand	Online	Self-paced	Free		Harvard University through edX												
Case Study: ChIP-seq Data Analysis. Basic Workflow for Analyzing ChIP-seq Datasets.	Expression Analysis; Languages	R; Bioconductor; ChIP-seq data analysis	This course is presented by Harvard University on edX. You'll learn how to analyze ChIP-seq datasets with step-by-step instructions in order to investigate relevant biological questions. *** This is a past/archived course on edX. At this time, you can only explore this course in a self-paced fashion. Certain features of this course may not be active, but many people enjoy watching the videos and working with the materials. Make sure to check for reruns of this course. In the PH525 case studies, we will explore the data analysis of an experimental protocol in depth, using various open source software, including R and Bioconductor. We will explain how to start with raw data, and perform the standard processing and normalization steps to get to the point where one can investigate relevant biological questions. Throughout the case studies, we will make use of exploratory plots to get a general overview of the shape of the data and the result of the experiment. We will learn the basic steps for analyzing ChIP-seq datasets, from read alignment, to peak calling, and assessing differential binding patterns across multiple samples. This course is part of a larger set of 8 total courses: PH525.1x: Statistics and R for the Life Sciences PH525.2x: Introduction to Linear Models and Matrix Algebra PH525.3x: Advanced Statistics for the Life Sciences PH525.4x: Introduction to Bioconductor PH525.5x: Case study: RNA-seq data analysis PH525.6x: Case study: Variant Discovery and Genotyping PH525.7x: Case study: ChIP-seq data analysis PH525.8x: Case study: DNA methylation data analysis	Bioinformatician	Intermediate	https://www.edx.org/course/case-study-chip-seq-data-analysis-harvardx-ph525-7x#!	edX, video	On-demand	Online	Self-paced	Free		Harvard University through edX												
Case Study: DNA Methylation Data Analysis. Basic Workflow for Analyzing DNA Methylation Data	Expression Analysis; Languages	R; Bioconductor; DNA methylation data analysis	This course is presented by Harvard University on edX. • You'll learn how to analyze DNA methylation data with step-by-step instructions in order to investigate relevant biological questions. *** This is a past/archived course on edX. At this time, you can only explore this course in a self-paced fashion. Certain features of this course may not be active, but many people enjoy watching the videos and working with the materials. Make sure to check for reruns of this course. In the PH525 case studies, we will explore the data analysis of an experimental protocol in depth, using various open source software, including R and Bioconductor. We will explain how to start with raw data, and perform the standard processing and normalization steps to get to the point where one can investigate relevant biological questions. Throughout the case studies, we will make use of exploratory plots to get a general overview of the shape of the data and the result of the experiment. We will learn the basic steps in analyzing DNA methylation data, including reading the raw data, normalization, and finding regions of differential methylation across multiple samples. This course is part of a larger set of 8 total courses: PH525.1x: Statistics and R for the Life Sciences PH525.2x: Introduction to Linear Models and Matrix Algebra PH525.3x: Advanced Statistics for the Life Sciences PH525.4x: Introduction to Bioconductor PH525.5x: Case study: RNA-seq data analysis PH525.6x: Case study: Variant Discovery and Genotyping PH525.7x: Case study: ChIP-seq data analysis PH525.8x: Case study: DNA methylation data analysis	Bioinformatician	Intermediate	https://www.edx.org/course/case-study-dna-methylation-data-analysis-harvardx-ph525-8x#!	edX, video	On-demand	Online	Self-paced	Free		Harvard University through edX												
Useful Links to Genomics Tools	Comparative Genomics	Genome Annotation; SSU rRNA Gene Data Analysis; Phylogenetic Data Analysis	Links to these webtools (contains no annotation): Tools and Databases for Genome Annotation and Comparative Analyses Artemis CAMERA CAZY GeneMark HMMER IMG InterPro KBase KEGG METACYC MUMMER NCBI PRODIGAL RAST UniProt Tools and Databases for SSU rRNA Gene Analyses Green Genes KeyDNATools Ribosomal Database Project Silva Tools for Phylogenetic Analyses ARB MABL MEGA	Bioinformatician	Intermediate	https://scgc.bigelow.org/resources/#br=useful_links	HTML	On-demand	Online	Self-paced	Free		Single Cell Genomics Center, Bigelow Laboratory for Ocean Sciences												
Microbial Genomics and Infectious Diseases	Microbiology	Microbial/Infectious Diseases Genomics	The ninth article in the New England Journal of Medicine series examining the past 10 years of accomplishments in screening, preventing and treating disease - Microbial Genomics and Infectious Diseases by David A. Relman, M.D. - discusses how advances in genomic technologies have permitted a better understanding of the biology of microbes, pathogenic or benign, and the effects of genomic information on our understanding of and response to microbial infections.	Bioinformatician	Introductory	http://www.nejm.org/doi/full/10.1056/NEJMra1003071	Article	On-demand	Online	Self-paced	Free		New England Journal of Medicine												

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Avaliable	Notes
New England Journal of Medicine Series on Genomic Medicine	**Comparative Genomics**	Genomics	The publication of the draft sequence of the human genome in 2000 heralded the promise of incorporating genomic knowledge into patient care. Ten years later, a new series of articles, beginning with the August 26, 2010 issue of the New England Journal of Medicine, is taking a comprehensive look at what has been accomplished in the quest to screen, prevent and treat disease in the new world of genomic medicine. These articles were published from 2010 to 2012. The series is edited by W. Gregory Feero, M.D., Ph.D., former special advisor to the director for genomic medicine, National Human Genome Research Institute, and Alan E. Guttmacher, M.D., director of the National Institute of Child Health and Human Development. Articles include: • Genomic Medicine: An Updated Primer • GWAS and Assessment of the Risk of Disease • New Therapeutic Approaches to Mendelian Disorders • Ancestry and Disease in the Age of Genomic Medicine • Genomics, Type 2 Diabetes, and Obesity • Genomics and the Continuum of Cancer Care • Genomics and Drug Response • Genomics and the Eye • Microbial Genomics and Infectious Diseases • Genomics, Health Care, and Society • Genomics and the Multifactorial Nature of Human Autoimmune Disease • Genomics of Cardiovascular Disease • Genomics and Perinatal Care • Genomics, Intellectual Disability, and Autism • An Editorial: Realizing Genomic Medicine	Bioinformatician	Introductory	http://www.genome.gov/27541912#al-9	Article	On-demand	Online	Self-paced	Free		New England Journal of Medicine												
What's Bugging You? The Intersection of Genomics and Infectious Disease	**Microbiology**	Microbial/Infectious Diseases Genomics	Genomics has revolutionized the tools used by clinicians to detect and treat infectious diseases. By sequencing the human microbiome, researchers have identified scores of previously unidentified species, which coexist with their human host, and exploration has begun to understand how disease states alter the host microbial flora. Genomic-based diagnostic testing is more rapid and accurate than traditional cultures, and dramatically changed the clinician and public health approach to sexually transmitted and hospital-acquired infections. Diseases like HIV and hepatitis C are managed using direct measures of viral burden, determined by genomics. Finally, microbial genomics has had a key role in understanding and responding to increased antibiotic resistance. Learning objectives: 1. Describe the human microbiome and its role in human health and disease. 2. Review the role of genomics based diagnostic testing in detecting infections. 3. Describe the impact of microbial and viral genomics in managing HIV, hepatitis C and other infections. 4. Review case studies of the role of genomics in epidemic investigations and understanding new pathogens. Jonathan Zenilman, M.D., Chief, Infectious Diseases Division, Johns Hopkins University, Bayview Medical Center	Bioinformatician	Introductory	http://www.genome.gov/27546022	Video, slides	On-demand	Online	1 hr 5 min	Free		Johns Hopkins												
Case Studies in Reproducible Research in Bioinformatics and Other Disciplines	**Reproducible Research**		This web page was created to provide convenient links to resources on reproducible research in bioinformatics. The term "reproducible research" is taken as a primitive to refer to a scheme of conducting and publishing quantitative research. Hallmarks of the scheme are: • publication of versioned instances of numerical and textual data and metadata underlying quantitative analyses; • publication of computer program code used to generate numerical summaries and statistical reports; • publication of documentation that links the programming task results to analytical report elements; • reasonable support for consumers of research who wish to recreate and, possibly, enhance published research findings. • It is clear that reproducible research activities involve considerable bookkeeping and coordination efforts for producers, and may require nontrivial computational resources and skills for consumers. It is also worth noting that the distinction between research producer and consumer is not always clear; adoption of reproducible research disciplines is often found to be useful in research production, regardless of the impact on research consumers, principally through auditing and archiving practices that support concrete reproducibility. It would be useful to establish categories of best practices in quantitative scientific work that contribute to efficiencies of reproducible research for both producers and consumers of research artifacts. The resources linked on this page represent concrete instances of reproducible research discipline, and literature describing the discipline. • Work of Coombs and Baggerly of M.D. Anderson Cancer Center shows how published reports can be carefully examined for validity; they use reproducible research discipline to document difficulties encountered in reproducing published findings. • Work of Gentleman and Temple Lang defines workflows and components for creating reproducible research artifacts. A link is included to Gentleman's compendium for the reproduction of a classic microarray analysis. • Work of Peng and colleagues constitutes a compendium for a large-scale epidemiologic study of air pollution and mortality. • Work and sites created in other disciplines is collected in the final link.	Bioinformatician	Introductory	http://www.hsph.harvard.edu/carey/REPRO/	HMTL, articles	On-demand	Online	Self-paced	Free		V. J. Carey, Harvard University												
Forum: Reproducible Research in High-Throughput Biology: Case Studies in Forensic Bioinformatics	**Reproducible Research**		A well delivered, highly entertaining lecture on the importance of reproducible research in high-throughput biology. Keith Baggerly walks us through an exercise in 'forensic bioinformatics.' Those with bioinformatics experience may find it entertaining and cringe inducing. Those new to the new field may find it illuminating and educational on the topics of classification, principle component analysis, gene expression estimation, etc. The data and analysis being dissected relate to the now famous Duke/Potti controversy described by the New York Times, 60 minutes and others in which the work of Biostatisticians Keith Baggerly and Kevin Coombes ultimately led to the retraction of ten papers by Potti, and the cancellation of clinical trials. A recent Nature article provides a follow-up and guidance for uncovering research misconduct. An interesting case study on the importance of being able to reproduce complicated computational analyses, how some very problematic work from an otherwise productive and potentially useful area of research (personalized chemotherapy prediction) went horribly wrong, and how we might use this experience to promote transparent, open source, and reproducible research in bioinformatics. For example, by using things like 'Sweave.'	Bioinformatician	Introductory	http://videolectures.net/cancerbioinformatics2010_baggerly_irrh/	Video, slides	On-demand	Online	30 min	Free		Keith Baggerly, M. D. Anderson Cancer Center												
Rosalind Python Village	**Languages**	**Python**	Rosalind is a platform for learning bioinformatics and programming through problem solving. You must establish a free account to log in. If you don't know anything about programming, you can start at the Python Village. For a collection of exercises to accompany Bioinformatics Algorithms book, go to the Textbook Track. Otherwise you can try to storm the Bioinformatics Stronghold right now. Python Village If you are completely new to programming, try these initial problems to learn a few basics about the Python programming language. You'll get familiar with the operations needed to start solving bioinformatics challenges in the Stronghold. Problem Titles Installing Python Variables and Some Arithmetic Strings and Lists Conditions and Loops Working with Files Dictionaries	Bioinformatician	Introductory	http://rosalind.info/problems/list-view/?location=python-village	Computer Exercises	On-demand	Online	Self-paced	Free		Rosalind												
Rosalind Bioinformatics Stronghold			Rosalind is a platform for learning bioinformatics and programming through problem solving. You must establish a free account to log in. If you don't know anything about programming, you can start at the Python Village. For a collection of exercises to accompany Bioinformatics Algorithms book, go to the Textbook Track. Otherwise you can try to storm the Bioinformatics Stronghold right now. Bioinformatics Stronghold Discover the algorithms underlying a variety of bioinformatics topics: computational mass spectrometry, alignment, dynamic programming, genome assembly, genome rearrangements, phylogeny, probability, string algorithms and others. Problem Titles Counting DNA Nucleotides Transcribing DNA into RNA Complementing a Strand of DNA Rabbits and Recurrence Relations Computing GC Content Counting Point Mutations Mendel's First Law Translating RNA into Protein	Bioinformatician	Introductory	http://rosalind.info/problems/list-view/	Computer Exercises	On-demand	Online	Self-paced	Free		Rosalind												
Rosalind Bioinformatics Armory			Rosalind is a platform for learning bioinformatics and programming through problem solving. You must establish a free account to log in. If you don't know anything about programming, you can start at the Python Village. For a collection of exercises to accompany Bioinformatics Algorithms book, go to the Textbook Track. Otherwise you can try to storm the Bioinformatics Stronghold right now. Bioinformatics Armory Ready-to-use software tools abound for bioinformatics analysis. Whereas in the Stronghold you implement algorithms on your own, in the Armory you solve similar problems by using existing tools Problem Titles Introduction to Protein Databases GenBank Introduction Data Formats New Motif Discovery Pairwise Global Alignment FASTQ format introduction Read Quality Distribution Protein Translation	Bioinformatician	Introductory	http://rosalind.info/problems/list-view/?location=bioinformatics-armory	Computer Exercises	On-demand	Online	Self-paced	Free		Rosalind												

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Row	Title	Topic	Keywords (Filter or Search)	Course Description
299	Rosalind Bioinformatics Textbook Track			Rosalind is a platform for learning bioinformatics and programming through problem solving. You must establish a free account to log in. If you don't know anything about programming, you can start at the Python Village. For a collection of exercises to accompany Bioinformatics Algorithms book, go to the Textbook Track. Otherwise you can try to storm the Bioinformatics Stronghold right now. Bioinformatics Textbook Track A collection of exercises to accompany Bioinformatics Algorithms: An Active-Learning Approach by Phillip Compeau & Pavel Pevzner. A full version of this text is hosted on stepic.org. Problem Titles Reverse Complement Problem Pattern Matching Problem Clump Finding Problem Minimum Skew Problem Approximate Pattern Matching Problem Frequent Words with Mismatches Problem Frequent Words with Mismatches and Reverse Complements Problem Protein Translation Problem
300	Rosalind Algorithmic Heights	Computer Science	Algorithms	Rosalind is a platform for learning bioinformatics and programming through problem solving. You must establish a free account to log in. If you don't know anything about programming, you can start at the Python Village. For a collection of exercises to accompany Bioinformatics Algorithms book, go to the Textbook Track. Otherwise you can try to storm the Bioinformatics Stronghold right now. Algorithmic Heights A collection of exercises in introductory algorithms to accompany "Algorithms", the popular textbook by Dasgupta, Papadimitriou, and Vazirani. Problem Titles Fibonacci Numbers Binary Search Degree Array Insertion Sort Double-Degree Array Majority Element Merge Two Sorted Arrays 2SUM Breadth-First Search
301	Emacs + org-mode + Python in Reproducible Research: SciPy 2013 Presentation	Reproducible Research	Python; Emacs; org-mode	The author presents his solution to tracking big data projects
302	Reproducible Research	Statistics; Languages; Reproducible Research	R	This Johns Hopkins course is offered through Coursera. Recommended background: • Some programming experience (in any language) • Working knowledge of mathematics and algebra (neither calculus or linear algebra are required) Data Science Specialization Certificate: • This course may be taken as a free stand-alone course, or as part of the Data Science specialization certificate (https://www.coursera.org/specialization/jhudatascience/1?utm_medium=courseDescripTop). • It is recommended, but not necessary, to take the courses in order. • To obtain the specialization certificate, you must complete 9 courses ($49 each). The cost to complete the 9 courses for the certificate is $470. The courses are offered multiple times a year. • Completion of a Data Science Capstone project is required to earn the specialization certificate. Course 5 in Data Science Specialization Certificate: Reproducible Research Duration: 4 weeks Estimated Workload: 4-9 hours/week In this course you will learn to write a document using R markdown, integrate live R code into a literate statistical program, compile R markdown documents using knitr and related tools, and organize a data analysis so that it is reproducible and accessible to others. The lectures from a past offering of this course are also on YouTube. Search "Roger Peng reproducible research" to retrieve all 15 lectures. Johns Hopkins also offers a Genomics Data Science Specialization Certificate through Coursera.
303	JGI Microbial Genomics & Metagenomics Workshop	Microbiology	Microbial/Infectious Diseases Genomics; Metagenomics	The U.S. Department of Energy Joint Genome Institute (DOE JGI) will be offering two five-day workshops on Microbial Genomics and Metagenomics during 2015. Each workshop will have a similar agenda and content, and will include seminars and extensive hands-on tutorials on how to use the IMG family of systems for comparative analysis of isolate genomes and metagenomes. Our goal is to provide you with training in microbial genomic and metagenomic analysis and demonstrate how the cutting-edge science and technology of DOE JGI can enhance your research.
304	An Introduction to Metagenomics Data Analysis	Metagenomics	Metagenomics	Vall d'Hebron Institut de Recerca's (VHIR) Metagenomics Training. Session 1. 2013/08/26. An Introduction to Metagenomics Data Analysis Outline Introduction to Metagenomics Basic Terminology Computational Approaches & Tools ☐ Whole Genome Shotgun 16S/ITS Community Surveys Recommended Tools ☐ MEGAN ☐mothur ☐QIIME ☐AXIOME & CloVR
305	Introduction to Metagenomics. Applications, Approaches and Tools (Bioinformatics for Biological Researchers Course - CSIC, Blanes)	Metagenomics		Vall d'Hebron Institut de Recerca (VHIR) 05/28/2014 Applications Basic Concepts Approaches & Workflows 1. Whole Genome Shotgun 2. 16S/ITS Community Surveys Analysis Tools 1. MEGAN 2. Mothur 3. Qiime 4. Axiome & CloVR 5. MG-RAST
306	Tools for Metagenomics with 16S/ITS and Whole Genome Shotgun Sequences	Metagenomics	16S/ITS; Whole Genome Shotgun Sequences	Presented at Cornell Symbiosis symposium. Workflow for processing amplicon based 16S/ITS sequences as well as whole genome shotgun sequences are described. Slides include short description and links for each tool.
307	Single-Cell Genomics		Single Cell Genomics; Fluidigm	17 collected videos on single-cell genomics, single-cell mRNA sequencing, single-cell gene expression, and other scientific applications performed on the Fluidigm C1 Single-Cell Auto Prep System.
308	Single Cell Research: An Overview of Recent Single Cell Research Publications Featuring Illumnia Technology		Single Cell Genomics; Illumina	This report was compiled by Illumina to market their technology, but it does contain some interesting information. Contents Applications Sample Preparation Data Analysis DNA Applications Epigenetics RNA Applications
309	UNIX Tutorial for Beginners	Languages	Unix; Linux	Introduction to the UNIX Operating System What is UNIX? Files and processes The Directory Structure Starting an UNIX terminal Tutorial One Listing files and directories Making Directories Changing to a different Directory The directories . and .. Pathnames More about home directories and pathnames Tutorial Two Copying Files Moving Files Removing Files and directories Displaying the contents of a file on the screen Searching the contents of a file Tutorial Three Redirection Redirecting the Output Redirecting the Input Pipes Tutorial Four
310	Bioconductor Courses and Conferences	Languages	Bioconductor	This is a list of courses and conference presentations on Bioconductor. Many of the links lead to course materials such as slides
311	Google Developers ' R Programming Video Lectures	Statistics; Languages	R	These videos provide a solid foundation for programming tools, data manipulation, and functions in the R language and software. The series of short videos is organized into four subsections: intro to R, loading data and more data formats, data processing and writing functions.
312	De Novo Genome Assembly	Comparative Genomics	Genome Assembly	Lex Nederbragt at the Norwegian Sequencing Center put together this course on de novo genome assembly and released all the course materials on Github under Creative Commons/Public Domain. Course material includes slideshow presentations and exercises (in the practicals directory), which give code examples from everything from quality control, assembly, and assembly evaluation.

Title	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters /PhD Program	Non-Degree Option Avaliable	Notes
Rosalind Bioinformatics Textbook Track	Bioinformatician	Introductory	http://rosalind.info/problems/list-view/?location=bioinformatics-textbook-track	Computer Exercises	On-demand	Online	Self-paced	Free		Rosalind												
Rosalind Algorithmic Heights	Bioinformatician	Introductory	http://rosalind.info/problems/list-view/?location=algorithmic-heights	Computer Exercises	On-demand	Online	Self-paced	Free		Rosalind												
Emacs + org-mode + Python in Reproducible Research: SciPy 2013 Presentation	Bioinformatician	Intermediate	https://www.youtube.com/watch?v=1-dUkyn_fZA	Video	On-demand	Online	21 min	Free		John Kitchen, Carnegie Mellon University												
Reproducible Research	Bioinformatician	Intermediate	https://www.coursera.org/course/repdata	Coursera course	July 6 to August 1, 2015; see schedule on website	Online	4 weeks, 4-9 hours/week	Free or can pay for certificate, $49 per course or $470 for 9 course certificate		Johns Hopkins on Coursera									Coursera certificate			
JGI Microbial Genomics & Metagenomics Workshop	Bioinformatician	Intermediate	http://mgm.jgi.doe.gov/	Lecture, Computer Exercises	September 14-18, 2015	Walnut CreekCA	5 days	425		U.S. Department of Energy Joint Genome Institute	Casey Rundles			CJRundles@lbl.gov		Walnut Creek	CA					
An Introduction to Metagenomics Data Analysis	Bioinformatician	Intermediate	http://www.slideshare.net/ueb52/bbr-31introduction-to-metagenomics?related=2	Slides	On-demand	Online	Self-paced	Free		Vall d'Hebron Institut de Recerca (VHIR)	Ferran Brianso			Ferran.Brianso@vhir.org								
Introduction to Metagenomics. Applications, Approaches and Tools (Bioinformatics for Biological Researchers Course - CSIC, Blanes)	Bioinformatician	Intermediate	http://www.slideshare.net/ueb52/bbr-31introduction-to-metagenomics?related=2	Slides	On-demand	Online	Self-paced	Free		Vall d'Hebron Institut de Recerca (VHIR)	Ferran Brianso			Ferran.Brianso@vhir.org								
Tools for Metagenomics with 16S/ITS and Whole Genome Shotgun Sequences	Bioinformatician	Intermediate	http://www.slideshare.net/suryasaha/surya-saha-metagenomics-tools?related=1	Slides	On-demand	Online	Self-paced	Free		Cornell University	Surya Saha	Research Associate/Bioinformatics Analyst										
Single-Cell Genomics	Bioinformatician	Intermediate	https://www.youtube.com/playlist?list=PL2C0B6CDF0716C47A	Video	On-demand	Online	Self-paced	Free		Fluidigm												
Single Cell Research: An Overview of Recent Single Cell Research Publications Featuring Illumnia Technology	Bioinformatician	Intermediate	http://www.illumina.com/content/dam/illumina-marketing/documents/products/research_reviews/single-cell-sequencing-research-review.pdf	Article	On-demand	Online	Self-paced	Free		Illumina												
UNIX Tutorial for Beginners	Bioinformatician	Introductory	http://www.ee.surrey.ac.uk/Teaching/Unix/	HTML	On-demand	Online	Self-paced	Free		University of Surrey	Michael Stonebank			m.stonebank@surrey.ac.uk								
Bioconductor Courses and Conferences	Bioinformatician	Intermediate	http://bioconductor.org/help/course-materials/	HTML	On-demand	Online	Self-paced	Free		Bioconductor												
Google Developers ' R Programming Video Lectures	Bioinformatician	Introductory	https://www.youtube.com/watch?v=iffR3fWv4xw&list=PLOU2XLYxmsIK9qQfztXeybpHvru-TrqAP	Video	On-demand	Online	Self-paced	Free		Google Developers												
De Novo Genome Assembly	Bioinformatician	Intermediate	https://github.com/lexnederbragt/	PDF	On-demand	Online	Self-paced	Free		University of Oslo	Lex Nederbragt											

Back to Brief View

Course Details for Advanced Molecular Detection and Bioinformatics Training Opportunities

Title	Topic	Keywords (Filter or Search)	Course Description	Audience: Laboratorian, Bioinformatician, Epidemiologist	Level (Introductory, Intermediate, Advanced)	Webpage	Format (Lecture, Online, etc.)	Date of Course	Location of Course	Duration of Course	Cost	Mechanism	Sponsor/Offerer/ Vendor	Vendor Contact Person	Title of Contact Person	Vendor Phone Number	Vendor Email/Contact Webpage	Vendor Street Address	Vendor City	Vendor State	Vendor Zip Code	Continuing Education Credit	Graduate Certificate/Masters/PhD Program	Non-Degree Option Available	Notes
Bioinformatics for Cancer Genomics (BICG) (2014)		Pathway Analysis; Cancer Genomics	Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. Cancer research has rapidly embraced high throughput technologies into its research, using various microarray, tissue array, and next generation sequencing platforms. The result has been a rapid increase in cancer data output and data types. Now more than ever, having the informatic skills and knowledge of available bioinformatic resources specific to cancer is critical. The CBW has developed a 5-day workshop covering the key bioinformatics concepts and tools required to analyze cancer genomic data sets. Participants will gain experience in genomic data visualization tools which will be applied throughout the development of the skills required to analyze cancer-omic data for gene expression, genome rearrangement, somatic mutations and copy number variation. The workshop will conclude with analyzing and conducting pathway analysis on the resultant cancer gene list and integration of clinical data. Target Audience This workshop is developed for clinical researchers, research scientists, post-doctoral fellows, and graduate students with cancer genomics research projects. Prerequisite: UNIX and R familiarity is required. Familiarity can be gained through online activities. You should be familiar with theseUNIX concepts (tutorial 1-2) and these R concepts (chapters 1-5)or review the past Statistics tutorials provided by CBW.	Bioinformatician	Intermediate	http://bioinformatics.ca/workshops/2014	Slides, PDF, MP4	On-demand	Online	Self-paced	Free		Bioinformatics.ca												
Exploratory Analysis of Biological Data Using R (2014)	Statistics; Languages	R	Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. Before we can begin to apply rigorous statistical tools to research data, we often need to approach our data intuitively, and look for meaningful associations, surprising patterns, or irregularities, to formulate hypotheses. This is commonly referred to as Exploratory Data Analysis–EDA. This workshop introduces the essential tools and strategies that are available through the free statistical workbench R. Participants should be able to modify the scripts and protocols we discuss for their research tasks, identify potential problems with their own data, and define their statistics needs for cases in which expert advice is required. Case studies with common research scenarios such as microarray data, and flow cytometry will emphasize practical skills. Writing your own R functions and analysis scripts will be introduced at the beginning of the workshop and skills will be gradually built on over the course of the lectures. Plotting and visualization is a key element of EDA and we will gradually build skills-from the elementary built-in routines via their (sometimes bewildering) array of parameters to sophisticated, publication-ready presentations. Target Audience Graduates, postgraduates and PIs who need to design and execute strategies for data analysis but have little or no formal prior training in statistics and /or familiarity with the R statistical workbench. Prerequisites: You need to complete our introductory R tutorial for the course beforehand. Please navigate to: Quick and Dirty Guide to R and complete up to and including "Descriptive Statistics". You need to spend some time with the tutorial – unless you are already a seasoned R expert – since this workshop is an introduction to data wrangling, not an R course per se. If you feel you would profit from a more in-depth introduction, we are offering an Introduction to R Workshop on the day before this one.	Bioinformatician	Intermediate	http://bioinformatics.ca/workshops/2014	Slides, PDF, MP4	On-demand	Online	Self-paced	Free		Bioinformatics.ca												
Informatics on High-Throughput Sequencing Data (2014)			Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. With the introduction of high-throughput sequencing platforms from Illumina, Roche and ABI, it is becoming feasible to consider sequencing approaches to address many research projects. However, knowing how to manage and interpret the large volume of sequence data resulting from such technologies is less clear. The CBW has developed a 2-day course covering the bioinformatics tools available for managing and interpreting high-throughput sequencing data. Beginning with an understanding of the workflow involved to move from platform images to sequence generation, participants will gain practical experience and skills to be able to • Assess sequence quality • Map sequence data onto a reference genome • Quantify sequence data • Integrate biological context with sequence information Target Audience This workshop is intended for graduate students, post-doctoral fellows, clinical fellows and investigators involved in analyzing data from HT sequencing platforms. Prerequisite: UNIX familiarity is required. Familiarity can be gained through online activities. You should be familiar with these UNIX concepts (tutorial 1-3).	Bioinformatician	Intermediate	http://bioinformatics.ca/workshops/2014	Slides, PDF, MP4	On-demand	Online	Self-paced	Free		Bioinformatics.ca												
Informatics and Statistics for Metabolomics (2014)	Metabolomics; Statistics		Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. The workshop will cover many topics ranging from understanding metabolomics technologies, data collection and analysis, using pathway databases, performing pathway analysis, conducting univariate and multivariate statistics, working with metabolomic databases and exploring chemical databases. Participants will be given various data sets and short assignments to assist with the learning process. Target Audience This course is intended for graduate students, post-doctoral fellows, clinical fellows and investigators who are interested in learning about both bioinformatic and cheminformatic tools to analyze and interpret metabolomics data. Prerequisite: Familiarity with R is required. Familiarity can be gained through online activities. You should be familiar with these R concepts (chapters 1-5) or review the past Statistics tutorials provided by CBW.	Bioinformatician	Intermediate	http://bioinformatics.ca/workshops/2014	Slides, PDF, MP4	On-demand	Online	Self-paced	Free		Bioinformatics.ca												
High-Throughput Biology: From Sequence to Networks (2015)			Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. *** The materials from the 2015 courses are anticipated to be placed on the website in 2016. With the introduction of next generation sequencing platforms, it is becoming feasible to consider sequencing approaches to address many research projects. Now more than ever, having knowledge of the available bioinformatic resources and the informatic skills to analyze such data is critical. The Canadian Bioinformatics Workshops, in collaboration withCold Spring Harbor and New York Genome Center, has developed a comprehensive 7-day course covering the key bioinformatics concepts and tools required to analyze DNA- and RNA-sequence reads using a reference genome. Participants will gain experience in cloud computing and data visualization tools, which will be applied throughout the course. Beginning with an understanding of the workflow involved to move from platform images to sequence generation, participants will gain practical experience and skills to be able to evaluate sequence read quality, map reads to a reference and analyze sequence reads for variation and expression level. The workshop will conclude with analyzing and conducting pathway and network analysis on the resultant 'gene' list. The tutorials are designed as self-contained units that include example data (e.g. Illumina paired-end data) and detailed instructions for installation of all required bioinformatics tools. Target Audience Graduates, postgraduates and PIs working with or about to embark on analysis of data from next generation sequencing platforms (Illumina focus). A reference genome is required. Prerequisites for attendance: Basic familiarity with Linux environment and S, R, or Matlab. Must be able to complete and understand the following simple Linux and R tutorials before attending: • Linux Guide for Beginners • Quick & Dirty Guide to R	Bioinformatician	Intermediate	http://bioinformatics.ca/workshops/2015	Slides, PDF, MP4	On-demand	Online	Self-paced	Free		Bioinformatics.ca												
Introduction to R (2015)	Languages	R	Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. ***The materials from the 2015 courses are anticipated to be placed on the website in 2016. R is rapidly becoming the most important scripting language for both experimental- and computational biologists. It is well designed, efficient, widely adopted and has a very large base of contributors who add new functionality for all modern aspects of data analysis and visualization. Moreover it is free and open source. However, R's great power and expressivity can at first be difficult to approach without guidance, especially for those who are new to programming. This workshop introduces the essential ideas and tools of R. We will work in a problem-based scenario in which we analyze a real world challenge in data handling. As we break down the problem into structured parts, we explore R syntax, functions and packages – and in general explore best practices for scientific computational work. Target Audience Graduates, postgraduates and PIs who design and execute strategies for data analysis but have little or no familiarity with the R statistical workbench. This workshop is designed to lead on to the two-day workshop on Exploratory Data Analysis, which follows it.	Bioinformatician	Intermediate	http://bioinformatics.ca/workshops/2015	Slides, PDF, MP4	On-demand	Online	Self-paced	Free		Bioinformatics.ca												
Microarray Expression Analysis (2015)	Expression Analysis	Microarrays	Bioinformatics.ca offers one- and two-week short courses in bioinformatics. Course materials from the previous year's workshops, available under a Creative Commons license, are placed on their website. ***The materials from the 2015 courses are anticipated to be placed on the website in 2016. Microarrays remain the most popular, most affordable, and best-established technique for functional genomics. Hundreds of thousands of datasets have been generated to address diverse aspects of biology. This workshop provides an overview of the analysis of microarray data ranging in size from one to two samples to hundreds of samples. The goal of this workshop is to provide procedures and analysis workflows for the analysis of microarray datasets. Discussions will include data-organization practices, data-annotation, normalization, pre-processing, and (briefly) downstream analysis. Comparison and data mining of results from different microarray datasets will also be discussed. This workshop provides an ideal entry to the "Pathway and Network Analysis of –omics Data " workshop. Target Audience This workshop is aimed at researchers who are working with mRNA expression microarray data and focuses on the popular Affymetrix platforms. However, many of the algorithms and techniques discussed will be applicable to non-mRNA and non-Affymetrix datasets. All practical analysis will employ the R statistical environment, with a combination of custom scripts and BioConductor libraries. Prerequisites: UNIX and R familiarity is required. Familiarity can be gained through online activities. You should be familiar with theseUNIX concepts (tutorial 1-3) and these R concepts (chapters 1-5) or review the past Statistics tutorials provided by CBW.	Bioinformatician	Intermediate	http://bioinformatics.ca/workshops/2015	Slides, PDF, MP4	On-demand	Online	Self-paced	Free		Bioinformatics.ca												
http://bioinformatics.ca/workshops/2014						http://bioinformatics.ca/workshops/2014	Slides, PDF, MP4	On-demand	Online	Self-paced	Free		Bioinformatics.ca												
http://bioinformatics.ca/workshops/2014						http://bioinformatics.ca/workshops/2014	Slides, PDF, MP4	On-demand	Online	Self-paced	Free		Bioinformatics.ca												