Appendix 1

PRAISE-HOB Consensus definition & Minimal dataset

This supplement describes the definition of hospital-onset bacteraemia and fungaemia (HOB) as defined by the PRAISE (Providing a Roadmap for Automated Infection Surveillance in Europe) network.

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PRAISE-HOB Consensus definition

The PRAISE-HOB definition classifies blood cultures of in inpatients according to standardized definitions.

Key concepts in the PRAISE-HOB algorithm and definition

Hospital admission	A hospital admission is defined as at least one overnight stay. The day of admission is considered day 0. An admission ends upon discharge.
Blood culture	Blood cultures are counted at the blood culture 'set' level (sample ID). Hence, 1 blood culture may consist of 1 or 2 vials. Sample date is considered day 0. Blood cultures are eligible if collected during hospital admission[1]. If a patient is readmitted on the same day, all blood cultures from that day are related to the prior admission.
Microorganism in blood culture	All microorganisms (bacteria and or fungi) isolated from eligible blood cultures.
Common commensals and pathogens	Common commensals are defined in line with the current CDC/NHSN classification[2]. All microorganisms not classified as common commensal are considered pathogens.
Microorganism event	Defined by either a pathogen in 1 blood culture OR the same common commensal (genus + species) in 2 blood cultures (different sample ID's) within 2 calendar days of each other (i.e., day 0, 1, 2). Results of antimicrobial susceptibility testing are not included in determining similarity. Date of microorganism event = sampling date of the 1st culture with pathogen or 1st culture with a common commensal that is part of a set of at least 2.
Microorganism episode	For each microorganism event, a subsequent 14-day period is defined, lasting from day 0 – 13 relative to the microorganism event OR until hospital discharge. The start date of a microorganism episode is the date of the microorganism event. The end date of the microorganism episode is 13 days after the microorganism event or at hospital discharge, whichever comes first.
Copy strains	All microorganisms of the same species isolated from blood cultures of the same patient and taken within the microorganism episode timeframe (and hence the same hospital admission) are classified as copy strains.
Solitary commensal	A common commensal that is not confirmed by a second blood culture within 2 calendar days (i.e. day 0, 1, or 2) AND is not a copy strain is classified as a solitary commensal.

Bacteraemia episode	One or several microorganism episodes can constitute a bacteraemia episode. Microorganism episodes with start dates within 2 calendar days (i.e. day 0, 1, or 2) of each other are grouped together as one bacteraemia episode. The start date of the bacteraemia episode is the date of the first microorganism episode. If there is only a single microorganism episode, this is a **monomicrobial** bacteraemia episode. In that case, the start and end date of the bacteraemia episode coincide with the dates of the microorganism episode. If there are 2 or more microorganism episodes within 2 calendar days (i.e., day 0, 1, or 2) of each other, these are **polymicrobial** bacteraemia episodes. Here, the start date of the bacteraemia episode is the start date of the first microorganism episode included, and the end date of the bacteraemia episode is the end date of the last included microorganism episode. Consequently, the maximum possible duration of a bacteraemia episode is 16 days. Of note, this does not influence copy strain elimination which happens at the microorganism episode level.
Hospital-onset bacteraemia	A bacteraemia episode qualifies as HOB if the start date of the bacteraemia episode is >=2 days after admission. Admissions start on day 0, so any bacteraemia episode starting on day 2 of admission or later is classified as a HOB.
Community-onset bacteraemia	Bacteraemia episodes starting on day 0 or 1 of admission are classified as community-onset bacteraemia.
Attributable ward	The bacteraemia episode is attributed to the ward where the patients was 2 calendar days prior to the start date of the bacteraemia episode. If the patient was transferred on that day, the ward where the patient was first is selected.
Ward specialty	Ward specialties are classified according to the ECDC ward specialty classification. Patient specialty classification is optional (see minimal dataset).
Patient days	For the denominator, patient days are calculated by ward specialty. This employs the midnight method, meaning that the ward where the patient was at midnight (00:00) is counted in the denominator (see example in MDS). The entire admission is included, also the first and last two days of admission.

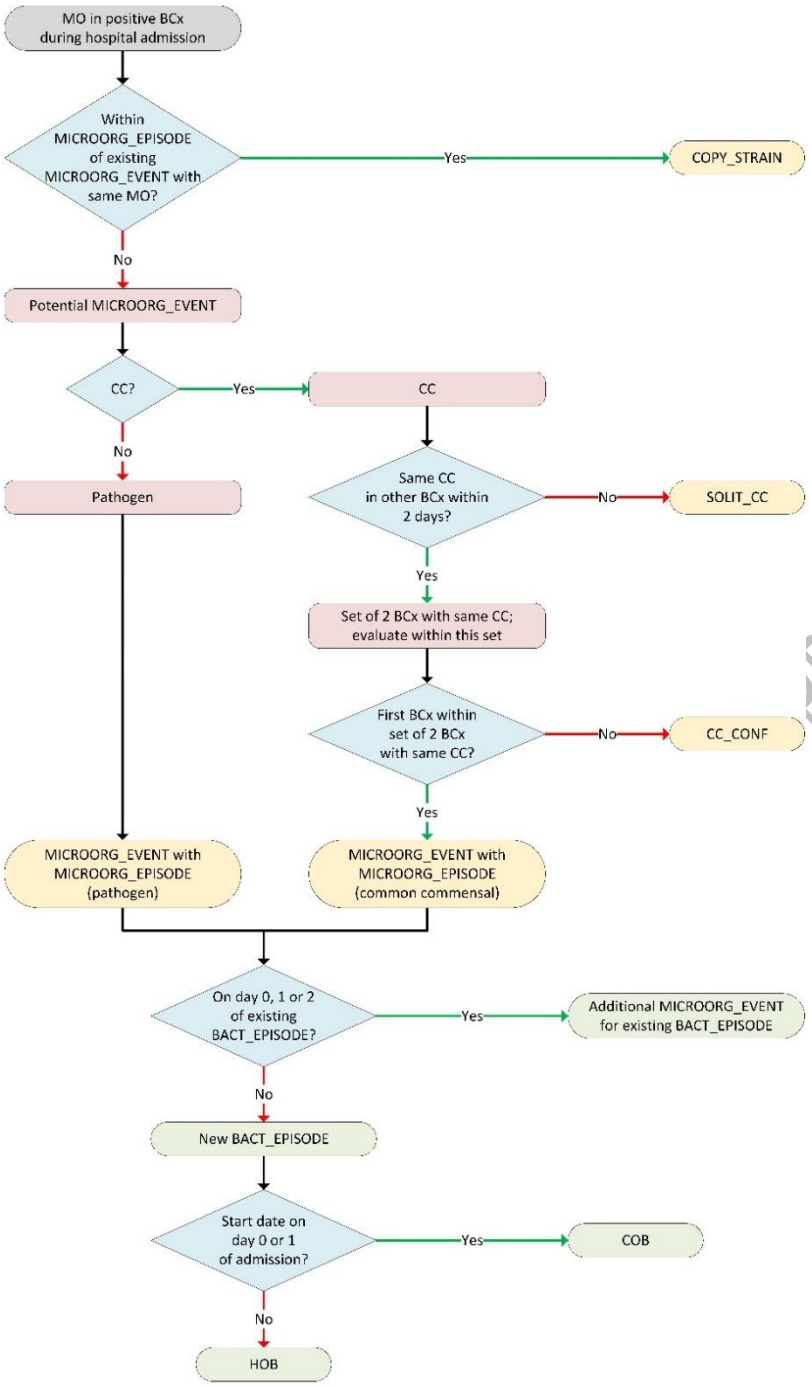
[1] Blood cultures taken in the emergency room are included within the hospital admission for the purpose of applying the algorithm.

[2] Common commensal classification used in this version is from 2023. We recommend using the most recent version when implementing algorithms.

Notes:

- Time intervals are counted in calendar days for reasons of feasibility.
- Some patients may have positive blood cultures in outpatient settings prior to admission, be transferred from other facilities with a prolonged bacteraemia, or be readmitted soon after discharge with positive blood cultures. These are relatively infrequent scenarios, and we did not include these for the sake of clarity of interpretation.
- In all place where bacteraemia is mentioned, this also includes fungaemia.

Flow chart of the PRAISE-HOB algorithm



Abbreviations/explanations
MO: microorganism, only bacteria and fungi, on genus and species level
BCx: blood culture (on cultureID level)
CC: common commensal, based on CDC/NHSN list
MICROORG_EVENT: microorganism event; pathogen in BCx or common commensal in BCx confirmed by second BCx with same common commensal within 2 calendar days (day 0, 1 & 2)
CC_CONF: common commensal confirmation BCx; second BCx with same common commensal within 2 days (day 0-2) of previous BCx to confirm MICROORG_EVENT for common commensal
COPY_STRAIN: repeated MO in BCx within MICROORG_EPISODE period of MICROORG_EVENT
MICROORG_EPISODE: microorganism episode; MICROORG_EVENT (first BCx), CC_CONF (second BCx for common commensal) and COPY STRAINs within 14-day period (day 0-13) of start MICROORG_EVENT
SOLIT_CC: solitary common commensal; common commensal in BCx without CC_CONF and not within MICROORG_EPISODE of MICROORG_EVENT
BACT_EPISODE: bacteraemia and fungaemia episode; MICROORG_EVENTS with their associated MICROORG_EPISODEs which occurred within 2 days of each other (day 0, 1 & 2)
COB: community-onset bacteraemia and fungaemia; BACT_EPISODE started on day 0 or 1 of admission
HOB: hospital-onset bacteraemia and fungaemia; BACT_EPISODE started on day 2 or later of admission

Notes:
This flowchart assumes that microorganism identified in blood cultures are processed independently and sorted in chronological order. This flowchart is not meant for real-time processing.

Examples of the PRAISE-HOB algorithm

The following examples illustrate the PRAISE-HOB algorithm in different scenarios. All examples are based on fictitious data.

1. HOB with a single microorganism

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10	11	12
Microorg. from BC				*E. coli*									
Ward name	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1 *Hospital discharge at 15:00*					
Ward specialty	MED	MED	MED	MED	MED	MED	MED	MED	x	x	x	x	x

Conclusion of algorithm: 1 HOB with *E. coli* attributable to Ward 1 of ward specialty MED. The HOB-episode starts on Day 3 and ends with hospital discharge on Day 7.

2. HOB with common commensal

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10	11	12
Microorg. from BC	*S. hominis*					*S. epidermidis in 2 BC sets*							
Ward name	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1 *Hospital discharge at 15:00*					
Ward specialty	MED	MED	MED	MED	MED	MED	MED	MED	x	x	x	x	x

Conclusion of algorithm: 1 HOB with *S. epidermidis* attributable to Ward 1 of ward specialty MED. The HOB-episode starts on Day 5 and ends with hospital discharge on Day 7.

Note: Both S. epidermidis and S. hominis are common commensals. Blood culture with S. hominis (on day 0, admission day) is considered a solitary commensal.

3. HOB with pathogen AND solitary commensal

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10	11	…	17	18
Microorg. from BC					*S. aureus* *S. epidermidis*										
Ward name	Ward 1	Ward 1	Ward 1 *Transfer to Ward 2 at 3 pm*	Ward 2	Ward 2	Ward 2 *Transfer to ward 1 at 16:00*	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	…	Ward 1	Ward 1 *Hospital discharge at 15:00*
Ward specialty	SUR	SUR	SUR	ICU	ICU	ICU	SUR	SUR	SUR	SUR	SUR	SUR	…	SUR	SUR

Conclusion of algorithm: 1 HOB with *S. aureus* attributable to Ward 1 of ward specialty SUR. The HOB-episode starts on Day 4 and ends on Day 17.
Note: The attribution to Ward 1 is due to the fact that, two days before the start of the HOB-episode, the patient was first present on Ward 1 and then on Ward 2. S. epidermidis is considered a solitary commensal.

4. Polymicrobial HOB with 2 pathogens, 2 days apart

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10	11	12	…	26	27
Microorg. from BC							*E. coli*		*S. marcescens*							
Ward name	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1 *Transfer to Ward 2 at 11:00*	Ward 2	Ward 2	Ward 2	Ward 2	Ward 2 *Transfer to Ward 1 at 12:00*	Ward 1	Ward 1	…	Ward 1	Ward 1 *Hospital discharge at 15:00*
Ward specialty	SUR	SUR	SUR	SUR	SUR	SUR	MIX	MIX	MIX	MIX	MIX	SUR	SUR	…	SUR	SUR

Conclusion of the algorithm: 1 polymicrobial HOB with *E. coli* and *S. marcescens* attributable to Ward 1 of ward specialty SUR. The HOB-episode starts on Day 6 and ends on Day 21.
Note: Since S. marcescens is part of a polymicrobial HOB-episode starting on Day 6, the whole episode is attributed to Ward 1 = SUR (-2 days relative to Day 6). The polymicrobial bacteraemia episode starts on day 6 with the microorganism episode of E. coli and terminates after the end of the microorganism episode of S. marcescens, which is on Day 21. Consequently, a new HOB with an E. coli microorganism episode on Day 20 or Day 21 would be possible despite still being within the timeframe of the HOB-episode. This is due to the fact that copy strain elimination happens on the microorganism episode level (see definition table).

5. Community-onset bacteraemia on admission, and cultures with the same pathogen identified later during admission.

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10	11	12
Microorg. from BC	*S. aureus*				*S. aureus*								
Ward name	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1 *Hospital discharge at 15:00*
Ward specialty	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED

Conclusion of algorithm: No HOB. *Note: This patient has a community-onset bacteraemia episode that started on Day 0, and hence is not hospital-onset. S. aureus on Day 4 is a copy strain in the bacteraemia episode starting on admission. The community-onset microorganism episode ends with hospital discharge on Day 12.*

6. Pre-existing bacteraemia on admission and new cultures with a different pathogen

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10
Microorg. from BC	*S. aureus*						*E. coli*				
Ward name	Ward 1	Ward 1	Ward 1 *Transfer to ward 2 at 10:00*	Ward 2	Ward 2	Ward 2	Ward 2	Ward 2	Ward 2	Ward 2	Ward 2 *Hospital discharge at 15:00*
Ward specialty	ICU	ICU	ICU	MED	MED	MED	MED	MED	MED	MED	MED

Conclusion of algorithm: 1 HOB with *E. coli* attributable to Ward 2 of ward specialty MED. The HOB-episode starts on Day 6 and ends with the hospital discharge on Day 10.

Note: Additionally, this patient has a community-onset bacteraemia episode with S. aureus that started on Day 0 and ends with hospital discharge on Day 10.

7. Prolonged bacteraemia

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	…	40
Microorg. from BC	*S. aureus*								*S. aureus*								*S. aureus*			
Ward name	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A *Hospital discharge at 15:00*
Ward specialty	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED

Conclusion of algorithm: 1 HOB with *S. aureus* attributable to Ward A of ward specialty MED. The HOB-episode starts on Day 16 and ends on Day 29.
Note: S. aureus on Day 8 is a copy strain within the microorganism episode on admission (community-onset bacteraemia episode). S. aureus on Day 8 does not extent the microorganism episode. Therefore, S. aureus on Day 16 occurs outside of the 14-day microorganism episode window and marks the start of a new microorganism episode.

8. Prolonged bacteraemia after a polymicrobial HOB (extreme example)

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
Microorg. from BC	*S. aureus*		*E. coli*												*E. coli* *S. aureus*					
Ward name	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A *Hospital discharge at 15:00*
Ward specialty	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED

Conclusion of algorithm: 1 HOB with *S. aureus* attributable to Ward A of ward specialty MED. The HOB-episode starts on Day 14 and ends with hospital discharge on Day 19.
Note: This patient has a polymicrobial community-onset bacteraemia episode with S. aureus and E. coli. The E. coli on Day 14 falls within the E. coli microorganism episode starting on Day 2. The E. coli on Day 14 is hence a copy strain. The S. aureus on Day 14 falls outside of the of S. aureus microorganism episode starting on Day 0, hence constitutes a HOB (and not a copy strain).

9. Polymicrobial HOB with two common commensals

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10
Microorg. from BC				*S. epidermidis*	*S. hominis* *S. epidermidis*		*S. hominis*				
Ward name	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1 *Transfer to Ward 2 at 14:00*	Ward 2	Ward 2	Ward 2	Ward 2	Ward 2	Ward 2 *Hospital discharge at 15:00*
Ward specialty	ICU	ICU	ICU	ICU	ICU	SUR	SUR	SUR	SUR	SUR	SUR

Conclusion of algorithm: 1 polymicrobial HOB with *S. epidermidis and S. hominis* attributable to Ward 1 of ward specialty ICU. The HOB-episode starts on Day 3 and ends with hospital discharge on Day 10.

Note: Both S. epidermidis and S. hominis are common commensals. The two microorganism episodes are merged into a polymicrobial HOB since they start within 2 days of each other.

10. Overlapping HOB-episodes

Hospital admission day	0	1	2	3	4	5	6	7	8	…	25
Microorg. from BC				*S. aureus*			*E. coli*				
Ward name	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1 *Transfer to Ward 2 at 10:00*	Ward 2	Ward 2	Ward 2	Ward 2	…	Ward 2 *Hospital discharge at 15:00*
Ward specialty	ICU	ICU	ICU	ICU	ICU	MED	MED	MED	MED	…	MED

Conclusion of algorithm: 2 HOB

1 HOB with *S. aureus* attributable to Ward 1 of ward specialty ICU. This HOB-episode starts on Day 3 and ends on Day 16.

1 HOB with *E. coli* attributable to Ward 1 of ward specialty ICU. This HOB-episode starts on Day 6 and ends on Day 19.

Note: The two microorganism episodes are not merged into a polymicrobial HOB because they do not start within 2 days of each other.

11. Polymicrobial HOB and overlapping HOB-episode.

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10	…	30
Microorg. from BC				*E. coli* *S. epidermidis* *S. epidermidis*	*S. aureus*	*S. hominis*				*S. hominis*	*S. hominis*		
Ward name	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1	…	Ward 1 *Hospital discharge at 15:00*
Ward specialty	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	…	MED

Conclusion of algorithm: 2 HOB

1 polymicrobial HOB with *E. coli*, *S. epidermidis* and *S. aureus* attributable to Ward 1 of ward specialty MED. This HOB-episode starts on Day 3 and ends on Day 17.

1 HOB with *S. hominis* attributable to Ward 1 of ward specialty MED. This HOB-episode starts on Day 9 and ends on Day 22.

Note: S. epidermidis and S. hominis are common commensals. The S. hominis on Day 5 is a solitary commensal. The polymicrobial bacteraemia episode starts on day 3 with the microorganism episodes of E. coli & S. epidermidis and terminates after the end of the microorganism episode of S. aureus, which is on Day 17. Consequently, a new HOB with an E. coli and/or S. epidermidis microorganism episode on Day 17 would be possible despite still being within the timeframe of the HOB-episode. This is due to the fact that copy strain elimination happens on the microorganism episode level (see definition table).

12. Solitary commensals do not make a HOB.

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10
Microorg. from BC							*S. epidermidis* *S. hominis*	*Micrococcus luteus*			
Ward name	Ward 1	Ward 1	Ward 1	Ward 1	Ward 1 *Transfer to Ward 2 at 10:00*	Ward 2	Ward 2	Ward 2	Ward 2	Ward 2	Ward 2 *Hospital discharge at 15:00*
Ward specialty	ICU	ICU	ICU	ICU	ICU	MED	MED	MED	MED	MED	MED

Conclusion of algorithm: 0 HOB. *Note: All identified microorganisms are common commensals. Different solitary commensals do not constitute a HOB. All identified microorganisms are considered solitary commensals.*

13. “A chain of positive BC” (extreme example)

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10	…	30
Microorg. from BC				*S. aureus*	*E. coli*		*P. aeruginosa*	*E. coli*		*K. pneumoniae*			
Ward name	Ward A	Ward A	Ward A	Ward A	Ward A	Ward A	Ward A	Ward A	Ward A	Ward A	Ward A	…	Ward A *Hospital discharge at 15:00*
Ward specialty	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	MED	…	MED

Conclusion of algorithm: 3 HOB.

1 polymicrobial HOB with *S. aureus* and *E. coli* attributable to Ward A of ward specialty MED. This HOB-episode starts on Day 3 and ends on Day 17.

1 HOB with *P. aeruginosa* attributable to Ward A of ward specialty MED. This HOB-episode starts on Day 6 and ends on Day 19.

1 HOB with *K. pneumoniae* attributable to Ward A of ward specialty MED. This HOB-episode starts on Day 9 and ends on Day 22.

Note: The polymicrobial bacteraemia episode starts on day 3 with the microorganism episodes of S. aureus and terminates after the end of the microorganism episode of E. coli, which is on Day 17. Consequently, a new HOB with an S. aureus microorganism episode on Day 17 would be possible despite still being within the timeframe of the HOB-episode. This is due to the fact that copy strain elimination happens on the microorganism episode level (see definition table).

P. aeruginosa is more than two days after the first microorganism episode of the polymicrobial HOB and therefore not added to it. E. coli on Day 7 is a copy strain and is therefore not merged with P. aeruginosa on Day 6 to form a polymicrobial HOB. K. pneumonia and P. aeruginosa are more than two days apart and therefore not merged into a polymicrobial episode.

14. No post-discharge surveillance

Hospital admission day	Jan 1	Jan 2	Jan 3	Jan 4	Jan 5	…	Jan 12	Jan 13	Jan 14	Jan 15	…	Jan 29
Microorg. from BC				*S. aureus*	*S. epidermidis in 2 BC sets*				*S. aureus*			
Ward name	Ward 1	Ward 1	Ward 1	Ward 1 *Transfer to other facility*			Ward 1 (*Hospital readmission)* *Then transfer to ICU at 17:00*	Ward 2	Ward 2 *Transfer to Ward 1 at 16:00*	Ward 1	…	Ward 1 *Hospital discharge at 15:00*
Ward specialty	MED	MED	MED	MED			MED	ICU	ICU	MED	…	MED

Conclusion of algorithm: 2 HOB.

1 HOB with *S. aureus* during the first hospital stay attributable to Ward 1 of ward specialty MED. This HOB-episode starts on January 4 and ends with the hospital discharge (transfer) on January 4.

1 HOB with *S. aureus* during the second hospital stay attributable to Ward 1 of ward specialty MED. This HOB-episode starts on January 14 and ends on January 27.

Note: The 2 S. epidermidis on January 5 are not considered because it was taken outside of an in-patient admission. S. aureus on January 14 is not a copy strain of the S. aureus HOB-episode of January 4 since these are separate hospital admissions and HOB-episodes are not “carried over” between separate admissions.

Minimal dataset (input) of the PRAISE-HOB algorithm

In the tables below we describe the minimal dataset agreed upon. This dataset describes the true minimum input to achieve the output file and allow for reporting as shown in the manuscript. An excel file describing the minimal dataset is also available.

Stage 1: this describes the minimal dataset for hospitals/data providers that cannot locally link data needed by the algorithm (e.g., linking of blood cultures to wards).

Stage 2: for hospitals/data providers able to perform linkage of data files: they can perform linkage locally and only provide the data needed by the algorithms.

Note: it is not envisioned to mix stage 1 and 2. It is advised to either provide stage 1 or stage 2 data.

Stage 1

Variable	Data type	Values or format (if applicable)	Optional?	Comments
PATIENTS.CSV				For each patient with HOB
patientId	string		MANDATORY	Should be pseudonymised
patientSex	string	M (male); F (female); X (not male not female); U (unknown)	MANDATORY	
patientBirthDate	date	YYYY/MM/DD	MANDATORY	For sharing purpose consider dummy
patientDeathDate	date	YYYY/MM/DD	Optional	
BLOODCULTURES.CSV	**(1 line per microorganism)**			*Includes positive AND negative blood cultures.*
bcId	string		MANDATORY	A unique identifier of BC microorganism. For example compound sampleId+isolateNumber. Must add isolateNumberfor unique identification purposes
sampleId	string		MANDATORY	one sample can have multiple isolates
patientId	string		MANDATORY	reference to Patient.patientId
sampleDate	date	YYYY/MM/DD	MANDATORY	
sampleWardId	string		OPTIONAL	Ward where the patient was on day of culture; if on multiple wards, take the first one.
isolateNumber	integer		MANDATORY	If posNeg = 0 (neg), set to 0
bcMicroorgLocalId	string		MANDATORY	Local ID of the microorganism in lab system (this serves as basis for the algorithm). Should curate this for example if determination for some species is unreliable (e.g. E. cloacae complex, B. cereus complex). Set to "NULL" if posNeg = 0 (neg)
posNeg	boolean	0 (neg); 1 (pos)	MANDATORY	

MOVEMENT.CSV				This should include all patient movements if it is also used to calculate the denominator[1]
movementId	string		MANDATORY	
patientId	string		MANDATORY	reference to Patient.patientId
wardId	string		MANDATORY	
admissionWardDate	date	YYYY/MM/DD	MANDATORY	
dischargeWardDate	date	YYYY/MM/DD	MANDATORY	Can be empty if patient is still admitted, i.e. no discharge date available
admissionHospDate	date	YYYY/MM/DD	MANDATORY	
dischargeHospDate	date	YYYY/MM/DD	MANDATORY	Can be empty if patient is still admitted, i.e. no discharge date available

[1]**:** Providing all patient movement data can be very voluminous and not easy to acquire. In that situation it may be considered to provide aggregated denominator data as described in Stage 2, complement with movement data of all patients with a blood culture taken

Stage 2

Variable	**Data type**	**Values or format (if applicable)**	**Optional?**	**Comments**
PATIENTS.CSV				
patientId	string		MANDATORY	Should be pseudonymised
patientSex	string	M (male); F (female); X (not male not female); U (unknown)	MANDATORY	
patientBirthDate	date	YYYY/MM/DD	MANDATORY	For sharing purpose consider dummy
patientDeathDate	date	YYYY/MM/DD	OPTIONAL	
BLOODCULTURES.CSV				*Only positive blood cultures are needed in stage 2*
bcId	string		MANDATORY	A unique identifier of BC microorganism. Example compound sampleId+isolateNumber. Must add isolateNumber for unique identification purposes
sampleId	string		MANDATORY	one sample can have multiple isolates
patientId	string		MANDATORY	reference to Patient.patientId
sampleDate	date	YYYY/MM/DD	MANDATORY	
sampleWardId	string		MANDATORY	Ward where culture was taken -> if not present in hospital data then ward where pt was admitted on day of culture; if pt was transferred on day of blood culture, take first ward (where patient came from)
isolateNumber	integer		MANDATORY	

bcMicroorgLocalId	string		MANDATORY	Local ID of the microorganism in lab system = basis for algo. Should curate this for example if determination for some species is unreliable (e.g. E. cloacae complex, B. cereus complex).
attributableWardId	string		MANDATORY	Ward where pt was 2 days prior to culture taken if patient was transferred on day of blood culture, take first ward (where patient came from)
admissionHospDate	date	YYYY/MM/DD	MANDATORY	
DENOMINATOR.CSV	**(aggregated data)**			**Denominator (calculated by data provider)** These are denominator data of all patients wardGroup under analysis. See examples below
wardGroupType	string	value_set HOSPITAL WARD LOCALWARD ECDCWARD	MANDATORY	Defines at what level the analysis will be done, for example enter hospital, individual wards, local ward groups or ECDCWard groups
wardGroupValue	string	value_set containing a values applicable to wardGroups	MANDATORY	Specifies the value options for the denominators.
patientDays	numeric		MANDATORY	Number of patient days in wardGroupValue within specified period type. Midnight method: assign patient day to ward where patient was at 00:00
periodType	value_set	Valueset DAY MONTH QUARTER YEAR	MANDATORY	If possible, DAY, else the lowest level feasible.
calendarDateStart	date	YYYY/MM/DD	MANDATORY	Start date to which the denominator value applies. If Period type is DAY, then calendarDateStart = calendarDateEnd
calendarDateEnd	Date	YYYY/MM/DD	MANDATORY	end date to which the denominator value applies (inclusive). If Period type is DAY, then calendarDateStart = calendarDateEnd
numberOfAdmissions	numeric		MANDATORY	Number of admissions to that specific WardGroupValue on specified period type
numberOfBloodCultureSamples	numeric		MANDATORY	Count distinct sampleID If available, else try to submit all BC's according to stage 1 (sampleWard, also for negative cultures)

See examples of denominator calculation below.

Look-up tables

WARDCLASSIFICATION.CSV				

wardId	string		MANDATORY	
wardECDCWard	string	value_set (ECDC classification list)	MANDATORY	ECDC ward specialty classification of ward
wardECDCWardPatient	string	value_set (ECDC classification list)	OPTIONAL	ECDC patient specialty classification of ward
wardLocalWardGroup	string	value_set (own ward classification hospital)	OPTIONAL	Local classification of ward. If wards have a 1:n relation with ward groups, the aggregate groups can be calculated from the output.
MICROCLASSIFICATION.CSV				
bcMicroorgLocalId	string		MANDATORY	Local ID of the microorganism in lab system = basis for algo. Should curate this; for example, if determination for some species is unreliable (e.g. E. cloacae complex, B. cereus complex).
bcMicroorgSnomedCTConceptId	string		OPTIONAL	If SNOMED CT code is not available, leave empty
bcMicroorgSpecifiedName	string	Description of the bacterial species	OPTIONAL	SNOMED CT label or local label
isCommCommensal	boolean	0 (no); 1 (yes)	MANDATORY if no SNOMED CT codes	If filled use this value; otherwise refer to CDC Common commensal classification, else treat as pathogen

Microorganism classification (based on CDC Common commensals).

- The algorithm runs on the microorganism ID's in place locally. They may be mapped to the CDC common commensal list by SNOMED CT code or manually.
- Local additions may be necessary, for example for new species or different local terminology.
- Please ensure correct grouping of difficult to distinguish pathogens if appropriate. For example, MALDI-ToF cannot reliably distinguish certain species of the *E. cloacae complex*. Reporting species names may lead to incorrect detection of repeat HOB's or polymicrobial HOB's with different species within this complex. Data providers may ensure that they report all relevant Enterobacter species as *E. cloacae complex.*
- Link to Common commensal list (most current version): [master-organism-com-commensals-lists.xlsx (live.com)]

Ward classification

- Wards are classified by ECDC ward specialty for reporting purposes.
- Data providers/hospitals may also perform analyses by ECDC patientSpecialty or a local ward classification system.
- Link to ECDC classification: European Centre for Disease Prevention and Control. Point prevalence survey of healthcare-associated infections and antimicrobial use in European acute care hospitals – protocol version 6.1. Stockholm: ECDC; 2022.: [Point prevalence survey of HAIs and antimicrobial use in European acute care hospitals, protocol version 6.1 (europa.eu)]

Minimal dataset (output) of the PRAISE-HOB algorithm

Notes:

The output file should at least have one line for each HOB microorganism event (line listing) hence there is more than 1 line per HOB possible (if polymicrobial event);
For debugging purposes, it is possible to allow for one line for each positive blood culture (see hobBcStatus)

Cardinality:

[1 … n]: one or more lines of data per patient
[0 … n]: may be left empty if not applicable or when de data is optional.

Variable	Data type	Values or format (if applicable)	Cardinality	Notes
HOBOUTPUT.CSV				
hobId	string		[1..n]	string composed of [patientId]_[hobEventDate in yyyyMMDD], so 1022_20220122
hobEventDate	date	YYYY/MM/DD	[1..n]	Date of the HOB (first positive BC finding within HOB episode)
patientId	string		[1..n]	
patientSex	string	M (male); F (female); X (not male not female); U (unknown)	[1..n]	
patientBirthDate	date	YYYY/MM/DD	[1..n]	
patientDeathDate	date	YYYY/MM/DD	[0..n]	
bcId	string		[1..n]	for example sampleId+IsolateNumber //=bloodCultureId
bcSampleDate	date	YYYY/MM/DD	[1..n]	
hobBcStatus	value_set	**MICROORG_EVENT**; COPY_STRAIN; CC_CONF; SOLIT_COMM	[1..n]	Value MICROORG_EVENT mandatory, other categories are optional but may be assigned for debugging purposes
bcMicroorgLocalId	string		[1..n]	
bcMicroorgSnomedCTConceptId	string	value_set	[0..n] or [1…n] if SNOMED CT	MANDATORY if SNOMED CT implemented, 1 microorganism per line
bcMicroorgSpecifiedName	string	label with belonging to SNOMED CT or localId	[0..n]	
bcIsCommCommensal	boolean	0 (no); 1 (yes)	[1..n]	
hobIsPolymicrobial	boolean	0 (no); 1 (yes)	[1..n]	if polymicrobial -> 1 = True = Yes
hobWithCommCommensal	boolean	0 (no); 1 (yes)	[1..n]	HOB contains a CSC

hobWithPathogen	boolean	0 (no); 1 (yes)	[1..n]	HOB contains a recognized pathogen
hobAttrWardId	string		[1..n]	WardID to which HOB is attributed
hobAttrWardECDCWard	string	value_set (ECDC classification list)	[1..n]	Ward type to what HOB is attributed: Consensus = ward type, patient specialty = optional.
hobAttrWardECDCWardPatient	string	value_set (ECDC classification list)	[0..n]	
hobAttrWardLocalWardGroup	string	value_set (locally defined)	[0..n]	
DENOMINATOR.CSV	**(aggregated data)**			**Denominator (intell in hospital/facility)** These are denominator data of all patients in the ward.
wardGroupType	string	value_set HOSPITAL WARD LOCALWARD ECDCWARD	MANDATORY	Defines at what level the analysis will be done, for example wardID, ECDCWard, or other local classifications
wardGroupValue	string	value_set containing a values applicable to wardGroups	MANDATORY	Specifies the value options for the denominators.
patientDays	numeric		MANDATORY	Number of patient days in wardGroupValue within specified period type. Midnight method: assign patient day to ward where patient was at 00:00
periodType	value_set	Value_set DAY MONTH QUARTER YEAR	MANDATORY	If possible DAY, else the lowest level feasible.
calendarDateStart	date	YYYY/MM/DD	MANDATORY	Start date to which the denominator value applies. If Period type is DAY, then calendarDateStart = calendarDateEnd
calendarDateEnd	Date	YYYY/MM/DD	MANDATORY	End date to which the denominator value applies (inclusive). If Period type is DAY, then calendarDateStart = calendarDateEnd
numberOfAdmissions	numeric		MANDATORY	Number of admissions to that specific WardGroupValue on specified period type
numberOfBloodCultureSamples	numeric		MANDATORY	Count distinct sampleID If available, else try to submit all BC's according to stage 1 (sampleWard, also for negative cultures)

Examples for denominator calculation

Example of the midnight method for use of patient days as denominator

Hospital admission day	0	1	2	3	4	5	6	7	8	9	10
Ward name	Ward 1 *Admission to ward 1 at 8:00*	Ward 1	Ward 1	Ward 1	Ward 1 *Transfer to Ward 2 at 10:00*	Ward 2	Ward 2	Ward 2 *Transfer to Ward 3 at 23:55*	Ward 3	Ward 3	Ward 3 *Hospital discharge at 15:00*
Ward specialty	ICU	ICU	ICU	ICU	ICU	MED	MED	MED	SUR	SUR	SUR
Count in denominator	none	ICU	ICU	ICU	ICU	MED	MED	MED	SUR	SUR	SUR

Notes: Day 0 is not counted in the denominator data because the patient was not yet in the ward at midnight (00:00), Day 4 is counted as ICU since the patient was in ICU at midnight.

Examples of denominator data analysis by wardGroupType and wardGroupValue

In the denominator data, different ward classification methods are included as possibilities to report HOB rates, hence giving different units of analysis. The choice of reporting unit may differ by purpose (e.g., sharing with external institution for trend monitoring vs. in-hospital reporting).

For each unit within the period type chosen (day, month, quarter, year), the denominator count is report per unit of analysis. And multiple aggregation levels may be included in one dataset.

This approach allows for flexible aggregation of output data.

In the following example, the hospital has 6 wards with different specialties, and each ward has 4 beds, and we assume they are always occupied.

The Look-up table may have this structure:

Ward name	**Description**	**wardECDCWard**	**wardECDCWardPatient**	**wardLocalWardGroup**
A1	ICU medical 1	ICU	ICUMED	ICU
B2	Internal A	MED	MEDHEMA	Medical tower
C3	Internal B	MED	MEDNEPH	Medical tower
D4	Neurology & neurosurgery	MIX	MIX	NEURO
E5	General surgery	SUR	SURGEN	Surgical tower
F6	Orthopaedic	SUR	SURGEN	Surgical Stepdown

Denominator data for the whole hospital (period type = DAY)

wardGroupType	wardGroupValue	patientDays	periodType	calendarDateStart	calendarDateEnd	numberOfWardGroupAdmissions	numberOfBloodCultureSamples
HOSPITAL	HOSP	24	DAY	2023/01/01	2023/01/01	5	10
HOSPITAL	HOSP	24	DAY	2023/01/02	2023/01/02	3	20
HOSPITAL	HOSP	24	DAY	2023/01/03	2023/01/03	5	15
HOSPITAL	HOSP	24	DAY	2023/01/04	2023/01/04	2	35

Denominator data by ECDCWard level grouping (period type = DAY)

wardGroupType	wardGroupValue	patientDays	periodType	calendarDateStart	calendarDateEnd	numberOfWardGroupAdmissions	numberOfBloodCultureSamples
ECDCWARD	MED	8	DAY	2023/01/01	2023/01/01	1	2
ECDCWARD	MED	8	DAY	2023/01/02	2023/01/02	0	5
ECDCWARD	MED	8	DAY	2023/01/03	2023/01/03	1	3
ECDCWARD	MED	8	DAY	2023/01/04	2023/01/04	0	8
ECDCWARD	SUR	8	DAY	2023/01/01	2023/01/01	0	2
ECDCWARD	SUR	8	DAY	2023/01/02	2023/01/02	1	5
ECDCWARD	SUR	8	DAY	2023/01/03	2023/01/03	1	3
ECDCWARD	SUR	8	DAY	2023/01/04	2023/01/04	0	8
ECDCWARD	MIX	4	DAY	2023/01/01	2023/01/01	2	3
ECDCWARD	MIX	4	DAY	2023/01/02	2023/01/02	1	5
ECDCWARD	MIX	4	DAY	2023/01/03	2023/01/03	2	3
ECDCWARD	MIX	4	DAY	2023/01/04	2023/01/04	1	10
ECDCWARD	ICU	4	DAY	2023/01/01	2023/01/01	2	3
ECDCWARD	ICU	4	DAY	2023/01/02	2023/01/02	0	5
ECDCWARD	ICU	4	DAY	2023/01/03	2023/01/03	1	6
ECDCWARD	ICU	4	DAY	2023/01/04	2023/01/04	1	9

Denominator data by Local grouping (period type = DAY)

wardGroupType	wardGroupValue	patientDays	periodType	calendarDateStart	calendarDateEnd	numberOfWardGroupAdmissions	numberOfBloodCultureSamples
LOCALWARD	Medical tower	8	DAY	2023/01/01	2023/01/01	1	2
LOCALWARD	Medical tower	8	DAY	2023/01/02	2023/01/02	0	5
LOCALWARD	Medical tower	8	DAY	2023/01/03	2023/01/03	1	3
LOCALWARD	Medical tower	8	DAY	2023/01/04	2023/01/04	0	8
LOCALWARD	Surgical tower	4	DAY	2023/01/01	2023/01/01	0	1
LOCALWARD	Surgical tower	4	DAY	2023/01/02	2023/01/02	1	3
LOCALWARD	Surgical tower	4	DAY	2023/01/03	2023/01/03	0	1
LOCALWARD	Surgical tower	4	DAY	2023/01/04	2023/01/04	0	4
LOCALWARD	Surgical stepdown	4	DAY	2023/01/01	2023/01/01	0	1
LOCALWARD	Surgical stepdown	4	DAY	2023/01/02	2023/01/02	0	2
LOCALWARD	Surgical stepdown	4	DAY	2023/01/03	2023/01/03	1	2
LOCALWARD	Surgical stepdown	4	DAY	2023/01/04	2023/01/04	0	4
LOCALWARD	NEURO	4	DAY	2023/01/01	2023/01/01	2	3
LOCALWARD	NEURO	4	DAY	2023/01/02	2023/01/02	1	5
LOCALWARD	NEURO	4	DAY	2023/01/03	2023/01/03	2	3
LOCALWARD	NEURO	4	DAY	2023/01/04	2023/01/04	1	10
LOCALWARD	ICU	4	DAY	2023/01/01	2023/01/01	2	3
LOCALWARD	ICU	4	DAY	2023/01/02	2023/01/02	0	5
LOCALWARD	ICU	4	DAY	2023/01/03	2023/01/03	1	6
LOCALWARD	ICU	4	DAY	2023/01/04	2023/01/04	1	9

Denominator data by single ward (period type = DAY)

wardGroupType	wardGroupValue	patientDays	periodType	calendarDateStart	calendarDateEnd	numberOfWardGroupAdmissions	numberOfBloodCultureSamples
WARD	B2	4	DAY	2023/01/01	2023/01/01	1	1
WARD	B2	4	DAY	2023/01/02	2023/01/02	0	2
WARD	B2	4	DAY	2023/01/03	2023/01/03	0	1
WARD	B2	4	DAY	2023/01/04	2023/01/04	0	4
WARD	C3	4	DAY	2023/01/01	2023/01/01	0	1
WARD	C3	4	DAY	2023/01/02	2023/01/02	0	3
WARD	C3	4	DAY	2023/01/03	2023/01/03	1	2
WARD	C3	4	DAY	2023/01/04	2023/01/04	0	4
WARD	E5	4	DAY	2023/01/01	2023/01/01	0	1
WARD	E5	4	DAY	2023/01/02	2023/01/02	1	3
WARD	E5	4	DAY	2023/01/03	2023/01/03	0	1
WARD	E5	4	DAY	2023/01/04	2023/01/04	0	4
WARD	F6	4	DAY	2023/01/01	2023/01/01	0	1
WARD	F6	4	DAY	2023/01/02	2023/01/02	0	2
WARD	F6	4	DAY	2023/01/03	2023/01/03	1	2
WARD	F6	4	DAY	2023/01/04	2023/01/04	0	4
WARD	D4	4	DAY	2023/01/01	2023/01/01	2	3
WARD	D4	4	DAY	2023/01/02	2023/01/02	1	5
WARD	D4	4	DAY	2023/01/03	2023/01/03	2	3
WARD	D4	4	DAY	2023/01/04	2023/01/04	1	10
WARD	A1	4	DAY	2023/01/01	2023/01/01	2	3
WARD	A1	4	DAY	2023/01/02	2023/01/02	0	5
WARD	A1	4	DAY	2023/01/03	2023/01/03	1	6
WARD	A1	4	DAY	2023/01/04	2023/01/04	1	9