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
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Generated on: 20 Mar 2024 17:01
Software version: 3.0 released on 20 MAR 2024

Generated by
AutoMated tool for Antimicrobial resistance Surveillance System (AMASS) version 3.0 (released on 20 MAR 2024)

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 date 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.

Content

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 AMR proportion and AMR frequency reports stratified by infection origin from routinely collected electronic databases. The application was built in 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 3.0 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 3.0 also separately generates Supplementary data indictors 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 Indictors report (in PDF and Excel format) to any party outside of the hospital without data security management and confidential agreement.

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 (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]: AMR proportion report

Introduction

An AMR proportion 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 3.0 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 faecalis*
– *Enterococcus faecium*
– *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:

857 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)
Staphylococcus aureus	***113***	***96***
Enterococcus faecalis	***0***	***0***
Enterococcus faecium	***0***	***0***
Streptococcus pneumoniae	***25***	***20***
***Salmonella* spp.**	***43***	***35***
Escherichia coli	***384***	***339***
Klebsiella pneumoniae	***135***	***120***
Pseudomonas aeruginosa	***56***	***48***
Acinetobacter baumannii	***101***	***90***
Total:	***857***	***748***

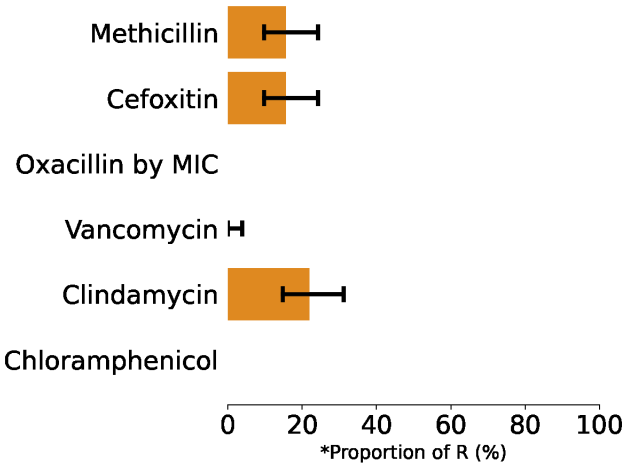
*The negative culture included data values specified as 'no growth' in the dictionary_for_microbiology_data file (details on data dictionary files are in the method section) to represent specimens with negative culture for any microorganism.
**Only the first isolate for each patient per specimen type, 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 resistant isolates.

Section [2]: AMR proportion report

Blood: *Staphylococcus aureus*

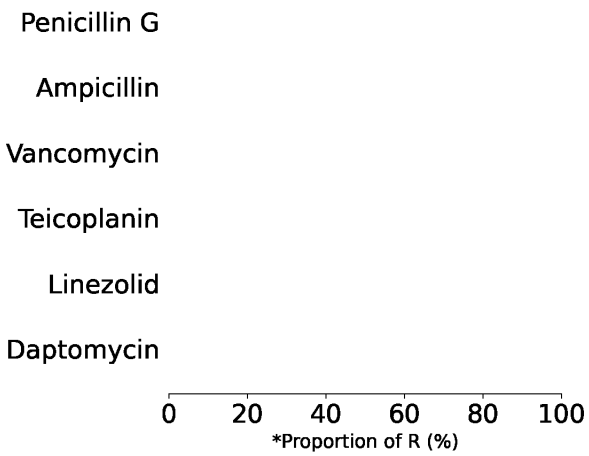
(No. of patients = 96)



Antibiotic agent	Proportion of R	95% CI
Methicillin	16% (15/96)	10% - 24%
Cefoxitin	16% (15/96)	10% - 24%
Oxacillin by MIC	NA	-
Vancomycin	0% (0/96)	0% - 4%
Clindamycin	22% (21/96)	15% - 31%
Chloramphenicol	NA	-

Blood: *Enterococcus faecalis*

(No. of patients = 0)

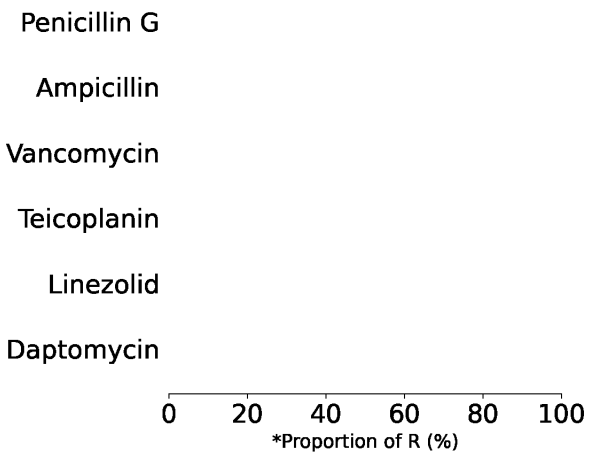


Antibiotic agent	Proportion of R	95% CI
Penicillin G	NA	-
Ampicillin	NA	-
Vancomycin	NA	-
Teicoplanin	NA	-
Linezolid	NA	-
Daptomycin	NA	-

*Proportion of R represents the number of patients with blood culture positive for resistant 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 AST unknown results are more than 30% of the total number of patients with blood culture positive for the organism. CI=confidence interval; NA=not available/reported/tested; Methicillin: cefoxitin or oxacillin by MIC

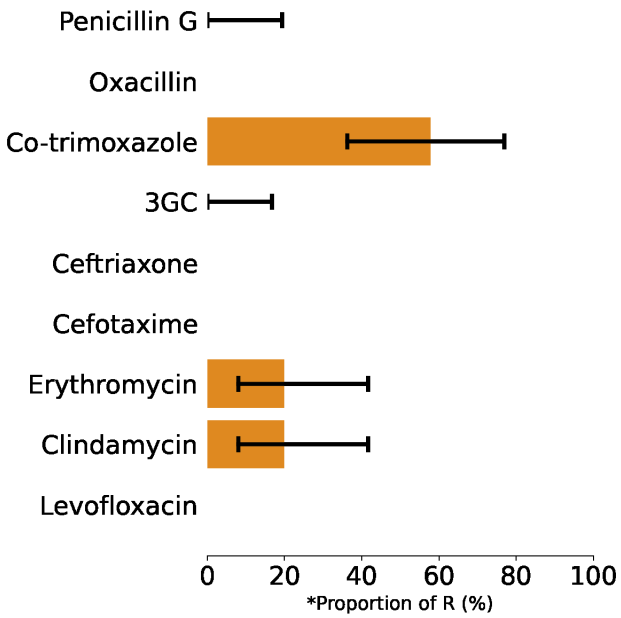
Section [2]: AMR proportion report

Blood: *Enterococcus faecium* *(No. of patients = 0)*



Antibiotic agent	Proportion of R	95% CI
Penicillin G	NA	-
Ampicillin	NA	-
Vancomycin	NA	-
Teicoplanin	NA	-
Linezolid	NA	-
Daptomycin	NA	-

Blood: *Streptococcus pneumoniae* *(No. of patients = 20)*

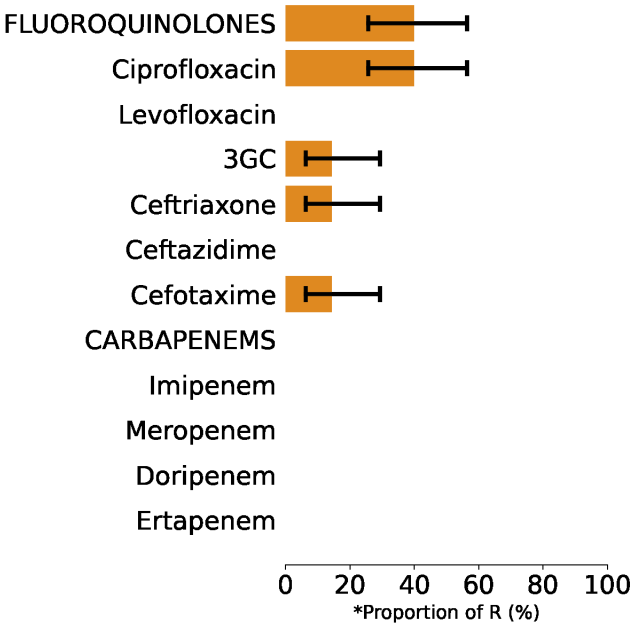


Antibiotic agent	Proportion of R	95% CI
Penicillin G	0% (0/16)	0% - 19%
Oxacillin	NA	-
Co-trimoxazole	58% (11/19)	36% - 77%
3GC	0% (0/19)	0% - 17%
Ceftriaxone	NA	-
Cefotaxime	NA	-
Erythromycin	20% (4/20)	8% - 42%
Clindamycin	20% (4/20)	8% - 42%
Levofloxacin	NA	-

*Proportion of R represents the number of patients with blood culture positive for resistant 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 AST unknown results are more than 30% 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

Section [2]: AMR proportion report

Blood: *Salmonella* spp. ***(No. of patients = 35)***

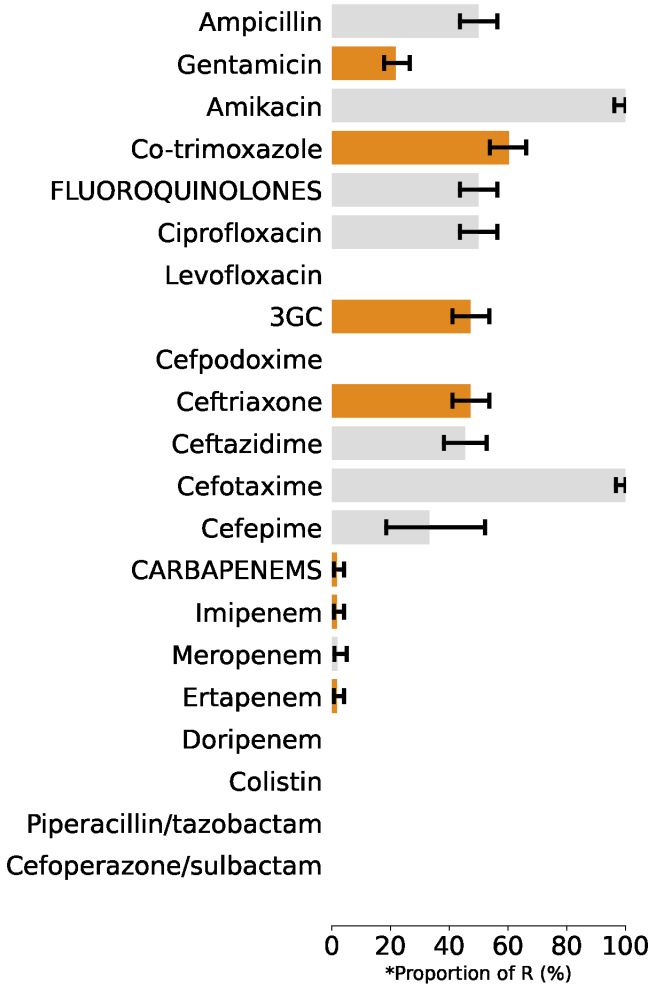


Antibiotic agent	Proportion of R	95% CI
FLUOROQUINOLONES	40% (14/35)	26% - 56%
Ciprofloxacin	40% (14/35)	26% - 56%
Levofloxacin	NA	-
3GC	14% (5/35)	6% - 29%
Ceftriaxone	14% (5/35)	6% - 29%
Ceftazidime	NA	-
Cefotaxime	14% (5/35)	6% - 29%
CARBAPENEMS	NA	-
Imipenem	NA	-
Meropenem	NA	-
Doripenem	NA	-
Ertapenem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

*Proportion of R represents the number of patients with blood culture positive for resistant 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 AST unknown results are more than 30% of the total number of patients with blood culture positive for the organism. CI=confidence interval; NA=not available/reported/tested; FLUOROQUINOLONES: ciprofloxacin or levofloxacin; 3GC=3rd–generation cephalosporin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

Section [2]: AMR proportion report

Blood: *Escherichia coli* *(No. of patients = 339)*

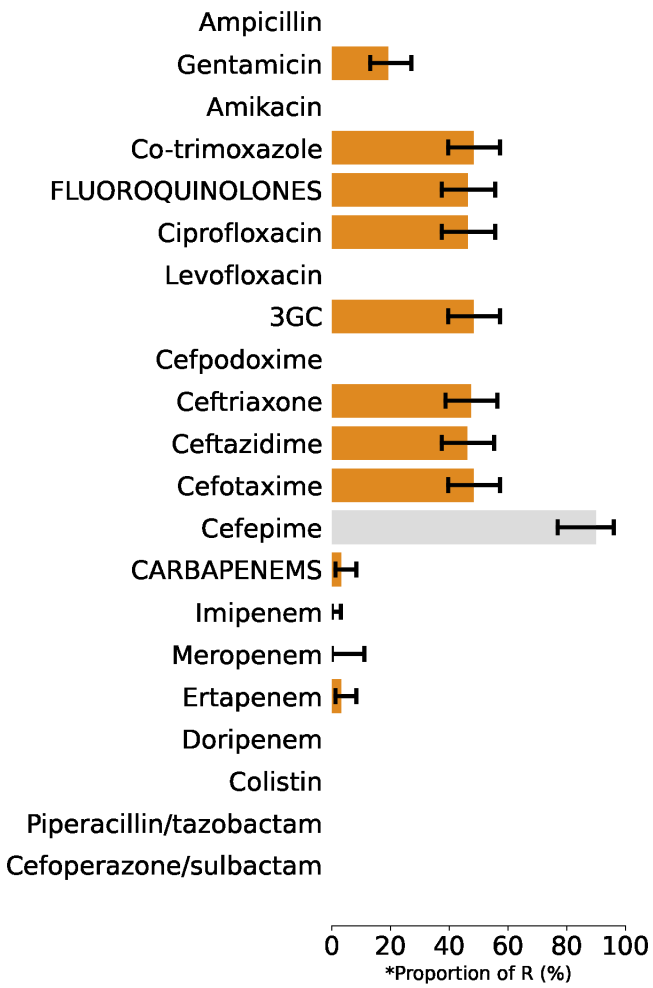


Antibiotic agent	Proportion of R	95% CI
Ampicillin	50% (118/236)	44% - 56%
Gentamicin	22% (74/339)	18% - 26%
Amikacin	100% (100/100)	96% - 100%
Co-trimoxazole	60% (144/239)	54% - 66%
FLUOROQUINOLONES	50% (118/236)	44% - 56%
Ciprofloxacin	50% (118/236)	44% - 56%
Levofloxacin	NA	-
3GC	47% (113/239)	41% - 54%
Cefpodoxime	NA	-
Ceftriaxone	47% (113/239)	41% - 54%
Ceftazidime	45% (79/174)	38% - 53%
Cefotaxime	100% (113/113)	97% - 100%
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	-
Piperacillin/tazobactam	NA	-
Cefoperazone/sulbactam	NA	-

*Proportion of R represents the number of patients with blood culture positive for resistant 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 AST unknown results are more than 30% of the total number of patients with blood culture positive for the organism. CI=confidence interval; NA=not available/reported/tested; FLUOROQUINOLONES: ciprofloxacin or levofloxacin; 3GC=3rd–generation cephalosporin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

Section [2]: AMR proportion report

Blood: *Klebsiella pneumoniae* ***(No. of patients = 120)***



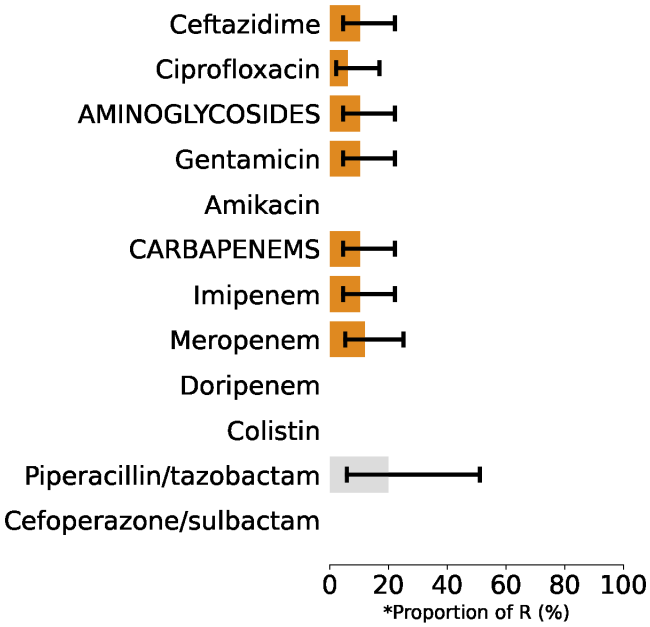
Antibiotic agent	Proportion of R	95% CI
Ampicillin	NA	-
Gentamicin	19% (23/120)	13% - 27%
Amikacin	NA	-
Co-trimoxazole	48% (58/120)	40% - 57%
FLUOROQUINOLONES	46% (52/112)	38% - 56%
Ciprofloxacin	46% (52/112)	38% - 56%
Levofloxacin	NA	-
3GC	48% (58/120)	40% - 57%
Cefpodoxime	NA	-
Ceftriaxone	48% (57/120)	39% - 56%
Ceftazidime	46% (54/117)	37% - 55%
Cefotaxime	48% (58/120)	40% - 57%
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	-
Piperacillin/tazobactam	NA	-
Cefoperazone/sulbactam	NA	-

*Proportion of R represents the number of patients with blood culture positive for resistant 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 AST unknown results are more than 30% of the total number of patients with blood culture positive for the organism. CI=confidence interval; NA=not available/reported/tested; FLUOROQUINOLONES: ciprofloxacin or levofloxacin; 3GC=3rd–generation cephalosporin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

Section [2]: AMR proportion report

Blood: *Pseudomonas aeruginosa*

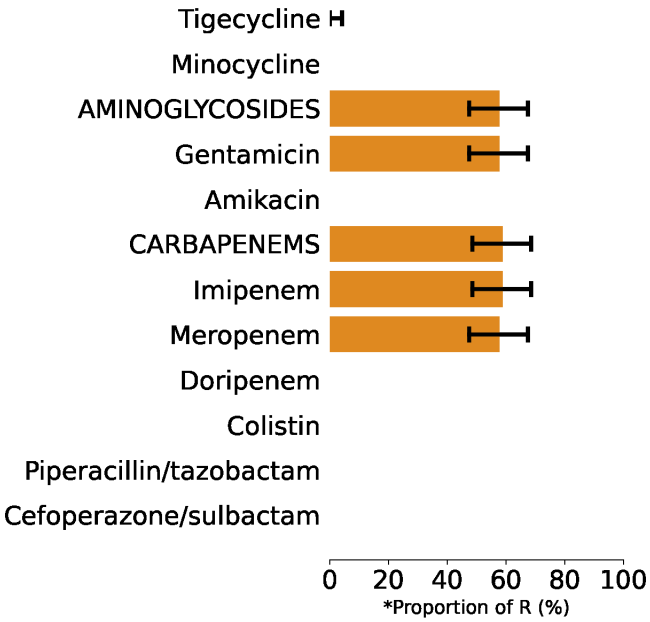
(No. of patients = 48)



Antibiotic agent	Proportion of R	95% CI
Ceftazidime	10% (5/48)	4% - 22%
Ciprofloxacin	6% (3/48)	2% - 17%
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	-
Piperacillin/tazobactam	20% (2/10)	6% - 51%
Cefoperazone/sulbactam	NA	-

Blood: *Acinetobacter baumannii*

(No. of patients = 90)



Antibiotic agent	Proportion of R	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	-
Piperacillin/tazobactam	NA	-
Cefoperazone/sulbactam	NA	-

*Proportion of R represents the number of patients with blood culture positive for resistant 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 AST unknown results are more than 30% of the total number of patients with blood culture positive for the organism. CI=confidence interval; NA=not available/reported/tested; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem; AMINOGLYCOSIDES: either gentamicin or amikacin

Section [3]: AMR proportion 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]: AMR frequency report

Introduction

For each pathogen and antibiotic under surveillance, the frequencies of patients with new infections are calculated per 100,000 tested patients.

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

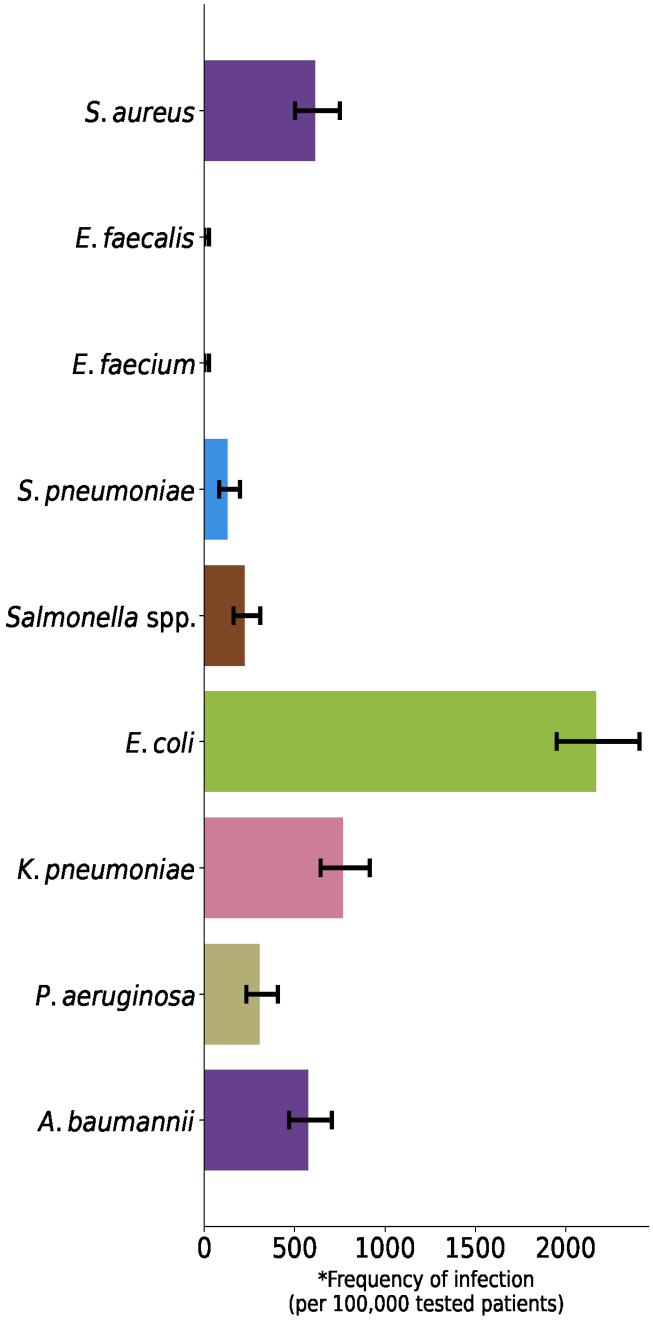
*Number of patients sampled for blood culture is used as denominator to estimate the frequency of infections per 100,000 tested patients

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

Section [4]: AMR frequency report

Blood: Pathogens

(No. of patients = 15638)



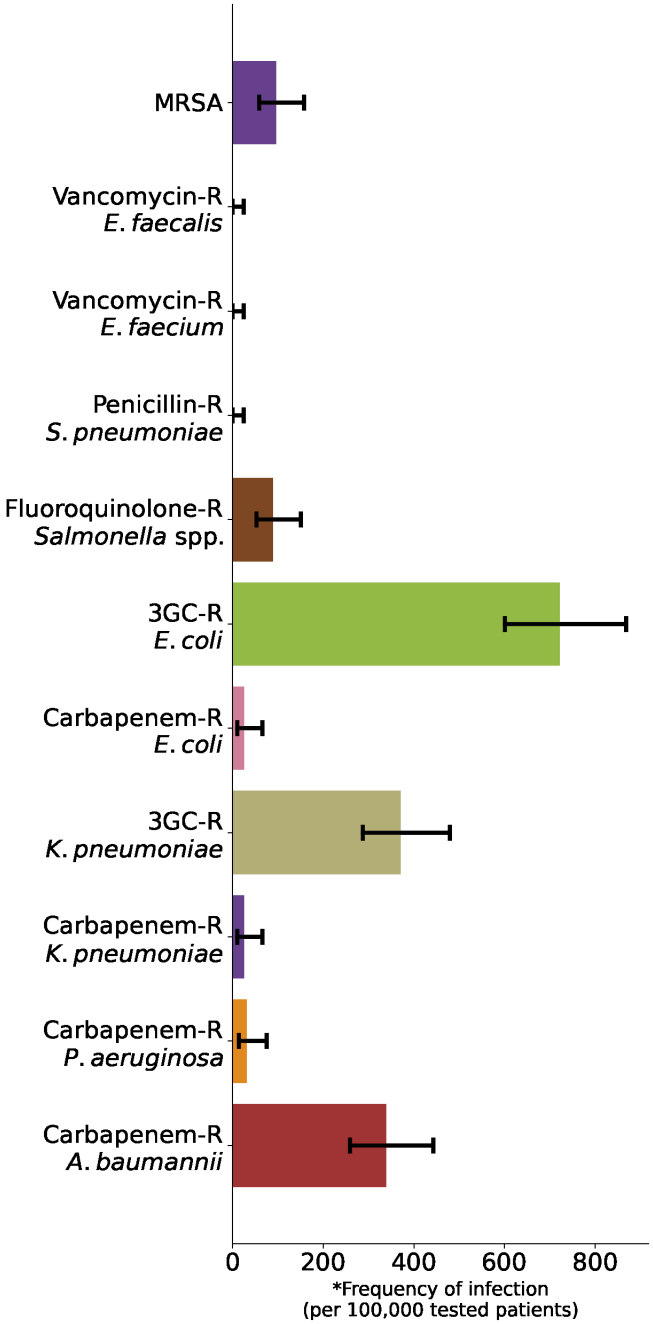
Pathogens	*Frequency of infection (per 100,000 tested patients; 95% CI)
S. aureus	614 (504-750)
E. faecalis	0 (0-25)
E. faecium	0 (0-25)
S. pneumoniae	128 (83-198)
Salmonella spp.	224 (161-312)
E. coli	2168 (1952-2409)
K. pneumoniae	768 (643-917)
P. aeruginosa	307 (232-407)
A. baumannii	576 (469-707)

*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; R=resistant; NA=not available/reported/tested

Section [4]: AMR frequency report

Blood: Resistant pathogens

(No. of patients = 15638)



Resistant (NS) pathogens	*Frequency of infection (per 100,000 tested patients; 95% CI)
MRSA	96 (59-159)
Vancomycin-R *E. faecalis*	0 (0-25)
Vancomycin-R *E. faecium*	0 (0-25)
Penicillin-R *S. pneumoniae*	0 (0-25)
Fluoroquinolone-R *Salmonella* spp.	90 (54-151)
3GC-R *E. coli*	723 (602-868)
Carbapenem-R *E. coli*	26 (10-66)
3GC-R *K. pneumoniae*	371 (288-480)
Carbapenem-R *K. pneumoniae*	26 (10-66)
Carbapenem-R *P. aeruginosa*	32 (14-75)
Carbapenem-R *A. baumannii*	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; R=resistant; NA=not available/reported/tested ; FLUOROQUINOLONES: ciprofloxacin or levofloxacin; 3GC=3rd–generation cephalosporin; CARBAPENEMS: imipenem, meropenem, ertapenem or doripenem

Report [5]: AMR frequency 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) notifiable bacterial infections and (A2) mortality involving notifiable bacterial infections. The AMR proportion 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

- *Burkholderia pseudomallei*
- *Brucella* spp.
- *Corynebacterium diphtheriae*
- *Neisseria gonorrhoeae*
- *Neisseria meningitidis*
- Non-typhoidal *Salmonella* spp.
- *Salmonella* Paratyphi
- *Salmonella* Typhi
- *Shigella* spp.
- *Streptococcus suis*
- *Vibrio* spp.

Note: The list of notifiable bacteria included in the AMASS application version 3.0 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: 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
B. pseudomallei	331	109	3	3	92	0	155	34
Brucella spp.	0	0	0	0	0	0	0	0
C. diphtheriae	0	0	0	0	0	0	0	0
N. gonorrhoeae	0	0	0	0	0	0	0	0
N. meningitidis	0	0	0	0	0	0	0	0
Non-typhoidal *Salmonella* spp.	60	35	0	0	0	54	0	0
S. Paratyphi	0	0	0	0	0	0	0	0
S. Typhi	0	0	0	0	0	0	0	0
Shigella spp.	0	0	0	0	0	0	0	0
S. suis	0	0	0	0	0	0	0	0
Vibrio 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 indictors 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

Annex C: Cluster signals

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

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, in case that 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 will then be generated.

Requirements:

– **Computer with Microsoft Windows 7 or higher**

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

– **AMASSv3.0.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 4 files (AMASS.bat, dictionary_for_microbiology_data.xlsx, dictionary_for_hospital_admission_data.xlsx, and dictionary_for_wards.xlsx), and 6 folders (Configuration, Example_Dataset_1_WHONET, Example_Dataset_2, Example_Dataset_3_longformat, Example_dataset_4_cluster_signals, and 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 in .csv or .xlsx file format)**

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 the AMASS application**

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

– **Python**

The download package (AMASSv3.0.zip) included 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 Python if the computer already has the programme installed. The user does not need to know how to use Python.

– **SaTScan**

The download package (AMASSv3.0.zip) included batch SaTScan. The user does not need to install SaTScan or any programme before using the AMASSv3.0. The user does not need to know how to use SaTScan. The user can configurate and edit the parameter values to run the cluster detection analyses through the file provided under the Configuration folder.

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. For example, please do not add an empty row before the row of the variable names, which are the first row in both files).

[3] For the first run, a 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-negative specimens is not available, only section one, two, and three 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 calculating the AMR frequency. 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.

To detect spatio-temporal clusters of antimicrobial resistant bacterial species, the AMASS-SaTScan used the retrospective space-time uniform model of the SaTScan (http://www.satscan.org). The cluster detection was based on the first hospital-origin resistant isolate per organism per patient per evaluation period. Analyses were conducted separately for each of the seven species-groups, including MRSA, VREfs, VREfm, CREC, CRKP, CRPA, and CRAB identified from blood specimens only and from all types of specimens. Both ward names (or ward identifiers) and resistant profiles were defined as “location” in the SaTScan to allow the detection of spatio-temporal cluster of periods with a higher than the expected frequency of a specific resistance profile. The AMASS-SaTScan assumed that each ward was independent. In case that the ward name variable is not available (or some of the ward names are not filled in the dictionary file for wards), the whole hospital (or the wards that had no data in the dictionary files for wards) would be considered as a single space. The total resistance isolates were used as the denominator. Hypothesis testing was conducted using Monte Carlo simulations.

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:

Variable names used in AMASS	**Variable names used in your microbiology data file**	**Requirements**
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
Values described in AMASS	**Values used in your microbiology data file**	**Requirements**
blood_specimen		Required

Please fill in your variable names as follows:

Variable names used in AMASS	**Variable names used in your microbiology data file**	**Requirements**
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
Values described in AMASS	**Values used in your microbiology data file**	**Requirements**
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 faecalis*
– *Enterococcus faecium*
– *Streptococcus pneumoniae*
– *Salmonella* spp.
– *Escherichia coli*
– *Klebsiella pneumoniae*
– *Pseudomonas aeruginosa*
– *Acinetobacter baumannii*

The eight organisms and antibiotics included in the report were selected based on the global priority list of antibiotic resistant bacteria and Global Antimicrobial Resistance Surveillance System (GLASS) of WHO [1,2].

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*.

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. (accessed on 3 Dec 2018)

Investigator team

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The AMASS application version 2.0 and 3.0 was developed by Chalida Rangsiwutisak, Preeyarach Klaytong, Prapass Wannapinij, Paul Tuner, John Stelling, Cherry Lim and Direk Limmathurotsakul.

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