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Evaluation of a web-based tool for labelling potential hospital outbreaks: a mixed methods study

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SUMMARY

Background: Labelling outbreaks in surveillance data is necessary to train advanced analytical methods for outbreak detection, but there is a lack of software tools dedicated to this task.

Aim: To evaluate the usability of a web-based tool by infection control practitioners for labelling potential outbreaks.

Methods: A mixed methods design was used to evaluate how 25 experts from France and Canada interacted with a web-based application to identify potential outbreaks. Each expert used the application to retrospectively review 11–12 1-year incidence time series from 23 different types of micro-organism. The interactions between the users and the application were recorded and analysed using mixed effect models. The users' comments were analysed via qualitative methods.

Findings: From the 240 reviews completed, 439 potential outbreaks were labelled, approximately half with a high probability. Significant heterogeneity was observed between users regarding their answers and behaviours (evaluation time, usage of the different options). A significant learning effect was also observed for the experts' interactions with the tool, but this did not seem to impact their answers. The content analysis of the comments highlighted the difficulty of early outbreak identification for practitioners, but also the potential utility of web applications such as that evaluated for routine surveillance.

Conclusion: The interactive web application was both usable and useful for infection control practitioners. Its implementation in routine practice could help professionals to identify potential outbreaks while creating data to train automated detection algorithms.

Introduction

In 1976, Lawrence Kunz wrote with enthusiasm about the coming of age of computerized microbiology [1], already envisaging what is now known as 'syndromic surveillance and predictive medicine'. The 1970s was an era of rapid development for both informatics and infection control, and the first computerized surveillance systems within hospitals were built during this period [2,3].

Since then, infection control professionals have continued to adapt computer science innovations to address problems in their field. Technologies in routine use now include complex

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computer algorithms [4], dedicated data warehouses [5] and cloud-based reporting systems [6]. This computational infrastructure is used for a variety of activities, such as monitoring nosocomial infections [7], identifying high-risk patients [8] and guiding antibiotic prescriptions [9].

However, outbreak detection — another area of computerized microbiology envisaged by Kunz — has not reached the same level of development. Although several attempts have been made in the last decades to implement automated detection systems within hospitals, their characteristics and evaluations have varied widely, and there is a lack of evidence about their practical utility [10]. A major barrier is the absence of data sets in which outbreak periods are clearly labelled, which could serve as reference standards.

In order to support the creation of such data sets for the evaluation of early outbreak detection methods, an interactive web tool was developed for experts to use for retrospective examination of available data and to indicate when outbreaks probably occurred. The aim of this study was to evaluate the tool's usability, analyse how users interacted with it, and try to understand what influenced their behaviours.

Materials and methods

Initial design of the web application

To serve its purpose, the tool had to meet several requirements. First, it had to display the necessary data. As the focus was on early outbreak detection, the data available prospectively are rather minimal; most clinical and microbiological data are usually gathered after an alert is issued, and would therefore not be relevant in this context. However, as outbreaks can spread more easily across wards with many patients, additional data were necessary to help users to understand how wards related to one another. Second, the tool had to be interactive in order to allow the users to explore the data and label potential outbreaks. Third, in addition to keeping track of these outbreaks, the tool also needed to record how users interacted with the data. Finally, it had to be accessible simultaneously to several users from different institutions in France and Canada.

To meet the requirements of accessibility, data visualization and interactivity, a web application based on the D3 JavaScript library for interactive data visualization was developed [11]. A screenshot of the application is available in Figure 1, as well as a video demonstration. Data visualization and interactivity were allowed via three panels (incidence, network and event list). The incidence panel mainly consisted of a bar chart presenting one year's worth of weekly incidence data for a given type of micro-organism, along with a moving average curve to help review time series that exhibited extensive variability in incidence. A red circle over a bar indicated that a notification about a potential outbreak was recorded in the hospital's notification system that week. A description of the notification was available by hovering the mouse over the circle.

A supplementary video related to this article can be found at https://doi.org/10.1016/j.jhin.2019.05.004.

The network panel was created to help users understand how the different wards were connected. The wards were represented as connected circles in a graph, laid out so that the distances reflected the number of patients transferred between wards in the previous year; the more patients transferred, the closer the wards were to each other.

The incidence and network panels interacted with each other. When a user selected a period within the bar chart, the wards with new cases during that period were highlighted in the network view. The user could hover the mouse over the nodes for these wards to obtain more information (type of

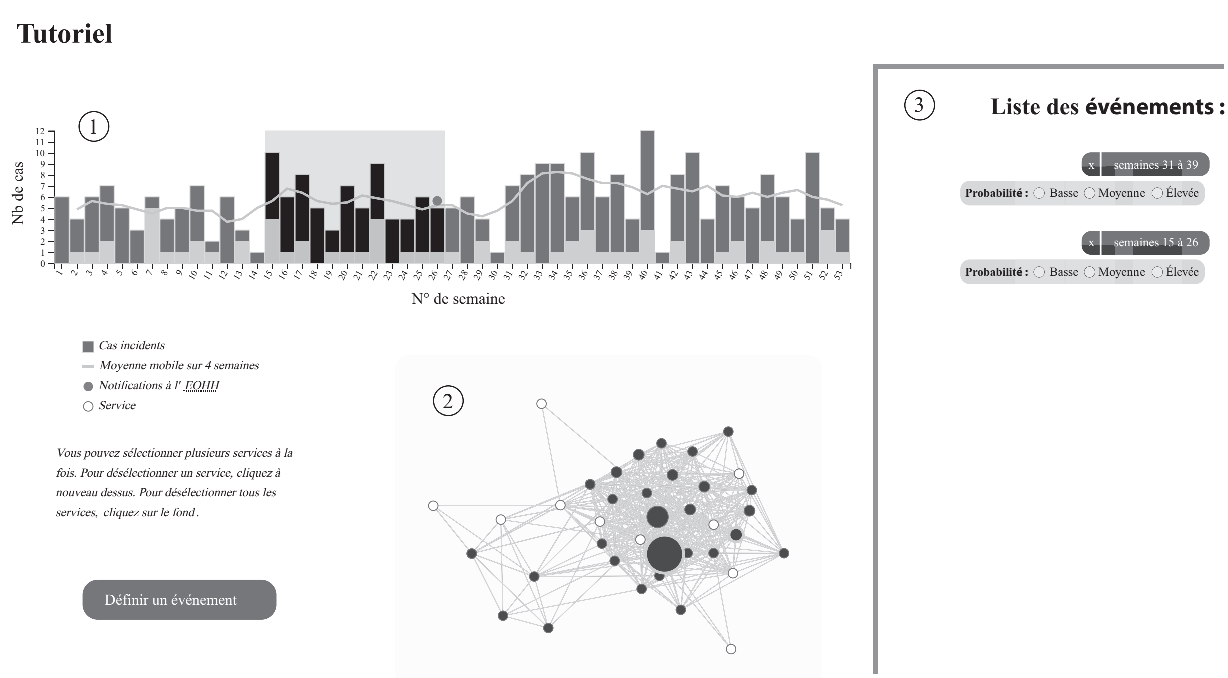

Figure 1. Screenshot of the web application (training version). The three main components of the application are the incidence panel (1), the network panel (2) and the event panel (3). The bars in light grey correspond to specific incidence data of the wards selected in the network view.

ward, number of cases), and could click on the nodes to see the incidence data for these wards appear as a new layer on the bar chart (Figure 1).

To label a selected period as a potential outbreak, the user had to click on a button to add the period to the third panel of the application: the event list. The user would then be asked to describe their certainty (low, medium or high) that the event corresponded to an actual outbreak.

At the end of a review, the user clicked on a validation button to save the created events to a PostgreSQL database. Using Google Analytics, data were also collected about the duration of the review, how many selections were made in the incidence view, and how many clicks and mouse hovering events were made in the network view.

Evaluation of the web application

Surveillance data

The surveillance focused on 23 types of micro-organism based on their frequency and potential harm for patients (Table I). A patient infected or colonized with one of these micro-organisms (i.e. presenting a positive bacteriological culture) for the first time within a year was considered as a case. Data from the bacteriological laboratory's information system were used to identify every case that occurred from 2013 to 2016 at Nantes University Hospital. The number of cases was aggregated by week for each type of micro-organism and each year, resulting in 92 time series.

Admission–transfer–discharge data were used to build the network view; this allowed the number of transfers for every pair of wards to be tallied. For each year, the network was based on the data from the preceding year. The distances on the graph were calculated based on these counts using the Kamada–Kawaii layout algorithm [12]. Potential outbreak notifications were gathered from the hospital's adverse events and incident reporting system, and a short summary was written for each of them.

Table I
List of the 23 types of micro-organism selected for surveillance

- Extended-spectrum beta-lactamase-producing Enterobacteriaceae
- Meticillin-resistant *Staphylococcus aureus*
- Carbapenemase-producing Enterobacteriaceae
- *Acinetobacter baumannii*
- *Staphylococcus aureus* (regardless of resistance profile)
- *Staphylococcus epidermidis*
- *Staphylococcus haemolyticus*
- Group B streptococcus
- *Streptococcus pneumoniae*
- *Enterococcus faecalis*
- *Enterococcus faecium*
- *Escherichia coli*
- *Pseudomonas aeruginosa*
- *Proteus mirabilis*
- *Enterobacter cloacae*
- *Klebsiella pneumoniae*
- *Klebsiella oxytoca*
- *Clostridium difficile*
- *Lactobacillus* spp.
- *Haemophilus influenza*
- *Citrobacter koseri*
- *Propionobacterium acnes*
- *Stenotrophomonas maltophilia*

Application trial

A convenience sample of 25 French and Canadian experts in infection control surveillance was asked to test the application. Each expert had to review 11–12 randomly assigned time series between October and December 2017. After receiving their consent to participate, the experts were emailed detailed instructions, login credentials, and links to the application and a video tutorial. Two follow-up emails were sent one and two months after the beginning of the study.

After their initial login, each user was asked about their position, specialty and years of experience in that field. They also self-rated their internet, computer and surveillance skills, and reported how many hours they spend on average in front of a computer each day. After completing all of their evaluations, they were asked to assess the application's usability using the System Usability Scale (SUS), a 10-item scale with a score ranging from 0 to 100 [13]. They also had the opportunity to give their opinion about the application in an open text field.

Analysis

In order to account for the repeated nature of the measures, potential variations between users and time series were estimated with random effect models, adjusting for characteristics of users and time series when necessary. To enable comparisons between the models, the sizes of the random effects are displayed in this article using intra-cluster correlations (ICCs), which represent the percentages of the overall model variance explained by the effects.

The number of events by time series was modelled using a Poisson model, after verifying the absence of overdispersion. The length of the events and data from the Google Analytics trackers were modelled using log-linear models. The probability of the event was modelled as a quantitative variable [from 0 (no outbreak) to 4 (high probability)], and was also modelled using a log-linear model. All statistical analyses were performed using R Version 3.5.1 [14].

The users' comments were examined via a qualitative content analysis using RQDA Version 0.3.1 within R [15]. Each comment was read thoroughly to identify the units of meaning, which were then coded and gathered into categories. In the article, verbatim citations of the comments are displayed within quotation marks, and modifications made for clarity are indicated with brackets.

Results

Users and participation

Of the 25 experts recruited, 23 evaluated at least one time series. Their characteristics are displayed in Table II. Most were infection control physicians or pharmacists (78.3%), had at least 20 years of experience in their field (52.2%), and considered themselves to have high or very high skills in disease surveillance (82.6%). The majority of the experts also reported having medium to high internet and computer skills (91.2% and 78.2%, respectively), and working, on average, $\geq$6 h on a computer every day (52.2%). Most of the experts reviewed all of

Table II
Characteristics of the 23 experts who reviewed at least one time series

Occupation	*N* (%)
Physician	21 (91.3)
Pharmacist	1 (4.3)
Scientist	1 (4.3)
Specialty	*N* (%)
Infection control	18 (78.3)
Infectious diseases	2 (8.7)
Epidemiology	2 (8.7)
Microbiology	1 (4.3)
Years of experience	
Range	3–30
Mean ± SD	16.2 ± 7.6
Median	20
Surveillance skills	*N* (%)
Very low	0 (0)
Low	2 (8.7)
Medium	2 (8.7)
High	14 (60.9)
Very high	5 (21.7)
Internet skills	*N* (%)
Very low	0 (0)
Low	3 (13)
Medium	3 (13)
High	15 (65.2)
Very high	2 (8.7)
Computer skills	*N* (%)
Very low	0 (0)
Low	1 (4.3)
Medium	8 (34.8)
High	13 (56.5)
Very high	1 (4.3)
Daily time spent on computer (h)	
Range	3–10
Median	6
Mean ± SD	5.7 ± 1.8

SD, standard deviation.

the time series they were assigned, and a total of 240 reviews were completed out of the 276 initially planned (87.0%). Five time series were reviewed once (5.4%), 26 were reviewed twice (28.3%), and 61 were reviewed three times (66.3%).

Application usage

It took the users between 16 min and 9 s to evaluate a time series, with a median of 2.7 min. During these evaluations, they made between one and 194 selections in the bar chart (median 24), hovered the mouse over the network nodes between one and 290 times (median 29), and clicked on the nodes to see ward-specific incidences between one and 146 times (median 14).

Part of these variations could be explained by significant differences in users' behaviour ($P<0.001$). Indeed, according to the ICC, the user effect accounted for 37% of the evaluation time variance. Similarly, differences among users explained one-quarter to one-third of the variances in the number of clicks (34%), the number of selections (28%) and the number of hover events (26%).

When a random effect was included for users, none of the recorded baseline user characteristics influenced the way in which the experts interacted with the application, except for average daily computer time and reported internet skills. Average daily computer time was positively correlated with the number of clicks on the network nodes ($P=0.02$), whereas reported internet skills was correlated with the number of selections in the bar chart ($P=0.047$).

The way in which users interacted with the application was also partly determined by the time series they had to review. Indeed, the nature of the time series significantly influenced how many selections the users made in the bar chart (ICC=21%, $P=0.047$) and how much time it took to complete the evaluation (ICC=22%, $P=0.02$). However, this did not significantly influence how the users interacted with the network. These significant variations between time series were almost completely due to differences in the type of micro-organism, with corresponding ICCs of 17% ($P=0.003$) for number of selections and 18% ($P=0.008$) for evaluation time.

Taking account of all of these significant effects, the way in which users interacted with the application was seen to change as they gained experience. The time to complete an evaluation decreased log-linearly with the number of time series evaluated, as did the number of selections, clicks and hover events (Figure 2).

The results of the final models are presented in Appendix 1.

Created events

Over the 240 evaluations completed, the users created 439 events, of which 196 were flagged with a high outbreak probability (44.6%), 167 with a medium outbreak probability (38.0%) and 76 with a low outbreak probability (17.3%). The number of events by time series varied from 0 to 15 (median 2) and the length of the events varied from 1 to 53 weeks (median 4). As shown in the examples in Figure 3, the number, length and estimated probability of the events varied significantly between users ($P<0.001$), with ICCs of 46%, 35% and 35%, respectively. These measures also varied significantly between the types of micro-organism, with ICCs of 20% ($P<0.001$), 7% ($P=0.003$) and 11% ($P<0.001$), respectively. With the random effects taken into account, these characteristics did not vary significantly as the users gained experience with the application, nor did they change with their baseline characteristics.

Application evaluation

All of the experts who completed their set of evaluations also completed the final questionnaire ($N=21$). They gave, on average, an SUS score of 67.33, with a median of 69. Out of 10, two items of the SUS score were graded less favourably by the users: Items 4 ('I think that I would need the support of a technical person to be able to use this app') and 9 ('I felt very confident using the app'). In their comments, several experts reported a 'very good general opinion' and highlighted how enjoyable their experience with the application was, even if 'understanding all of [its] subtleties [was] necessary to use it at its full potential'. Many experts expressed their desire to see the future developments of this work.

Besides the application itself, some experts felt that the task they were assigned was too complex, either because of the difficulty of envisaging what a potential outbreak could be ('I sometimes had trouble understanding what you meant by

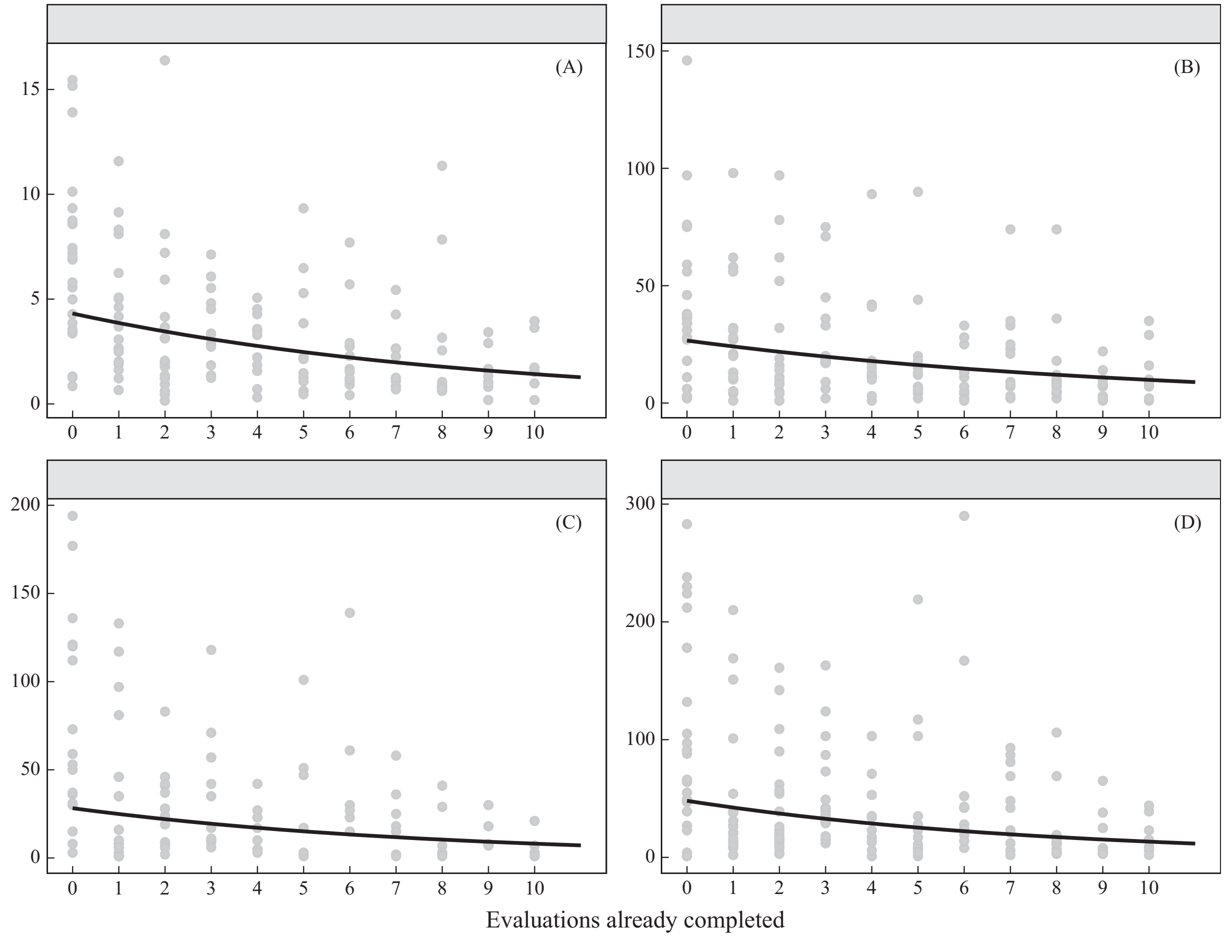

Figure 2. Users' behaviour over time. (A) Evaluation time (in min). (B) Number of selections in the bar chart. (C) Number of hover events in the graph. (D) Number of clicks in the graph. The points represent the observations for each review, and the lines represent the estimations from the log-linear mixed models.

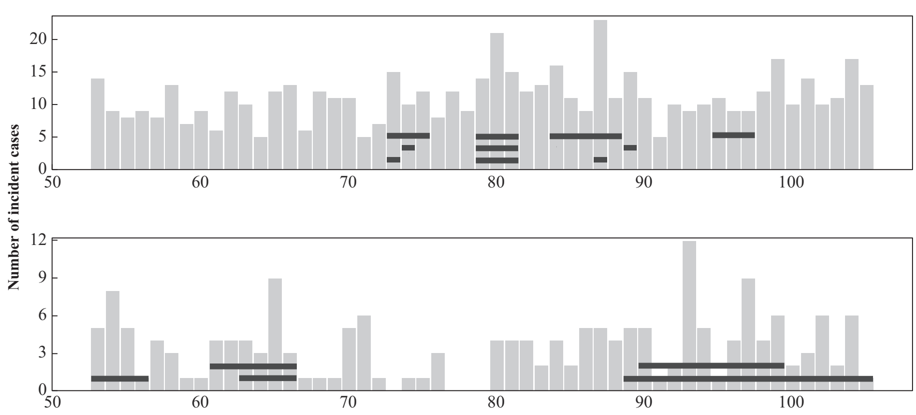

Figure 3. Examples of time series evaluations. The horizontal bars represent the events created by the experts. The events at the same height are from the same user.

'event'') or because of the difficulty of estimating the outbreak probability ('the main challenge for me was to understand the level of likelihood of each scenario'). The main difficulty, however, seemed to be identifying the underlying 'endemic trend' because 'the background noises [were] too important'. To help them in this task, several experts suggested adding features such as ward-specific statistics. For some experts, the task would have been easier with additional microbiological and clinical data, such as antibiotic resistance profiles, type of infection and case-mix of each ward. As these data were not available, one expert noted that he had 'little confidence in the answers [he had] given', and another had doubts about the reproducibility of the evaluations.

Ultimately, many experts noted the potential usefulness of the application in the context of routine surveillance. As one expert stated, 'if this application could work in real time, it would be very interesting for infection control practitioners to identity wards with potential outbreaks'. In this context, the lack of clinical and microbiological data was considered less critical because 'in real life [practitioners] would already have this information'. Indeed, as stated by another expert, 'this tool is surely very useful when used in one's own hospital, with knowledge of the different wards and of the background microbial epidemiology'.

Discussion

Building surveillance data in which outbreaks are correctly labelled is necessary to evaluate algorithms for early outbreak detection. This study showed that the application developed for this task was both usable and useful; it allowed experts to review incidence charts in less than 3 min and to identify dozens of potential outbreaks. The comments were, generally, positive and encouraging, with several experts expressing their wish to see the application developed further. However, the application's usability was only average on the SUS score [16]; users did not feel extremely confident using it and felt that they needed technical support. Even if approximately half of the events were categorized with a high probability, several users expressed a lack of confidence in the answers they had given. The qualitative analysis of the comments was particularly useful to explore these apparent contradictions; it seemed that the difficulties lay in the task that the users were assigned rather than in use of the application.

Identifying outbreaks is complex, notably because there is no clear definition. Textbooks usually describe outbreaks as localized increases in the incidence of a disease [17,18], but more practical definitions acknowledge that they cannot be reduced to mere statistical events. In practice, as Buehler *et al*. wrote, 'the confirmation of an outbreak is a judgment that depends on past experience [...], the severity [and] communicability of the condition, confidence in the diagnosis [...], public health concern about outbreaks at the time, having options for effective prevention or control, and the resources required and available to respond' [19]. To summarize, identifying outbreaks requires much information, and the definition is susceptible to change depending on the context and the persons involved. This probably explains the significant amount of heterogeneity observed among users. Provision of more data, as some experts suggested, may have compensated for the lack of a formal definition, and improved the overall homogeneity of the answers. However, it would have been incompatible with the goal of building data for outbreak identification at an early stage when specific data are not yet available. This lack of specificity is common in early detection systems which usually identify situations that require human scrutiny or further investigation. Sensitivity and timeliness are priorities for such systems. With regards to timeliness, clinical and biological signs are the first data to be available, and they constitute the theoretical basis of what is called 'syndromic surveillance'. As data on clinical symptoms are not yet routinely computerized, this tool relied primarily on bacteriological test results. In the future, additional data could be incorporated in the tool, but for this study, the reliance on bacteriological results is a potential limitation. However, infections are sometimes treated empirically without bacteriological documentation, and even if bacteriological tests are performed, they do not have perfect sensibility and specificity.

Knowledge can also come from experience rather than data. This study only included experts without any prior knowledge of the local context to ensure blinded evaluations and to achieve a reasonable sample size. It is possible that local users would have identified different, possibly more relevant, events. Experience with the tool itself could also influence the answers given by the experts; the events identified by novices might be different from those identified by more advanced users. This study did identify a change in users' behaviours as they gained experience, but this learning effect did not influence their answers significantly.

Unfortunately, it was not possible to compare these results with those of other studies, as few tools are available to support outbreak labelling. To the authors' knowledge, the only tool was proposed by Debin *et al*. for determining influenza outbreak periods at a national level [20]. However, this tool is not suitable for labelling hospital-acquired infection outbreaks, because they are less predictable than seasonal influenza outbreaks which have one incidence peak per winter season.

One particularly encouraging result from the qualitative analysis was that many experts emphasized the great potential of the application for routine surveillance. Although it was not its initial purpose, the application could easily be integrated with a hospital information system and used in daily infection control practice, notably by letting the user decide the microorganism and antibiotic resistance profile for which they want to explore the incidence trends. With the addition of other readily available data (e.g. antibiograms, patient transfer history), it could help practitioners to investigate outbreaks.

This evolution of the tool from ad-hoc outbreak labelling to routine surveillance could be very useful for automated outbreak detection. Infection control practitioners could record outbreaks prospectively, generating true data with good face validity [21] that could be used to refine the algorithms continuously. This strategy of 'reinforcement learning' [22] could be an excellent example of a learning healthcare system [23], where data on performance are analysed routinely to produce knowledge that can guide future decisions.

Of course, all of these efforts to computerize infection control surveillance are not simply about integrating new technologies. They are part of a continuous process of automating some of the most demanding tasks to allow practitioners to reinvest their time in prevention activities [24]. With hindsight, the relative delay in the automation of hospital outbreak detection is understandable: the task is difficult and the data are hard to gather. For Kunz, more than 40 years ago, the main problem with outbreak surveillance was that 'the significant data [...] are not readily available; they are buried in masses of routine background data not immediately applicable to the problem'. Today, informatics can help with the complex preprocessing [25]. However, effort is still needed to improve the way in which relevant data are presented to practitioners and to facilitate outbreak detection overall — a complex but highly beneficial task for both practitioners and patients.

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Conflict of interest statement
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Appendix 1. Results of the mixed models

	Estimate	*P*-value	Variance
Evaluation time (in min)			
Intercept	1.57	<0.001	–
Evaluation rank	−0.11	<0.001	–
Type of micro-organism	–	–	0.04
User	–	–	0.30
Residual	–	–	0.46
Number of hover events in the graph			
Intercept	4.00	<0.001	–
Evaluation rank	−0.13	<0.001	–
User	–	–	0.41
Residual	–	–	1.07
Number of clicks in the graph			
Intercept	1.86	0.03	–
Evaluation rank	−0.12	0.002	–
Average daily time spent working on a computer (h)	0.32	0.03	–
User	–	–	0.41
Residual	–	–	1.15
Number of selections in the bar chart			
Intercept	2.74	<0.001	–
Evaluation rank	−0.09	0.002	–
High informatics skills (0 = no, 1 = yes)	0.64	0.03	–
User	–	–	0.26
Type of micro-organism	–	–	0.10
Residual	–	–	0.71

Estimates and *P*-values are provided for the fixed effects, as well as the estimated variances for the random effects. The evaluation rank refers to the position of the review in the expert's list (1 = first review, 2 = second review, etc.).

References

[1] Kunz LJ. Computerization in microbiology. Hum Pathol 1976;7:169–75.
[2] Gooch JJ, Wood DD. Computerized system analyzes epidemiological data. Hospitals 1976;50:95–6.
[3] Phillips S. Application of clinical laboratory database for monitoring infection control and antibiotic control. Proc Annu Symp Comput Appl Med Care 1979:561–4.
[4] Trick WE, Zagorski BM, Tokars JI, Vernon MO, Welbel SF, Wisniewski MF, et al. Computer algorithms to detect bloodstream infections. Emerg Infect Dis 2004;10:1612–20.
[5] Wisniewski MF, Kieszkowski P, Zagorski BM, Trick WE, Sommers M, Weinstein RA. Development of a clinical data warehouse for hospital infection control. J Am Med Inform Assoc 2003;10:454–62.
[6] Wang M-H, Chen H-K, Hsu M-H, Wang H-C, Yeh Y-T. Cloud computing for infectious disease surveillance and control: development and evaluation of a hospital automated laboratory reporting system. J Med Internet Res 2018;20:e10886.
[7] Atreja A, Gordon SM, Pollock DA, Olmsted RN, Brennan PJ. Opportunities and challenges in utilizing electronic health records for infection surveillance, prevention, and control. Am J Infect Control 2008;36:S37–46.
[8] Escobar GJ. The neonatal 'sepsis work-up': personal reflections on the development of an evidence-based approach toward newborn infections in a managed care organization. Pediatrics 1999;103:360–73.
[9] Lee BY. Digital decision making: computer models and antibiotic prescribing in the twenty-first century. Clin Infect Dis 2008;46:1139–41.
[10] Leclère B, Buckeridge DL, Boëlle P-Y, Astagneau P, Lepelletier D. Automated detection of hospital outbreaks: a systematic review of methods. PloS One 2017;12:e0176438.
[11] Bostock M. D3.js – data-driven documents. Available at: https://d3js.org/[last accessed February 2019].
[12] Kamada T, Kawai S. An algorithm for drawing general undirected graphs. Inf Process Lett 1989;31:7–15.
[13] Brooke J. SUS – a quick and dirty usability scale. In: Usability evaluation in industry. London: Taylor and Francis; 1996.
[14] R Core Team. R: a language and environment for statistical computing. Vienna: R Foundation for Statistical Computing; 2018.
[15] Huang Ronggui. RQDA: R-based qualitative data analysis. R package version 0.3-1. 2018. Available at: http://rqda.r-forge.r-project.org.
[16] Brooke J. SUS: a retrospective. J Usability Stud 2013;8:29–40.
[17] Porta MP. Outbreak. A dictionary of epidemiology. Oxford: Oxford University Press; 2016.
[18] Horsburgh JrJr, Mahon BE. Infectious disease epidemiology. In: Modern epidemiology. 3rd ed. Philadelphia: Lippincott Williams & Wilkins; 2008. p. 549–63.
[19] Buehler JW, Hopkins RS, Overhage JM, Sosin DM, Tong V; CDC Working Group. Framework for evaluating public health surveillance systems for early detection of outbreaks: recommendations from the CDC Working Group. MMWR Recomm Rep Morb Mortal Wkly Rep Recomm Rep Cent Dis Control 2004;53:1–11.
[20] Debin M, Souty C, Turbelin C, Blanchon T, Boëlle P-Y, Hanslik T, et al. Determination of French influenza outbreaks periods between 1985 and 2011 through a web-based Delphi method. BMC Med Inform Decis Mak 2013;13:138.
[21] Buckeridge DL, Burkom H, Campbell M, Hogan WR, Moore AW. Algorithms for rapid outbreak detection: a research synthesis. J Biomed Inform 2005;38:99–113.
[22] Sutton RS, Barto AG. Reinforcement learning: an introduction. Cambridge, MA: MIT Press; 2018.
[23] Olsen L, Aisner D, McGinnis JM. Roundtable on evidence-based medicine. In: The learning healthcare system: workshop summary. Washington, DC: National Academies Press; 2007.
[24] Russo PL, Shaban RZ, Macbeth D, Carter A, Mitchell BG. Impact of electronic healthcare-associated infection surveillance software on infection prevention resources: a systematic review of the literature. J Hosp Infect 2018;99:1–7.
[25] Shmueli G, Burkom H. Statistical challenges facing early outbreak detection in biosurveillance. Technometrics 2010;52:39–51.