Walking through Nextstrain trees

COVID-19 Genomic Epidemiology Toolkit: Module 3.4

Krisandra Allen, MPH, MB(ASCP)
Molecular Epidemiologist
Washington State Department of Health
Part 1: Introduction

1.1 What is genomic epidemiology?
1.2 The SARS-CoV-2 genome
1.3 How to read phylogenetic trees
1.4 Emerging variants of SARS-CoV-2

Part 2: Case Studies

2.1 SARS-CoV-2 sequencing in Arizona
2.2 Healthcare cluster transmission
2.3 Community transmission

Part 3: Implementation

3.1 Getting started with Nextstrain
3.2 Getting started with MicrobeTrace
3.3 Phylogenetics with UShER
3.4 Walking through Nextstrain trees
What is Nextstrain?

- Powerful analytics and interactive visualization tool (Module 3.1)
  - Designed to aid epidemiological understanding, improve outbreak response, and provide real-time snapshots of evolving pathogen populations

- Currently used to support SARS-CoV-2 genomic epidemiology at local, state, and national levels

- Many SARS-CoV-2 builds available to the public
  - https://nextstrain.org/sars-cov-2/
  - https://nextstrain.org/groups/spheres
Complex phylogenetic trees
Tree Terminology

Genetic Distance
Live - Demo

- Tutorial MetaData File - demo_metadata.tsv (URL)
- Tutorial Newick File - https://nextstrain.org/groups/blab/ncov/tutorial
Locate Tips of Interest using the 'Filter' Function
Locate Tips of Interest using the 'Filter' Function
Locate Individual Outbreaks using 'Color By' Function
Advanced Functionality - Combining filters
Advanced Functionality - Changing Tip Labels on a Zoomed-in View
Advanced Functionality - Switching Between Time and Divergence Trees
Exporting filtered data

- After sequences of interest are selected on the tree, they can be exported for additional exploratory analyses in tools such as MicrobeTrace and auspice.us
Interoperability with Auspice.us and MicrobeTrace

- Exported filtered data viewed in Auspice.us or MicrobeTrace for different perspectives

https://auspice.us/
Summary

- NextStrain can assist exploration of genomic and epidemiologic data
  - Filtering, sorting, zooming, and overlaying

- Complete trees or filtered datasets can be exported
  - Analysis and visualization with other tools, such as MicrobeTrace and Auspice.us
Module 3.4 Hands-On Material

- NextStrain Tutorial
  - https://nextstrain.org/groups/blab/ncov/tutorial

- Metadata File
  - Module 3.4 - demo_metadata.tsv
Learn more

- Other modules in Part 3: Implementation
  - Getting Started with Nextstrain—Module 3.1
  - Getting Started with MicrobeTrace—Module 3.2
  - Phylogenetics with USHER—Module 3.3

- COVID-19 Genomic Epidemiology Toolkit
  - Find further reading
  - Subscribe to receive updates on new modules as they are released
  - go.usa.gov/xAbMw
For more information, contact CDC
1-800-CDC-INFO (232-4636)

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.