**Supplementary table 1 Computer algorithm for HA-bacteraemia**

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| **Data preparation** | | |
| 1 | The initial extract from MiBa was based on the following MDS codes (Microbiological Diagnosis System)35 for specimen material:   * 10001 Whole blood; 10002 Whole blood from peripheral vein; 10003 Whole blood from catheter; 10160 Blood (blood culture bottle); 10164 Blood from umbilical cord (blood culture bottle); 10165 Blood from peripheral vein (blood culture bottle); 10166 Blood from catheter (blood culture bottle); 10167 Blood from artery (blood culture bottle). | MiBa |
| 2 | Relevant specimen were subsequently identified through the following MDS codes for the requested microbiological test: 10002 Aerobic culture (bacteria); 10003 Aerobic and anaerobic culture (bacteria); 10011 Culture and resistence; 10040 Anaerobic culture (bacteria); 10045 Aerobic and anaerobic culture in blood culture bottle; 10122 Staphylococcus aureus (MRSA) (culture); 10190 Listeria monocytogenes (culture); 10410 Actinomyces (culture); 12127 Staphylococcus aureus (MRSA) (DNA/RNA and culture); 17000 General bacterial investigation (=culture) and bacterial DNA/RNA; 20001 Culture (mould); 20010 Culture (yeast); 59015 Staphylococcus aureus (MRSA) (investigation for); 12129 and 12300 - not mapped in MiBa, but included not to miss important information. | MiBa |
| 3 | Records with an incorrect result in the field that indicates the microorganisms found in a blood culture were excluded. | MiBa |
| 4 | The date for the bacteraemia was determined, using the sampling date.   * If the sampling date was missing, then the date of receipt in the Department of Clinical Microbiology was used. * If the sampling date was more than 7 days before the date of receipt then the date of receipt was used. * If the sampling date was after the date of receipt, the date of receipt was used. | MiBa |
| 5 | The time for bacteraemia was determined, using the time of sampling.   * If the sampling time was not available, and the date of sampling and receipt were the same then the time of sampling was set to 4 hours (parameter) before receipt. * If the time of sampling was still missing, then it was set at 08:00. | MiBa |
| 6 | The number of samples with a sampling time at 08:00 was calculated by Department of Clinical Microbiology, but only for those that initially had information on the time of sampling. If there was an increase of >75% on one day, then those above 75% were set to 09:00, but only those that originally did not have information on the time of sampling. | MiBa |
| 7 | If there were more than one sample for the same person at the same time, then they were merged into one. Information on the microorganism(s) and the original laboratory identification numbers was kept. | MiBa |
| 8 | All observations with at least one pathogenic bacterium or fungus were marked as having bacteraemia. Pathogens were classified as all those **not** in the following list:   * *Acinetobacter* spp., *Aerococcus* spp. (except *A. urinae*), *Bacillus* spp. (except *B. anthracis*, *B. cereus*), *Corynebacterium* spp. (except *C. diphtheriae*), *Lactobacillus* spp., *Lactococcus* spp, *Micrococcus* spp., *Moraxella* spp. (except *M. catarrhalis*), *Neisseria* spp. (except *N. meningitides, N. gonorrhoeae, N. elongate, N. animaloris*, *N. canis*, and *N. zoodegmatis*), *Propionibacterium acnes*, *Staphylococcus* spp. (except *S. aureus*, *S. saprophyticus*, *S. lugdunensis* and *S. schleiferi*). *Streptococcus* spp. and non-haemolytic streptococci.   **Comment:** *Streptococcus* spp. and non-haemolytic streptoccocci are usually determined on species level, especially in those situations where the microorganism is considered the etiological agent. Reporting at genus level is taken to be a sign that the Department of Clinical Microbiology did not consider the microorganism to be the etiological agent and such reports were therefore assessed as contaminants in our algorithm. | MiBa |
| 9 | Course of admission was determined using an algorithm that linked related records to each other (manuscript submitted).26 | DNPR |
| 10 | For courses of admission the risk time was indicated (≥48 hours after admission up to 48 hours after discharge). | DNPR |
| 11 | 14 days were marked before the admission to be able to identify blood cultures taken during this period, indicating that there was a (suspicion of) bacteraemia before admission. | DNPR |
| **Constructing the algorithm** | |  |
| 12 | A bacteraemia was counted on the date and time of sampling. A bacteraemia was counted as a new bacteraemia if the sample date and time was >14 days (in hours) after a previous one. If a positive blood culture was found ≤14 days after a previous one, a new 14-day window started during which no new bacteraemia was counted. | HAIBA |
| 13 | In order to calculate the prevalence, it was defined that each bacteraemia episode lasted for 14 days, starting from the date and time of sampling. | HAIBA |
| 14 | Data from MiBa were combined with data from DNPR if the CPR-number was the same and the sample date fell within the period of 14 days before admission and 48 hours after discharge. | HAIBA |
| 15 | A bacteraemia was counted as hospital-acquired if it occurred within the period between >48 hours after admission and 48 hours after discharge, and no positive blood culture was found during the 14 days before admission nor within the first 48 hours of admission. | HAIBA |
| 16 | For incidence calculations, only the first HA-bacteraemia per course of admission was counted. For prevalence calculations, also further bacteraemias within a course of admission were included. | HAIBA |
| 17 | The number of risk days for incidence calculation was calculated as the number of days in the period between 48 hours after admission and 48 hours after discharge. | HAIBA |
| 18 | The number of risk days for prevalence was calculated as the number of days in the period from  >48 hours after admission until 48 hours after discharge. | HAIBA |