



Antimicrobial Resistance (AR) Option Benchmark Metrics: Standardized Resistant Infection Ratio (SRIR) & Pathogen-specific Standardized Infection Ratio (pSIR)

Erin O'Leary, MPH
Senior Data Analyst
Lantana Consulting Group

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Objectives

- Provide an overview of new AR Option benchmark metrics
- Describe methods used to develop SRIRs and pSIRs
- Describe statistical model details
- Interpret forthcoming SRIR and pSIR reports in NHSN

Overview of SRIRs and pSIRs

Overview

- We developed two new AR benchmark metrics in 2021/2022 using 2019 as the baseline year
 - SRIR: Standardized Resistant Infection Ratio
 - pSIR: pathogen-specific Standardized Infection Ratio
- Both are observed-to-predicted ratios (like SAARs, SIRs, SURs)

SRIR Overview

- **SRIRs** allow facilities to compare their number of observed hospital-onset* (HO) resistant infections for eligible phenotypes, to the number predicted, based on 2019 baseline risk-adjusted AR models

$$SRIR = \frac{\textit{Observed Resistant Infections}}{\textit{Predicted Resistant Infections}}$$

*Hospital-onset is defined as a specimen collected in an inpatient location on or after day 4 (where day 1 is date of admission)

Target SRIR Antimicrobial Resistant Phenotypes

- **Observed** resistant infections are the number of resistant HO isolates reported to NHSN for the following phenotypes*:
 - Carbapenem-resistant *Enterobacterales*
 - Extended-spectrum cephalosporin-resistant *Enterobacterales*
 - Fluoroquinolone-resistant *Enterobacterales*
 - Vancomycin-resistant *Enterococcus*
 - Fluoroquinolone-resistant *P. aeruginosa*
 - Multi-drug-resistant *P. aeruginosa*
 - Methicillin-resistant *S. aureus*
- **Predicted** resistant infections are the number of resistant HO isolates for a particular phenotype, predicted for a hospital based on negative binomial regression modeling applied to nationally aggregated 2019 AR data

*Phenotype definitions can be found in the AUR Module Protocol: <https://www.cdc.gov/nhsn/pdfs/pscmanual/11pscaurcurrent.pdf>

Criteria for Generating SRIRs

- Facility-wide SRIRs can be calculated for three specimen sources:
 - Blood
 - Urine
 - Lower respiratory tract (LRT)
- For a facility to calculate a SRIR, they must have reported:
 - At least one HO isolate for the eligible organism from the correct specimen source during the specified time period of interest
 - Example SRIR for 2022 Q3 Vancomycin-resistant *Enterococcus* in blood: the facility must report at least one HO *Enterococcus* from blood in month 7, 8, or 9 of 2022

pSIR Overview

- **pSIRs** allow facilities to compare their number of observed HO infections for eligible organisms, to the number predicted, based on 2019 baseline risk-adjusted AR models

$$pSIR = \frac{\textit{Observed Infections}}{\textit{Predicted Infections}}$$

Target pSIR Organisms

- **Observed** infections are the number of HO isolates reported to NHSN for the following four eligible pathogens/pathogen groups:
 - *Enterobacterales*
 - *Enterococcus*
 - *Pseudomonas aeruginosa*
 - *Staphylococcus aureus*
- **Predicted** infections are the number of HO isolates for a particular pathogen/pathogen group, predicted for a hospital based on negative binomial regression modeling applied to nationally aggregated 2019 AR data

Criteria for Generating pSIRs

- Facility-wide pSIRs can be calculated for three specimen sources:
 - Blood
 - Urine
 - Lower respiratory tract
- For a facility to calculate a pSIR, they must have reported:
 - At least one HO isolate (any organism) from the correct specimen source during the specified time period of interest
 - Example pSIR 2022 Q3 Enterococcus in blood: the facility must report at least one HO isolate from blood in month 7, 8, or 9 of 2022

Why were these metrics developed?

- SRIRs and pSIRs enable hospitals to compare their rates of resistant HO infections and HO infections to a national average
- Using incidence and prevalence instead of % susceptible for benchmarking minimizes the bias of selective/cascade antimicrobial susceptibility testing/reporting* in some hospitals
 - *<https://doi.org/10.1128/spectrum.01646-22>

How were phenotypes/organisms selected?

- Selected by a group of internal subject matter experts
- Target phenotypes were relatively common AR threats that could spread widely in hospital settings
 - Of interest to hospital infection prevention and antimicrobial stewardship programs
 - Benchmarking metrics for selected phenotypes can enable inter-facility comparisons
 - Rare AR phenotypes were not prioritized for benchmarking but worth investigating if seen in other NHSN reports

Methods used to develop SRIRs and pSIRs

Methods

- Data Sources:
 - 2019 AR Option data (reported as of August 2021)
 - 2019 Patient Safety Component Annual Survey data
- Level of aggregation for model development:
 - Facility-year

Exclusion criteria

- Exclusions:
 - Facilities reporting <9 months of AR data in 2019
 - Facilities missing patient days
 - Facilities reporting admissions=0*
 - For each specimen source type, facilities missing antimicrobial susceptibility results for >10% of HO isolates for the organism in question*
 - Records where susceptibility results were missing*

*SRIR models only

Facility-level factors assessed for risk adjustment

- Facility type
- Number of beds
- Number of ICU beds
- Percentage of ICU beds
- Medical school affiliation
- Medical school affiliation type (i.e., undergrad, grad, major teaching)
- Hospital length of stay (annual # patient days / annual # admissions)
- Community-onset (CO) prevalence* (# resistant CO isolates / 10,000 admissions)

*Only assessed in SRIR models

Source: NHSN Annual Hospital Survey; except CO prevalence which is calculated from AR Option data

Statistical modeling

- We used negative binomial regression to assess associations between rates of *resistant* HO infections and potential risk-factors (SRIR models) and rates of HO infections and potential risk-factors (pSIR models)
- Models were created for each phenotype (SRIR models) or pathogen/group of pathogens (pSIR models) for each specimen source (blood, lower respiratory tract, urine)
- This resulted in development of 21 SRIR models and 12 pSIR models
 - SRIRs: 7 phenotypes * 3 specimen sources = 21 models
 - pSIRs: 4 pathogens/pathogen groups * 3 specimen sources = 12 models

Referent population

- The number of hospitals included in each analytic dataset differs depending on which phenotype or pathogen the hospital reports from each specimen source type
- Facility types represented in 2019 AR data include: critical access, children's, general acute care, long-term acute care, oncology, psychiatric, inpatient rehabilitation, surgical, women's, and women's and children's hospitals
- Not all of these facility types are represented in the referent population for all models

Isolate summary for SRIR models

Pathogen	Drug-resistance	Specimen source	Number of facilities in analytic dataset	Number of drug resistant isolates	Number of tested isolates	Total patient-days	Pooled resistant isolate rate, per 1000 patient-days	Resistant isolate rate per 1000 patient-days, Median (Q1, Q3)
<i>Enterobacteriales</i> *	Carbapenem-resistant	Blood	181	91	2,370	12,977,061	0.007	0.000 (0.000, 0.000)
		LRT	203	190	5,641	13,924,473	0.014	0.000 (0.000, 0.015)
		Urine	241	168	12,596	14,367,796	0.012	0.000 (0.000, 0.009)
	Extended-spectrum cephalosporin-resistant	Blood	237	873	3,036	17,153,552	0.051	0.027 (0.000, 0.052)
		LRT	242	1,837	7,017	16,832,810	0.109	0.077 (0.031, 0.127)
		Urine	291	3,165	15,246	17,450,730	0.181	0.125 (0.057, 0.207)
	Fluoroquinolone-resistant	Blood	274	907	3,130	18,631,133	0.049	0.024 (0.000, 0.046)
		LRT	289	1,255	7,098	18,577,764	0.068	0.043 (0.016, 0.085)
		Urine	343	4,167	16,410	19,147,673	0.218	0.165 (0.082, 0.260)

*Enterobacteriales defined as *E. coli*, *Klebsiella pneumoniae*, *K. oxytoca*, and *Enterobacter* isolates. *Enterobacter* isolates includes *Enterobacter*, *Enterobacter aerogenes*, *Enterobacter amnigenus*, *Enterobacter asburiae*, *Enterobacter cancerogenus*, *Enterobacter cloacae*, *Enterobacter cloacae* complex, *Enterobacter cloacae* subspecies *dissolvens*, *Enterobacter hormaechei*, *Enterobacter intermedius*, *Enterobacter kobei*, *Enterobacter ludwigii*.

Isolate summary for SRIR models

Pathogen	Drug-resistance	Specimen source	Number of facilities in analysis dataset	Number of drug resistant isolates	Number of tested isolates	Total patient-days	Pooled resistant isolate rate, per 1000 patient-days	Resistant isolate rate per 1000 patient-days, Median (Q1, Q3)
<i>Enterococcus</i>	Vancomycin-resistant	Blood	232	478	1,405	17,949,216	0.027	0.011 (0.000, 0.027)
		LRT	115	45	321	10,135,289	0.004	0.000 (0.000, 0.008)
		Urine	317	1,425	6,183	19,480,228	0.073	0.035 (0.000, 0.085)
<i>Pseudomonas aeruginosa</i>	Fluoroquinolone-resistant	Blood	184	114	718	15,553,181	0.007	0.000 (0.000, 0.013)
		LRT	296	1,307	5,640	19,080,975	0.068	0.041 (0.000, 0.082)
		Urine	294	535	3,092	19,022,668	0.028	0.017 (0.000, 0.043)
	Multidrug-resistant	Blood	191	96	783	16,286,620	0.006	0.000 (0.000, 0.008)
		LRT	306	1,084	6,109	20,327,428	0.053	0.027 (0.000, 0.066)
		Urine	316	329	3,383	20,806,708	0.016	0.000 (0.000, 0.022)
<i>Staphylococcus aureus</i>	Methicillin-resistant	Blood	285	971	2,330	19,364,507	0.050	0.040 (0.018, 0.067)
		LRT	308	3,865	7,856	20,238,799	0.191	0.160 (0.085, 0.242)
		Urine	207	312	599	16,159,309	0.019	0.018 (0.000, 0.033)

Enterococcus includes *Enterococcus faecalis*, *Enterococcus faecium*, and *Enterococcus*

Isolate summary for pSIR models

Pathogen/Pathogen-Group	Specimen source	Number of facilities in analysis dataset	Number of isolates	Total patient-days	Pooled isolate rate, per 1000 patient-days	Resistant isolate rate per 1000 patient-days, Median (Q1, Q3)
<i>Enterobacterales</i>	Blood	352	3,557	22,026,801	0.161	0.169 (0.102, 0.223)
	LRT	353	8,399	21,694,825	0.387	0.257 (0.125, 0.430)
	Urine	389	19,035	22,073,214	0.862	0.723 (0.518, 1.007)
<i>Enterococcus</i>	Blood	352	1,527	22,026,801	0.069	0.034 (0.000, 0.066)
	LRT	353	399	21,694,825	0.018	0.000 (0.000, 0.016)
	Urine	389	6,854	22,073,214	0.311	0.229 (0.132, 0.373)
<i>Staphylococcus aureus</i>	Blood	352	2,524	22,026,801	0.115	0.093 (0.051, 0.140)
	LRT	353	8,161	21,694,825	0.376	0.271 (0.143, 0.415)
	Urine	389	633	22,073,214	0.029	0.016 (0.000, 0.037)
<i>Pseudomonas aeruginosa</i>	Blood	352	822	22,026,801	0.037	0.017 (0.000, 0.043)
	LRT	353	6,207	21,694,825	0.286	0.200 (0.104, 0.332)
	Urine	389	3,460	22,073,214	0.157	0.129 (0.052, 0.198)

Model details

High-level risk-adjustment summary

SRIR - Standardized Resistant Infection Ratio											
Pathogen	Drug-resistance	Specimen source	Facility type	Number of beds	Number of ICU beds	Percentage of ICU beds	Medical school affiliation	Affiliation type	Hospital length of stay	Community-onset prevalence	
<i>Enterobacteriales</i>	Carbapenem-resistant	Blood								✓	
		LRT							✓	✓	
		Urine							✓	✓	
	Extended-spectrum cephalosporin-resistant	Blood								✓	✓
		LRT			✓						✓
		Urine								✓	✓
	Fluoroquinolone-resistant	Blood			.					✓	✓
		LRT			✓						✓
		Urine								✓	✓
<i>Enterococcus</i>	Vancomycin-resistant	Blood							✓	✓	
		LRT*				.			.	.	
		Urine								.	✓
<i>Pseudomonas aeruginosa</i>	Fluoroquinolone-resistant	Blood								✓	
		LRT			.	✓				✓	
		Urine									✓
	Multidrug-resistant	Blood					✓				.
		LRT					.				✓
		Urine								.	✓
<i>Staphylococcus aureus</i>	Methicillin-resistant	Blood			✓				✓	✓	
		LRT							✓	✓	
		Urine					✓				✓

High-level risk-adjustment summary

pSIR - pathogen-specific Standardized Infection Ratio									
Pathogen/Pathogen-Group	Specimen source	Facility type	Number of beds	Number of ICU beds	Percentage of ICU beds	Medical school affiliation	Affiliation type	Hospital length of stay	Community-onset prevalence
<i>Enterobacterales</i>	Blood	.	.	✓				✓	n/a
	LRT	.	.	✓				.	n/a
	Urine	✓			.			✓	n/a
<i>Enterococcus</i>	Blood	.	✓	.				✓	n/a
	LRT	.	.	.				✓	n/a
	Urine	.	.		.			✓	n/a
<i>Staphylococcus aureus</i>	Blood	.	.	✓				✓	n/a
	LRT	.		✓				✓	n/a
	Urine	.		.	.			✓	n/a
<i>Pseudomonas aeruginosa</i>	Blood	.	.	✓				✓	n/a
	LRT	.	.	✓				.	n/a
	Urine	✓			.			✓	n/a

SRIR and pSIR reports in NHSN

SRIR and pSIR Reports

- We plan for SRIR and pSIR reports to be included in the NHSN application later this calendar year
- The release will add two new reports:
 - One with 21 SRIR tables
 - One with 12 pSIR tables
- Reports will default to facility-quarter level but will also be available at the half-year, year, and cumulative levels
- Once released, facilities that report eligible AR data will be able to generate SRIRs and pSIRs back to January 2019

Interpreting SRIR and pSIR values

- As ratios, SRIR and pSIR values are always greater than or equal to 0
- Similar to SIRs, lower values are considered better
- SRIR interpretations:
 - A value <1 indicates the rate of resistant HO infection was less than predicted
 - A value $=1$ indicates the rate of resistant HO infection was equal to predicted
 - A value >1 indicates the rate of resistant HO infection was greater than predicted
- pSIR interpretations:
 - A value <1 indicates the rate of HO infection was less than predicted
 - A value $=1$ indicates the rate of HO infection was equal to predicted
 - A value >1 indicates the rate of HO infection was greater than predicted

Example SRIR calculation

- Facility A reports 4 HO vancomycin-resistant *Enterococcus* (VRE) events in blood during Q1 of 2022
- 6 HO VRE events in blood are predicted for Facility A for Q1 of 2022
- Facility A's blood HO VRE SRIR for Q1 2022 would be calculated as:
 - $SRIR = 4 \text{ observed} / 6 \text{ predicted} = 0.667$
- SRIR interpretation: Facility A's number of hospital-onset vancomycin-resistant *Enterococcus* isolates from blood in Q1 of 2022 is 0.7 times what is predicted

Situations where a SRIR=0

- SRIR=0 indicates a facility reported the organism of interest from the specimen source of interest during the correct time period, but the organism was NOT resistant to the drug(s) specified
- For example, for HO VRE in blood, if a hospital reports 10 HO Enterococcus isolates from blood during the time of interest and all 10 are reported to be susceptible to vancomycin, the HO VRE blood SRIR would be 0 because there were 0 observed resistant infection events

Reasons a SRIR could be missing

- There were no specimens collected from the specimen source of interest during the time period of interest
- There were no organisms of interest isolated from the specimen source of interest during that time period
- The minimum precision criteria (for the number of predicted AR events) was not met
 - Minimum precision criteria: <0.3 predicted events

Example pSIR calculation

- Facility A reports 100 HO *Staphylococcus aureus* (SA) events in blood during 2022
- Facility A has 50 HO SA events in blood predicted for that year
- Their blood HO SA pSIR for 2022 would be calculated as:
 - $\text{pSIR} = 100 \text{ observed} / 50 \text{ predicted} = 2.000$
- pSIR interpretation: Facility A's number of hospital-onset *Staphylococcus aureus* isolates in blood in 2022 is 2 times what is predicted

pSIRs=0 and reasons a pSIR value could be missing

- Using the example of SA in blood, a pSIR=0 indicates a facility reported at least one blood specimen in 2022, but no SA was isolated
- Reasons a pSIR value could be missing:
 - There were no specimens collected from the specimen source of interest during the time period of interest
 - There were no HO isolates (any organisms) from the specimen source of interest during the time period of interest
 - The minimum precision criteria (for the number of predicted infections) was not met
 - Minimum precision criteria: <0.3 predicted events

Questions?

NHSN@cdc.gov

Thank you!

For more information, contact CDC
1-800-CDC-INFO (232-4636)
TTY: 1-888-232-6348 www.cdc.gov

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.

