THE NHSN STANDARDIZED RESISTANT INFECTION RATIO (SRIR) AND PATHOGEN-SPECIFIC STANDARDIZED INFECTION RATIO (pSIR)

A Guide to the SRIR and pSIR

Centers for Disease Control and Prevention
National Center for Emerging and Zoonotic Infectious Diseases

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Intended Audience

- This document serves as guidance for hospitals, health systems, and health departments interested in monitoring antimicrobial resistance (AR) and understanding what the Standardized Resistant Infection Ratio (SRIR) and Pathogen-specific Standardized Infection Ratio (pSIR) are, how the National Healthcare Safety Network (NHSN) develops SRIRs and pSIRs, and how they can use the SRIR and pSIR for intervention.
- The SRIR and the pSIR are risk-adjusted measures of AR and infections associated with specific pathogens. The SRIR and pSIR are available to acute care hospitals participating in the NHSN AR Option.
- Hospitals can use the SRIR to compare their rates of drug-resistant hospital-onset infections to a national benchmark and can use the pSIR to compare their rates of hospital-onset infections associated with specific pathogens to a national benchmark.
- Health systems and health departments can use the SRIR and pSIR to better understand these issues across and between facilities in their system or jurisdiction.

Overview of the Standardized Resistant Infection Ratio (SRIR) and the Pathogen-specific Standardized Infection Ratio (pSIR)

What is the Standardized Resistant Infection Ratio (SRIR)?

The SRIR is a metric developed by CDC to enable facilities to compare their rates of drug-resistant hospital-onset (HO)[a] infections to a national benchmark. In the NHSN AR Option, culture-positive AR Option Events are considered proxies for clinical infections. NHSN originally developed the metric in 2022, using national AR Option data reported in 2019, as a quantitative tool for hospitals, health systems, and health departments to make comparisons of AR within and across facilities and thereby help guide infection prevention and antimicrobial stewardship efforts. The SRIR compares observed resistant HO infections to predicted resistant HO infections for pathogens or pathogen groups resistant to specific drug categories identified in inpatient locations.

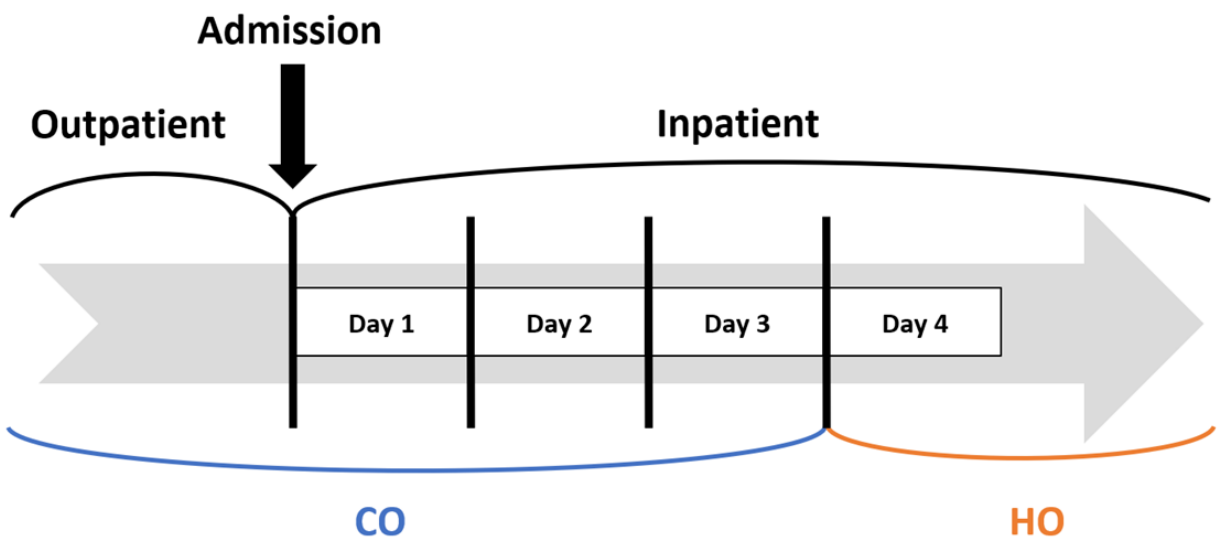
The SRIR can be generated for seven AR Option phenotypes from three specimen sources (blood, urine, and lower respiratory tract), for a total of 21 possible SRIRs (see Appendix A). The drug-resistant pathogens eligible for SRIR calculation were determined by CDC with input from external experts, including infectious disease physicians and pharmacists caring for adult, pediatric, and neonatal patients. The seven AR Option phenotypes are listed in Table 1 with their definitions.

Table 1. NHSN AR Option SRIR Phenotype Definitions

Phenotype Name	Phenotype Definition
Carbapenem-resistant Enterobacterales	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to at least one of the following: imipenem, meropenem, doripenem, ertapenem, meropenem/vaborbactam, or imipenem/relebactam
Extended-spectrum cephalosporin-resistant Enterobacterales	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to at least one of the following: cefepime, ceftriaxone, cefotaxime, ceftazidime, ceftazidime-avibactam, or ceftolozane-tazobactam
Fluoroquinolone-resistant Enterobacterales	Any *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp. that has tested resistant (R) to at least one of the following: ciprofloxacin, levofloxacin, or moxifloxacin
Vancomycin-resistant *Enterococcus*	Any *Enterococcus* spp. that has tested resistant (R) to vancomycin
Fluoroquinolone-resistant *Pseudomonas aeruginosa*	*Pseudomonas aeruginosa* that has tested resistant (R) to at least one of the following: ciprofloxacin or levofloxacin
Multidrug-resistant *Pseudomonas aeruginosa*	*Pseudomonas aeruginosa* that has tested either intermediate (I) or resistant (R) to at least one drug in at least three of the following six categories: 1. Extended-spectrum cephalosporin (cefepime, ceftazidime, ceftazidime-avibactam, ceftolozane-tazobactam) 2. Fluoroquinolones (ciprofloxacin, levofloxacin) 3. Aminoglycosides (amikacin, gentamicin, tobramycin) 4. Carbapenems (imipenem, meropenem, doripenem, imipenem/relebactam) 5. Piperacillin/tazobactam 6. Cefiderocol
Methicillin-resistant *Staphylococcus aureus*	*Staphylococcus aureus* that has tested resistant (R) to at least one of the following: oxacillin or cefoxitin

[a]**Note:** NHSN classifies AR Option Events as hospital-onset (HO) or community-onset (CO) based on the specimen collection date and date of admission (Figure 1). Facility admission date is considered Day 1. If the specimen was collected in an outpatient location or in an inpatient location on Days 1, 2, or 3, the AR Option Event is classified as CO. If the specimen was collected in an inpatient location on Day 4 or after, the AR Option Event is classified as HO.

Figure 1. How NHSN Classifies AR Option Events as Hospital-onset or Community-onset



How does NHSN calculate the SRIR?

NHSN calculates the SRIR by dividing the number of observed resistant HO infections by predicted resistant HO infections. NHSN calculates predicted resistant HO infections by risk-adjusting for facility-level factors and other risk factors found to be statistically significantly associated with rates of resistant infections among the SRIR referent population. The referent population comes from nationally aggregated AR Option data reported to NHSN during the baseline time period (2019).

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

- Observed Resistant Infections: The number of HO AR Option Events isolated from the specified specimen source that met the resistance definition for the specified AR Option phenotype and reported to the AR Option.
- Predicted Resistant Infections: The number of HO AR Option Events predicted for that same specimen source and AR Option phenotype. NHSN calculates the predicted number of resistant HO infections using risk-adjusted SRIR predictive models.

A SRIR greater than 1.0 indicates that a greater number of resistant HO infections were observed than predicted. A SRIR less than 1.0 indicates that fewer resistant HO infections were observed than predicted. A SRIR of 0 indicates a facility reported the HO pathogen of interest from the specimen source of interest during the correct time period, but the pathogen was not resistant to the drug(s) specified. For example, using the example of HO VRE in urine, if a hospital reports 10 HO *Enterococcus* isolates from urine during the time period of interest, and all 10 are reported to be susceptible to vancomycin, the HO VRE Urine SRIR would be 0 because there were 0 observed resistant infection events.

The NHSN application will not generate a SRIR value (*i.e.*, the SRIR will appear missing) when no HO isolates of the pathogen of interest were reported from the given specimen source during the time period, or a HO isolate of the pathogen of interest was reported from the given specimen source but <0.3 events were predicted (minimum precision criteria for the number of predicted antimicrobial-resistant infections was not met). Using the example of HO VRE in urine, a facility would receive a missing value for a SRIR if:

1. No HO *Enterococcus* was reported in a urine specimen or,
2. HO *Enterococcus* was reported from urine during the time period of interest but there were <0.3 HO VRE events predicted for that time period.

SRIRs for extended-spectrum cephalosporin-resistant Enterobacterales are not available to those facilities that reported "No" to the question "Has the laboratory implemented revised breakpoints recommended by CLSI for cephalosporin and monobactam breakpoints for Enterobacterales in 2010" in the NHSN Patient Safety Annual Hospital Survey for that year. SRIRs for carbapenem-resistant Enterobacterales are not available to those facilities that reported "No" to the annual hospital survey question "Has the laboratory implemented revised breakpoints recommended by CLSI for carbapenem breakpoints for Enterobacterales in 2010" for that year. For these two scenarios, the number of predicted resistant HO infections and the SRIR will appear missing when running the report in NHSN.

What is the pathogen-specific Standardized Infection Ratio (pSIR)?

Similar to the SRIR, the pSIR is a metric developed by CDC to enable facilities to compare their rates of HO infections associated with a specific pathogen to a national benchmark. The pSIR compares observed HO infections to predicted HO infections associated with specific pathogens or pathogen groups identified in inpatient locations.

The pSIR can be generated for four pathogens or pathogen groups from three specimen sources (blood, urine, and lower respiratory), for a total of twelve possible pSIRs (see Appendix B).

- Enterobacterales: includes *Escherichia coli, Klebsiella aerogenes, Klebsiella oxytoca, Klebsiella pneumoniae, or Enterobacter* spp.
- *Enterococcus*: includes all *Enterococcus* spp.
- *Staphylococcus aureus*
- *Pseudomonas aeruginosa*

How does NHSN calculate the pSIR?

NHSN calculates the pSIR as the number of observed HO infections associated with specific pathogens divided by the number of predicted HO infections associated with specific pathogens. NHSN calculates the predicted number of infections associated with specific pathogens by risk-adjusting for facility-level factors and other risk factors found to be statistically significantly associated with rates of infections among the pSIR referent population. The

referent population comes from nationally aggregated AR Option data reported to NHSN during the baseline time period (2019).

$$pSIR = \frac{\boldsymbol{Observed}\ Infections\ of\ Specific\ Pathogens}{\boldsymbol{Predicted}\ Infections\ of\ Specific\ Pathogens}$$

- Observed Infections of Specific Pathogens: The number of HO AR Option Events of a specific pathogen or pathogen group isolated from the specified specimen source and reported to the AR Option.
- Predicted Infections of Specific Pathogens: The number of HO AR Option Events predicted for that pathogen or pathogen group and same specimen source. NHSN calculates predicted HO infections using risk-adjusted pSIR predictive models.

A pSIR greater than 1.0 indicates that a greater number of infections were observed than predicted. A pSIR less than 1.0 indicates that fewer infections were observed than predicted. A pSIR value of 0 indicates a facility reported at least one HO isolate from the specimen source of interest during the time period of interest, but the pathogen of interest was not isolated. For example, for HO *Enterococcus* in urine, if a facility reported one or more HO isolates (any pathogen) from urine during the time period of interest, but no HO *Enterococcus* was isolated, the facility would receive a pSIR of 0.

The NHSN application will not generate a pSIR value (*i.e.*, pSIR will appear missing) when no positive culture grew reportable pathogens from the given specimen source during the time period, or an HO pathogen of interest was reported for the specimen source but <0.3 events were predicted (the minimum precision criteria for the number of predicted infections was not met). Using the example of HO *Enterococcus* in urine, a facility would receive a missing value for a pSIR if:

1. No HO positive culture grew reportable pathogens from a urine specimen, or
2. At least one HO pathogen of interest was isolated from urine during the time period of interest but there were <0.3 HO *Enterococcus* events predicted for that time period.

pSIRs are available to facilities that have submitted at least one HO pathogen in the correct specimen source during the specified time period of interest.

Why risk-adjust?

Risk adjustment is used to enhance fair comparison of infection incidence rates across facilities that potentially have different patient populations and therefore different risks for incident HO infections. There are many factors accounting for differences in the risk of infection, including but not limited to the overall patient demographics, underlying diseases, procedures and devices, antimicrobial exposure, and the prevalence of colonization or carriage of antimicrobial-resistant organisms among patients. Ideally, all predictive factors would be taken into consideration when developing NHSN metrics like the SRIR and pSIR; however, there is a trade-off between the

added burden on hospitals to collect such data and the potential improvement gained in the models' predictive abilities. At present, only selected facility-level data reported in the NHSN Patient Safety Component Annual Hospital Survey are available for risk-adjustment in SRIR and pSIR models. Rates of CO antimicrobial-resistant infections reported to the AR Option are also available for risk-adjustment in the SRIR models as proxies for AR burden in the communities served by the hospital.

SRIR and pSIR Model Development

Defining the referent population

A SRIR and pSIR referent population, which NHSN uses to develop SRIR and pSIR predictive models, is data reported to the AR Option for a particular year, specifically the baseline year (2019). NHSN assesses reporting volume for each facility type to ensure sample size is large enough for inclusion in SRIR and pSIR models. Associations between infection incidence and risk factors identified in the referent population are later applied to the larger universe of eligible facility types and if these associations were based on a small number of records, they may not be representative of all facilities. The greater the sample size NHSN includes in the predictive models, the more precise the SRIR and pSIR estimates, or adjustments. SRIR and pSIR referent populations include facilities that report for at least nine months of the baseline year.

SRIR referent populations were further limited to only include facilities reporting the HO organism (specific to each model) isolated from the specimen source for which the model is being developed. For each specimen source type, we excluded the records from facilities where >10% of their HO isolates were missing antimicrobial susceptibility results for resistance pattern determination. pSIR referent populations were further limited to only include facilities reporting at least one HO organism (any pathogen) isolated from the specimen source type for which the model was being developed. Once the referent population was finalized, we aggregated data to the facility/year-level for model development.

Defining SRIR Phenotypes and pSIR Pathogens

With input from external experts, including infectious disease physicians and pharmacists caring for adult, pediatric, and neonatal patients, NHSN determined the most notable drug-resistant pathogens to include in the SRIR modeling to allow facilities to compare their rates of drug-resistant HO infections to a national benchmark. Seven SRIR phenotypes and four pSIR pathogens/pathogen groups were chosen to be included in the 2019 baseline final models. Separate predictive models were developed for each drug-resistant pathogen (SRIR) or pathogen/pathogen group (pSIR) and specimen source (blood, urine, and lower respiratory).

Identifying potential risk-factors

After defining referent populations and drug-resistant pathogens and pathogen categories, NHSN identified candidate facility-level factors to consider as risk-adjustments in SRIR predictive models by 1) listing factors reported to NHSN by *all* hospitals, 2) consulting experts to identify which of these available and uniformly reported factors could explain differences in infection incidence. Facility-level data are collected through the NHSN Patient Safety Component Annual Hospital Survey.

Factors assessed in 2019 baseline SRIR predictive models:

- Facility type
- Medical school affiliation
- Type of medical school affiliation
- Total number of hospital beds
- Number of ICU beds
- Percentage of ICU beds, calculated as (ICU beds/total hospital beds) x 100
- Average facility length of stay (LOS), calculated as annual patient days/annual survey admissions
- CO prevalence, calculated as (number of resistant CO isolates/admissions*) x 10,000

*Admissions used in the CO prevalence calculation comes from AR Option Summary data submitted monthly

Factors assessed in 2019 baseline pSIR predictive models:

- Facility type
- Medical school affiliation
- Type of medical school affiliation
- Total number of hospital beds
- Number of ICU beds
- Percentage of ICU beds, calculated as (ICU beds/total hospital beds) x 100
- Average facility length of stay (LOS), calculated as annual patient days/annual survey admissions

The predictive model development process

After identifying factors to assess, NHSN began the SRIR and pSIR model development process to determine which factors (and in what form) were associated with infection rates for each SRIR and pSIR type. NHSN used negative binomial regression to assess these associations; first, by assessing each factor alone in univariate models and then, by assessing factors that statistically significantly predicted rates in univariate models together in multivariate models. NHSN used forward selection, a stepwise method of fitting regression models, to identify a final predictive model that risk adjusted for all factors predictive of infection for each SRIR and pSIR type. NHSN assessed variables in multiple forms and grouped levels with similar risk estimates together. Continuous variables, such as number of beds, were assessed as deciles, quintiles, quartiles, tertiles, and at the median.

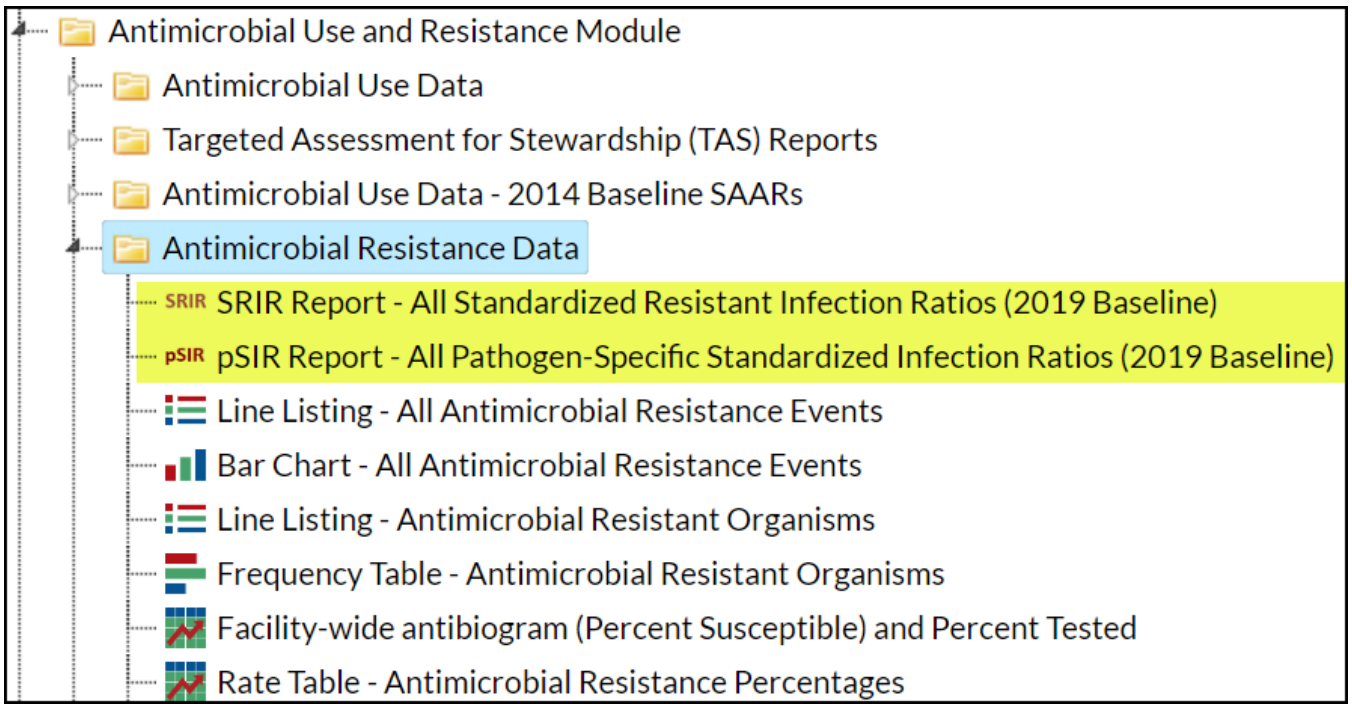
Details about SRIR and pSIR model development will be made publicly available in future NHSN published manuscripts.

High-level methodology and model details can be found in the 2023 NHSN Annual Training Video: https://www.youtube.com/watch?v=qEmKo8GpczU and Slides: https://www.cdc.gov/nhsn/pdfs/training/2023/New-AR-Option-Benchmark-Metrics-508.pdf.

SRIRs and pSIRs in NHSN

Finding and reading SRIR and pSIR reports

Users can find reports in the NHSN Analysis Reports within the Antimicrobial Use and Resistance (AUR) Module folder.



The SRIR reports include the following variables: NHSN Facility Org ID (orgID), Time Period (summaryYQ, summaryYH, summaryYr), SRIR Type (SRIR_Type), Resistant Hospital-Onset Isolates (numResistant_HO), Predicted Resistant Hospital-Onset Isolates (numResistant_HO_Predicted), Patient Days from AR Option Summary (numPatDaysAR), SRIR, SRIR p-value (SRIR_pval), and 95% Confidence Interval (SRIR95CI).

- **SRIR Type:** The SRIR type variable indicates the abbreviated name of the SRIR type. You can find the full name in the table title.
- **Resistant Hospital-Onset Isolates:** Resistant HO isolates include the number of HO AR Option Events isolated from the specified specimen source that met the resistance definition for the specified AR Option phenotype. Resistant HO isolates are the SRIR numerator.

- **Predicted Resistant Hospital-Onset Isolates:** Predicted resistant HO isolates are the number of HO AR Option Events predicted for each SRIR type through predictive modeling applied to nationally aggregated AR Option data. Predicted resistant HO isolates are the SRIR denominator.

- **Patient Days from AR Option Summary:** Patient days include the aggregate number of patients present in the facility at the same time on each day of the month, summed across all days in the month. Users should verify the accuracy of their patient days counts because NHSN uses patient days to calculate predicted values.

- **SRIR:** The SRIR is a ratio comparing observed resistant HO isolates (infections) to resistant HO isolates (infections) predicted by a referent, or baseline, population.

- **SRIR p-value:** The SRIR p-value is a statistical measure that indicates if observed resistant HO isolates (infections) is statistically significantly different from predicted resistant HO isolates (infections).

- **95% Confidence Interval:** The 95% confidence interval is the range of values in which NHSN has a high degree of confidence that the true SRIR value lies. However, the SRIR is the most likely value.

The pSIR reports include the following variables: NHSN Facility Org ID (orgID), Time Period (summaryYQ, summaryYH, summaryYr), pSIR Type (pSIR_Type), Hospital-Onset Isolates (numIsolates_HO), Predicted Hospital-Onset Isolates (numIsolates_HO_Predicted), Patient Days from AR Option Summary (numPatDaysAR), pSIR, pSIR p-value (pSIR_pval), and 95% Confidence Interval (pSIR95CI).

- **pSIR Type:** The pSIR type variable indicates the abbreviated name of the pSIR type. You can find the full name in the table title.

- **Hospital-Onset Isolates:** HO isolates include the number of HO AR Option Events isolated from the specified specimen source. HO isolates are the pSIR numerator.

- **Predicted Hospital-Onset Isolates:** Predicted HO isolates are the number of HO AR Option Events predicted for each pSIR type through predictive modeling applied to nationally aggregated AR Option data. Predicted HO isolates are the pSIR denominator.

- **Patient Days from AR Option Summary:** Patient days include the aggregate number of patients present in the facility at the same time on each day of the month, summed across all days in the month. Users should verify the accuracy of their patient days counts because NHSN uses patient days to calculate predicted values.

- **pSIR:** The pSIR is a ratio comparing observed HO isolates (infections) to HO isolates (infections) predicted by a referent, or baseline, population.

- **pSIR p-value:** The pSIR p-value is a statistical measure that indicates if observed HO isolates (infections) is statistically significantly different from predicted HO isolates (infections).

- **95% Confidence Interval:** The 95% confidence interval is the range of values in which NHSN has a high degree of confidence that the true pSIR value lies. However, the pSIR is the most likely value.

Interpreting the SRIR and pSIR

The SRIR is a ratio comparing observed resistant HO infections to resistant HO infections predicted by a referent, or baseline, population. In general:

- A SRIR > 1.0 indicates a greater number of resistant HO infections were observed than predicted.
- A SRIR = 1.0 indicates the number of observed resistant HO infections were equivalent to the number predicted.
- A SRIR < 1.0 indicates fewer resistant HO infections were observed than predicted.

The pSIR is a ratio comparing observed HO infections to HO infections predicted by a referent, or baseline, population. In general:

- A pSIR > 1.0 indicates a greater number of HO infections were observed than predicted.
- A pSIR = 1.0 indicates the number of observed HO infections were equivalent to the number predicted.
- A pSIR < 1.0 indicates fewer HO infections were observed than predicted.

As with the Standardized Infection Ratios (SIRs), the target value for SRIRs and pSIRs is always 0 because facilities strive to prevent all hospital-associated infections (HAIs). However, a SRIR and pSIR value of 1.0 or less than 1.0 does not necessarily mean it is ideal. Please refer to the Using the SRIR and pSIR for Action section to learn more about possible explanations for your high or low SRIRs and/or pSIRs.

Two statistical measures, the p-value and 95% confidence interval, accompany the SRIR and pSIR and aid in their interpretation. The p-value and 95% confidence interval will always indicate the same statistical significance and users can interpret them interchangeably.

SRIR p-value: The SRIR p-value indicates if observed or reported resistant HO infections are statistically significantly different from predicted resistant HO infections. Users should interpret SRIR p-values with caution, as statistical significance does not necessarily translate to clinical significance.

- A SRIR p-value ≤ 0.05 (an arbitrary and conveniently used cut point) indicates the number of reported resistant HO infections is statistically significantly different (greater or fewer) from the number of predicted resistant HO infections.
- A SRIR p-value > 0.05 indicates the number of reported resistant HO infections is **not** statistically significantly different from the number of predicted resistant HO infections.

SRIR 95% confidence interval: The SRIR 95% confidence interval is the range of values in which we have a high degree of confidence the true SRIR value lies. However, the SRIR is the most likely value.

- If the 95% confidence interval does not include 1.0 (for example: 95% CI = [0.85, 0.92]), the SRIR is statistically significantly different than 1.0 (specifically, the number of reported resistant HO infections is

statistically significantly different from the number of predicted resistant HO infections), and the p-value will be ≤ 0.05.

- If the 95% confidence interval does include 1.0 (for example: 95% CI = [0.85, 1.24]), the SRIR is **not** statistically significantly different than 1.0 (specifically, the number of reported resistant HO infections is not statistically significantly different from the number of predicted resistant HO infections), and the p-value will be > 0.05.

pSIR p-value: The pSIR p-value indicates if the number of observed or reported infections is statistically significantly different from the number of predicted HO infections. Users should interpret pSIR p-values with caution, as statistical significance does not necessarily translate to clinical significance.

- A pSIR p-value ≤ 0.05 (an arbitrary and conveniently used cut point) indicates the number of reported HO infections is statistically significantly different (more or fewer) from the number of predicted HO infections.
- A pSIR p-value > 0.05 indicates the number of reported infections is **not** statistically significantly different from the number of predicted HO infections.

pSIR 95% confidence interval: The pSIR 95% confidence interval is the range of values in which we have a high degree of confidence the true pSIR value lies. However, the psIR is the most likely value.

- If the 95% confidence interval does not include 1.0 (for example: 95% CI = [0.85, 0.92]), the pSIR is statistically significantly different than 1.0 (specifically, the number of reported HO infections is statistically significantly different from the number of predicted HO infections), and the p-value will be ≤ 0.05.
- If the 95% confidence interval does include 1.0 (for example: 95% CI = [0.85, 1.24]), the pSIR is **not** statistically significantly different than 1.0 (specifically, the number of reported HO infections is not statistically significantly different from the number of predicted HO infections), and the p-value will be > 0.05.

Users should interpret p-values and 95% CI with caution, as statistical significance does not necessarily translate into clinical significance. For example, a rapid increase of resistant infection events compared to the facility's baseline or a cluster of events in a short period of time and patient care locations may already warrant investigation even if the SRIR or pSIR is not statistically significantly higher than the national benchmark.

Circumstances under which NHSN *cannot* generate SRIR or pSIR reports or SRIR or pSIR values:

SRIRs and pSIRs are not available for AR Option data with specimen collection dates before January 2019. NHSN does not generate a SRIR or pSIR when the number of predicted infections is less than 0.3 to enforce a minimum precision criterion and avoid statistically imprecise SRIRs or pSIRs, which typically have extreme values.

For additional circumstances under which NHSN cannot generate SRIR or pSIR reports or SRIR or pSIR values, which are listed below, users will receive either a "No Records Met Your Criteria" error message or a missing SRIR or pSIR value (SRIR or pSIR = ".").

SRIR:

- No HO isolates of the pathogen of interest were reported from the given specimen source during the time period
- Facilities that responded 'N' to the "Carbapenem breakpoints for Enterobacterales in 2010" question on the NHSN Annual Facility Survey will not receive a predicted value or SRIR for the Carbapenem-resistant Enterobacterales (CRE) SRIR types for the survey year of the AR Option data
- Facilities that responded 'N' to the "Cephalosporin and monobactam breakpoints for Enterobacterales in 2010" question on the NHSN Annual Facility Survey will not receive a predicted value or SRIR for the Extended-spectrum cephalosporin-resistant Enterobacterales (ESCE) SRIR types for the survey year of the AR Option data

pSIR:

- No HO positive culture grew reportable pathogens from the given specimen source during the time period

Example SRIR interpretation

As an example, here is an interpretation of one row of a sample SRIR report for HO extended-spectrum cephalosporin-resistant Enterobacterales in urine specimens.

National Healthcare Safety Network
SRIR Table - All Standardized Resistant Infection Ratios (2019 Baseline)
As of: September 7, 2023 at 5:33 PM
Date Range: AR_ALL_SRIR_2019 summaryYr 2020 to 2022
if (((SRIR_Type = "HO_ESCEall_Urine")))
Hospital-onset (HO) Extended-spectrum cephalosporin-resistant Enterobacterales in urine specimens

Facility Org ID	Summary Yr/Qtr	SRIR Type	Resistant Hospital-Onset Isolates	Predicted Resistant Hospital-Onset Isolates	Patient days from AR Summary	SRIR	SRIR p-value	95% Confidence Interval
13860	2020Q1	HO_ESCEall_Urine	0	0.339	7226	0.000	0.713	., 8.837
13860	2020Q3	HO_ESCEall_Urine	0	0.902	19208	.	.	
13860	2020Q4	HO_ESCEall_Urine	0	0.170	3618	.	.	
13860	2021Q2	HO_ESCEall_Urine	0	0.221	4700	.	.	
13860	2021Q3	HO_ESCEall_Urine	0	0.615	13100	0.000	0.541	., 4.871
13860	2021Q4	HO_ESCEall_Urine	2	0.355	7550	5.634	0.056	0.945, 18.613

Note: *This example uses fictitious data for illustrative purposes only.*

During the fourth quarter (Q4) of 2021, this facility reported 2 HO cephalosporin-resistant Enterobacterales in urine specimens for patients contributing 7,550 patient days. NHSN applied risk-adjustments based on the 2019 baseline SRIR predictive model to calculate 0.355 predicted resistant HO isolates for this facility during 2021Q4. NHSN calculated the SRIR as 2 divided by 0.355, for a SRIR value of 5.634. With a p-value of 0.056 and a 95% confidence interval that contains 1.0 (0.945, 18.613), the number of observed resistant HO isolates was NOT statistically significantly different from the number of predicted resistant HO isolates during 2021Q4.

Example SRIR calculation

NHSN uses negative binomial regression for risk adjustment. The model uses a set of fixed parameters (adjustment variables) for each SRIR type to predict the risk of resistant infection incidence by specimen source. Below is the general formula for a negative binomial model:

$$log\ (\lambda) = \alpha + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_i X_i\text{, where:}$$

α = Intercept

β_i = Parameter estimate

X_i = Value of risk factor (categorical variables: 1 if present, 0 if not present)

i = Number of predictors

Exponentiating the solution (specifically, $e^{log\ (\lambda)}$), and multiplying by the number of patient days provides an estimate for predicted number of resistant HO isolates.

As an example, the table below represents the negative binomial regression model used to calculate the number of predicted resistant isolates for HO extended-spectrum cephalosporin-resistant Enterobacterales in urine specimens (Table 2).

Table 2. Risk factors used in the 2019 baseline SRIR predictive model for hospital-onset extended-spectrum cephalosporin-resistant Enterobacterales in urine specimens

Factor	Parameter Estimate	P-value
Intercept	-9.9663	<.0001
Community-onset Prevalence >47.3	0.9689	<.0001
Community-onset Prevalence 20.7 - 47.3	0.5580	<.0001
Hospital Length of Stay (LOS) >4.2	0.5912	<.0001

Note: CO prevalence less than 20.7 and hospital length of stay less than or equal to 4.2 which are NOT shown in the table above are part of a referent group (parameter estimate = 0.0000).

We can put the model details from Table 1 into the negative binomial regression model formula:

 # predicted resistant hospital-onset isolates = Exp [-9.9663
+ 0.9689 (Community-onset Prevalence: >47.3)
+ 0.5580 (Community-onset Prevalence: 20.7 - 47.3)
+ 0.5912 (Hospital Length of Stay: > 4.2 days)
] x # AR Option Patient Days

For each variable shown in parentheses above, replace the variable name with (and, therefore, multiply each parameter estimate by) a "1" or "0" depending on whether that factor is present (Yes="1", No="0").

Let's walk through an example of calculating predicted HO extended-spectrum cephalosporin-resistant Enterobacterales in urine specimens for a facility that reported 15,000 annual patient days and 2,500 annual admissions on the 2022 NHSN Annual Hospital Survey, so the average hospital length of stay was 6 days (15,000 annual patient days / 2,500 annual admissions). The hospital also reported 2 HO extended-spectrum cephalosporin-resistant Enterobacterales in urine specimens, 4 CO extended-spectrum cephalosporin-resistant Enterobacterales in urine specimens, 4,200 AR Option patient days, and 650 AR Option admissions in 2022Q4. The CO prevalence was 61.5 (4 CO resistant isolates / 650 AR Option admissions x 10,000).

In our example, the completed formula looks like this:

 # predicted resistant hospital-onset isolates = Exp [-9.9663
+ 0.9689 (Community-onset Prevalence: >47.3) ⟶ (1)
+ 0.5580 (Community-onset Prevalence: 20.7 - 47.3) ⟶ (0)
+ 0.5912 (Hospital Length of Stay: > 4.2 days) ⟶ (1)
] x # AR Option Patient Days

= $e^{[-9.9663+0.9689+0.5912]}$ **x 4,200 patient days**
= $e^{[-7.8482]}$ **x 4,200 patient days**
= 0.00039045 x **4,200 patient days**
= **1.6399 predicted resistant hospital-onset isolates**

Since the facility fell into the CO prevalence >47.3 category, the formula did not include the other CO prevalence categories (others received 0). This location received an adjustment of 0.9689 for having a CO prevalence >47.3 and an adjustment of 0.5912 for having an average length of stay >4.2 days. To calculate predicted resistant HO isolates, sum the adjustments (0.9689 and 0.5912) and intercept (-9.9663), exponentiate that sum, and multiply by 4,200 patient days, which results in 1.6399 resistant HO isolates for extended-spectrum cephalosporin-resistant Enterobacterales in urine specimens for 2022Q4. To calculate the SRIR, divide observed resistant HO isolates by predicted resistant HO isolates. In our example:

$$\boldsymbol{SRIR = \frac{2\ observed\ resistant\ hospital\text{-}onset\ isolates}{1.6399\ predicted\ resistant\ hospital\text{-}onset\ isolates} = 1.220}$$

Example pSIR interpretation

As an example, here is an interpretation of one row of a sample pSIR report for HO Enterobacterales in blood specimens.

National Healthcare Safety Network
pSIR Table - All Pathogen-Specific Standardized Infection Ratios (2019 Baseline)
As of: October 12, 2023 at 4:43 PM
Date Range: AR_ALL_PSIR_2019 summaryYQ After and Including 2020Q1

Hospital-onset (HO) Enterobacterales in blood specimens

Facility Org ID	Summary Yr/Qtr	pSIR Type	Hospital-Onset Isolates	Predicted Hospital-Onset Isolates	Patient days from AR Summary	pSIR	pSIR p-value	95% Confidence Interval
33617	2020Q1	HO_Enterobacterales_Blood	5	0.522	3601	9.579	0.0002	3.510, 21.231
33617	2020Q2	HO_Enterobacterales_Blood	0	0.522	3601	0.000	0.5933	., 5.739
33617	2020Q3	HO_Enterobacterales_Blood	0	0.522	3601	.	.	
33617	2020Q4	HO_Enterobacterales_Blood	0	0.524	3618	.	.	
33617	2021Q1	HO_Enterobacterales_Blood	2	0.507	5824	3.945	0.1073	0.661, 13.033
33617	2021Q2	HO_Enterobacterales_Blood	0	0.417	4785	.	.	
33617	2021Q3	HO_Enterobacterales_Blood	0	0.936	10750	.	.	
33617	2021Q4	HO_Enterobacterales_Blood	0	0.383	4400	0.000	0.6818	., 7.822
33617	2022Q1	HO_Enterobacterales_Blood	3	0.501	5750	5.988	0.0162	1.523, 16.297
33617	2022Q3	HO_Enterobacterales_Blood	0	0.075	861	.	.	
33617	2022Q4	HO_Enterobacterales_Blood	0	1.091	12525	0.000	0.3359	., 2.746
33617	2023Q1	HO_Enterobacterales_Blood	0	0.601	6900	0.000	0.5483	., 4.985
33[illegible]	23Q[illegible]	HO_[illegible]erales_Blo[illegible]	0.1[illegible]		[illegible]00			

Note: *This example uses fictitious data for illustrative purposes only.*

During the first quarter (Q1) of 2022, this facility reported 3 HO Enterobacterales in blood specimens for patients contributing 5,750 patient days. NHSN applied risk-adjustments based on the 2019 baseline pSIR predictive model to calculate 0.501 predicted HO isolates for this facility during 2022Q1. NHSN calculated the pSIR as 3 divided by 0.501, for a pSIR value of 5.988. With a p-value of 0.0162 and a 95% confidence interval that does not contain 1.0 (1.523, 16.297), observed HO isolates was statistically different from predicted HO isolates during 2022Q1.

Example pSIR calculation

NHSN uses negative binomial regression for risk adjustment. The model uses a set of fixed parameters (adjustment variables) for each pSIR type to predict the risk of infection incidence by specimen source. Below is the general formula for a negative binomial model:

$$log\ (\lambda) = \alpha + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_i X_i\text{, where:}$$

α = Intercept
β_i = Parameter estimate
X_i = Value of risk factor (categorical variables: 1 if present, 0 if not present)
i = Number of predictors

Exponentiating the solution (specifically, $e^{log\ (\lambda)}$), and multiplying by the number of patient days provides an estimate for predicted HO isolates.

As an example, the table below represents the negative binomial regression model used to calculate the number of predicted HO isolates for HO Enterobacterales in blood specimens (Table 3).

Table 3. Risk factors used in the 2019 baseline pSIR predictive model for hospital-onset Enterobacterales in blood specimens

Factor	Parameter Estimate	P-value
Intercept	-9.3485	<.0001
Number of ICU Beds ≥96	0.6452	<.0001
Number of ICU Beds 64–95	0.3013	0.0023
Hospital Length of Stay (LOS) ≥5.0	0.5095	<.0001
Hospital Length of Stay (LOS) 4.3–4.9	0.1974	0.0243

Note: Number of ICU beds less than 64 and hospital length of stay less than 4.3 which are NOT shown in the table above are part of a referent group (parameter estimate = 0.0000).

We can put the model details from Table 1 into the negative binomial regression model formula:

 # predicted hospital-onset isolates = Exp [-9.3485
+ 0.6452 (Number of ICU Beds: ≥96)
+ 0.3013 (Number of ICU Beds: 64 - 95)
+ 0.5095 (Hospital Length of Stay: ≥5.0 days)
+ 0.1974 (Hospital Length of Stay: 4.3 - 4.9 days)
] x # AR Option Patient Days

For each variable shown in parentheses above, replace the variable name with (and, therefore, multiply each parameter estimate by) a "1" or "0" depending on whether that factor is present (Yes="1", No="0").

Let's walk through an example of calculating predicted HO Enterobacterales in blood specimens for a facility that reported 65 ICU beds, 15,000 annual patient days, and 2,500 annual admissions on the 2022 NHSN Annual Hospital Survey, so the average hospital length of stay was 6 days (15,000 annual patient days / 2,500 annual admissions). The hospital also reported 4 HO Enterobacterales in blood specimens and 4,200 AR Option patient days in 2022Q4.

In our example, the completed formula looks like this:

 # predicted hospital-onset isolates = Exp [-9.3485
+ 0.6452 (Number of ICU Beds: ≥96) → (0)
+ 0.3013 (Number of ICU Beds: 64 - 95) → (1)
+ 0.5095 (Hospital Length of Stay: ≥5.0 days) → (1)
+ 0.1974 (Hospital Length of Stay: 4.3 - 4.9 days) → (0)
] x # AR Option Patient Days

= $e^{[-9.3485+0.3013+0.5095]}$ **x 4,200 patient days**

= $e^{[-8.5377]}$ **x 4,200 patient days**

= 0.00019594 x **4,200 patient days**

= **0.8230 predicted hospital-onset isolates**

This location received an adjustment of 0.3013 for having 65 ICU beds and an adjustment of 0.5095 for having an average length of stay >5.0 days. To calculate predicted HO isolates, sum the adjustments (0.3013 and 0.5095) and intercept (-9.3485), exponentiate that sum, and multiply by 4,200 patient days, which results in 0.8230 HO isolates for Enterobacterales in blood specimens for 2022Q4. To calculate the pSIR, divide observed HO isolates by predicted HO isolates. In our example:

$$\boldsymbol{SRIR = \frac{4\ observed\ hospital\text{-}onset\ isolates}{0.8230\ \ predicted\ hospital\text{-}onset\ isolates} = 4.860}$$

Additional notes regarding risk-adjustment:

- NHSN separates some risk-adjustment variables into different levels, or categories. For example, NHSN breaks down continuous variables into categories based on decile, quintile, quartile, tertile, and median values. NHSN may group levels further if risk estimates are not statistically significantly different.
- For variables with more than one level, one level is the referent category (specifically, the category to which all other levels are compared). The analyst developing the model can select the referent group. For risk of AR, it is often easier to understand which factors are associated with increased infection incidence, rather than decreased infection incidence and, when possible, we select the group with the lowest risk as the referent category.
- Parameter estimates reflect the nature of the relationship between the variable and the risk of infection incidence. A positive estimate means the risk of resistant infection incidence for the associated group is greater than the referent group. A negative estimate means the risk of resistant infection incidence for the associated group is less than the referent group.
- Standard errors reflect the precision of parameter estimates, where smaller standard errors indicate a greater level of precision than larger standard errors.
- You can find model details for the 2019 baseline SRIR models and the 2019 baseline pSIR models at the end of this document.

Analysis Guidance

Scalability of the SRIR and pSIR – how to aggregate SRIR and pSIR data

Scalability means that hospitals can calculate SRIRs and pSIRs at various levels of aggregation. For example, in pre-filtered reports, NHSN calculates SRIRs and pSIRs at the facility- and quarter-level. Users can modify reports to display half-yearly, yearly, or cumulative SRIRs and pSIRs. NHSN does not have a built-in option to generate SRIRs and pSIRs for multiple facilities, however, users can manually pool data to calculate SRIRs and pSIRs at different levels of aggregation.

Examples of how users can aggregate SRIR and pSIR data:

- Across time (quarters, half-years, years, or cumulative)
- Across facilities, health systems, or health department jurisdictions

To calculate a pooled SRIR or pSIR for aggregation levels not available in NHSN, users can export their SRIR or pSIR data and manually sum observed HO infections across desired levels of aggregation, sum predicted HO infections across those same levels, and then divide the pooled observed HO infections by pooled predicted HO infections. For example, you can calculate a pooled SRIR for HO extended-spectrum cephalosporin-resistant Enterobacterales in urine specimens across two different facilities.

Hospital-onset (HO) Extended-spectrum cephalosporin-resistant Enterobacterales in urine specimens

Facility Org ID	Summary Yr	SRIR Type	Resistant Hospital-Onset Isolates	Predicted Resistant Hospital-Onset Isolates	Patient days from AR Summary	SRIR	SRIR p-value	95% Confidence Interval
10036	2022	HO_ESCEall_Urine	0	0.142	1680	.	.	
33617	2022	HO_ESCEall_Urine	3	0.927	19736	3.236	0.082	0.823, 8.808

Note: *This example uses fictitious data for illustrative purposes only.*

For the year 2022, you can calculate a pooled HO extended-spectrum cephalosporin-resistant Enterobacterales in urine specimens (HO_ESCEall_Urine) SRIR for these two hospitals using the following formula:

$$\boldsymbol{Pooled\ HO\_ESCEall\_Urine\ SRIR} = \frac{\boldsymbol{orgID\ 10036\ observed\ resistant\ HO\ isolates + orgID\ 33617\ observed\ resistant\ HO\ isolates}}{\boldsymbol{orgID\ 10036\ predicted\ resistant\ HO\ isolates + orgID\ 33617\ predicted\ resistant\ HO\ isolates}}$$

$$\boldsymbol{Pooled\ HO\_ESCEall\_Urine\ SRIR} = \frac{\mathbf{0 + 3}}{\mathbf{0.142 + 0.927}}$$

$$\textbf{\textit{Pooled HO\_ESCEall\_Urine SRIR}} = \mathbf{2.806}$$

Note: This example is an appropriate use of aggregation because we are pooling within the same SRIR Type (HO_ESCEall_Urine). We would NOT want to pool across SRIR Types such as HO_ESCEall_Urine data with HO_CREall_Urine data.

While scaling SRIR and pSIR data can be useful for many infection prevention efforts, there are limitations that users must keep in mind. The more scaling that occurs, the more uncertainty you introduce and the greater the likelihood that additional factors (not included in risk adjustments) will account for observed changes. The more you aggregate, the more likely the groups you are comparing will differ in certain factors, leading to a loss in proportionality. This concept of proportionality can be found in the 2nd Volume of Breslow and Day's Statistical Methods in Cancer Research: https://publications.iarc.fr/Book-And-Report-Series/Iarc-Scientific-Publications/Statistical-Methods-In-Cancer-Research-Volume-II-The-Design-And-Analysis-Of-Cohort-Studies-1986.

State, territorial, and local health departments, as well as hospital systems, can generate SRIRs and pSIRs for all hospitals in their jurisdiction using the NHSN Group Function. The NHSN Group Function allows users to access multiple facilities' NHSN data with their permission or, in the case of state, territorial and local health departments, through a data use agreement. The Group is managed centrally and, while facilities share data with the group, individual facilities cannot see data from other group members. You can find more information about the NHSN Group Function on the NHSN Group Function website: https://www.cdc.gov/nhsn/group-users/index.html. State, territorial, and local health departments can find more information on obtaining NHSN data from facilities in their jurisdiction on the Data Use Agreement (DUA) website: https://www.cdc.gov/nhsn/about-nhsn/dua.html.

Survey data and risk-adjustment

NHSN uses Patient Safety Component Annual Hospital Survey data for facility-level risk-adjustment in SRIR and pSIR models; survey year is matched to the year of the AR Option data (*e.g.*, 2022 survey values are used when risk adjusting 2022 AR Option data). However, because hospitals complete surveys annually while reporting AR Option data monthly, there is a period of 12+ months where NHSN risk-adjusts SRIR/pSIR using the previous year's survey data. For example, facilities complete their survey each March, so they completed their 2022 surveys in early 2023 using data from the complete 2022 calendar year. If the facility reports AR Option data monthly, in February 2023, NHSN calculates their 2022 and 2023 SRIRs and pSIRs using 2021 survey data (specifically, the most recent survey data available).

Hospitals and health systems may track SRIRs and pSIRs on an ongoing basis and may notice shifts in their SRIR and pSIR values once current survey data replace old survey data for risk-adjustment in calculations. The likelihood

and magnitude of shifts in SRIRs and pSIRs due to survey updates depends on the number and types of risk-adjustments made in each predictive model. For example, the SRIR model for multidrug-resistant *Pseudomonas aeruginosa* in urine specimens only risk-adjusts for CO prevalence which uses AR Option data and is, therefore, not affected by survey updates, while the pSIR model for *Pseudomonas aeruginosa* in urine specimens risk-adjusts for facility type and average length of stay, and is therefore susceptible to shifts in pSIR calculations if a hospital changes one or more facility-level factors that cause it to shift risk-adjustment categories. These survey variables are used in at least one SRIR or pSIR model, so make sure your annual hospital surveys reflect what actually occurred in your facility and laboratory during the survey year.

Example: *How changes to surveys can affect 2019 baseline Staphylococcus aureus in blood specimens pSIR*

The pSIR model for *Staphylococcus aureus* in blood specimens risk-adjusts for length of stay and number of ICU beds.

In 2022, the facility reports:

- Length of stay (LOS) – 5.2 days
- Number of ICU beds – 32 beds

In 2023, the facility reports:

- Length of stay (LOS) – 4.5 days
- Number of ICU beds – 28 beds

pSIR *Staphylococcus aureus* in Blood Specimens	**Estimate**
Intercept	-9.5228
Number of ICU beds, facility-wide	
≥30	0.3814
<30	REF
Average length of stay, facility-wide (in days)	
≥5.0	0.2635
<5.0	REF

Based on changes in the facility's average LOS and bed size between 2022 and 2023, they can expect changes in their 2023 pSIR for *Staphylococcus aureus* in blood specimens once their 2023 survey data replaces their 2022 survey data for pSIR calculations. For LOS, they reported 5.2 days in 2022, which falls in the highest risk category (≥5.0 days), and 4.5 days in 2023, which falls in the lowest risk category (<5.0 days). For number of ICU beds, they reported 32 ICU beds in 2022, which falls in the highest risk category (≥30 ICU beds), and 28 ICU beds in 2023, which falls in the lowest-risk category (<30 ICU beds). Changes in LOS and ICU bed-size will affect estimates for predicted HO isolates and total risk-adjustment will be lower using 2023 survey data compared with 2022 survey data:

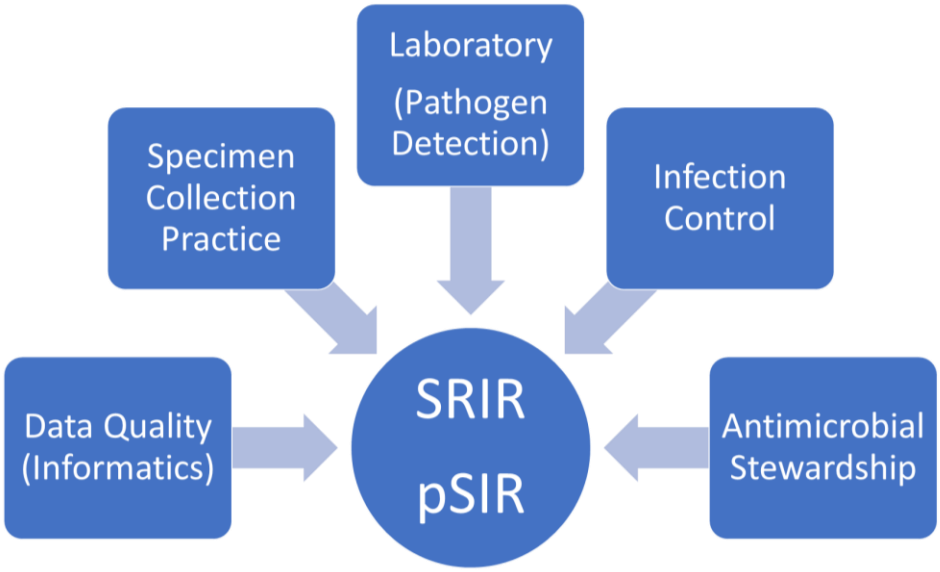
- LOS estimate 2022 vs. 2023: 0.2635 → 0.0000
- Number of ICU beds estimate 2022 vs. 2023: 0.3814 → 0.0000
- Predicted HO isolates using 2023 survey data will decrease by:
  - $= e^{(-0.2635 - 0.3814)}$ x number of days present
  - $= e^{(-0.6449)}$ x number of days present
  - = 0.525 x number of days present
- Because 0.525 is less than 1.0, this change in estimation will result in a *smaller* number of predicted HO isolates and, therefore, a higher pSIR value.

Using the SRIR and pSIR for Action

The SRIR and pSIR are measures that are intended to help facilities better understand the role of specific pathogens (resistant or sensitive) on their HO infections; this information might help inform decisions about infection control and antimicrobial stewardship. This section provides possible explanations for high or low SRIR or pSIR values, guidance on how to differentiate among these possible explanations, and potential solutions for addressing unexpected values.

Possible explanations for a high or low SRIR or pSIR

SRIRs and pSIRs are generated based on the data your facility submitted to the NHSN AR Option. In addition to inherent risk for infections of patients, the following modifiable factors can contribute to a high or low SRIR or pSIR: data quality, sampling (specimen collection) technique and strategy, methods and reporting practice of the clinical microbiology laboratory, and the rates of susceptible and drug-resistant infections.



- Data Quality (Informatics): The flow of the data and connections between your hospital's information and surveillance systems could affect the quality of your AR Option data. For example, you may receive an inaccurate SRIR or pSIR if the terminology used to report eligible organism(s), drug(s), or specimen(s) were not mapped properly to a reportable NHSN term. To ensure the accuracy of these metrics, review your data following the NHSN AR Option Data Validation Protocol prior to interpreting SRIR/pSIR results. SRIR and pSIR values can be affected by the following:
    - Selective or cascade reporting may lead to a low SRIR. This happens when antimicrobial susceptibility testing (AST) results of certain drug(s) were revealed to prescribers conditionally or only for certain isolates, and partially reported data were submitted to NHSN, therefore AR Option data do not reflect the original drug panel tested. For example, if fluoroquinolone data are suppressed for isolates

obtained from pediatric patients, the incidence of fluoroquinolone-resistant Enterobacterales and *P. aeruginosa* can potentially be underestimated. Check the percentage tested (%tested) using the analysis report available in the NHSN application (AR Facility-wide Antibiogram and Percent Tested Quick Reference Guide). Selective or cascade reporting is an antimicrobial stewardship strategy in which only AST results of selected antimicrobials are available to clinicians based off an algorithm built into AST instruments, the laboratory information system, or electronic health records. It is possible to submit complete AST data to the NHSN AR Option while keeping selective and cascade reporting for antimicrobial stewardship purposes. If your microbiology laboratory routinely tests the drug(s) that are used to determine the resistance phenotype, yet the results are not shown for all isolates, reach out to your information technology department and surveillance vendor for troubleshooting.

- Specimen collection and/or culture utilization issues (sampling) may lead to variability of clinical isolates (AR and susceptible)
    - Specimen quality (high SRIR or pSIR): A high number of positive cultures from non-sterile specimen sources (especially urine samples) could be due to inappropriate specimen collection technique, for example, urine samples taken from urinary bags instead of from the port of a urinary catheter. Alternatively, there may be delayed transit of urine cultures to the laboratory for processing with storage at room temperature (leading to outgrowth) or poor blood culture collection technique leading to contamination.
    - Culture utilization strategy (low or high SRIR or pSIR): SRIR and pSIR were calculated based on the baseline population's incidence of culture-positive specimens, ideally taken from patients with suspected clinical infections. A high pSIR, sometimes in concordance with a high SRIR associated with the same specimen type(s), could be due to oversampling. For example, urine cultures submitted for patients regardless of clinical suspicion of urinary tract infections. Conversely, SRIR/pSIR could be underestimated if cultures are underused. Additionally, for SRIR, because it is adjusted for the hospital's CO infections, if cultures are frequently obtained in ER or 24-hour observation units, it is possible that the same hospital would receive a higher number of predicted HO events for all phenotypes, *i.e.*, lower HO SRIRs. This phenomenon may be more significant in SRIRs for non-sterile sites (*i.e.*, urine and lower respiratory tract) than in blood SRIRs.
- Shifts in laboratory processes (Low SRIR or pSIR).
    - The AR Option currently captures events based on culture-based pathogen identification and AST. If not all clinical isolates went through culture-based organism identification (pSIR and SRIR) or AST (SRIR), these ratios could be underestimated. For example, if instead of cultures, specimens or isolates were tested only using culture-independent tests, the facility's pSIR and/or SRIR could appear lower, compared to facilities which use only culture-based pathogen identification and antimicrobial susceptibility tests.
    - SRIR could be underestimated if a facility does not routinely perform AST for the antimicrobial(s) that are required to determine the SRIR phenotype. For example, if phenotypic fluoroquinolone susceptibility test(s) are not performed for all *P. aeruginosa* isolates for the specimen type of interest,

the fluoroquinolone-resistant *P. aeruginosa* SRIR could be underestimated. Our 2019 AR Option baseline population were restricted to the data from facilities that submitted susceptibility test results for ≥90% isolates. Check the percentage tested (%tested) for the pathogen-antimicrobial(s) involved in the phenotype using the analysis report available in the NHSN application (AR Facility-wide Antibiogram and Percent Tested Quick Reference Guide).

- Infection Control (High SRIR or pSIR): High incidence rates of HO infections associated with specific pathogens/phenotypes and specimen types could result in a high SRIR or pSIR. Facilities should consider further investigating the relevant epidemiology to identify potential causes. If horizontal transmission of a single strain is suspected, consider if laboratory evaluation (*e.g.*, whole genome sequencing) is warranted to evaluate clonality. Consider reaching out to your health department's HAI/AR Program or public health laboratory for further recommendations.
- Antimicrobial Stewardship (high SRIR): A high SRIR means a high incidence of culture-positive infection for the AR Option phenotype compared to the baseline population after adjusting for CO prevalence of resistance and other facility-level factors. If the pSIR of the corresponding organism is not high, this disproportionately high rate of AR could signify an opportunity for antimicrobial stewardship. Overuse/misuse of antimicrobials can create selective pressure for certain AR Option phenotype(s). Review your facility's use of antimicrobial(s) that can potentially create a selection pressure for the phenotype with high SRIR. For example, review the rates and appropriateness of vancomycin use in your facility if the SRIR for vancomycin-resistant enterococci (VRE) was high. If your facility also reports data to the NHSN Antimicrobial Use Option, the corresponding Standardized Antimicrobial Administration Ratios (SAAR) can also be helpful.

Before interpreting SRIRs or pSIRs, we recommend checking data quality by following the steps recommended in the NHSN AR Option Data Validation tool to ensure accurate terminology mapping and complete AST data submission. If data quality is not an issue, then to navigate through possible explanations, in addition to inherent patient risk factors, for SRIRs and/or pSIRs that are significantly lower or higher than the national benchmark, we recommend the following steps:

1. In the situation of high pSIR with or without high SRIR, review specimen collection strategies and techniques to rule out the possibility of inappropriate culture collection technique and/or overutilization of cultures. (Figure 2 and Figure 3)
2. In the situation of low pSIR, review specimen collection strategies and laboratory testing methods for bacterial pathogen detection to ensure the pSIR truly reflects low rates of HO infections. (Figure 3)
3. If a high pSIR (with or without a high SRIR) is not due to data quality or sampling issues, this indicates that compared to the national benchmark, your facility had a higher rate of HO infections associated with the respective organism. Investigate possible reasons for high infection rate(s) and consider appropriate interventions. (Figure 2)
4. In the situation of a high SRIR, in addition to step 3, review the facility's antibiotic use and consider potential antimicrobial stewardship interventions. (Figure 2)

Figure 2. Differentiating possible explanations and actions for high Standardized Resistant Infection Ratios (SRIR) and/or Pathogen-specific Standardized Infection Ratios (pSIR)

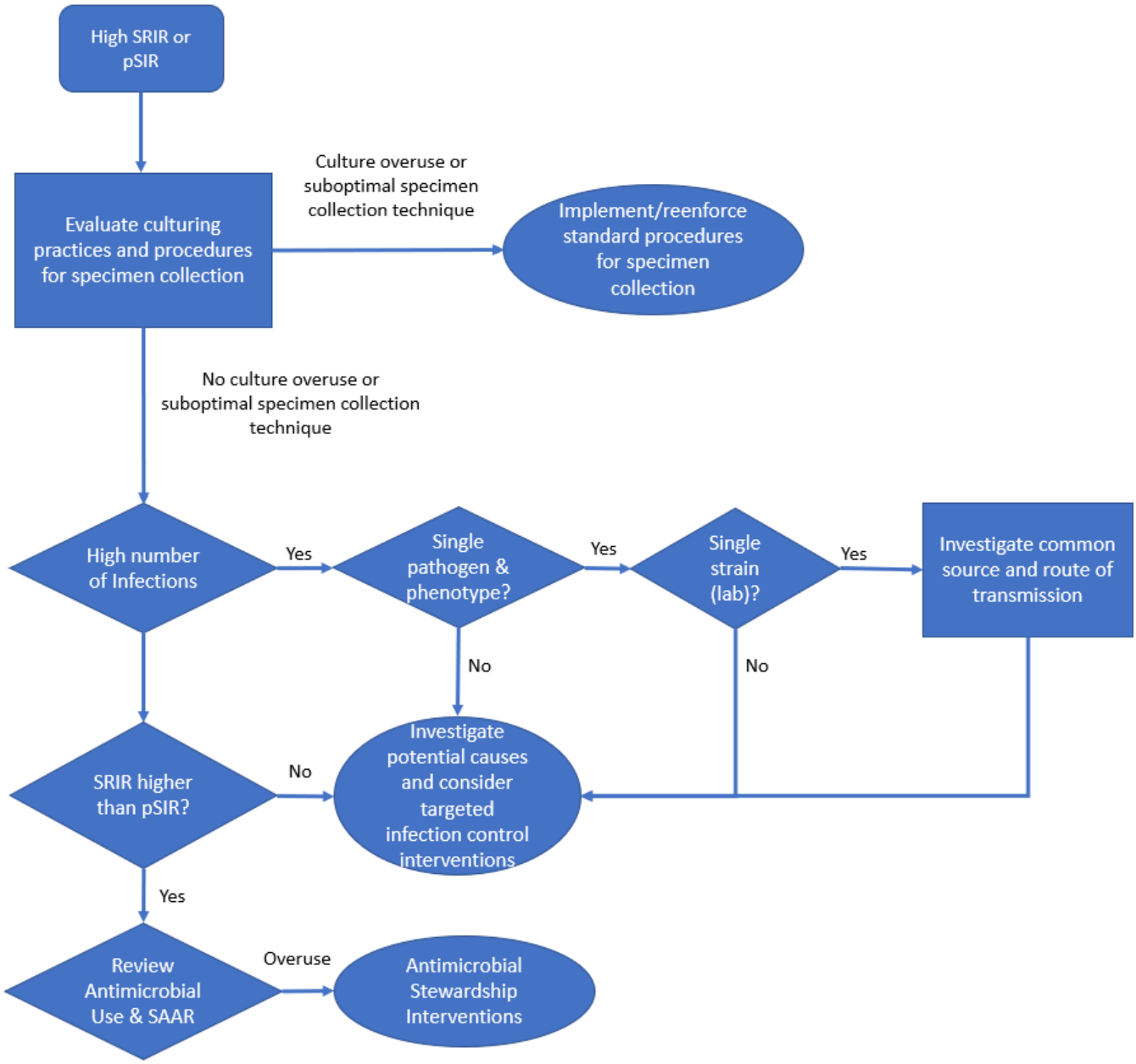


Figure 2 Acronyms:

- pSIR: Pathogen-specific Standardized Infection Ratio
- SRIR: Standardized Resistant Infection Ratio
- SAAR: Standardized Antimicrobial Administration Ratio

Figure 3. Differentiating possible explanations and actions for low Standardized Resistant Infection Ratios (SRIR) and/or Pathogen-specific Standardized Infection Ratios (pSIR)

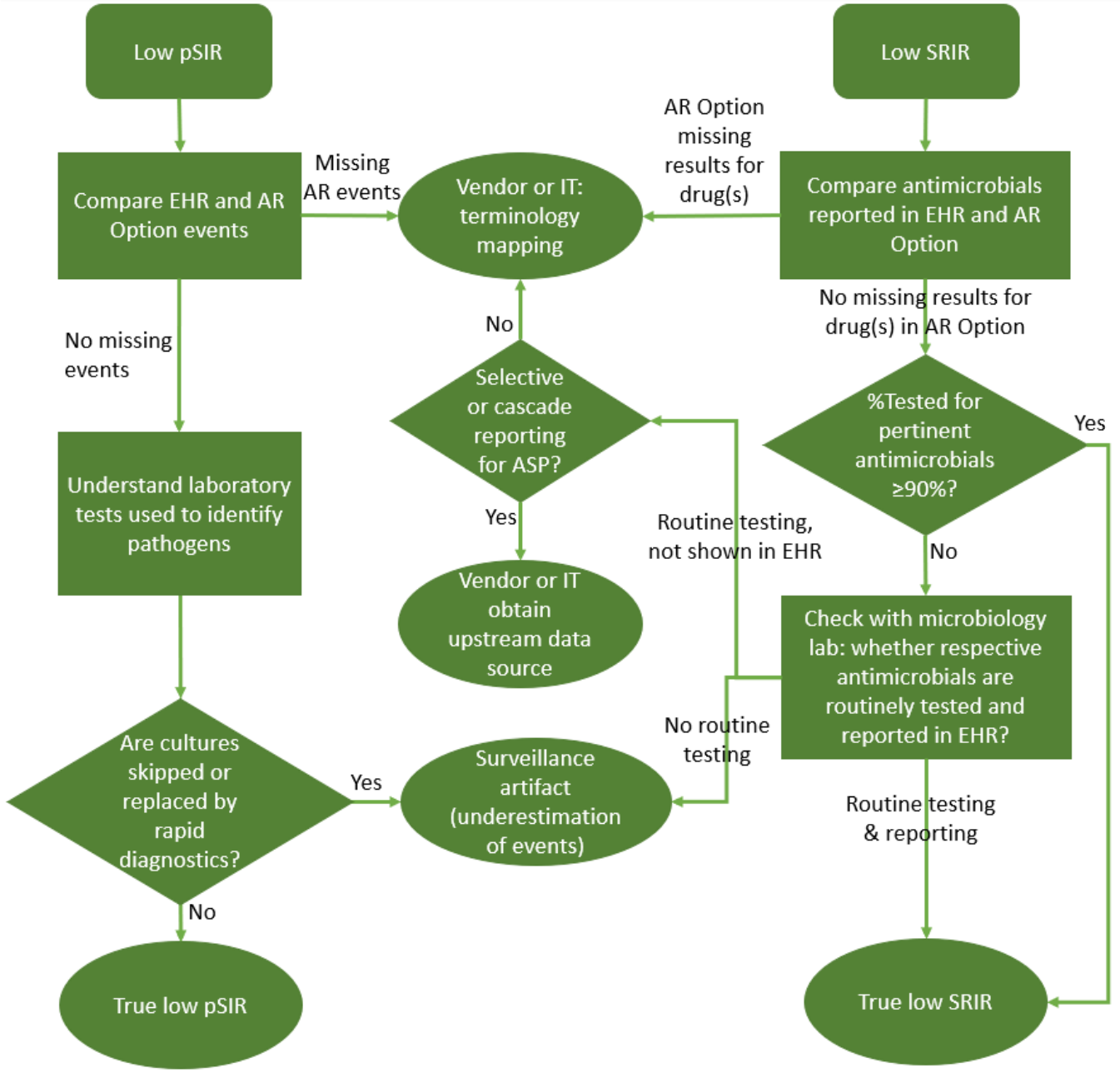


Figure 3 Acronyms:

- AR: Antimicrobial Resistance
- ASP: Antimicrobial Stewardship Program
- EHR: Electronic Health Records
- IT: Information Technology
- pSIR: Pathogen-specific Standardized Infection Ratio
- SRIR: Standardized Resistant Infection Ratio

Evaluating potential high rates of infections

The SRIR report or pSIR report may help facilities identify potential increases in rates of infection. If the SRIR for a drug-resistant pathogen is higher than expected, facilities can run a line list to further investigate the infections and identify potential clusters. We will walk through an example using fictitious data of how the SRIR report can be used to identify potential clusters.

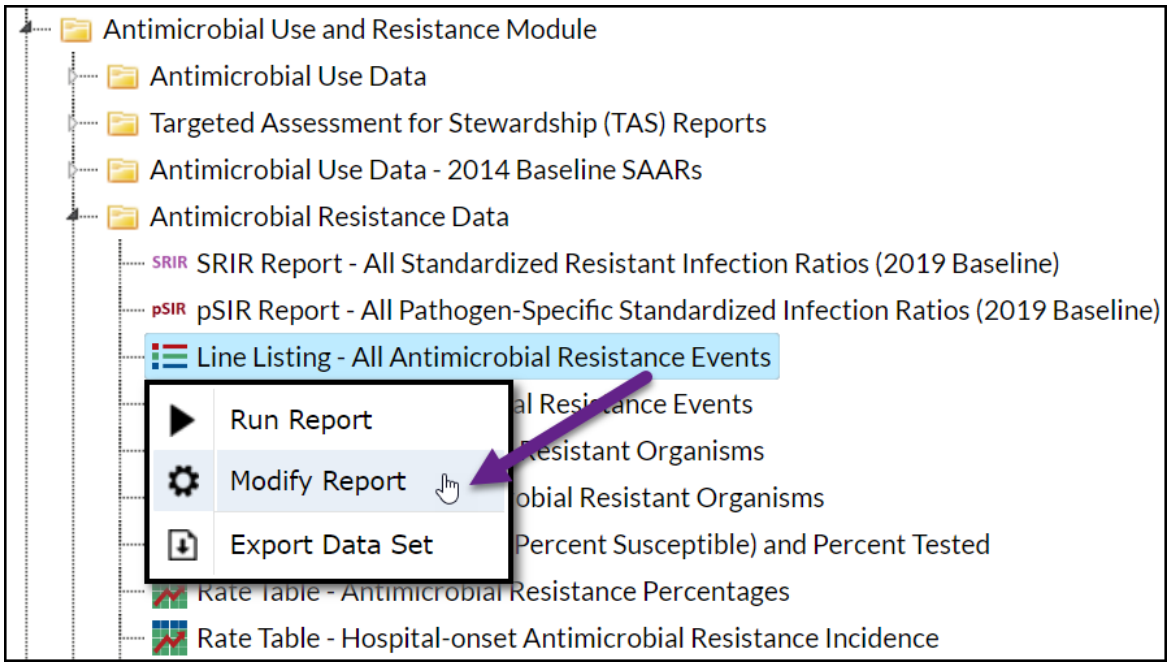
For example, let's say we ran the SRIR report for our facility by year. We noticed that we reported seven HO vancomycin-resistant *Enterococcus* collected from blood specimens in 2021, while we reported zero for 2019, 2020, and 2022. The SRIR for VRE in blood specimens for 2021 was 7.202 which is over seven times more than predicted. We want to find out more information on these seven bloodstream VRE infections from 2021.

National Healthcare Safety Network
SRIR Table - All Standardized Resistant Infection Ratios (2019 Baseline)
As of: September 22, 2023 at 4:25 PM
Date Range: All AR_ALL_SRIR_2019

Hospital-onset (HO) Vancomycin-resistant Enterococcus in blood specimens

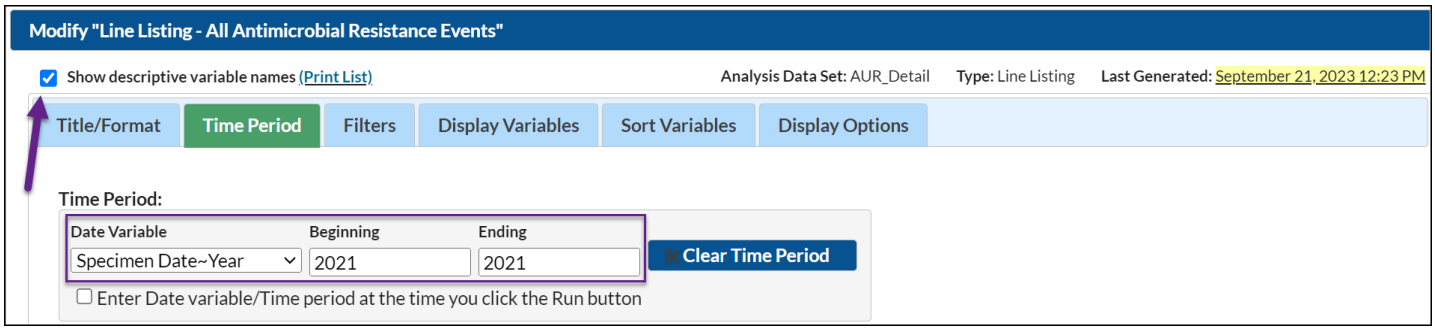
Facility Org ID	Summary Yr	SRIR Type	Resistant Hospital-Onset Isolates	Predicted Resistant Hospital-Onset Isolates	Patient days from AR Summary	SRIR	SRIR p-value	95% Confidence Interval
33617	2019	HO_VRE_Blood	0	0.130	14404	.	.	
33617	2020	HO_VRE_Blood	0	0.130	14421	.	.	
33617	2021	HO_VRE_Blood	7	0.972	25759	7.202	0.000	3.150, 14.246
33617	2022	HO_VRE_Blood	0	0.173	19136	.	.	

In NHSN, we can run a line list report to gather more information on these seven AR Option Events. Click Analysis > Reports > Antimicrobial Use and Resistance Module > Antimicrobial Resistance Data. Select the report, "Line Listing – All Antimicrobial Resistance Events" and a pop-up box will appear that will allow you to "Run Report," "Modify Report," or "Export Data Set." Select "Modify Report" to customize your report.

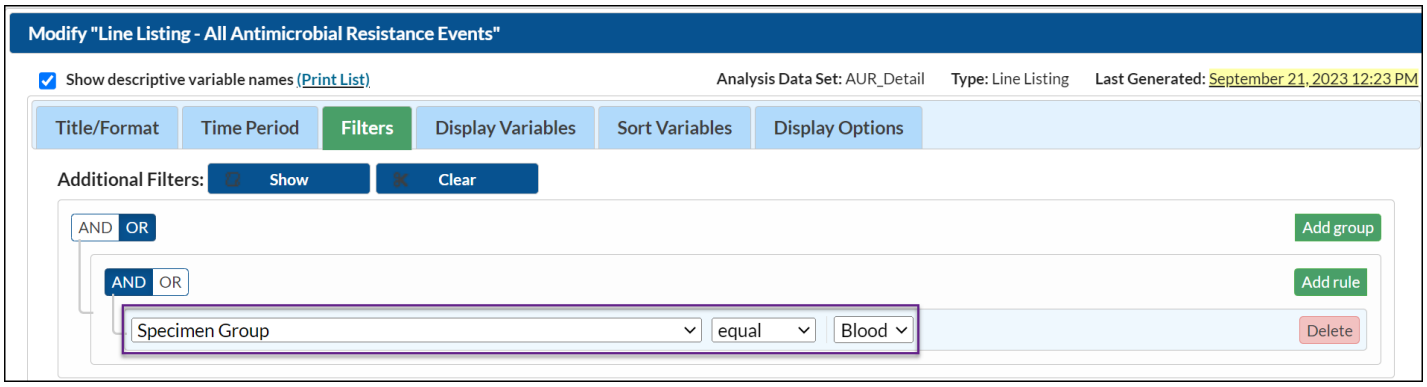


When you choose to modify the report, the modification screen appears showing multiple tabs containing available modifications for the given report. The "Title/Format" tab allows you to update the report title and select the format in which you want the report displayed, such as HTML or PDF. To filter the data by time period, choose the "Time Period" tab at the top of the page. To display data for 2021, select Specimen Date~Year with a beginning date of 2021 and an ending date of 2021.

Tip: For more descriptive variable labels on your report, check the box "Show descriptive variable names" that appears near the top of the modification window (recommended).



The "Filters" tab allows you to filter the data displayed in the report. For our example, we want to filter the report to show all the isolates that were collected from blood specimens. Select Specimen Group as the variable and use the "equal" operator. Use the drop-down menu to select "Blood".



The line list was exported to an Excel spreadsheet where we further filtered the onset to "HO" which indicates hospital-onset and Drug Description to "VANC – Vancomycin" since we are looking for vancomycin-resistant isolates.

Facility Org ID	Event ID	Patient ID	Fac Admission Date	Date Specimen Collected	Location	Isolate ID	Specimen Group	Drug Description	Final interpretation Description	Onset
33617	44768157	ENTDISBLD	12/25/2020	1/4/2021	MSICU	0121_Entero Dis BLD	Blood	VANC - Vancomycin	R - Resistant	HO
33617	44768158	ENTGILVBLD	12/22/2020	1/3/2021	ICU-A	0121_EnteroGilv BLD	Blood	VANC - Vancomycin	R - Resistant	HO
33617	44768160	ENTMORBLD	12/29/2020	1/3/2021	MSICU	0121_Entero Mora BLD	Blood	VANC - Vancomycin	R - Resistant	HO
33617	44768161	ENTPHOENBLD	12/21/2020	1/5/2021	ICU-A	0121_Entero Phoen BLD	Blood	VANC - Vancomycin	R - Resistant	HO
33617	44768162	ENTRATBLD	12/20/2020	1/1/2021	ICU-A	0121_Entero Ratti Bld	Blood	VANC - Vancomycin	R - Resistant	HO
33617	44768163	ENTVILLBLD	12/27/2020	1/3/2021	MEDWARD	0121_Entero Vill BLD	Blood	VANC - Vancomycin	R - Resistant	HO
33617	44768159	ENTHIRALRI	12/27/2020	1/5/2021	MEDWARD	0121_Entero Hirae BLD	Blood	VANC - Vancomycin	R - Resistant	HO

From the spreadsheet, we can see that three of the HO VRE bloodstream infections were reported from the facility's Surgical Critical Care unit (ICU-A), two were from the Medical Ward (MEDWARD), and two were from the

Medical-Surgical Critical Care (MSICU). All seven specimens were collected within five days of each other from January 1-January 5, 2021. With this information, the facility can review information about these patients in the Electronic Health Record (EHR) and determine if there were commonalities between them, including shared staff, shared equipment, or other factors.

Determine whether AR Option Events are also device-associated events

It might be helpful for facilities to compare their AR Option data with the data that have been submitted for other areas of NHSN such as the HAI Device-Associated Module. The Device-Associated Module includes central line-associated bloodstream infections (CLABSI), catheter-associated urinary tract infections (CAUTI), and ventilator-associated events (VAE). Please note that the locations under surveillance in the AR Option and the HAI Device-Associated Module may differ so there could be fewer HAI Events reported compared to AR Option Events.

Using the same example as above, we now know which AR Option Events we want to investigate further. We can assess whether these AR Option Events also meet HAI device-associated definitions, specifically for this example, if they were also CLABSIs or VAEs. We can then compare line lists for the same time period. The Device-Associated line listing reports can be found by selecting Device-Associated (DA) Module > Central Line-Associated BSI > Line Listing – All CLAB Events or Ventilator-Associated Events > Line Listing – All VAE. If you were looking at infections identified in urine and wanted to compare to the CAUTI line list, select Urinary Catheter-Associated UTI > Line Listing – All CAU Events. You would need to match the patient ID, date of birth, and admit date from the AR Option Event line listing to the line listing for device-associated events. If the AR Option Events were also determined to be device-related, we could tap into those specific infection prevention tools and resources to address any gaps.

Additional Resources

General AR Option Materials:

AUR Module Protocol:
https://www.cdc.gov/nhsn/pdfs/pscmanual/11pscaurcurrent.pdf

FAQs for the Antimicrobial Resistance Option:
https://www.cdc.gov/nhsn/faqs/faq-ar.html

NHSN AUR Module Training Presentations:
https://www.cdc.gov/nhsn/training/patient-safety-component/aur.html

NHSN AR Option Data Validation Protocol: https://www.cdc.gov/nhsn/pdfs/ps-analysis-resources/aur/ar-validation-508.pdf

SRIR and pSIR Specific Materials:

SRIR Quick Reference Guide: https://www.cdc.gov/nhsn/pdfs/ps-analysis-resources/aur/AR-Option-SRIR-Report_QRG_FINAL.pdf

pSIR Quick Reference Guide: https://www.cdc.gov/nhsn/pdfs/ps-analysis-resources/aur/AR-Option-pSIR-Report_QRG_FINAL.pdf

2023 NHSN Annual Training Video: https://www.youtube.com/watch?v=qEmKo8GpczU

2023 NHSN Annual Training Slides: https://www.cdc.gov/nhsn/pdfs/training/2023/New-AR-Option-Benchmark-Metrics-508.pdf

2024 NHSN Annual Training Video: https://www.youtube.com/watch?v=wat71p9bZZ0

General NHSN Materials:

NHSN Location Mapping:
https://www.cdc.gov/nhsn/pdfs/pscmanual/15locationsdescriptions_current.pdf

NHSN Annual Hospital Survey:
https://www.cdc.gov/nhsn/forms/57.103_pshospsurv_blank.pdf

Instructions for NHSN Annual Hospital Survey:
https://www.cdc.gov/nhsn/forms/instr/57_103-toi.pdf

NHSN Codes and Variables and Statistical Tools:
https://www.cdc.gov/nhsn/ps-analysis-resources/index.html

NHSN Data Dictionary:
https://www.cdc.gov/nhsn/xls/analysis/nhsn-data-dictionary.xlsx

NHSN Group Function:
https://www.cdc.gov/nhsn/group-users/index.html

NHSN Data Use Agreement (DUA):
https://www.cdc.gov/nhsn/about-nhsn/dua.html

Antimicrobial Resistance and Patient Safety Portal:
https://arpsp.cdc.gov/

Appendix A: SRIR Model Details

Table 1. Hospital-onset SRIRs

SRIR	Specimen Source	SRIR Type in NHSN
Hospital-onset Carbapenem-resistant Enterobacterales	Blood	HO_CREall_Blood
	Lower Respiratory Tract	HO_CREall_LRT
	Urine	HO_CREall_Urine
Hospital-onset Extended-spectrum cephalosporin-resistant Enterobacterales	Blood	HO_ESCEall_Blood
	Lower Respiratory Tract	HO_ESCEall_LRT
	Urine	HO_ESCEall_Urine
Hospital-onset Fluoroquinolone-resistant Enterobacterales	Blood	HO_FQE_Blood
	Lower Respiratory Tract	HO_FQE_LRT
	Urine	HO_FQE_Urine
Hospital-onset Vancomycin-resistant *Enterococcus*	Blood	HO_VRE_Blood
	Lower Respiratory Tract	HO_VRE_LRT
	Urine	HO_VRE_Urine
Hospital-onset Fluoroquinolone-resistant *Pseudomonas aeruginosa*	Blood	HO_FQPA_Blood
	Lower Respiratory Tract	HO_FQPA_LRT
	Urine	HO_FQPA_Urine
Hospital-onset Multidrug-resistant *Pseudomonas aeruginosa*	Blood	HO_MDR_PA_Blood
	Lower Respiratory Tract	HO_MDR_PA_LRT
	Urine	HO_MDR_PA_Urine
Hospital-onset Methicillin-resistant *Staphylococcus aureus*	Blood	HO_MRSA_Blood
	Lower Respiratory Tract	HO_MRSA_LRT
	Urine	HO_MRSA_Urine

NHSN included 2019 baseline Standardized Resistance Infection Ratio (SRIR) risk models by drug-resistant pathogen and specimen source below.

Table 2. Hospital-onset Carbapenem-resistant Enterobacterales

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
BLOOD						
Intercept	-12.4225	0.2247	-12.8629	-11.9821	3056.48	<.0001
CO Prevalence >0	0.8500	0.3167	0.2293	1.4707	7.20	0.0073
CO Prevalence =0	REF	.	.	.	.	.
Dispersion	1.6335	0.5519	0.8424	3.1676		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
URINE						
Intercept	-13.7045	0.4300	-14.5474	-12.8616	1015.58	<.0001
CO Prevalence >1.3	1.5200	0.2781	0.9749	2.0651	29.87	<.0001
CO Prevalence ≤1.3	REF	.	.	.	.	.
Hospital LOS ≥4.0	1.3151	0.3836	0.5632	2.0670	11.75	0.0006
Hospital LOS <4.0	REF	.	.	.	.	.
Dispersion	0.6333	0.2186	0.3219	1.2457		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
LRT						
Intercept	-12.2678	0.3174	-12.8899	-11.6458	1494.00	<.0001
CO Prevalence >0	0.8087	0.2231	0.3714	1.2461	13.14	0.0003
CO Prevalence =0	REF	.	.	.	.	.
Hospital LOS ≥4.0	0.8263	0.3343	0.1712	1.4815	6.11	0.0134
Hospital LOS <4.0	REF	.	.	.	.	.
Dispersion	0.6769	0.2223	0.3556	1.2884		

Table 3. Hospital-onset Extended-spectrum cephalosporin-resistant Enterobacterales

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
BLOOD						
Intercept	-10.7032	0.0983	-10.8957	-10.5106	11867.30	<.0001
CO Prevalence >13.3	0.7053	0.1287	0.4530	0.9576	30.03	<.0001
CO Prevalence ≤13.3	REF	.	.	.	.	.
Hospital LOS >5.4	0.9502	0.1550	0.6464	1.2541	37.57	<.0001
Hospital LOS 4.9-5.4	0.4933	0.1485	0.2021	0.7844	11.03	0.0009
Hospital LOS <5.4	REF	.	.	.	.	.
Dispersion	0.4252	0.0789	0.2956	0.6116		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
URINE						
Intercept	-9.9663	0.1611	-10.2821	-9.6506	3826.76	<.0001
CO Prevalence >47.3	0.9689	0.1581	0.6591	1.2788	37.57	<.0001
CO Prevalence 20.7 - 47.3	0.5580	0.1761	0.2128	0.9032	10.04	0.0015
CO Prevalence <20.7	REF	.	.	.	.	.

Hospital LOS >4.2	0.5912	0.0861	0.4224	0.7599	47.13	<.0001
Hospital LOS ≤4.2	REF	.	.	.	.	.
Dispersion	0.2537	0.0360	0.1920	0.3351		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
LRT						
Intercept	-9.9369	0.0980	-10.1289	-9.7448	10284.20	<.0001
CO Prevalence >3.8	0.9309	0.1190	0.6978	1.1641	61.24	<.0001
CO Prevalence 2.2 - 3.8	0.5327	0.1255	0.2868	0.7786	18.03	<.0001
CO Prevalence ≤2.1	REF	.	.	.	.	.
Number of Beds >239	0.4864	0.1040	0.2826	0.6902	21.87	<.0001
Number of Beds ≤239	REF	.	.	.	.	.
Dispersion	0.3305	0.0515	0.2435	0.4487		

Table 4. Hospital-onset Fluoroquinolone-resistant Enterobacterales

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
BLOOD						
Intercept	-10.7757	0.1031	-10.9777	-10.5736	10925.50	<.0001
CO Prevalence >13.7	0.7715	0.1276	0.5214	1.0216	36.57	<.0001
CO Prevalence ≤13.7	REF	.	.	.	.	.
Hospital LOS ≥5.5	0.8344	0.1511	0.5382	1.1307	30.48	<.0001
Hospital LOS <5.5	REF	.	.	.	.	.
Dispersion	0.5716	0.0938	0.4144	0.7885		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
URINE						
Intercept	-9.2554	0.1063	-9.4637	-9.0471	7583.16	<.0001
CO Prevalence >171.8	0.3183	0.0780	0.1655	0.4712	16.66	<.0001
CO Prevalence ≤171.8	REF	.	.	.	.	.
Hospital LOS >3.4	0.7441	0.1109	0.5267	0.9615	44.99	<.0001
Hospital LOS ≤3.4	REF	.	.	.	.	.
Dispersion	0.2505	0.0316	0.1957	0.3208		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
LRT						
Intercept	-10.3816	0.0986	-10.5750	-10.1883	11078.30	<.0001
CO Prevalence >7.4	1.2855	0.1413	1.0086	1.5624	82.79	<.0001
CO Prevalence 2.6-7.4	0.7652	0.0983	0.5725	0.9578	60.58	<.0001
CO Prevalence <2.6	REF	.	.	.	.	.
Number of Beds >228	0.3818	0.1007	0.1845	0.5791	14.38	0.0001
Number of Beds ≤228	REF	.	.	.	.	.
Dispersion	0.2398	0.0458	0.1650	0.3486		

Table 5. Hospital-onset Vancomycin-resistant *Enterococcus*

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
BLOOD						
Intercept	-11.6162	0.1242	-11.8596	-11.3729	8752.15	<.0001
CO Prevalence ≥2.3	1.4314	0.1759	1.0866	1.7761	66.23	<.0001
CO Prevalence 1.1 - 2.2	0.7994	0.1921	0.4228	1.1759	17.31	<.0001
CO Prevalence <1.1	REF	.	.	.	.	.
Hospital LOS ≥5.4	0.5908	0.1638	0.2696	0.9119	13.00	0.0003
Hospital LOS <5.4	REF	.	.	.	.	.
Dispersion	0.4313	0.1114	0.2600	0.7155		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
URINE						
Intercept	-10.8789	0.1357	-11.1448	-10.6130	6429.54	<.0001
CO Prevalence >9.7	1.8227	0.1576	1.5138	2.1316	133.73	<.0001
CO Prevalence 3.2 - 9.7	1.0742	0.1561	0.7683	1.3801	47.38	<.0001
CO Prevalence ≤3.1	REF	.	.	.	.	.
Dispersion	0.3987	0.0670	0.2869	0.5541		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
LRT						
Intercept	-12.3249	0.1763	-12.6705	11.9793	4885.62	<0.0001
Scale	1.1828	0.0000	1.1828	1.1828		
***POISSON WITH SCALE=PEARSON						

Table 6. Hospital-onset Fluoroquinolone-resistant *Pseudomonas aeruginosa*

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
BLOOD						
Intercept	-11.9903	0.1313	-12.2476	-11.7331	8344.85	<.0001
CO Prevalence ≥1.5	0.7268	0.2675	0.2025	1.2510	7.38	0.0066
CO Prevalence <1.5	REF	.	.	.	.	.
Dispersion	0.5945	0.2613	0.2512	1.4070		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
URINE						
Intercept	-11.1614	0.1238	-11.4041	-10.9187	8122.51	<.0001
CO Prevalence >10.3	1.0308	0.1527	0.7315	1.3301	45.57	<.0001
CO Prevalence 5.2-10.3	0.7261	0.1497	0.4327	1.0196	23.53	<.0001
CO Prevalence ≤5.1	REF	.	.	.	.	.
Dispersion	0.2113	0.0717	0.1087	0.4107		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
LRT						
Intercept	-11.0471	0.1796	-11.3991	-10.6951	3783.38	<.0001
CO Prevalence >10.3	1.8338	0.1918	1.4580	2.2097	91.45	<.0001
CO Prevalence 1.8-10.3	0.9992	0.1378	0.7291	1.2693	52.56	<.0001
CO Prevalence ≤1.7	REF	.	.	.	.	.
Number of ICU Beds >14	0.5341	0.1492	0.2417	0.8264	12.82	0.0003
Number of ICU Beds ≤14	REF	.	.	.	.	.
Dispersion	0.3713	0.0610	0.2691	0.5123		

Table 7. Hospital-onset Multidrug-resistant *Pseudomonas aeruginosa*

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
BLOOD						
Intercept	-12.3284	0.1704	-12.6624	-11.9944	5235.03	<0.0001
Percent ICU Beds >19.8	0.6047	0.2625	0.0903	1.1192	5.31	0.0212
Percent ICU Beds ≤19.8	REF	.	.	.	.	.
Dispersion	0.8265	0.3617	0.3505	1.9489		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
URINE						
Intercept	-12.6195	0.3510	-13.3075	-11.9315	1292.51	<0.0001
CO Prevalence >1.9	1.8095	0.3604	1.1031	2.5159	25.21	<0.0001
CO Prevalence 0.7-1.9	0.9290	0.3942	0.1563	1.7016	5.55	0.0184
CO Prevalence ≤0.6	REF	.	.	.	.	.
Dispersion	0.4015	0.1160	0.2279	0.7075		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
LRT						
Intercept	-10.0791	0.0728	-10.2217	-9.9365	19184.40	<.0001
CO Prevalence >7.3	1.0633	0.2128	0.6463	1.4803	24.97	<.0001
CO Prevalence ≤7.3	REF	.	.	.	.	.
Dispersion	0.9369	0.1287	0.7157	1.2264		

Table 8. Hospital-onset Methicillin-resistant *Staphylococcus aureus*

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
BLOOD						
Intercept	-10.4323	0.0953	-10.6191	-10.2455	11976.00	<.0001
CO Prevalence >15.3	0.3476	0.0821	0.1867	0.5084	17.93	<.0001
CO Prevalence ≤15.3	REF	.	.	.	.	.
Number of ICU Beds >36	0.2933	0.0922	0.1127	0.4740	10.13	0.0015
Number of ICU Beds ≤36	REF	.	.	.	.	.
Hospital LOS ≥5.0	0.2493	0.0830	0.0865	0.4120	9.01	0.0027
Hospital LOS <5.0	REF	.	.	.	.	.
Dispersion	0.1112	0.0354	0.0596	0.2074		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
URINE						
Intercept	-11.6552	0.1597	-11.9683	-11.3422	5325.49	<.0001
CO Prevalence >6.3	0.5204	0.1347	0.2565	0.7844	14.93	0.0001
CO Prevalence ≤6.3	REF	.	.	.	.	.
Percent ICU Beds <20.4	0.5622	0.1514	0.2654	0.8590	13.79	0.0002
Percent ICU Beds ≥20.4	REF	.	.	.	.	.
Dispersion						

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
LRT						
Intercept	-10.4437	0.1882	-10.8126	-10.0748	3078.94	<.0001
CO Prevalence >13.9	1.9979	0.1841	1.6370	2.3588	117.72	<.0001
CO Prevalence 6.4 - 13.9	1.5333	0.1826	1.1753	1.8912	70.48	<.0001
CO Prevalence 1.9 - 6.3	1.0986	0.1906	0.7250	1.4723	33.21	<.0001
CO Prevalence ≤1.8	REF	.	.	.	.	.
Hospital LOS >3.7	0.3321	0.0907	0.1544	0.5099	13.42	0.0002
Hospital LOS <3.7	REF	.	.	.	.	.
Dispersion	0.1683	0.0235	0.1279	0.2213		

Appendix B: pSIR Model Details

Table 1. Hospital-onset pSIRs

pSIR	Specimen Source	pSIR Type in NHSN
Hospital-onset Enterobacterales	Blood	HO_Enterobacterales_Blood
	Lower Respiratory Tract	HO_Enterobacterales_LRT
	Urine	HO_Enterobacterales_Urine
Hospital-onset *Enterococcus*	Blood	HO_Enterococcus_Blood
	Lower Respiratory Tract	HO_Enterococcus_LRT
	Urine	HO_Enterococcus_Urine
Hospital-onset *Staphylococcus aureus*	Blood	HO_SA_Blood
	Lower Respiratory Tract	HO_SA_LRT
	Urine	HO_SA_Urine
Hospital-onset *Pseudomonas aeruginosa*	Blood	HO_PA_Blood
	Lower Respiratory Tract	HO_PA_LRT
	Urine	HO_PA_Urine

NHSN included 2019 baseline Pathogen-specific Standardized Infection Ratio (pSIR) risk models by pathogen and specimen source below.

Table 2. Hospital-onset Enterobacterales

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
BLOOD						
Intercept	-9.3485	0.0645	-9.4749	-9.2220	20997.40	<.0001
Number of ICU Beds ≥96	0.6452	0.0965	0.4560	0.8344	44.66	<.0001
Number of ICU Beds 64 - 95	0.3013	0.0987	0.1079	0.4948	9.32	0.0023
Number of ICU Beds <64	REF	.	.	.	.	.
Hospital LOS ≥5.0	0.5095	0.0872	0.3386	0.6804	34.13	<.0001
Hospital LOS 4.3 - 4.9	0.1974	0.0876	0.0256	0.3691	5.07	0.0243
Hospital LOS <4.3	REF	.	.	.	.	.
Dispersion	0.2204	0.0309	0.1675	0.2901		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
URINE						
Intercept	-7.6367	0.0686	-7.7711	-7.5023	12401.90	<.0001
Hospital LOS ≥4.5	0.6408	0.0758	0.4923	0.7893	71.51	<.0001

Hospital LOS 3.5 - 4.4	0.3327	0.0818	0.1723	0.4931	16.53	<.0001
Hospital LOS <3.5	REF	.	.	.	.	.
Facility Type CAH, ONC, REHAB	1.0049	0.1100	0.7894	1.2204	83.52	<.0001
Facility Type CHLD, GEN, LTAC, PSYCH, SURG, WOM, WOMCHILD	REF	.	.	.	.	.
Dispersion	0.1894	0.0173	0.1583	0.2265		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
LRT						
Intercept	-9.3992	0.2988	-9.9849	-8.8135	989.24	<.0001
Number of ICU Beds ≥93	1.8213	0.3162	1.2015	2.4411	33.17	<.0001
Number of ICU Beds 29 - 92	1.5131	0.3040	0.9173	2.1089	24.78	<.0001
Number of ICU Beds 12 - 28	1.1398	0.3084	0.5354	1.7443	13.66	0.0002
Number of ICU Beds 6 - 11	0.8286	0.3169	0.2076	1.4497	6.84	0.0089
Number of ICU Beds <6	REF	.	.	.	.	.
Dispersion	0.3916	0.0378	0.3241	0.4732		

Table 3. Hospital-onset *Enterococcus*

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
BLOOD						
Intercept	-10.6162	0.1247	-10.8605	-10.3718	7252.45	<.0001
Number of Beds ≥469	0.8387	0.1342	0.5757	1.1018	39.06	<.0001
Number of Beds 269 - 468	0.3351	0.1130	0.1136	0.5567	8.79	0.003
Number of Beds <269	REF	.	.	.	.	.
LOS ≥5.3	0.8700	0.1561	0.5641	1.1759	31.07	<.0001
LOS 4.0 - 5.2	0.4678	0.1441	0.1853	0.7503	10.54	0.0012
LOS <4.0	REF	.	.	.	.	.
Dispersion	0.3386	0.0519	0.2507	0.4571		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
URINE						
Intercept	-8.5735	0.0631	-8.6971	-8.4499	18488.00	<.0001
Hospital LOS ≥6.5	0.9199	0.1370	0.6515	1.1884	45.12	<.0001
Hospital LOS 4.2 - 6.4	0.5119	0.0777	0.3597	0.6641	43.46	<.0001
Hospital LOS <4.2	REF	.	.	.	.	.
Dispersion	0.3514	0.0346	0.2897	0.4262		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
LRT						
Intercept	-11.4261	0.1633	-11.7462	-11.1060	4894.40	<.0001
Hospital LOS ≥4.5	0.6743	0.2027	0.2770	1.0715	11.07	0.0009
Hospital LOS <4.5	REF	.	.	.	.	.
Dispersion	1.7909	0.2827	1.3143	2.4403		

Table 4. Hospital-onset *Staphylococcus aureus*

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
BLOOD						
Intercept	-9.5228	0.0600	-9.6404	-9.4051	25163.60	<.0001
Number of ICU Beds ≥30	0.3814	0.0677	0.2488	0.5140	31.77	<.0001
Number of ICU Beds <30	REF	.	.	.	.	.
Hospital LOS ≥5.0	0.2635	0.0603	0.1453	0.3818	19.08	<.0001
Hospital LOS <5.0	REF	.	.	.	.	.
Dispersion	0.1048	0.0219	0.0696	0.1580		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
URINE						
Intercept	-11.1682	0.1856	-11.5320	-10.8045	3621.60	<.0001
Hospital LOS ≥3.7	0.7579	0.1929	0.3799	1.1359	15.44	<.0001
Hospital LOS <3.7	REF	.	.	.	.	.
Dispersion	0.2254	0.0673	0.1255	0.4048		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
LRT						
Intercept	-9.8210	0.3132	-10.4348	-9.2072	983.51	<.0001
Number of ICU Beds ≥38	1.8075	0.3106	1.1987	2.4163	33.86	<.0001
Number of ICU Beds 12 - 37	1.5059	0.3118	0.8947	2.1170	23.32	<.0001
Number of ICU Beds 6 - 11	1.1365	0.3220	0.5054	1.7675	12.46	0.0004
Number of ICU Beds <6	REF	.	.	.	.	.
Hospital LOS ≥3.9	0.2502	0.0866	0.0804	0.4200	8.34	0.0039
Hospital LOS <3.9	REF	.	.	.	.	.
Dispersion	0.2901	0.0286	0.2392	0.3519		

Table 5. Hospital-onset *Pseudomonas aeruginosa*

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
BLOOD						
Intercept	-11.3590	0.2386	-11.8266	-10.8914	2266.66	<0.0001
Hospital LOS ≥4.5	0.5701	0.1269	0.3213	0.8189	20.17	<0.0001
Hospital LOS <4.5	REF	.	.	.	.	.
Number of ICU Beds ≥59	0.8840	0.2481	0.3977	1.3704	12.69	0.0004
Number of ICU Beds 12 - 58	0.5490	0.2444	0.0700	1.0279	5.05	0.0247
Number of ICU Beds <12	REF	.	.	.	.	.
Dispersion	0.4980	0.0929	0.3456	0.7177		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
URINE						
Intercept	-10.4926	0.2704	-11.0225	-9.9626	1506.03	<.0001
Facility type CAH, LTAC, PYSCH, REHAB	2.1974	0.2958	1.6177	2.7771	55.20	<.0001
Facility type GEN, SURG, ONC	1.1045	0.2483	0.6178	1.5912	19.78	<.0001
Facility type CHLD, WOM, WOMCHILD	REF	.	.	.	.	.
Hospital LOS ≥4.5	0.7095	0.1219	0.4705	0.9485	33.86	<.0001
Hospital LOS 3.5 - 4.4	0.3816	0.1305	0.1257	0.6374	8.55	0.0035
Hospital LOS <3.5	REF	.	.	.	.	.
Dispersion	0.2464	0.0321	0.1909	0.3181		

Parameter	Estimate	Standard Error	Wald 95% Confidence Limits		Wald χ2	χ2 P-Value
LRT						
Intercept	-8.8433	0.0915	-9.0226	-8.6639	9339.91	<.0001
Number of ICU Beds ≥46	0.8324	0.1123	0.6122	1.0526	54.91	<.0001
Number of ICU Beds 14 - 45	0.5158	0.1139	0.2926	0.7390	20.51	<.0001
Number of ICU Beds <14	REF	.	.	.	.	.
Dispersion	0.4664	0.0455	0.3851	0.5648		