

CDC Antimicrobial Resistance Threats Report

Infections and Deaths Aggregation Methods

The Antimicrobial Resistance Threats Report provides estimates of infections and deaths for 19 bacterial and fungal pathogens that threaten human health in the United States. Because CDC used the best available data for each pathogen, estimates were generated from multiple data sources, each with a different approach for calculating the total number of infections or deaths and the uncertainty surrounding the estimate.

A two-step approach was used to determine the total number of infections and deaths with credible intervals (range of values likely to include the true value) for all 19 pathogens. First, a probability distribution was created for each pathogen that reflected the underlying estimation methods. Next, the included probability distributions were combined, or convolved, into one overall distribution. Using this overall distribution, the median and 95% quantile range were used to estimate the combined infections and deaths with credible intervals (the range of values likely to include the true value) included in this report.

Distributions for each pathogen

Because of the large number of reported infections, a normal distribution was assumed for certain pathogens based on the reported mean and standard deviation. An empirical distribution was assumed for pathogens that used models to estimate the number of infections or deaths. The infection or death counts were used as input data. Finally, on occasion it was assumed that all infections were reported for certain pathogens, and their point estimates were added to the final combined estimate. See the table below describing the assumed distribution for each pathogen in the latest combined estimates of infections and deaths. When combined, carbapenem-resistant Enterobacterales (CRE) infections were removed from the extended-spectrum cephalosporin-resistant Enterobacterales (ESC-RE) infections. *Candida auris* pathogen estimates were not included in the combined estimate because hospitalized, drug-resistant *Candida auris* infections are included in drug-resistant *Candida* estimates.

Combined distribution (convolution)

To estimate the total number of infections or deaths, the distributions of all included pathogens were combined/convolved [1]. Importantly, it was assumed that all included pathogen distributions were independent; this assumption allowed the distributions to be combined. To combine the distributions, all the values were converted into discrete numbers. A metadistribution was then produced based on how frequently each value appeared using a Fourier transform.

Analysis and code availability

Analyses were conducted using Python 3.9.6.

Table: Included pathogens and assumed distributions for convolution

Pathogen	Assumed distribution*
<i>Candida auris</i> (<i>C.auris</i>)**	Not Applicable
Carbapenem-resistant <i>Acinetobacter</i>	Empirical
Carbapenem-resistant Enterobacterales (CRE)	Empirical
Drug-resistant <i>Neisseria gonorrhoeae</i>	Empirical (infections) / Point estimate (deaths)
<i>Clostridioides difficile</i> (<i>C. diff</i>)	Normal
Drug-resistant <i>Campylobacter</i>	Empirical
Drug-resistant <i>Candida</i>	Empirical
Drug-resistant <i>Mycobacterium tuberculosis</i>	Point estimate
Drug-resistant <i>Neisseria meningitidis</i>	Empirical
Drug-resistant nontyphoidal <i>Salmonella</i>	Empirical
Drug-resistant <i>Salmonella</i> Typhi	Empirical
Drug-resistant <i>Shigella</i>	Empirical
Drug-resistant <i>Streptococcus pneumoniae</i>	Empirical
Extended-spectrum cephalosporin-resistant Enterobacterales (ESC-RE)**	Empirical
Methicillin-resistant <i>Staphylococcus aureus</i> (MRSA)	Empirical
Multidrug-resistant <i>Pseudomonas aeruginosa</i>	Empirical
Vancomycin-resistant <i>Enterococcus</i> (VRE)	Empirical
Drug-resistant group A <i>Streptococcus</i> (GAS)	Empirical
Clindamycin-resistant group B <i>Streptococcus</i> (GBS)	Empirical

* Distribution assumed to be the same for infections and deaths, except as noted for drug-resistant *Neisseria gonorrhoeae*.

** When estimates of infections were combined, CRE infections were removed from ESC-RE infections. *C. auris* pathogen estimates were not included in the combined estimate because hospitalized, drug-resistant *C. auris* is included in drug-resistant *Candida* estimates.

References

1. Ruckdeschel P, Kohl M. General Purpose Convolution Algorithm in S4 Classes by Means of FFT. *J Stat Soft*. 2014;59(4):1-25. <https://doi.org/10.18637/jss.v059.i04>



For more information on the Antimicrobial Resistance Threats Report, visit: <https://arthreats.cdc.gov>



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