

# Antimicrobial Resistance (AMR)

## Surveillance report

Hospital name: **Hypothetical Hospital**

Country name: **Hypothetical Country**

Data from:

**02 Jan 2016 to 10 Jan 2017**

Contact person: **xxx\_Can be changed in the dictionary\_of\_variable\_data.csv\_xxx**

Contact address: **xxx\_Can be changed in the dictionary\_of\_variable\_data.csv\_xxx**

Contact email: **xxx@xxx.xxx**

Generated on: **07 Nov 2022**

**Generated by**

AutoMated tool for Antimicrobial resistance Surveillance System (AMASS) version 2.0  
(released on 16 May 2022)

The AMASS application is available under the Creative Commons Attribution 4.0 International Public License (CC BY 4.0). The application can be downloaded at :  
<https://www.amass.website>

The AMASS application used microbiology\_data and hospital\_admission\_data files that are stored in the same folder as the application (AMASS.bat) to generate this report.

The goal of the AMASS application is to enable hospitals with microbiology data available in electronic formats to analyze their own data and generate AMR surveillance reports promptly. If hospital admission data are available, the reports will additionally be stratified by infection origin (community–origin or hospital–origin). If mortality data (such as patient discharge outcome data) are available, a report on mortality involving AMR infection will be added.

This automatically generated report has limitations, and requires users to understand those limitations and use the summary data in the report with careful interpretation.

A valid report could have local implications and much wider benefits if shared with national and international organizations.

This automatically generated report is under the jurisdiction of the hospital to copy, redistribute, and share with any individual or organization.

This automatically generated report contains no patient identifier, similar to standard reports on cumulative antimicrobial susceptibility.

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**Suggested title for citation:**

Antimicrobial resistance surveillance report, Hypothetical Hospital,  
Hypothetical Country, 02 Jan 2016 to 10 Jan 2017.

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# Introduction

Antimicrobial resistance (AMR) is a global health crisis [1]. The report by Lord Jim O'Neill estimated that 700,000 global deaths could be attributable to AMR in 2015, and projected that the annual death toll could reach 10 million by 2050 [1]. However, data of AMR surveillance from low and middle-income countries (LMICs) are scarce [1,2], and data of mortality associated with AMR infections are rarely available. A recent study estimated that 19,000 deaths are attributable to AMR infections in Thailand annually, using routinely available microbiological and hospital databases [3]. The study also proposed that hospitals in LMICs should utilize routinely available microbiological and hospital admission databases to generate reports on AMR surveillance systematically [3].

Reports on AMR surveillance can have a wide range of benefits [2]; including

- characterization of the frequency of resistance and organisms in different facilities and regions;
- prospective and retrospective information on emerging public health threats;
- evaluation and optimization of local and national standard treatment guidelines;
- evaluation of the impact of interventions beyond antimicrobial guidelines that aim to reduce AMR; and
- data sharing with national and international organizations to support decisions on resource allocation for interventions against AMR and to inform the implementation of action plans at national and global levels.

When reporting AMR surveillance results, it is generally recommended that (a) duplicate results of bacterial isolates are removed, and (b) reports are stratified by infection origin (community-origin or hospital-origin), if possible [2]. Many hospitals in LMICs lack time and resources needed to analyze the data (particularly to deduplicate data and to generate tables and figures), write the reports, and to release the data or reports [4].

AutoMated tool for Antimicrobial resistance Surveillance System (AMASS) was developed as an offline, open-access and easy-to-use application that allows a hospital to perform data analysis independently and generate isolate-based and sample-based surveillance reports stratified by infection origin from routinely collected electronic databases. The application was built in R, which is a free software environment. The application has been placed within a user-friendly interface that only requires the user to double-click on the application icon. The AMASS application can be downloaded at: <https://www.amass.website>

The AMASS version 2.0 additionally generates reports on notifiable bacterial diseases in Annex A and on data indicators (including proportion of contaminants and discordant AST results) in Annex B for the "microbiology\_data" file that is used to generate this report. A careful review of the Annex B could help readers and data owners to identify potential errors in the microbiology data used to generate the report.

The AMASS version 2.0 also separately generates Supplementary data indicators report (in PDF and Excel formats) in a new folder "Report\_with\_patient\_identifiers" to support users to check and validate records with notifiable bacteria, notifiable antibiotic-pathogen combinations, infrequent phenotypes or potential errors in the AST results at the local level. The identifiers listed include hospital number and specimen collection date. The files are generated in a separate folder "Report\_with\_patient\_identifiers" so that it is clear that users should not share or transfer the Supplementary Data Indicators report (in PDF and Excel format) to any party outside of the hospital without data security management and confidential agreement.

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#### References:

- [1] O'Neill J. (2014) Antimicrobial resistance: tackling a crisis for the health and wealth of nations. Review on antimicrobial resistance. <http://amr-review.org>. (accessed on 3 Dec 2018).
- [2] World Health Organization (2018) Global Antimicrobial Resistance Surveillance System (GLASS) Report. Early implantation 2016–2017. <http://apps.who.int/iris/bitstream/handle/10665/259744/9789241513449-eng.pdf>. (accessed on 3 Dec 2018)
- [3] Lim C., et al. (2016) Epidemiology and burden of multidrug-resistant bacterial infection in a developing country. *Elife* 5: e18082.
- [4] Ashley EA, Shetty N, Patel J, et al. Harnessing alternative sources of antimicrobial resistance data to support surveillance in low-resource settings. *J Antimicrob Chemother*. 2019; 74(3):541–546.
- [5] Clinical and Laboratory Standards Institute (CLSI). Analysis and Presentation of Cumulative Antimicrobial Susceptibility Test Data, 4th Edition. 2014. (accessed on 21 Jan 2020)
- [6] European Antimicrobial Resistance Surveillance Network (EARS-Net). Antimicrobial resistance (AMR) reporting protocol 2018. (accessed on 21 Jan 2020)
- [7] European Committee on Antimicrobial Susceptibility Testing (EUCAST). [www.eucast.org](http://www.eucast.org) (accessed on 21 Jan 2020)

## Section [1]: Data overview

### Introduction

An overview of the data detected by the AMASS application is generated by default. The summary is based on the raw data files saved within the same folder as the application file (AMASS.bat).

Please review and validate this section carefully before proceeds to the next section.

### Results

The microbiology\_data file (stored in the same folder as the application file) had:

**50404** specimen data records with collection dates ranging from  
**02 Jan 2016** to **10 Jan 2017**

The hospital\_admission\_data file (stored in the same folder as the application file) had:

**NA** admission data records with hospital admission dates ranging from  
**NA** to **NA**

The total number of patient-days was **NA**.

The total number of patient-days at risk of BSI of hospital-origin was **NA**.

### Note:

[1] If the periods of the data in microbiology\_data and hospital\_admission\_data files are not similar, the automatically-generated report should be interpreted with caution. The AMASS generates the reports based on the available data.

[2] A patient is defined as at risk of BSI of hospital-origin when the patient is admitted to the hospital for more than two calendar days with calendar day one equal to the day of admission.

## Reporting period by months:

Data was stratified by month to assist detection of missing data, and verification of whether the month distribution of data records in microbiology\_data file and hospital\_admission\_data file reflected the microbiology culture frequency and admission rate of the hospital, respectively. For example if the number of specimens in the microbiology\_data file reported below is lower than what is expected, please check the raw data file and data dictionary files.

Month	Number of specimen data records in microbiology_data file	Number of admission data records in hospital_admission_data file
January	4197	
February	4059	
March	4332	
April	4269	
May	4317	
June	4022	
July	4301	
August	4296	
September	3975	
October	4302	
November	4131	
December	4203	
Total	50404	NA

### Note:

[1] Additional general demographic data will be made available in the next version of the AMASS application.

## Section [2]: Isolate-based surveillance report

### Introduction

An isolate-based surveillance report is generated by default, even if the hospital\_admission\_data file is unavailable. This is to enable hospitals with only microbiology data available to utilize the de-duplication and report generation functions of AMASS. This report is without stratification by origin of infection.

The report generated by the AMASS application version 2.0 includes only blood samples. The next version of AMASS will include other specimen types, including cerebrospinal fluid (CSF), urine, stool, and other specimens.

### Organisms under this survey:

- *Staphylococcus aureus*
- *Enterococcus* spp.
- *Streptococcus pneumoniae*
- *Salmonella* spp.
- *Escherichia coli*
- *Klebsiella pneumoniae*
- *Pseudomonas aeruginosa*
- *Acinetobacter baumannii*

### Results

The microbiology\_data file had:

*Sample collection dates ranged from **02 Jan 2016** to **10 Jan 2017***

*Number of records of blood specimens collected within the above date range:*

**15878 blood specimens records**

*Number of records of blood specimens with \*negative culture (no growth):*

**13315 blood specimens records**

*Number of records of blood specimens with culture positive for a microorganism:*

**2563 blood specimens records**

*Number of records of blood specimens with culture positive for organism under this survey:*

**910 blood specimens records**



The AMASS application de-duplicated the data by including only the first isolate per patient per specimen type per evaluation period as described in the method. The number of patients with positive samples is as follows:

Organism	Number of records of blood specimens culture positive for the organism	**Number of patients with blood culture positive for the organism (de-duplicated)
<i>Staphylococcus aureus</i>	113	96
<i>Enterococcus</i> spp.	53	47
<i>Streptococcus pneumoniae</i>	25	20
<i>Salmonella</i> spp.	43	35
<i>Escherichia coli</i>	384	339
<i>Klebsiella pneumoniae</i>	135	120
<i>Pseudomonas aeruginosa</i>	56	48
<i>Acinetobacter baumannii</i>	101	90
<b>Total:</b>	<b>910</b>	<b>795</b>

\*The negative culture included data values specified as 'no growth' in the dictionary\_for\_microbiology\_data file (details on data dictionary files are in the method section) to represent specimens with negative culture for any microorganism.

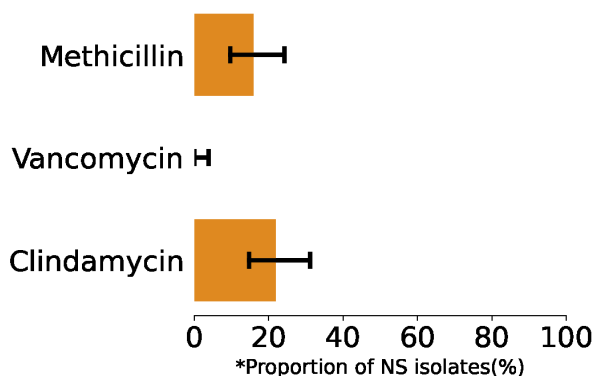
\*\*Only the first isolate for each patient per specimen type, per pathogen, and per evaluation period was included in the analysis.

The following figures and tables show the proportion of patients with blood culture positive for antimicrobial non-susceptible isolates.

## Section [2]: Isolate-based surveillance report

**Blood: *Staphylococcus aureus***

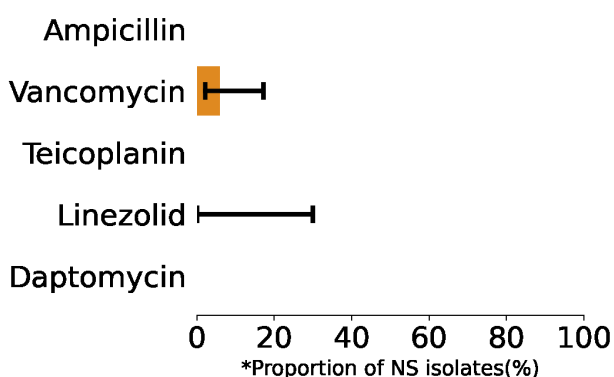
( No. of patients = 96 )



Antibiotic agent	Proportion of NS isolates (n)	95% CI
Methicillin	16% (15/96)	10% - 24%
Vancomycin	0% (0/96)	0% - 4%
Clindamycin	22% (21/96)	15% - 31%

**Blood: *Enterococcus* spp.**

( No. of patients = 47 )



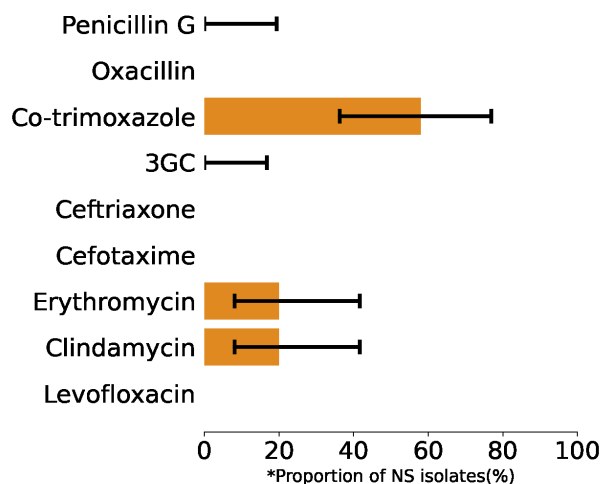
Antibiotic agent	Proportion of NS isolates (n)	95% CI
Ampicillin	NA	-
Vancomycin	6% (3/47)	2% - 17%
Teicoplanin	NA	-
Linezolid	0% (0/9)	0% - 30%
Daptomycin	NA	-

\*Proportion of non-susceptible (NS) isolates represents the number of patients with blood culture positive for non-susceptible isolates (numerator) over the total number of patients with blood culture positive for the organism and the organism was tested for susceptibility against the antibiotic (denominator). The AMASS application de-duplicated the data by including only the first isolate per patient per specimen type per evaluation period. Grey bars indicate that testing with the antibiotic occurred for less than 70% of the total number of patients with blood culture positive for the organism. CI=confidence interval; NA=Not available/reported/tested; Methicillin: methicillin, oxacillin, or ceftiofur

## Section [2]: Isolate-based surveillance report

### Blood: *Streptococcus pneumoniae*

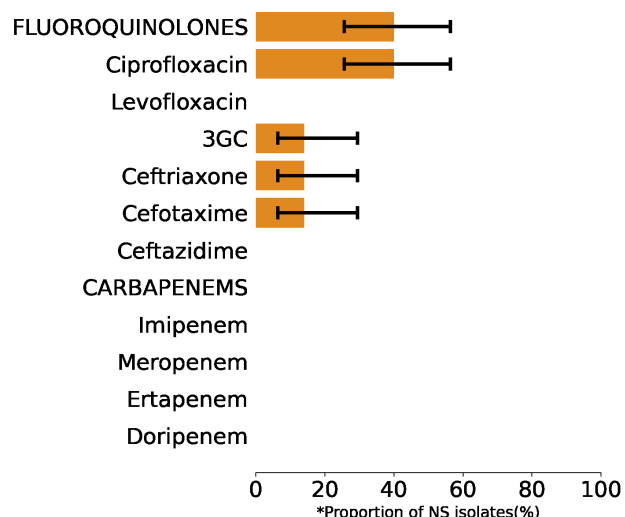
( No. of patients = 20 )



Antibiotic agent	Proportion of NS isolates (n)	95% CI
Penicillin G	0% (0/16)	0% - 19%
Oxacillin	NA	-
Co-trimoxazole	58% (11/19)	36% - 77%
3GC	0% (0/19)	0% - 17%
Ceftriaxone	NA	-
Cefotaxime	NA	-
Erythromycin	20% (4/20)	8% - 42%
Clindamycin	20% (4/20)	8% - 42%
Levofloxacin	NA	-

### Blood: *Salmonella* spp.

( No. of patients = 35 )



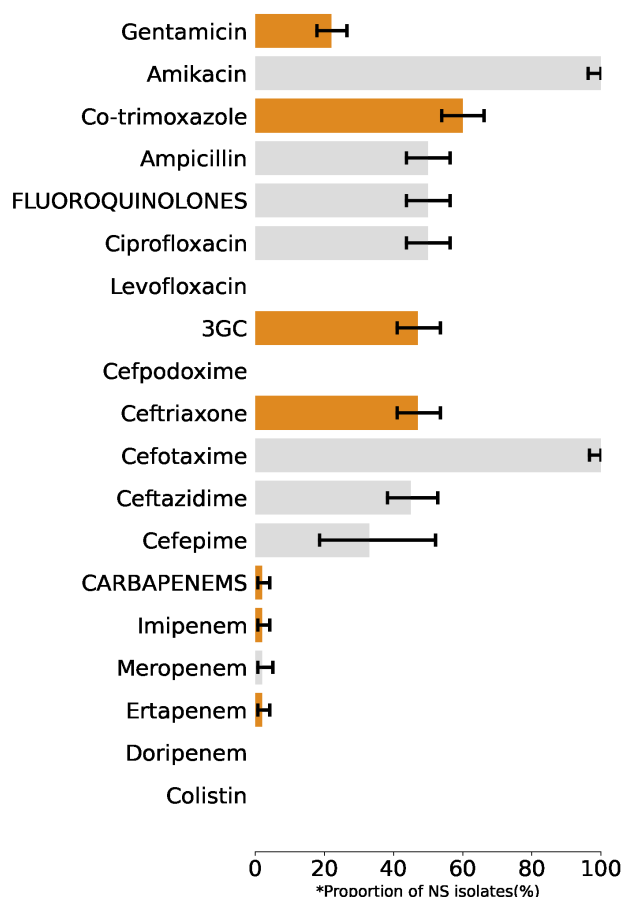
Antibiotic agent	Proportion of NS isolates (n)	95% CI
FLUOROQUINOLONES	40% (14/35)	26% - 56%
Ciprofloxacin	40% (14/35)	26% - 56%
Levofloxacin	NA	-
3GC	14% (5/35)	6% - 29%
Ceftriaxone	14% (5/35)	6% - 29%
Cefotaxime	14% (5/35)	6% - 29%
Ceftazidime	NA	-
CARBAPENEMS	NA	-
Imipenem	NA	-
Meropenem	NA	-
Ertapenem	NA	-
Doripenem	NA	-

\*Proportion of non-susceptible (NS) isolates represents the number of patients with blood culture positive for non-susceptible isolates (numerator) over the total number of patients with blood culture positive for the organism and the organism was tested for susceptibility against the antibiotic (denominator). The AMASS application de-duplicated the data by including only the first isolate per patient per specimen type per evaluation period. Grey bars indicate that testing with the antibiotic occurred for less than 70% of the total number of patients with blood culture positive for the organism. CI=confidence interval; NA=Not available/reported/tested; 3GC=3rd-generation cephalosporin; FLUOROQUINOLONES: ciprofloxacin or levofloxacin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

## Section [2]: Isolate-based surveillance report

**Blood: *Escherichia coli***

( No. of patients = 339 )



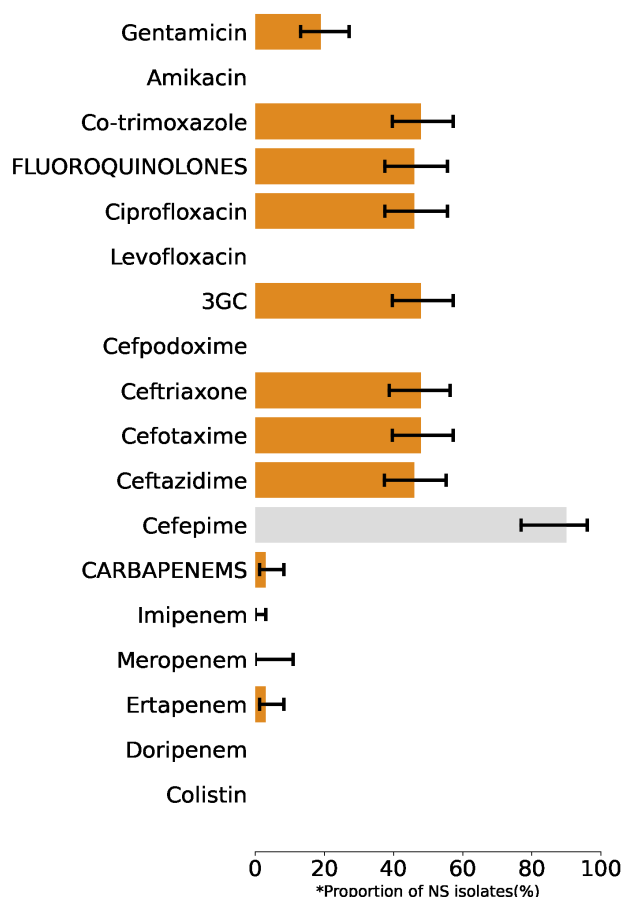
Antibiotic agent	Proportion of NS isolates (n)	95% CI
Gentamicin	22% (74/339)	18% - 26%
Amikacin	100% (100/100)	96% - 100%
Co-trimoxazole	60% (144/239)	54% - 66%
Ampicillin	50% (118/236)	44% - 56%
FLUOROQUINOLONES	50% (118/236)	44% - 56%
Ciprofloxacin	50% (118/236)	44% - 56%
Levofloxacin	NA	-
3GC	47% (113/239)	41% - 54%
Cefpodoxime	NA	-
Ceftriaxone	47% (113/239)	41% - 54%
Cefotaxime	100% (113/113)	97% - 100%
Ceftazidime	45% (79/174)	38% - 53%
Cefepime	33% (9/27)	19% - 52%
CARBAPENEMS	2% (4/239)	0.7% - 4%
Imipenem	2% (4/239)	0.7% - 4%
Meropenem	2% (4/199)	0.8% - 5%
Ertapenem	2% (4/239)	0.7% - 4%
Doripenem	NA	-
Colistin	NA	-

\*Proportion of non-susceptible (NS) isolates represents the number of patients with blood culture positive for non-susceptible isolates (numerator) over the total number of patients with blood culture positive for the organism and the organism was tested for susceptibility against the antibiotic (denominator). The AMASS application de-duplicated the data by including only the first isolate per patient per specimen type per evaluation period. Grey bars indicate that testing with the antibiotic occurred for less than 70% of the total number of patients with blood culture positive for the organism. CI=confidence interval; NA=Not available/reported/tested; 3GC=3rd-generation cephalosporin; FLUOROQUINOLONES: ciprofloxacin or levofloxacin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

## Section [2]: Isolate-based surveillance report

**Blood: *Klebsiella pneumoniae***

**( No. of patients = 120 )**



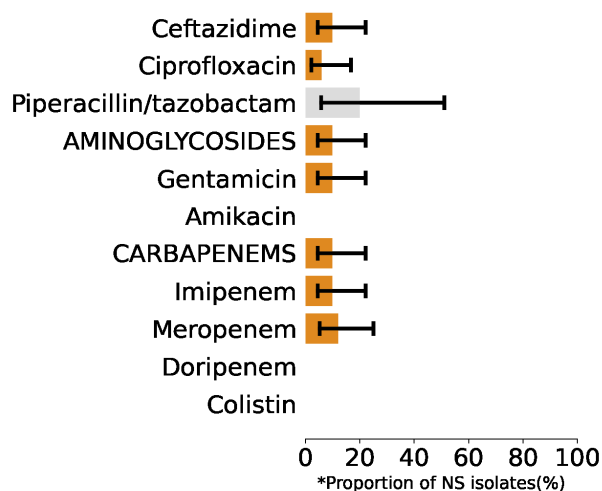
Antibiotic agent	Proportion of NS isolates (n)	95% CI
Gentamicin	19% (23/120)	13% - 27%
Amikacin	NA	-
Co-trimoxazole	48% (58/120)	40% - 57%
FLUOROQUINOLONES	46% (52/112)	38% - 56%
Ciprofloxacin	46% (52/112)	38% - 56%
Levofloxacin	NA	-
3GC	48% (58/120)	40% - 57%
Cefpodoxime	NA	-
Ceftriaxone	48% (57/120)	39% - 56%
Cefotaxime	48% (58/120)	40% - 57%
Ceftazidime	46% (54/117)	37% - 55%
Cefepime	90% (36/40)	77% - 96%
CARBAPENEMS	3% (4/120)	1% - 8%
Imipenem	0% (0/120)	0% - 3%
Meropenem	0% (0/31)	0% - 11%
Ertapenem	3% (4/120)	1% - 8%
Doripenem	NA	-
Colistin	NA	-

\*Proportion of non-susceptible (NS) isolates represents the number of patients with blood culture positive for non-susceptible isolates (numerator) over the total number of patients with blood culture positive for the organism and the organism was tested for susceptibility against the antibiotic (denominator). The AMASS application de-duplicated the data by including only the first isolate per patient per specimen type per evaluation period. Grey bars indicate that testing with the antibiotic occurred for less than 70% of the total number of patients with blood culture positive for the organism. CI=confidence interval; NA=Not available/reported/tested; 3GC=3rd-generation cephalosporin; FLUOROQUINOLONES: ciprofloxacin or levofloxacin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

## Section [2]: Isolate-based surveillance report

### Blood: *Pseudomonas aeruginosa*

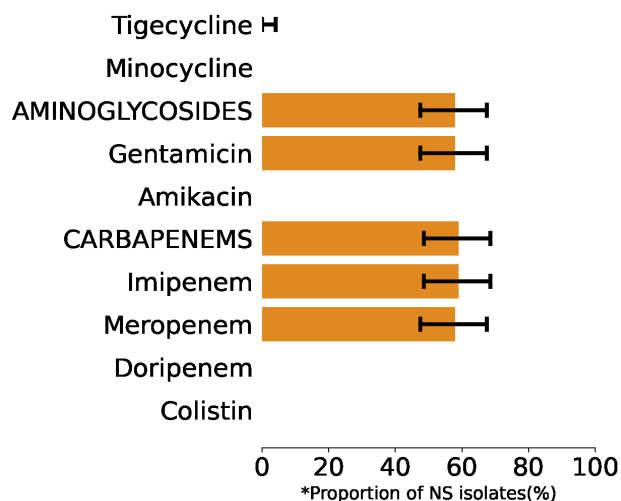
( No. of patients = 48 )



Antibiotic agent	Proportion of NS isolates (n)	95% CI
Ceftazidime	10% (5/48)	4% - 22%
Ciprofloxacin	6% (3/48)	2% - 17%
Piperacillin/tazobactam	20% (2/10)	6% - 51%
AMINOGLYCOSIDES	10% (5/48)	4% - 22%
Gentamicin	10% (5/48)	4% - 22%
Amikacin	NA	-
CARBAPENEMS	10% (5/48)	4% - 22%
Imipenem	10% (5/48)	4% - 22%
Meropenem	12% (5/42)	5% - 25%
Doripenem	NA	-
Colistin	NA	-

### Blood: *Acinetobacter baumannii*

( No. of patients = 90 )



Antibiotic agent	Proportion of NS isolates (n)	95% CI
Tigecycline	0% (0/90)	0% - 4%
Minocycline	NA	-
AMINOGLYCOSIDES	58% (52/90)	48% - 68%
Gentamicin	58% (52/90)	48% - 68%
Amikacin	NA	-
CARBAPENEMS	59% (53/90)	49% - 68%
Imipenem	59% (53/90)	49% - 68%
Meropenem	58% (52/90)	48% - 68%
Doripenem	NA	-
Colistin	NA	-

\*Proportion of non-susceptible (NS) isolates represents the number of patients with blood culture positive for non-susceptible isolates (numerator) over the total number of patients with blood culture positive for the organism and the organism was tested for susceptibility against the antibiotic (denominator). The AMASS application de-duplicated the data by including only the first isolate per patient per specimen type per evaluation period. Grey bars indicate that testing with the antibiotic occurred for less than 70% of the total number of patients with blood culture positive for the organism. CI=confidence interval; NA=Not available/reported/tested; AMINOGLYCOSIDES: either gentamicin or amikacin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

## **Section [3]: Isolate-based surveillance report with stratification by infection origin**

Proportions of antimicrobial-resistance infection stratified by origin of infection is not calculated because hospital admission date data is not available and infection origin variable is not available.

## Section [4]: Sample-based surveillance report

### Introduction

A sample-based surveillance report is generated if data of culture negative is available.

The sample-based approach involves the collection of data on all blood samples taken for microbiological testing and includes information on the number of positive blood samples for a specific specimen type (both pathogens under the survey and other bacteria) as well as number of negative (no microbial growth) samples. After removal of duplicate results and assuming that routine blood culture testing is applied systematically, we can use the number of tested patients as a proxy for a number of patients with new cases of bloodstream infection (BSI).

### Results

The microbiology\_data file had:

*Specimen collection dates ranged from **02 Jan 2016** to **10 Jan 2017***

*Number of records on blood specimen collected within the above date range:*

**15878 blood specimen records**

*\*Number of patients sampled for blood culture within the above date range:*

**15638 patients sampled for blood culture**

### Note

\*Number of patients sampled for blood culture is used as denominator to estimate the frequency of infections per 100,000 tested patients

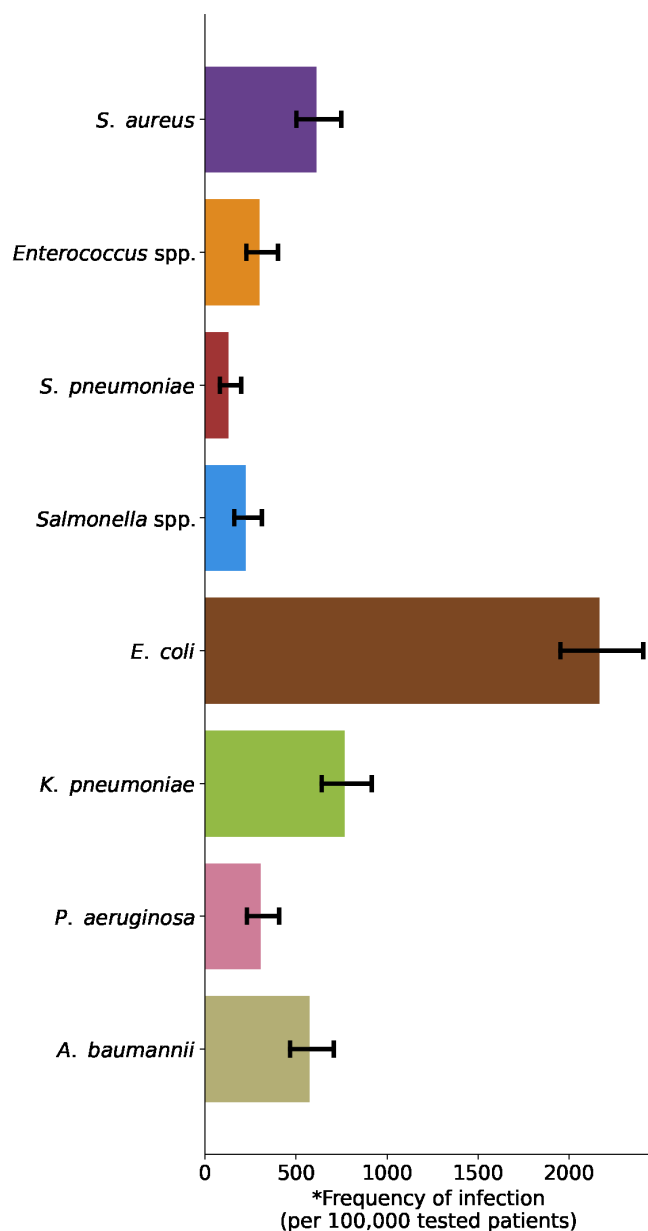
The following figures show the frequency of infections for patients with blood culture tested.



## Section [4]: Sample-based surveillance report

### Blood: Pathogens

( No. of patients = 15638 )



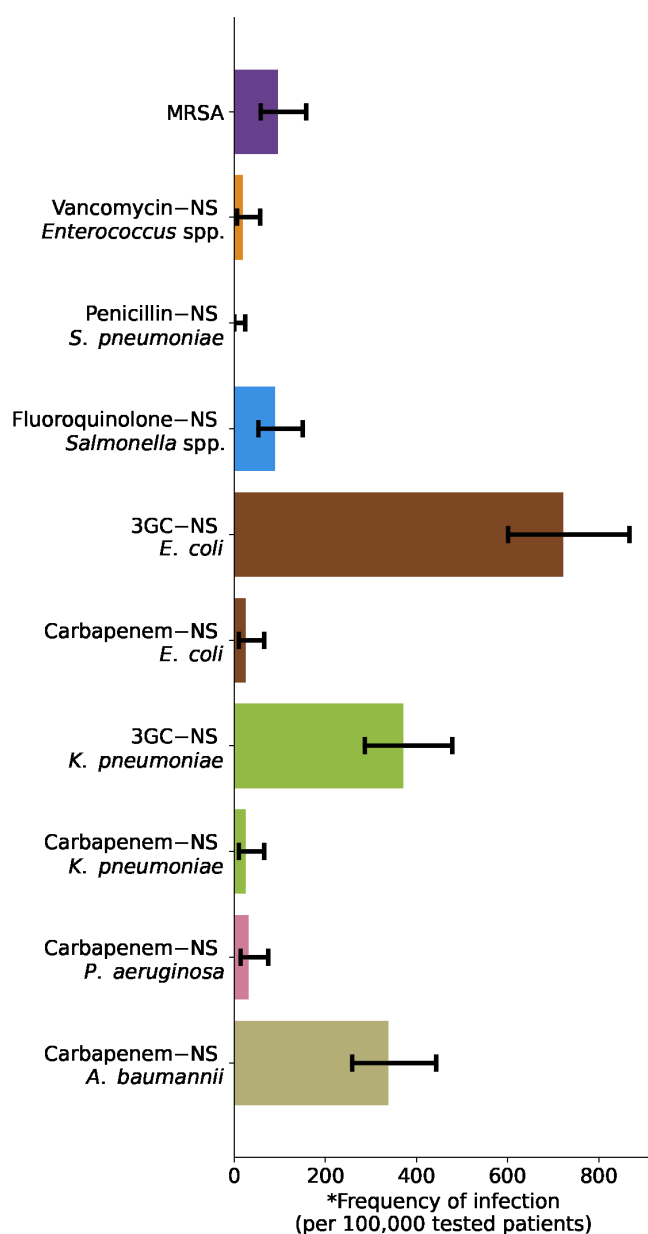
Pathogens	*Frequency of infection (per 100,000 tested patients; 95% CI)
<i>S. aureus</i>	614 (504-750)
<i>Enterococcus</i> spp.	301 (227-400)
<i>S. pneumoniae</i>	128 (83-198)
<i>Salmonella</i> spp.	224 (161-312)
<i>E. coli</i>	2168 (1952-2409)
<i>K. pneumoniae</i>	768 (643-917)
<i>P. aeruginosa</i>	307 (232-407)
<i>A. baumannii</i>	576 (469-707)

\*Frequency of infection per 100,000 tested patients represents the number of patients with blood culture positive for a pathogen (numerator) over the total number of tested patients (denominator). The AMASS application de-duplicates the data by included only the first isolate of each patient per specimen type per reporting period. CI=confidence interval; NS=non-susceptible; NA=Not available/reported/tested; 3GC=3rd-generation cephalosporin

## Section [4]: Sample-based surveillance report

### Blood: Non-susceptible pathogens

( No. of patients = 15638 )



Non-susceptible (NS) pathogens	*Frequency of infection (per 100,000 tested patients; 95% CI)
MRSA	96 (59-159)
Vancomycin-NS <i>Enterococcus</i> spp.	20 (7-57)
Penicillin-NS <i>S. pneumoniae</i>	0 (0-25)
Fluoroquinolone-NS <i>Salmonella</i> spp.	90 (54-151)
3GC-NS <i>E. coli</i>	723 (602-868)
Carbapenem-NS <i>E. coli</i>	26 (10-66)
3GC-NS <i>K. pneumoniae</i>	371 (288-480)
Carbapenem-NS <i>K. pneumoniae</i>	26 (10-66)
Carbapenem-NS <i>P. aeruginosa</i>	32 (14-75)
Carbapenem-NS <i>A. baumannii</i>	339 (260-444)

\*Frequency of infection per 100,000 tested patients represents the number of patients with blood culture positive for a pathogen (numerator) over the total number of tested patients (denominator). The AMASS application de-duplicates the data by included only the first isolate of each patient per specimen type per reporting period. CI=confidence interval; NS=non-susceptible; NA=Not available/reported/tested; 3GC=3rd-generation cephalosporin

## **Report [5]: Sample-based surveillance report with stratification by infection origin**

Incidence of infections per 100,000 tested population stratified by infection origin is not calculated because data on blood specimen with no growth is not available, or stratification by origin of infection cannot be done (due to hospital admission date variable is not available).

## **Report [6] Mortality in AMR antimicrobial–susceptible infections**

Not applicable because hospital\_admission\_data.csv file is not available, or in–hospital outcome (in hospital\_admission\_data.csv file) is not available.

# Annex A: Supplementary report on notifiable bacterial infections

## Introduction

This supplementary report has two parts; including (A1) isolate-based notifiable bacterial infections and (A2) mortality involving notifiable bacterial infections. The isolate-based notifiable bacterial infections supplementary report is generated by default, even if the hospital\_admission\_data file is unavailable. This is to enable hospitals with only microbiology data available to utilize the de-duplication and report generation functions of AMASS.

Please note that the completion of this supplementary report is strongly associated with the availability of data (particularly, all bacterial pathogens and all types of specimens) and the completion of the data dictionary files to make sure that the AMASS application understands the notifiable bacteria and each type of specimens.

Annex A includes various type of specimens including blood, cerebrospinal fluid (CSF), respiratory tract specimens, urine, genital swab, stool and other or unknown sample types. The microorganisms in this report were initially selected from common notifiable bacterial diseases in Thailand.

## Notifiable bacteria under the survey

- |  |                               |
|--|-------------------------------|
| - <i>Burkholderia pseudomallei</i>     | - <i>Salmonella</i> Paratyphi |
| - <i>Brucella</i> spp.                 | - <i>Salmonella</i> Typhi     |
| - <i>Corynebacterium diphtheriae</i>   | - <i>Shigella</i> spp.        |
| - <i>Neisseria gonorrhoeae</i>         | - <i>Streptococcus suis</i>   |
| - <i>Neisseria meningitidis</i>        | - <i>Vibrio</i> spp.          |
| - Non-typhoidal <i>Salmonella</i> spp. |                               |

Note: The list of notifiable bacteria included in the AMASS application version 2.0 was generated based on the literature review and the collaboration with Department of Disease Control, Ministry of Public Health, Thailand. The list could be expanded or modified in the next version of AMASS.

## Annex A1: Isolated-based notifiable bacterial infections

### Results

The microbiology\_data file had:

*Sample collection dates ranged from 02 Jan 2016 to 10 Jan 2017*

*Number of records of clinical specimens collected with culture positive for a notifiable bacteria under this survey:*

*615 specimen records (176 , 3 , 3 , 99 , 125 , 175 , 34 were blood, CSF, genital swab, respiratory tract specimens, stool, urine, and other or unknown sample types, respectively)*

The AMASS application de-duplicated the data by including only the first isolate per patient per specimen type per evaluation period as described in the method. The number of patients with positive samples is as follows:

Pathogens	Total number of patients*	Blood	CSF	Genital swab	RTS	Stool	Urine	Others
<i>B. pseudomallei</i>	331	109	3	3	92	0	155	34
<i>Brucella</i> spp.	0	0	0	0	0	0	0	0
<i>C. diphtheriae</i>	0	0	0	0	0	0	0	0
<i>N. gonorrhoeae</i>	0	0	0	0	0	0	0	0
<i>N. meningitidis</i>	0	0	0	0	0	0	0	0
Non-typhoidal <i>Salmonella</i> spp.	60	35	0	0	0	54	0	0
<i>S. Paratyphi</i>	0	0	0	0	0	0	0	0
<i>S. Typhi</i>	0	0	0	0	0	0	0	0
<i>Shigella</i> spp.	0	0	0	0	0	0	0	0
<i>S. suis</i>	0	0	0	0	0	0	0	0
<i>Vibrio</i> spp.	16	12	0	0	0	16	0	0
Total	407	156	3	3	92	70	155	34

\*Some patients may have more than one type of clinical specimen culture positive for the notifiable bacteria under the survey, and some may have more than one notifiable organism per evaluation period.

CSF = Cerebrospinal fluid; RTS = Respiratory tract specimens; Others = Other or unknown sample types;

NA = Not applicable (i.e. the specimen type is not available or identified in the microbiology\_data file)

## **Annex A2: Mortality involving notifiable bacterial infections**

Mortality involving the notifiable bacterial diseases is not applicable because hospital\_admission\_data.csv file is not available, or in-hospital outcome (in hospital\_admission\_data.csv file) is not available.

## Annex B: Supplementary report on data indicators

### Introduction

This supplementary report is generated by default, even if the `hospital_admission_data` file is unavailable. The management of clinical and laboratory practice can be supported by some data indicators such as blood culture contamination rate, proportion of notifiable antibiotic-pathogen combinations, and proportion of isolates with infrequent phenotypes or potential errors in AST results. Isolates with infrequent phenotypes or potential errors in AST results include (a) reports of organisms which are intrinsically resistant to an antibiotic but are reported as susceptible and (b) reports of organisms with discordant AST results.

This supplementary report could support the clinicians, policy makers and the laboratory staff to understand their summary data quickly. The laboratory staff could also use "Supplementary\_data\_indicators\_report.pdf" generated in the folder "Report\_with\_patient\_identifiers" to check and validate individual data records further.

**This supplementary report was estimated from data of blood specimens only.** Please note that the data indicators do not represent quality of the clinical or laboratory practice.

### Results

Indicators	Number of observations			
	Total (n)	Critical priority (n)	High priority (n)	Medium priority (n)
Blood culture contamination rate*	5% (742/15878)	NA	NA	5% (742/15878)
Proportion of notifiable antibiotic-pathogen combinations**	30% (308/1017)	27% (275/1017)	3% (33/1017)	0% (0/1017)
Proportion of isolates with infrequent phenotypes or potential errors in AST results***	10% (100/1017)	NA	NA	10% (100/1017)

\*Blood culture contamination rate is defined as the number of raw contaminated cultures per number of blood cultures received by the laboratory per reporting period. Blood culture contamination rate will not be estimated in case that the data of negative culture (specified as 'no growth' in the `dictionary_for_microbiology_data` file) is not available. \*\*Notifiable antibiotic-pathogen combinations and their classifications are defined as WHO list of AMR priority pathogen published in 2017. \*\*, \*\*\*The proportion is estimated per number of blood specimens culture positive for any organisms with AST result in the raw microbiology data. \*, \*\*, \*\*\*Details of the criteria are available in Table 3 and Table 4 of "Supplementary\_data\_indicators\_report.pdf", and "list\_of\_indicators.xlsx" in the folder "Configuration". NA = Not applicable



## Annex B: Supplementary report on data indicators

### Reporting period by months

Data was stratified by month to assist detection of missing data and understand the change of indicators by months.

Month	Blood culture contamination rate (n)*	Proportion of notifiable antibiotic-pathogen combinations (n)**	Proportion of isolates with infrequent phenotypes or potential errors in AST results (n)***
January	4% (59/1316)	32% (29/92)	13% (12/92)
February	6% (69/1256)	33% (28/85)	7% (6/85)
March	4% (53/1331)	28% (23/81)	6% (5/81)
April	4% (53/1382)	29% (21/73)	8% (6/73)
May	4% (57/1345)	32% (24/76)	5% (4/76)
June	4% (56/1269)	23% (15/66)	11% (7/66)
July	4% (58/1361)	31% (32/103)	10% (10/103)
August	5% (70/1344)	32% (30/94)	10% (9/94)
September	5% (58/1261)	43% (34/79)	9% (7/79)
October	4% (60/1365)	26% (28/108)	12% (13/108)
November	6% (78/1301)	28% (22/78)	15% (12/78)
December	5% (71/1347)	27% (22/82)	11% (9/82)

\*Blood culture contamination rate is defined as the number of raw contaminated cultures per number of blood cultures received by the laboratory per reporting period. Blood culture contamination rate will not be estimated in case that the data of negative culture (specified as 'no growth' in the dictionary\_for\_microbiology\_data file) is not available. \*\*Notifiable antibiotic-pathogen combinations and their classifications are defined as WHO list of AMR priority pathogen published in 2017. \*\*, \*\*\*The proportion is estimated per number of blood specimens culture positive for any organisms with AST result in the raw microbiology data. \*, \*\*, \*\*\*Details of the criteria are available in Table 3 and Table 4 of "Supplementary\_data\_indicators\_report.pdf", and "list\_of\_indicators.xlsx" in the folder "Configuration". NA = Not applicable

## Methods used by the AMASS application

### Data source:

For each run (double-click on AMASS.bat file), the AMASS application used the microbiology data file (microbiology\_data) and the hospital admission data file (hospital\_admission\_data) that were stored in the same folder as the application file. Hence, if the user would like to update, correct, revise or change the data, the data files in the folder should be updated before the AMASS.bat file is double-clicked again. A new report based on the updated data would then be generated.

### Requirements:

#### – Computer with Microsoft Windows 7 or 10

AMASS may work in other versions of Microsoft Windows and other operating systems. However, thorough testing and adjustment have not been performed.

#### – AMASSv2.0.zip package file

The AMASS application is to be downloaded from <https://www.amass.website>, and unzipped to generate an AMASS folder that could be stored under any folder in the computer. The AMASS folder contains 3 files (AMASS.bat, dictionary\_for\_microbiology\_data.xlsx, and dictionary\_for\_hospital\_admission\_data.xlsx), and 5 folders (Configuration, Example\_Dataset\_1\_WHONET, Example\_Dataset\_2, Example\_Dataset\_3\_longformat, Programs).

#### – Microbiology data file (microbiology\_data in .csv or .xlsx file format)

The user needs to obtain microbiology data, and then copy & paste this data file into the same folder as the AMASS.bat file.

#### – [Optional] Hospital admission data file (hospital\_admission\_data)

If available, the user could obtain hospital admission data, and then copy & paste this data file into the same folder as the AMASS.bat file.

### Not required:

#### – Internet to run AMASS application

The AMASS application will run offline. No data are transferred while the application is running and reports are being generated; the reports are in PDF format (do not contain any patient identifier) and can be shared under the user's jurisdiction.

#### – R and Python

The download package (AMASSv2.0.zip) included R portable, Python portable and their libraries that the AMASS application requires. The user does not need to install any programme before using the AMASS. The user also does not have to uninstall R or Python if the computer already has the programme installed. The user does not need to know how to use R and Python.

**Note:**

- [1] Please ensure that the file names of microbiology data file (microbiology\_data) and the hospital admission data file (hospital\_admission\_data) are identical to what is written here. Please make sure that all are lower-cases with an underscore '\_' at each space.
- [2] Please ensure that both microbiology and hospital admission data files have no empty rows before the row of the variable names (i.e. the variable names are the first row in both files).
- [3] For the first run, an user may need to fill the data dictionary files to make sure that the AMASS application understands your variable names and values.

AMASS uses a tier-based approach. In cases when only the microbiology data file with the results of culture positive samples is available, only section one and two would be generated for users. Section three would be generated only when data on admission date are available. This is because these data are required for the stratification by origin of infection. Section four would be generated only when data of specimens with culture negative (no microbial growth) are available in the microbiology data. This is because these data are required for the sample-based approach. Section five would be generated only when both data of specimens with culture negative and admission date are available. Section six would be generated only when mortality data are available.

Mortality was calculated from the number of in-hospital deaths (numerator) over the total number of patients with blood culture positive for the organism (denominator). Please note that this is the all-cause mortality calculated using the outcome data in the data file, and may not necessarily represent the mortality directly due to the infections.

**How to use data dictionary files**

In cases when variable names in the microbiology and hospital admission data files were not the same as the one that AMASS used, the data dictionary files could be edited. The raw microbiology and hospital admission data files were to be left unchanged. The data dictionary files provided could be edited and re-used automatically when the microbiology and hospital admission data files were updated and the AMASS.bat were to be double-clicked again (i.e. the data dictionary files would allow the user to re-analyze data files without the need to adjust variable names and data value again every time).

For example:

If variable name for 'hospital number' is written as 'hn' in the raw data file, the user would need to add 'hn' in the cell next to 'hospital\_number'. If data value for blood specimens is defined by 'Blood–Hemoculture' in the raw data file, then the user would need to add 'Blood–Hemoculture' in the cell next to 'blood\_specimen'.

**Dictionary file (dictionary\_for\_microbiology\_data.xlsx) may show up as in the table below:**

<b>Variable names used in AMASS</b>	<b>Variable names used in your microbiology data file</b>	<b>Requirements</b>
Don't change values in this column, but you can add rows with similar values if you need	Change values in this column to represent how variable names are written in your raw microbiology data file	
hospital_number		Required
<b>Values described in AMASS</b>	<b>Values used in your microbiology data file</b>	<b>Requirements</b>
blood_specimen		Required

**Please fill in your variable names as follows:**

<b>Variable names used in AMASS</b>	<b>Variable names used in your microbiology data file</b>	<b>Requirements</b>
Don't change values in this column, but you can add rows with similar values if you need	Change values in this column to represent how variable names are written in your raw microbiology data file	
hospital_number	hn	Required
<b>Values described in AMASS</b>	<b>Values used in your microbiology data file</b>	<b>Requirements</b>
blood_specimen	Blood–Hemoculture	Required

Then, save the file. For every time the user double-clicked AMASS.bat, the application would know that the variable named 'hn' is similar to 'hospital\_number' and represents the patient identifier in the analysis.

**Organisms included for the AMR Surveillance Report:**

- *Staphylococcus aureus*
- *Enterococcus* spp.
- *Streptococcus pneumoniae*
- *Salmonella* spp.
- *Escherichia coli*
- *Klebsiella pneumoniae*
- *Pseudomonas aeruginosa*
- *Acinetobacter baumannii*

**Definitions:**

The definitions of infection origin proposed by the WHO GLASS was used [1]. In brief, community–origin bloodstream infection (BSI) was defined for patients in the hospital within the first two calendar days of admission when the first blood culture positive specimens were taken. Hospital–origin BSI was defined for patients in the hospital longer than the first two calendar days of admission when the first blood culture positive specimens were taken. In cases when the user had additional data on infection origin defined by infection control team or based on referral data, the user could edit the data dictionary file (variable name 'infection\_origin') and the AMASS application would use the data of that variable to stratify the data by origin of infection instead of the above definition. However, in cases when data on infection origin were not available (as in many hospitals in LMICs), the above definition would be calculated based on admission date and specimen collection date (with cutoff of 2 calendar days) and used to classify infections as community–origin or hospital–origin.

**De–duplication:**

When more than one blood culture was collected during patient management, duplicated findings of the same patient were excluded (de–duplicated). Only one result was reported for each patient per sample type (blood) and surveyed organisms (listed above). For example, if two blood cultures from the same patient had *E. coli*, only the first would be included in the report. If there was growth of *E. coli* in one blood culture and of *K. pneumoniae* in the other blood culture, then both results would be reported. One would be for the report on *E. coli* and the other one would be for the report on *K. pneumoniae*.

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**References:**

- [1] World Health Organization (2018) Global Antimicrobial Resistance Surveillance System (GLASS) Report. Early implantation 2016–2017. <http://apps.who.int/iris/bitstream/handle/10665/259744/9789241513449-eng.pdf>. (accessed on 3 Dec 2018)
- [2] World Health Organization (2017) Global priority list of antibiotic–resistant bacteria to guide research, discovery, and development of new antibiotics. [https://www.who.int/medicines/publications/WHO-PPL-Short\\_Summary\\_25Feb-ET\\_NM\\_WHO.pdf](https://www.who.int/medicines/publications/WHO-PPL-Short_Summary_25Feb-ET_NM_WHO.pdf). (accessed on 3 Dec 2018)

## Investigator team

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AMASS version 2.0 is being developed by Chalida Rangsiwutisak, Cherry Lim, Paul Tuner, John Stelling and Direk Limmathurotsakul.

AMASS version 1.0 was funded by the Wellcome Trust (grant no. 206736 and 101103). C.L. is funded by a Research Training Fellowship (grant no. 206736) and D.L. is funded by an Intermediate Training Fellowship (grant no. 101103) from the Wellcome Trust.

AMASS version 2.0 was funded by the Wellcome Trust Institutional Translational Partnership Award- MORU

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