Original Article

Transmission visualizations of healthcare infection clusters: A scoping review

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Abstract

Objective: To evaluate infectious pathogen transmission data visualizations in outbreak publications.

Methods: Medline was searched for outbreak investigations of infectious diseases within healthcare facilities that included ≥1 data visualization of transmission using data observable by an infection preventionist showing temporal and/or spatial relationships. Abstracted data included the nature of the cluster(s) (pathogen, scope of transmission, and individuals involved) and data visualization characteristics including visualization type, transmission elements, and software.

Results: From 1,957 articles retrieved, we analyzed 30 articles including 37 data visualizations. The median cluster size was 20.5 individuals (range, 7–1,963) and lasted a median of 214 days (range, 12–5,204). Among the data visualization types, 10 (27%) were floor-plan transmission maps, 6 (16%) were timelines, 11 (30%) were transmission networks, 3 (8%) were Gantt charts, 4 (11%) were cluster map, and 4 (11%) were other types. In addition, 26 data visualizations (70%) contained spatial elements, 26 (70%) included person type, and 19 (51%) contained time elements. None of the data visualizations contained contagious periods and only 2 (5%) contained symptom-onset date.

Conclusions: The data visualizations of healthcare-associated infectious disease outbreaks in the systematic review were diverse in type and visual elements, though no data visualization contained all elements important to deriving hypotheses about transmission pathways. These findings aid in understanding the visualizing transmission pathways by describing essential elements of the data visualization and will inform the creation of a standardized mapping tool to aid in earlier initiation of interventions to prevent transmission.

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To stop pathogen transmission during a healthcare-associated outbreak, transmission pathways need to be hypothesized. Once potential routes of transmission are defined, whether they are probable or confirmed through person, place, and time, intervention measures can be initiated or continued to interrupt pathogen spread. Transmission pathways may be complex; the type of contact that occurred and the time and space in which the event occurred may not be completely clear. Compared to traditional epidemiological case investigations using only line-list data, visualizing transmission pathways can improve hypothesized relationships in time and space and can, therefore, promote more timely initiation of infection prevention and control measures.

No standard data visualization tool exists for describing transmission pathways. Typically, line lists comprising patient characteristics, event dates, and elements of clinical care provided are used to generate hypotheses of transmission pathways, with or without accompanying bed traces. Infection surveillance software allows users to review admission locations during the hospital stay, which can provide basic information about shared time and space and therefore transmission opportunities. However, transmission may occur even when patients do not share a proximate admission location at, or close to, the same time.

Tools for data visualization of transmission pathways have been described for use by healthcare-associated infection prevention teams for cluster investigation, and the extent of use these tools is not known. Two examples include Dotmapper and HospMapper: Dotmapper was developed by researchers as an

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easily accessible interactive mapping tool to visualize infection clusters over large geographic regions using Geographic Information Systems (GIS) (Esrí, California).4 HospMapper was developed for nosocomial transmission and can show data for patients who have a positive test for a pathogen, with outputs of an epidemic curve, a timeline, and a schematic ward plan.3

Furthermore, no guidelines or standards have been established to evaluate data visualization tools for transmission events. Salinas et al6 provided advice for best practices when creating a data visualization. In a systematic review published in 2014, Carroll et al7 found that usability and utility were important functions when determining helpfulness of a data visualization tool. Davis et al8 contemporaneously reported that 15% of published outbreak investigations included spatiotemporal analyses.

In infection prevention and hospital epidemiology, there is a need not only to describe the data visualizations that can be used to generate hypotheses about transmission pathways but also a critical analysis of the characteristics of each data visualization, as well as the software used to create them. Such an analysis would allow infection prevention and hospital epidemiology teams to choose a most effective data visualization tool for the cluster being investigated, to generate hypotheses about transmission pathways more effectively and therefore improve cluster investigations, to implement interventions to interrupt transmission more quickly to ultimately better prevent patient harm.

In this scoping review, we have evaluated the infectious-pathogen transmission data visualizations used in healthcare settings to determine which methods and elements of visualizing transmission in healthcare settings are effective at generating hypotheses regarding transmission pathways.

Methods

Published evidence eligibility criteria

Articles eligible for inclusion in the scoping review were peer reviewed, written in English, and published after 1985 (when infection preventionists (IPs) first documented using electronic surveillance including electronic medical records and information technology tools that allow for automated data collection).9,10 All eligibility criteria were selected in the search algorithm.

Articles were excluded if they did not contain patient data with a methodology appropriate for evaluating a healthcare-associated infectious disease or infectious pathogen cluster, such as observational cluster investigation methods.5 Therefore, cost–benefit analyses, meta-analyses, randomized control trials, community outbreaks, and other nonhealthcare studies were not included in the review.

Full article review used the following 4 inclusion criteria to select screened articles for data abstraction: (1) Infectious diseases met healthcare-associated infection definitions using National Healthcare Safety Network criteria (NHSN)12 but could be an infectious disease not defined using NHSN healthcare-associated infection criteria if ≥1 transmission event occurred within a healthcare facility. This was done to capture all potential pathogen transmission in the healthcare setting. (2) The source described an infectious disease cluster. Multiple clusters in an outbreak or publication were included if each cluster was contained in 1 healthcare facility. (3) The results contained 1 or more data visualizations demonstrating pathogen transmission pathways with data observable by an infection preventionist showing temporal and/or spatial relationships using patient health data and epidemiological data. For example, data visualizations could not contain only a phylogenetic tree, which alone would not include various person type data (ie, patients, healthcare workers) or test positive dates; however, a phylogenetic tree could serve as a data visualization if it incorporated other nongenetic epidemiologically relevant data. (4) The facilities where transmission occurred was considered a healthcare facility. Healthcare facilities were defined as structures whose primary purpose was designed to provide care to individuals where person-to-person transmission can occur and where healthcare personnel are present. Healthcare facilities include long-term care facilities, acute-care facilities, rehabilitation facilities, and behavioral health facilities.

Information sources and search strategy

Medline (Ovid) was searched by a health sciences librarian (H.M.V.V.) with systematic review experience. The date of the search was August 24, 2021. Concepts that comprised the search were healthcare-acquired infections and cluster analysis or geographic mapping. A combination of MeSH terms and title, abstract, and keywords was used to develop the Medline search that was checked against a known set of studies (Supplementary Table S1 online). Articles were also considered for review if they were cited as references within the papers found through the original Medline search and appeared to have relevance for this review.

Citations were uploaded from EndNote (Clarivate, UK) to DistillerSR (Evidence Partners, Canada) for the study selection process. All study selection decisions were stored in DistillerSR. Two authors (M.B.B. and J.F.W.) conducted the title, abstract, and full-article eligibility screening. When a consensus on article eligibility could not be reached, a third investigator (G.M.S.) independently reviewed the citation, abstract, and manuscript to determine eligibility. The data charting was completed by 3 reviewers (M.B.B., J.F.W., and N.J.R.) for articles that passed the full-text screening process. The protocol was published on Open Science Framework prior to beginning the literature search.12

Data abstraction

Data abstraction was completed independently by 3 reviewers (M.B.B., J.F.W., and N.J.R.) from the eligible articles using DistillerSR using a data abstraction form developed by the investigators. The data abstracted included the nature of the cluster(s) including pathogen, scope of transmission, and individuals involved. Characteristics of the transmission pathway data visualization(s) included type of visualization, elements of transmission incorporated into the visualization, and software used in the visualization (Supplementary Table S2).

Data visualization categorization

Data visualization categories were defined data visualization types within specified categories of hypothetical examples (Fig. 1). If data visualizations were unable to be grouped within the established example types, new categories were added to ensure that all data visualizations were incorporated and analyzed.

Statistical analysis

Statistical analysis, the calculations of means, medians, and totals, were performed using Excel. Characteristics of the studies and data visualizations are described using aggregate averages. The project, including a subsequent evaluation and implementation of a software tool for data visualization, underwent formal
review and was granted ethical approval (Project 3405) as a quality improvement project by University of Pittsburgh Medical Center’s Quality Improvement Review Committee.

Results

Study characteristics

With the exclusion of 1 duplicate article, 1,957 articles were identified through the Ovid Medline database search (Fig. 2) and 1,707 (87.2%) articles were included after review of the citation and abstract. Among the articles that were excluded, 335 did not include an infectious pathogen, 829 were not human studies, and 1,691 used nonpertinent study methodology. The remaining 250 (12.7%) articles underwent full text review, of which 220 did not meet ≥1 inclusion criteria: 13 did not study an NHSN-defined or healthcare-associated organism, 95 did not describe an infectious diseases cluster, 200 did not include ≥1 data visualization, 40 did not occur in a healthcare facility, and 1 reported an outbreak in >1 facility. The remaining 30 articles (1.5%) fulfilled the eligibility criteria and were included in data abstraction and analysis.

The 30 analyzed studies were conducted in healthcare facilities in North America,14–18 South America,19 Europe,20–31 Africa,32,33 Asia,34–42 and Australia43 (Table 1). Fourteen studies (46.7%) described outbreaks occurring in acute-care facilities,15,16,19,21,25,29,32,34–38 and 11 (36.7%) studies were conducted in a tertiary-care hospital.14,18,22–24,27,28,33,40,42,43 Of the remaining studies, 2 studies took place in a community hospital,17,41 2 studies took place in a long-term care facility with a rehabilitation care ward,20 Of the 30 studies, 17 (56.6%) were prospective studies.15,17,21,23,24,26,28–31,33,35,37,38,40–42

The 30 studies described clusters with a median cluster size of 20.5 individuals (range, 7 to 1,963) and a median duration of 214 days (range, 12–5,204) (Table 1). Also, 15 (50%) of the causative pathogens described in clusters were viral,14,15,17,20,21,25,29,31,34,35,37,38,40,42 10 (33.3%) were bacterial,16,18,19,23,24,32,33,36,41,43 (10, 33.3%), and 5 (16.6%) were other organism types.22,25,28,30,39 Of the 30 studied clusters, 17 (56.6%) had ≥1 case occurring in an acute-care facility, and 1 reported an outbreak in >1 facility. The remaining 30 articles (1.5%) fulfilled the eligibility criteria and were included in data abstraction and analysis.

Data visualization types and elements

In total, 37 data visualizations were reported in the 30 eligible articles (Supplementary Table S3), with up to 2 visualizations per study. More than half of the data visualizations contained spatial elements.14–16,19,22–27,31,33–37,39–42,45 and/or person type.14,15,17–22,24–32,34–36,39,40 and half contained time elements.15–17,21,22,24–28,30,31,34,36,39,43 Case type (confirmed, probable, or suspected)14,17,19,23,24,27,28,33,35,36,39,43 and pathway type were less frequently incorporated.17,22,28–31,34,36 None of the data visualizations contained contagious periods, and very few contained symptom-onset date (Table 2).14,36

Fig. 1. Examples of data visualization types from reported healthcare-associated infectious diseases outbreaks. Note: Citations for information for the data visualizations: heat map,46 dot maps,50 timelines,50 Gantt chart, transmission networks, and social networks.17 All visualizations are hypothetical examples created by the author this year.
Timeline-type data visualizations were more likely to include person type but more than half of timelines included spatial elements and test positivity date. Among floor-plan transmission maps, time elements were only included in 20% of the studies. All 3 cluster maps prioritized spatial elements; however, 1 cluster map successfully incorporated person type, case type, transmission pathways, symptom-onset date, and positive test date. Transmission trees and social networks successfully incorporated person types. For the heat map and case proximity map analyses, spatial elements were included. However, transmission networks were more variable in the type of elements included to display transmission events; more than half contained time elements and/or person types.

Only 2 studies reported the software used to create data visualizations (2 [5.4%] of 37 data visualizations). The following software programs were used to create data visualizations: AutoCAD, QGIS, and Pajek 4.90 (Supplementary Table S5).

Discussion

In this scoping review of 1,957 articles, 30 studies with 37 data visualizations were identified that described clusters of infections in healthcare settings. Across the 37 data visualizations, more than half included spatial elements and patients, and half included time. Almost half contained case type and none included contagious periods. Overall, this scoping review has demonstrated the wide range of data visualization practices used in characterizing outbreaks. Although none of the data visualizations analyzed in this review incorporated all data elements (ie, contagious period, healthcare workers, pathways, symptom onset date, and test positive date), several types of visualizations incorporated multiple elements.

We observed significant variability the data elements included across visualization types. With the wide range of data elements included in each of the visualizations analyzed for this review, an infection preventionist should explore different data visualization types to analyze the specific circumstance of the cluster most effectively. This variability also suggests an opportunity to develop a...
| Study            | Year | Country     | Study Type | Setting                                         | Scope of Outbreak                                                                 | Infectious Pathogen | Cluster Duration | Cluster Size |
|------------------|------|-------------|------------|-------------------------------------------------|------------------------------------------------------------------------------------|---------------------|------------------|--------------|
| Abbas et al      | 2021 | Switzerland | Case–Control | Long-term care facility | Palliative care ward, rehabilitation care ward                                   | SARS-CoV-2           | 35 d             | 37            |
| Burns et al      | 2011 | Ireland     | Prospective | Acute care                                      | Entire healthcare facility                                                        | Hepatitis B virus   | 425 d            | 7             |
| Borges et al     | 2021 | Portugal     | Prospective | Acute care                                      | Internal medicine, hemodialysis units                                             | SARS-CoV-2           | 25 d             | 48            |
| Charpentier et al| 2017 | France      | Case–control | Tertiary care                                   | Transplant unit, surgical cardiology outpatient clinic, echocardiography, transplant outpatient clinic, nephrology unit | Pneumocystis jirovecii | 61 d             | 12            |
| Cherifi et al    | 2006 | Belgium     | Prospective | Tertiary care                                   | Geriatric ward                                                                  | Clostridioides difficile | 731 d            | 21            |
| Duong et al      | 2011 | Vietnam     | Prospective | Acute care                                      | Intensive and non-intensive care units                                          | Klebsiella pneumoniae | 365 d            | 24            |
| Furusyo et al    | 2004 | Japan       | Prospective | Acute care                                      | Hemodialysis unit                                                              | Hepatitis C virus   | 720 d            | 11            |
| Gandhi et al     | 2013 | South Africa | Retrospective | Acute care                                      | General medicine ward                                                        | Mycobacterium tuberculosis | 700 d            | 148           |
| Jacobson et al   | 2015 | South Africa | Prospective | Tertiary care                                   | Hematology ICU                                                                | Klebsiella pneumoniae | 30 d             | 8             |
| Javaid et al     | 2021 | USA         | Prospective | Acute care                                      | Cardiac surgery unit                                                            | Clostridioides difficile | 792 d            | 20            |
| Klompas et al    | 2021 | USA         | Retrospective | Tertiary care                                   | 4 inpatient units                                                             | SARS-CoV-2            | 90 d             | 52            |
| Kosso et al      | 2019 | Germany     | Prospective | Tertiary care                                   | Obstetrics department, neonatal department                                       | Staphylococcus aureus | 401 d            | 8             |
| Lee et al        | 2021 | Korea       | Retrospective | Acute care                                      | Neurosurgery ICU, neurosurgery ward, radiology, bank, intervention room, echo lab, general internal medicine wards, | SARS-CoV-2          | 36 d             | 36            |
| Marmor et al     | 2020 | Australia   | Retrospective | Tertiary care                                   | Renal unit, surgical unit, ICU, hematology unit                                | Enterobacteriaceae   | 1,827 d          | 17            |
| Moldovan et al   | 2019 | Canada      | Case–control | Tertiary care                                   | 3 campuses                                                                     | Staphylococcus aureus | 426 d            | 547           |
| Nevez et al      | 2018 | France      | Case–control | Acute care                                      | Nephrology department                                                          | Pneumocystis jirovecii | 402 d            | 25            |
| Pagani et al     | 2015 | Switzerland | Prospective | Geriatric hospital                              | Hematology ICU                                                                | Influenza virus      | 90 d             | 69            |
| Pai et al        | 2020 | USA         | Retrospective | Acute care                                      | Across inpatient units                                                         | Clostridioides difficile | 2,526 d          | 1,963         |
| Perez-Lago et al | 2021 | Spain       | Retrospective | Tertiary care                                   | Gastroenterology ward                                                        | SARS-CoV-2            | 27 d             | 18            |
| Rabodoninina et al | 2004 | France     | Prospective | Tertiary care                                   | Entire healthcare facility                                                   | Pneumocystis jirovecii | 1,080 d          | 45            |
| Shen et al       | 2003 | China       | Prospective | Acute care                                      | Entire healthcare facility                                                   | SARS-CoV-1            | 4,621 d          | 77            |
| Spada et al      | 2008 | Italy       | Prospective | Acute care                                      | Hemodialysis unit                                                              | Hepatitis C virus   | 184 d            | 14            |
| Tsutsumi et al   | 2005 | Japan       | Retrospective | Geriatric hospital                              | Dementia ward                                                                 | Sarcoptes scabiei   | 216 d            | 20            |
| Varia et al      | 2003 | Canada      | Prospective | Community hospital                              | Entire healthcare facility                                                   | SARS-CoV-1            | 52 d             | 128           |
| Vindrios et al   | 2017 | France      | Prospective | Acute care                                      | Cardiac surgery unit                                                          | Pneumocystis jirovecii | 185 d            | 7             |

(Continued)
data visualization software tool that incorporates all the elements or has the capability to create different visualizations from the same cluster data set. The very infrequent reporting of software programs in these clusters did not allow us to evaluate whether a specific program could create hypothesized transmission pathways using different visualization types.

Among all data visualizations, 26 (70%) used spatial elements\(^1\) and 19 (51%) included time elements. 15\(^1\) The high frequency of these data element types may be related to accessibility and availability of information at a given healthcare facility. Less frequently utilized data visualization elements, such as contagious period and symptom-onset date, may relate to data accessibility. Despite the additional burden that collection of these elements place on healthcare facilities, symptom-onset dates and contagious periods should be collected and considered important features in cluster-transmission visualizations. For contact tracing and the development of hypotheses of transmission, these types of elements are essential to fully understanding the extent of the transmission event.

Specific data elements including patient information, microbiology cultures, as well as locations of patients and/or healthcare workers in space fit into the way in which standard outbreak investigations are conducted by infection preventionists. However, these data may not necessarily be in a form extractable directly from electronic health records (EHR). Thus, a standardized data visualization tool would need to be aware of the data infection preventionists have readily available. Additionally, the adoption of data visualization tools must include the consideration of data integration because EHR data may be difficult to extract and the software must work in tandem. EHR data mining has been effective at identifying transmission routes in healthcare outbreaks.\(^{46}\) A data visualization tool that can be used to visualize and hypothesize transmission routes and that seamlessly integrates with the existing EHR could aid in informing interventions to stop transmission. However, data visualization tools need operational data integration to be effective.

Within the 37 data visualizations we analyzed, the frequency of spatial elements and time elements was higher than the 15% frequency of spatiotemporal elements reported among data visualizations in 2014.\(^5\) Of the eligible articles, 19 of the 30 were published after 2014, which may account for some of the change. Of these 19 articles, 11 included spatial and time elements in data visualizations. The increased inclusion of spatiotemporal elements may be an indicator of improving data visualization utility over time.

We observed a slight pattern in the types of visualizations used to analyze droplet versus contact transmission. Infection clusters due to bacteria, most commonly requiring contact precautions, used case-proximity maps, floor-plan transmission maps, and transmission networks more frequently. In contrast, clusters due to viruses, more likely requiring droplet precaution isolation (excepting hepatitis B and C viruses), used timelines, cluster maps, Gantt charts, and transmission networks most often. In addition, many of the viral cluster visualizations included patients and healthcare workers, whereas bacterial cluster visualizations mostly included patients. Inclusion of both healthcare workers and patients in viral cluster visualizations may be due to transmission patterns of respiratory pathogens such as SARS-CoV-2 and influenza A.\(^{47,48}\) Data visualizations used for different infectious pathogens and the data elements used to describe the clusters could be tailored to the mechanisms of transmission of the pathogen under investigation.

Only 2 of the evaluated visualizations described the type of software used. Software such as R and GIS require training to use; other software created to aid in cluster visualization, such as DotMapper and HospMapper, require specific software knowledge and have technological limitations including data formatting (Supplementary Table S5). An ideal data visualization software program would not only be easily integrated into the current infection prevention workflow but would also be accessible for those with minimal programming expertise.

All the outbreaks in the articles were described after the outbreak occurred within the healthcare facility and after infection prevention measures were initiated. The data visualizations contained within these articles illustrated the transmission events and pathways that were already known. Therefore, the ability of these software tools to derive hypotheses about transmission pathways is limited, and this feature is essential when an outbreak is first identified to advance the investigation. Other limitations of this analysis include a small sample size of only 30 publications and 37 data visualizations, with most studies describing outbreaks in acute-care facilities. The common elements found in these articles may not be generalizable to other healthcare facilities seeking to visualize transmission pathways, such as long-term care facilities, behavioral health facilities, or psychiatric facilities. Our review may have been affected by publication bias toward acute-care facilities, which have better data accessibility, and by bias toward reporting larger outbreaks. Our findings may

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**Table 1. (Continued)**

| Study | Year | Country | Study Type | Setting | Scope of Outbreak | Infectious Pathogen | Cluster Duration | Cluster Size |
|-------|------|---------|------------|---------|-------------------|---------------------|-----------------|--------------|
| Wee et al | 2020 | Singapore | Prospective | Tertiary care | Campus-wide | SARS-CoV-2 | 212 d | 14 |
| Wong et al | 2010 | China | Prospective | Tertiary care | General medicine ward | Influenza virus | 16 d | 9 |
| Yang et al* | 2010 | Taiwan | Prospective | Community hospital | Respiratory care ward | Haemophilus influenzae | 25 d | 12 |

Note: End date of cluster in calculation (1 day was added).

*Article did not describe the type of care provided at the healthcare facility so acute care was marked.
Table 2. Types of Data Elements Included Across 37 Transmission Visualizations Grouped by Data Visualization Type in the 30 Eligible Articles Reviewed

| Study            | Infectious Pathogen | Data Visualization Type | Elements Included in the Data Visualization | Timeline Subtotal no. (%) | Gantt Chart Subtotal, no. (%) |
|------------------|---------------------|-------------------------|---------------------------------------------|---------------------------|--------------------------------|
| Javaid et al     | Influenza A virus   | Timeline                | ✓ ✓ ✓                                      | 5 (83) 5 (83) 3 (50) 2 (33) 1 (17) 4 (67) 6 (100) | 3 (100) 3 (100) 2 (67) 1 (33) |
| Javaid et al     | Influenza A virus   | Timeline                | ✓ ✓ ✓                                      |                           |                                |
| Jia et al        | Clostridoides difficile | Timeline             | ✓ ✓ ✓                                      |                           |                                |
| Kossow et al     | Staphylococcus aureus | Timeline              | ✓ ✓ ✓                                      |                           |                                |
| Pagani et al     | Influenza virus     | Timeline                | ✓ ✓ ✓                                      |                           |                                |
| Rabodonirina et al | Pneumocystis jirovecii | Timeline           | ✓ ✓ ✓                                      |                           |                                |
| Borges et al     | SARS-CoV-2          | Gantt chart             | ✓ ✓ ✓                                      |                           |                                |
| Borges et al     | SARS-CoV-2          | Gantt chart             | ✓ ✓ ✓                                      |                           |                                |
| Burns et al      | Hepatitis B virus   | Gantt chart             | ✓ ✓ ✓                                      |                           |                                |
| Cherifi et al    | Clostridoides difficile | Floor plan transmission map | ✓ ✓ ✓                                      |                           |                                |
| da Silva et al   | Klebsiella pneumoniae | Floor plan transmission map | ✓ ✓ ✓                                      |                           |                                |
| Furusyo et al    | Hepatitis C Virus   | Floor plan transmission map | ✓ ✓ ✓                                      |                           |                                |
| Jacobson et al   | Klebsiella pneumoniae | Floor plan transmission map | ✓ ✓ ✓                                      |                           |                                |
| Pérez-Lago et al | SARS-CoV-2          | Floor plan transmission map | ✓ ✓ ✓                                      |                           |                                |
| Tsutsumi et al   | Sarcoptes scabiei   | Floor plan transmission map | ✓ ✓ ✓                                      |                           |                                |
| Wong et al       | Influenza A virus   | Floor plan transmission map | ✓ ✓ ✓                                      |                           |                                |
| Yang et al       | Haemophilus influenzae | Floor plan transmission map | ✓ ✓ ✓                                      |                           |                                |
| Lee et al        | SARS-CoV-2          | Floor plan transmission map | ✓ ✓ ✓                                      |                           |                                |
| Floor plan transmission map subtotal, no. (%) | 5 (50) 5 (50) ... 6 (60) 1 (10) 10 (100) 2 (20) 1 (10) 2 (20) |                                |
| Klompas et al    | SARS-CoV-2          | Cluster map             | ✓ ✓ ✓                                      |                           |                                |
| Lee et al        | SARS-CoV-2          | Cluster map             | ✓ ✓ ✓                                      |                           |                                |
| Javaid et al     | Influenza A virus   | Cluster map             | ✓ ✓ ✓                                      |                           |                                |

(Continued)
| Study               | Infectious Pathogen    | Data Visualization Type | Elements Included in the Data Visualization |
|--------------------|-----------------------|-------------------------|---------------------------------------------|
|                    |                       |                         | Person Type | Patients | Healthcare workers | Other | Case Type | Pathway | Spatial Element | Time Element | Symptom Onset Date | Test Positive Date | Contagious Period |
| Cluster map subtotal, no. (%) |                       |                          | 2 (67)      | 2 (67)   | 2 (67)            | ...   | 3 (33)    | 1 (33) | 3 (100)       | --             | 1 (33)           | 1 (33)           | --               |
| Gandhi et al       | Mycobacterium tuberculosis | Transmission network      | ✓            | ✓        | ...               | ...   | ✓         | ...    | --             | ...           | ...              | ...              | ...              |
| Marmor et al       | Enterobacteriaceae     | Transmission network      | ...          | ...      | ...               | ...   | ✓         | ...    | ✓             | ✓             | ...              | ...              | ...              |
| Pérez-Lago et al   | SARS-CoV-2             | Transmission network      | ✓            | ✓        | ...               | ...   | ✓         | ✓      | ...           | ...           | ...              | ...              | ...              |
| Shen et al         | SARS-CoV-1             | Transmission network      | ...          | ...      | ...               | ...   | ...       |         | ...           | ...           | ...              | ...              | ...              |
| Spada et al        | Hepatitis C virus      | Transmission network      | ✓            | ✓        | ...               | ...   | ...       | ...    | ...           | ...           | ...              | ...              | ...              |
| Varia et al        | SARS-CoV-1             | Transmission network      | ✓            | ✓        | ✓                 | ✓     | ✓         | ...    | ✓             | ...           | ...              | ...              | ...              |
| Charpentier et al  | Pneumocystis jirovecii | Transmission network      | ✓            | ✓        | ...               | ...   | ✓         | ✓      | ...           | ...           | ...              | ...              | ...              |
| Duong et al        | Hepatitis C virus      | Transmission network      | ✓            | ✓        | ...               | ...   | ...       | ✓      | ✓             | ...           | ...              | ...              | ...              |
| Jia et al          | Clostridioides difficile| Transmission network      | ✓            | ✓        | ...               | ...   | ✓         | ✓      | ✓             | ✓             | ...              | ...              | ...              |
| Nevez et al        | Pneumocystis jirovecii | Transmission network      | ✓            | ✓        | ...               | ...   | ✓         | ...    | ...           | ...           | ...              | ...              | ...              |
| Vindrios et al     | Pneumocystis jirovecii | Transmission network      | ✓            | ✓        | ...               | ...   | ...       | ✓      | ✓             | ...           | ...              | ...              | ...              |
| Transmission network subtotal, no. (%) |                       |                          | 9 (82)      | 9 (82)   | 1 (9)             | 1 (9) | 5 (45)   | 4 (36) | 5 (45)       | 8 (73)        | --               | 2(18)            | --               |
| Abbas et al        | SARS-CoV-2             | Transmission tree         | ✓            | ✓        | ✓                 | ✓     | ...       | ...    | ...           | ...           | ...              | ...              | ...              |
| Transmission tree subtotal, no. (%) |                       |                          | 1 (100)     | 1 (100)  | 1 (100)           | ...   | ...       | ...    | ...           | ...           | ...              | ...              | ...              |
| Moldovan et al     | Staphylococcus aureus  | Social network*           | ✓            | ✓        | ✓                 | ...   | ...       | ...    | ...           | ...           | ...              | ...              | ...              |
| Social network analysis subtotal, no. (%) |                       |                          | 1 (100)     | 1 (100)  | 1 (100)           | ...   | ...       | ...    | ...           | ...           | ...              | ...              | ...              |
| Pai et al          | Clostridioides difficile| Case proximity graph      | ...          | ...      | ...               | ...   | ...       | ✓      | ✓             | ...           | ...              | ...              | ...              |
| Spatial proximity map, no. (%) |                       |                          | ...          | ...      | ...               | ...   | ...       | ...    | ...           | ...           | ...              | ...              | ...              |
| da Silva et al     | ...                   |                          | ...          | ...      | ...               | ...   | ...       | ✓      | ...           | ...           | ...              | ...              | ...              |
| Heat map subtotal, no. (%) |                       |                          | ...          | ...      | ...               | ...   | ...       | ...    | ...           | ...           | ...              | ...              | ...              |
| Totals N=37, no. (%) |                       |                          | 26 (70)     | 26 (70)  | 11 (30)           | 3 (8) | 14 (39)  | 7 (19) | 26 (70)      | 19 (51)       | 2(5)             | 9(24)            | --               |

*aData visualizations with specific software stated, see Supplementary Table 5.*
underrepresent smaller outbreaks and investigations in lower-resourced facilities. Although the findings of this study included outbreaks reported internationally, limiting the search to English language and 1 database may have excluded less readily accessible and non-peer-reviewed data.

The data gathered from these articles will be used to inform the creation of a standardized visualization tool that can aid in current SARS-CoV-2 cluster investigations, with the overall goal of allowing for visualization of other infectious pathogen clusters in healthcare settings to reduce nosocomial transmission. Data visualization should include spatial elements, time elements, and elements that inform the exposure window and incubation period, as well as epidemiologic characteristics potentially associated with transmission such as healthcare worker type. No single data visualization may capture all informative elements, however. By understanding the types of common data visualization elements utilized in transmission visualizations, IPs can develop a generalized understanding of the types of possible data visualizations and data elements that can be included for different infectious pathogens. This study also highlights the need for a standardized data visualization that can utilize electronic medical records to allow for the generation of hypotheses regarding transmission and, therefore, improve public health measures and patient safety through faster infection prevention and control interventions to interrupt transmission.

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