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Original Article

Integrating patient in-hospital transfer patterns into automated outbreak detection systems: a single-center retrospective study

Susanne Pinto PhD, Marieke A.M. Harmelink-de Zoete MSc and Maaike S.M. van Mourik MD, PhD
Department of Medical Microbiology and Infection Control, University Medical Centre Utrecht: Universitair Medisch Centrum Utrecht, Netherlands

Abstract

Objectives: Timely detection of pathogen-related outbreaks in hospitals is important for preventing onward transmission and can be supported by automated outbreak detection systems (AODS). Many methods overlook in-hospital patient transfers and focus only on patient locations at the time of sampling. This study compares three approaches for incorporating patient transfers into AODS.

Design: Two existing AODS frameworks, a local percentile-based system and a statistical modeling-based system were extended to include patient transfers: 1) grouping wards into communities based on frequent patient exchange, 2) including prior ward visits in the past 14 days, and 3) including both prior ward visits and time spent on wards. Alerts generated were reviewed for clinical relevance.

Setting: Data from January 2014 to December 2021 from a University Medical Center in the Netherlands.

Results: Using the percentile-based approach, the baseline scenario detected 99 possible outbreaks. Extension with ward community groupings, prior ward visits, and prior ward visits accounting for time spent in each ward increased this number with 16 (+15%), 42 (+42%), and 106 (+110%) possible outbreaks, respectively. Of the alerts generated by including individual patient transfer history, 35% were judged as requiring investigation. The trade-off between increased detection and relevance was less favorable for the other approaches. Similar findings were found for statistical modeling-based methods.

Conclusions: Inclusion of patient transfer data in AODS improved sensitivity, at the cost of increasing the alert burden. Therefore, ongoing refinement should further optimize the balance between accurate outbreak detection and a manageable alert burden.

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Introduction

Automated outbreak detection systems (AODS) support infection control departments in timely identification of possible outbreaks.[1,2] Current AODS usually count the number of newly detected colonized or infected patients with targeted microorganisms at a specific hospital location at the time of sampling.[3] Two examples are the percentile-based system (P75),[3] currently employed in our tertiary care hospital, and the statistics-based CLuster AleRt system (CLAR),[1] implemented in several German hospitals. P75 signals a potential outbreak when the prespecified threshold is exceeded, while CLAR applies statistical models to detect significant temporal outbreak signals, adjusting for baseline incidence and variation.

However, given the sometimes prolonged incubation periods and frequent patient transfers within healthcare facilities, incorporating the patient's in-hospital movement pathway into the AODS may also be relevant for outbreak detection. Previous studies have shown that certain departments can function as central hubs within the hospital network,[4,5] and can significantly influence the likelihood of transmission events.[6] In the context of hospital surveillance, groups of medical services and hospital wards, such as internal medicine or oncology, can be considered as epidemiologically linked units.[7,8]

This study aims to improve AODS by accounting for patient transfer history within healthcare facilities when identifying possible outbreaks. Earlier studies have shown that P75 and CLAR yield comparable results, but it remains unclear how their performance changes when patient transfers are incorporated.[3] In this study, P75 and CLAR were extended with three methods to account for patient in-hospital transfers. First, we determined if communities of epidemiologically linked wards, when integrated into AODS, contributed to more sensitive and timely identification of potential outbreaks than individual wards. Second, we incorporated individual patient's movement history data into the AODS, by assigning newly detected colonizations or infections to both current and previously visited inpatient locations,

Corresponding author: Maaike S.M. van Mourik; Email: m.s.m.vanmourik-2@umcutrecht.nl

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Table 1. Microorganism–phenotype–ward combinations of interest and selected for this study for AODS evaluation

Organism	Resistence phenotype	Ward	Selected for AODS evaluation
Acinetobacter spp.	Meropenem I/R	All wards	No
	Quinolone R Aminoglycoside R	All wards	No
	All isolates	(N/P)ICU	Yes, for ICU and for all ICU epidemiologically linked wards
Escherichia coli	Ciprofloxacin I/R	Hematology	No
	ESBL	All wards	Yes, for NICU, pediatric, and neurology and for all NICU, pediatric, and neurology epidemiologically linked wards
Citrobacter freundii	Ciprofloxacin I/R	Hematology	No
Enterobacter cloacae	ESBL	All wards	No
Klebsiella pneumoniae	ESBL	All wards	Yes, for NICU, pediatric, internal medicine, and neurology and for all NICU, pediatric, internal medicine, and neurology epidemiologically linked wards
Klebsiella oxytoca	ESBL	All wards	No
Serratia marcescens	All isolates	(N)ICU	Yes, for NICU and pediatric and for all NICU and pediatric epidemiologically linked wards
Pseudomonas aeruginosa	MDR I/R 3 (>= classes)	All wards	Yes, for ICU and for all ICU epidemiologically linked wards
	All isolates	(N/P)ICU	No
Stenotrophomonas maltophila	Cotrimoxazole I/R	(P)ICU	No
	All isolates	NICU	No
Enterobacteriaceae	Meropenem I/R	All wards	No
	Quinolone R Aminoglycoside R	All wards	No
Candida norvegensis	All isolates	Hematology	No
Aspergillus fumigatus	All isolates	ICU	No
Bacillus spp.	All isolates	NICU	No
PRSP	All isolates	All wards	No
MRSA	All isolates	All wards	Yes, for (N)ICU, pediatric, and neurology, and for all (N)ICU, pediatric, and neurology epidemiologically linked wards
MSSA	All isolates	(N/P)ICU	No
Vancomycin-resistant enterococci	All isolates	All wards	Yes, for internal medicine for all and internal medicine epidemiologically linked wards

Note: Antibiotic resistance and susceptibility were qualitatively described as "resistant'"(R), "intermediate'"(until 2020), or from 2021 onwards as "susceptible, increased exposure'"(I), and "susceptible'"(S), based on minimum inhibitory concentration (MIC) test results. All classifications followed EUCAST guidelines. Up until 2021 I and R classes were taken together as resistant, afterward the category I was considered susceptible. Abbrevations: ESBL - extended spectrum beta-lactamase, ICU - intensive care unit, MDR - multidrug resistant, MRSA - methicillin resistant *Staphylococcus aureus*, MSSA - methicillin susceptible *Staphylococcus aureus*, NICU - neonatal intensive care unit, PICU - pediatric intensive care unit, PRSP - penicillin resistant *Streptococcus pneumoniae*.

with a final extension additionally accounting for time spent in each ward.

Methods

Study setting

This single-center retrospective cohort study used data from the University Medical Center Utrecht, a tertiary care hospital in the Netherlands with approximately 1,100 beds. The hospital comprises multiple specialized units, including hematology, oncology, neurosurgery, and cardiothoracic surgery. It also includes a dedicated pediatric hospital with pediatric and neonatal intensive care units (ICUs).

Study population

This study includes all patients admitted to inpatient locations between January 1, 2014, and December 31, 2021. Patients who objected to the use of their data for research purposes were excluded, as were patients with admissions lasting less than 4 hours and admissions to the emergency room, psychiatry, or military wards.

Data collection

Data on patient admission, discharge, and transfers were collected from the electronic health record (EHR) databases. For each admission and transfer, this included patient pseudo-ID, admission pseudo-ID, transfer-ID, patient age in years, admission and discharge dates, department names, code, and description. Transfers within a single department and specific bed or room numbers were not collected.

Data on all isolates obtained from microbiological cultures were collected from the laboratory information system and included both clinical and screening cultures. Data included patient pseudo-ID, specimen number, specimen date, specimen type, isolate number, and antibiotic susceptibility testing results. Susceptibility results were used to identify microorganism–phenotype combinations of interest (Table 1). For each patient, only the first isolate of a specific microorganism–phenotype combination per year

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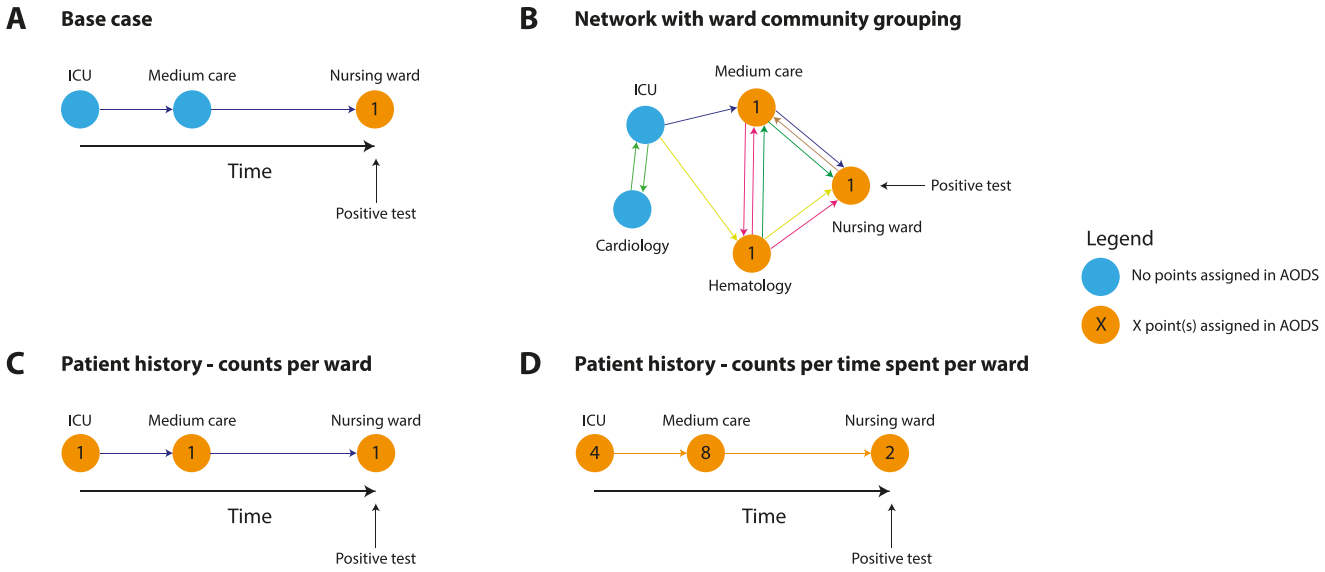


Figure 1. Overview of the different AODS variants using a hypothetical example of a single patient (A, C, D) or a hypothetical network of patient transfers (B). The colors indicate whether a microorganism finding is assigned to a ward and included in the AODS (orange) or not (blue). The number inside each circle represents the score assigned to that ward within the AODS. (A) The base case AODS. (B) All findings within wards in a ward community group are added together (as being one epidemiological unit). (C) Individual patient history—scoring based on each previously visited ward. (D) Individual patient history—time spent per ward. Scoring based on the number of days spent at previously visited wards.

was included, and all repeat findings within 365 days after the first finding were excluded.

Automated outbreak detection systems

The outbreak detection algorithms used are the P75 and the CLAR system.[1,3,9] The P75 system summarizes the monthly counts of new detections of a specific microorganism (and prespecified microorganism–phenotype combinations and/or wards under surveillance). The alert threshold is based on the 75th percentile of monthly counts for the preceding year and is recalculated annually. If a subsequent monthly count exceeds the threshold, an alert for a possible outbreak is generated.

The CLAR system was developed in-house by Charité University Hospital in Berlin and uses data from the previous 15 months to calculate a baseline incidence for organisms of interest.[9] This baseline is then compared to the counts from the preceding 30 days. The CLAR system employs six different algorithms relying on different probability distributions, and an alert is generated when any threshold is exceeded.

In both systems, alerts are generated for individual wards. To distinguish between first and repeated alerts related to the same possible outbreak, each alert was assigned an alert series identifier. Alerts occurring within 30 days of a previous alert were considered part of the same series. The earliest alert in a series was labeled as the first alert, and any subsequent alerts were labeled as repeated alerts.

Grouping ward communities

Communities of wards with frequent patient exchanges were identified using network analysis. An undirected graph was generated, with edges representing patient transfers between hospital departments (the nodes). Hospital admissions were used as the unit of analysis. Network analyses were performed separately for the adult and pediatric hospital buildings, as exchange between these facilities is very uncommon. Patients without transfers were excluded from the network analysis. Wards with few admissions and ambulatory care wards, such as the clinical IVF treatment center, were also excluded.

Incorporating patient transfers

To assess the influence of patient transfers on the detection of potential outbreaks, we extended the P75 and CLAR AODS systems, which included only the ward at the time of culture, with three alternative system configurations (Figure 1).

In the first extension, individual wards were grouped into ward communities (ie, epidemiologically linked wards with frequent patient transfers) using Louvain clustering.[10] Ward groupings from the preceding year were incorporated into the AODS as predefined epidemiologically linked units.

In the second extension, individual patient transfer history was incorporated by assigning the cultures to all wards visited within the previous 14 days. Each previously visited location received a count of 1, regardless of the duration of stay.

In the third extension, each previously visited location received a score equal to the number of days the patient had spent there within the previous 14 days, such that longer stays resulted in higher cumulative scores.

To assess the impact of our extensions we simulated prospective use of each approach using retrospective data for a selection of micro-organisms and ward types (Table 1) that we consider representative to interpret the performance. Each system version was run for each calendar week using data known up to that timepoint, and for each week generated alerts were documented.

All analyses were performed in R using RStudio (version 4.4.1 (2024.06.14)). Network analyses used the *cluster_louvain* function from the *igraph* R package.[11,12] R code and a detailed description of ward grouping and patient transfer extensions are available on Github (https://github.com/susannepinto/AODS_patient_movements).

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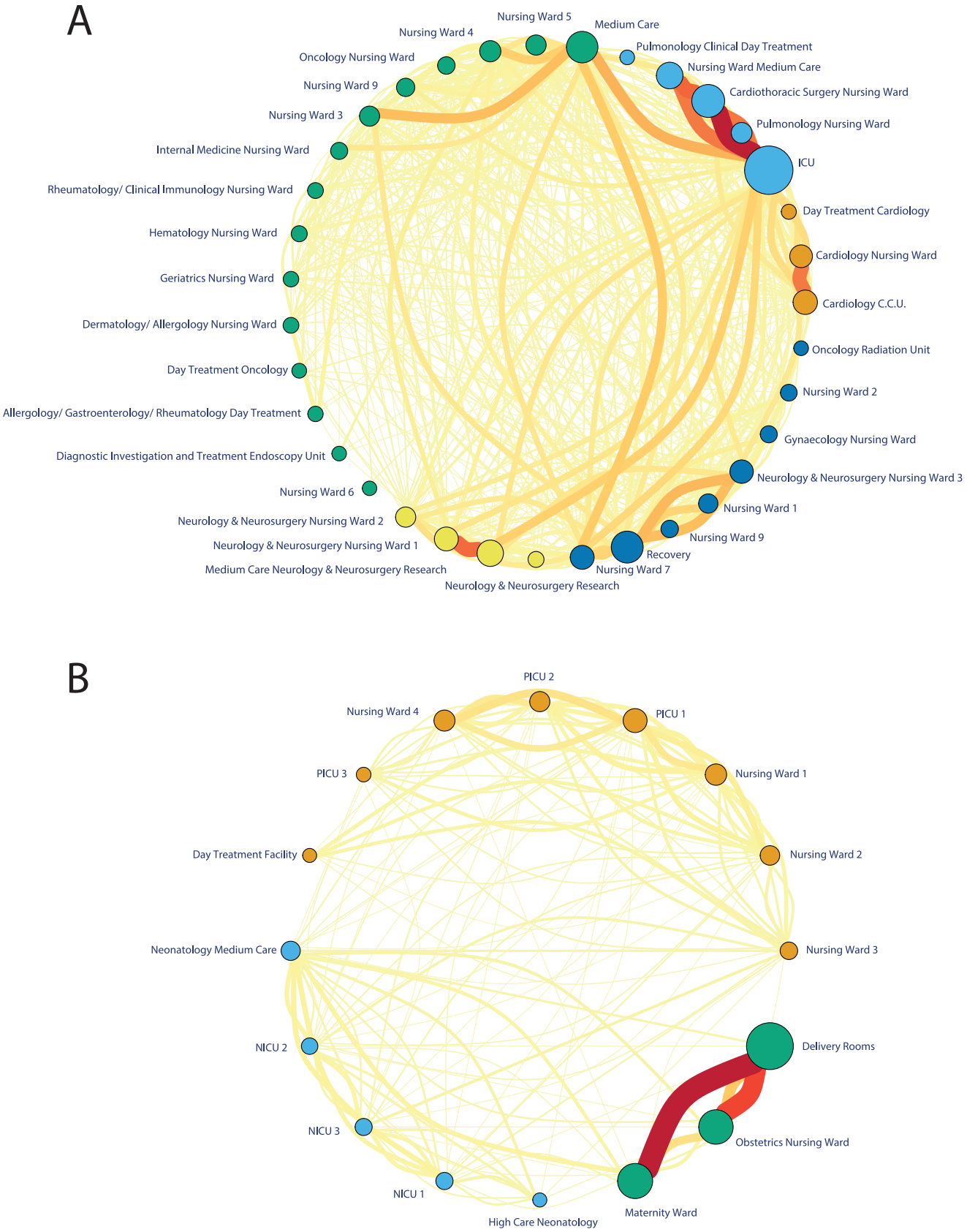


Figure 2. Networks of the adult (A) and pediatric (B) locations for 2019, grouping the wards has been performed with the Louvain clustering approach. Nodes represent wards, with color codes per ward grouping, edges represent patient transfers, with color scale and with indicating the number of transfers.

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Table 2. Summary table showing the alert characteristics for different selected AODS methods and extensions. These result include the micro-organisms selected for AODS evaluation see Table 1 *(last column)*

System	Data set	Total number of alerts	Number of alerts not in base case P75	Number of patients (mean and SD)	Alert duration time (mean and SD)	% repeated alerts
P75	**Base case**	99	0	5.3 (3.7)	43.5 (30)	50.1
	Ward community grouping	205	137	7.4 (6.9)	46.1 (31)	54.6
	Patient history (counts per ward)	115	31	6.0 (4.4)	46.5 (28)	54.8
	Patient history (counts per time spend per ward)	141	69	4.8 (3.2)	53.2 (29)	61.0
CLAR	**Base case**	141	54	4.8 (3.3)	53.2 (37.7)	61.0
	Ward community grouping	270	190	11.4 (12.5)	80.6 (54.8)	68.9
	Patient history (counts per ward)	196	112	5.5 (4.7)	63.4 (54.3)	60.7
	Patient history (counts per time spend per ward)	297	206	8.7 (12.7)	136.2 (167)	72.7

Note: Average alert duration is calculated as the mean time difference between the earlier and latest date associated with an alert.

Assessment of AODS extensions

Differences between AODS variants were assessed descriptively and by expert-opinion assessment from infection prevention experts for a selection of microorganisms (Table 1).

Descriptive assessment of alerts

To compare alerts generated by the eight AODS variants, both the number of identical alerts and the number of distinct alerts were quantified. Alerts were considered identical if they matched in microorganism–phenotype combination, location, and alert date. We specifically examined alerts not identified by the base case P75 system. Performance metrics included the mean number of alerts, mean number of patients per alert, average alert duration, and, where applicable, the percentage of repeated alerts. These analyses could not be performed for 2014 because the systems require data from the preceding year as baseline.

Assessment by infection prevention experts

A randomized selection process was used to curate a balanced sample of alerts for expert review. This sample included unique alerts from each AODS variant for selected microorganism–phenotype combinations (Table 1) and alerts generated by patient transfer-based systems that were not present in the base case P75 method.

Selected alerts were then divided into two sets. Four infection prevention experts, including two in training, independently reviewed one set in random order. Alerts were scored as:

1. Not relevant
2. Good to know (monitor for new cases)
3. Good to investigate (review patients or create an epidemiological curve)
4. Immediate action required (implement additional measures)

For interpretation, scores 3 and 4 were combined. Agreement was assessed using heatmaps and Cohen's Kappa, calculated with the *kappa2* function from the *irr* R package.[13] Differences in scoring were tested using a linear model with the *glm* function from the *stats* R package.[14]

Results

Patient transfers and network analysis

The data set included approximately 150,000 patients, of whom around 27,500 (~18%) had at least one positive microbiological culture between 2014 and 2021. A total of 486 patients objected to the use of their data and were excluded. The median length of stay per ward was 5.5 days, and patients had on average 3.7 transfers during their hospital stay. The data set used for network analyses (excluding short admissions, patients without transfers, and within-ward transfers) contained about 210,000 patient transfers for the entire study period.

Yearly ward communities were identified by Louvain clustering. For example, in 2019, five ward groups were identified for the adult building: one group consisting of wards connected to the adult ICU, one comprising cardiothoracic wards, one including internal medicine wards, one grouping neurology, and neurosurgery wards, and a remaining group containing several nursing wards. At the pediatric location, wards are grouped into three groups: one including mothers pre and postdelivery, a second including neonates and the NICU, and a third including all other pediatric wards (Figure 2). Because wards have been opened and closed over time, these groupings changed across years. However, ward group membership remained largely stable (S1 Figure and S2 Figure).

Descriptive assessment of AODS alerts

The total number of alerts differed between all AODS variants (Table 2 and S1 Table). The base case P75 generated the fewest alerts, whereas the CLAR AODS incorporating patient transfer history weighted by time spent per ward generated the most unique alerts. Despite generating the highest number of alerts, 73% were repeated alerts (Table 2). The CLAR system extended with ward community grouping included more patients per alert on average than the other systems (Table 2). When stratified by microorganism, these patterns showed only minor variation (S1 Table).

Overall, CLAR-based AODS generated substantially more unique alerts than P75-based AODS (S3 Figure). The highest number of unique alerts was generated AODS incorporating ward community grouping, for both P75 and CLAR (S3 to S5 Figure). Computation time was longer for CLAR-based systems than for

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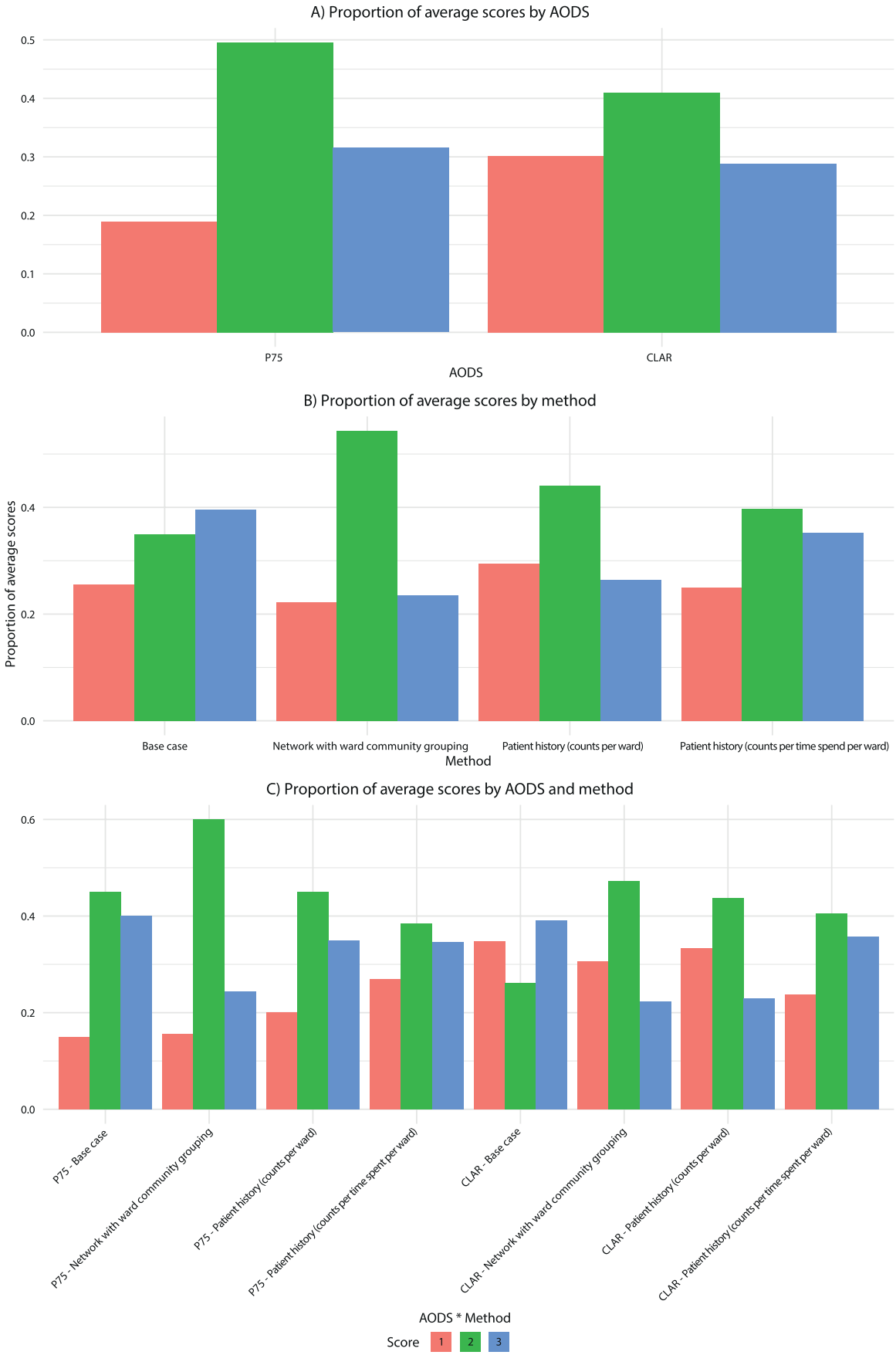


Figure 3. Results of alert judgment by infection prevention experts of the study hospital for A) differences between AODS framework, B) differences between patient transfer incorporation methods, and C) differences between the combination of AODS and patient transfer incorporation method. A score of 1: the alert is scored as "not relevant/ suspicious," a score of 2: "good to know (wait and observe for new findings)," a score of 3: "good to research (looking up patients or making an epi-curve) or immediate action required (intervention with additional measures)."

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P75-based systems and for AODS incorporating patient transfer history compared to the base case and ward community grouping approaches.

Assessment of AODS alerts

The interrater agreement among experts assessing selected possible outbreaks was moderate and statistically significant ($P < .01$), with Kappa values of 0.631 for the first selection and 0.429 for the second. In both selections, the more experienced infection prevention expert judged alerts as more relevant than the expert in training (S6 Figure).

Figure 3 shows the differences in alert scoring by AODS, method, and their combination. Both base case P75 and CLAR systems included a proportion of alerts scored as not relevant. The P75 AODS incorporating ward community grouping had the lowest proportion of non-relevant alerts, but also the fewest highly relevant alerts (Figure 3C). Only alerts unique to each system were evaluated, which limited direct comparability.

According to the first two experts, the best-performing systems were the P75 AODS incorporating patient transfer history (counts per ward) and the CLAR AODS incorporating time-weighted patient transfer history (counts per day per ward). In contrast, the second pair of experts identified the P75 base case as the top-performing method (S7 Figure). Repeated alerts were generally rated as more relevant than first alerts (S7 Figure).

Discussion

This study demonstrates that incorporating patient transfer history into AODS can increase the detection of possible outbreaks requiring follow-up or investigation. Extending a percentile-based AODS to include individual patient transfer history (wards visited in the prior 14 days) had the most favorable balance between increased detection and alert relevance.

One of the challenges when extending AODS to improve detection of previously unnoticed potential outbreaks is the increase in false positive alerts. These additional alerts increase workload for infection prevention experts, who must assess each alert to distinguish true outbreaks from noise. A higher alert burden may contribute to alert fatigue and reduce the effectiveness of alert response. Incorporating additional data therefore requires careful calibration to ensure that AODS remain practical for routine use.

Prolonged outbreaks with low case numbers present a particular challenge for AODS based on statistical or threshold methods, as such systems may fail to recognize slow-moving transmission patters. Accurately defining and incorporating microorganism-specific transmission and incubation periods remains a challenge and warrants further investigation. In this study, we used a fixed 14-day look-back window for inpatient transfers, although this may not be optimal for all organisms. Depending on the microorganism, patient characteristics, and culture practices, shorter or longer look-back periods may improve accuracy.

Possible outbreaks identified in this study were not routinely confirmed using bacterial sequencing or typing. Previous studies incorporating molecular typing or resistance-profile matching have shown that only a subset of algorithmically detected outbreaks represent true clonal transmission events.[15–18] Real-time whole-genome surveillance may further improve validation and prioritization of alerts. Additionally, AODS operate at species level, hence it overlooks outbreaks driven by horizontal transfer of antimicrobial resistance genes across species.[19]

Several AODS exist beyond P75 and CLAR. For example, WHONET integrated with SaTScan has also been used to detect space–time potential outbreaks in laboratory data.[17] Although this approach offers a standardized and widely used framework, our earlier comparative evaluation demonstrated that WHONET-SaTScan was less sensitive to increases above baseline than P75 and CLAR, resulting in fewer detected potential outbreaks.[3] For this reason, it was not further evaluated in the present study. Another important consideration is the choice of network clustering technique used to group hospital wards. Although ward community grouping improved detection of previously overlooked possible outbreaks, results are likely influenced by hospital-specific structures and patient flow patterns. No single clustering approach is universally optimal, and future work should explore which methods perform best under varying institutional conditions.

This study focused exclusively on bacteria and fungi. Findings may not be generalizable to nosocomial transmission of viral pathogens, which differ in incubation periods, transmissibility, and are often identified through syndromic rather than culture-based surveillance. Moreover, threshold-based systems depend on historical data, meaning that prior events can influence thresholds and bias detection in subsequent years. Finally, handling repeated alerts remains a challenge. Although repeated alerts increase workload, they often involve a higher number of patients and are frequently necessary to recognize potential outbreaks. This also underscores that balancing sensitivity with alert burden remains an important consideration for AODS design.

In sum, integrating patient transfer data into AODS improved the detection of potential hospital outbreaks. Further refinement of system parameters, including microorganism-specific look-back periods and context-specific configuration of AODS may improve precision and usability. Systematic evaluation of generated alerts will support ongoing optimalization and contribute to more effective infection prevention practices.

Supplementary material. The supplementary material for this article can be found at https://doi.org/10.1017/ice.2026.10485.

Data availability statement. R code is available via GitHub (https://github.com/susannepinto/AODS_patient_movements). Data are not made publicly available due to sensitive data fields containing that could lead to indirect patient identification.

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Author contributions. SP and MvM were involved with study conception and design, data collection, and analysis. MvM was involved with ethics approval. SP, MAMH-dZ, and MvM were involved with interpretation of results and manuscript preparation.

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Competing interests. The authors report no competing interests.

Ethical standard. Ethics approval and consent to participate: Waiver of consent was obtained from institutional review board for use of all data. However, for purposes of this study, persons who registered an objection to the use of their medical data were excluded.

Declaration of generative AI and AI-assisted technologies in the manuscript preparation process. During the preparation of this manuscript, the authors used generative AI to improve the English language and correct spelling and grammatical errors. After using this tool, the authors carefully reviewed and edited the text and take full responsibility for the content of the published article.

Consent for publication. Not applicable.

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