Presentation Type:
Poster Presentation

Comparative Usability of Three Platforms for Collecting Standard Precautions Surveillance Data

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Background: Although standard precautions are considered a building block in the prevention of healthcare-associated infections (HAIs) and bloodborne pathogen (BBP) exposures, little is known about the rate of adherence to standard precautions among healthcare workers in US acute-care hospitals and the processes used for measurement and surveillance. **Methods:** We evaluated the development and usability of electronic platforms to collect standard precautions surveillance data in support of the Simulation to Improve Infection Prevention and Patient Safety (SIPPS) Trial. SIPPS is a 5-year group-randomized group-interventional study to develop and test a simulation intervention to improve provider performance of standard precautions and prevent HAIs and occupational BBP exposures. In the pilot study, standard precautions adherence data were collected and validated using the Standard Precautions Observational Tool (SPOT) in a paper format. Adherence was measured using 10 indicators across the categories of hand hygiene, personal protective equipment, linen handling, and sharps disposal. The SPOT allows users to observe healthcare workers providing routine care and to record when an SP action is indicated and whether it was completed or missed. The data did not contain personally identifiable information or protected health information. The aim of this project was to design an electronic version of the SPOT that is simple and affordable to create, allows for rapid and structured data collection, and can be disseminated for broad standardization of standard precautions surveillance. **Results:** Three electronic platforms, including 2 survey-based platforms (Qualtrics and REDCap) and 1 website-based platform (Google), were evaluated for the following characteristics: (1) design interface, (2) customizability, (3) data entry speed, (4) accessibility, and (5) total cost. Both survey platforms performed well in design interface, allowing for a no- or low-code design and offered mobile-friendly formats. Rigid survey formats created obstacles in customization and rapid data collection, involving large amounts of scrolling or screen advancement. Survey-based platforms also required a subscription or access fee. Conversely, the website-based platform had a more challenging design interface but was easily customizable with low-level knowledge of hypertext mark-up language (HTML) and application programming interface deployment. The website platform allowed for a single screen view, mobile-phone–friendly design, and rapid data collection. It was developed using freely available resources. **Conclusions:** A website-based HTML form allows for faster data collection and a higher level of customization than survey-based platforms and can be designed and implemented free of cost using minimal web-development skills. This surveillance methodology will be field tested for fidelity of implementation and for broad use in surveillance.

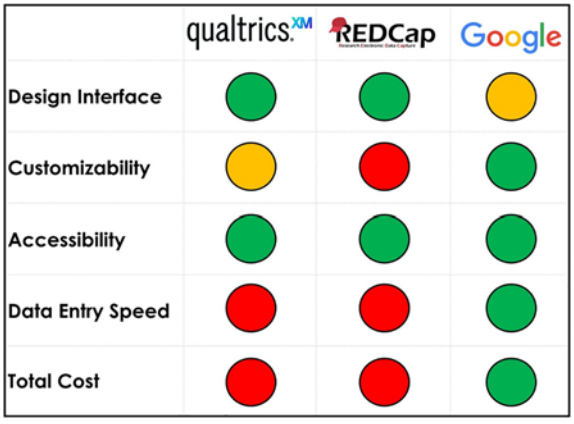

Fig. 1

Funding: The Agency for Healthcare Research and Quality provided **Funding:** for this study (grant no. 1R18HS026418).
Disclosures: Amanda Hessels reports that she is the primary investigator for the studies titled "Impact of Patient Safety Climate on Infection Prevention Practices and Healthcare Worker and Patient Outcomes" (grant no. DHHS/CDC/NIOSH 1K01OH011186 to Columbia University) and "Simulation to Improve Infection Prevention and Patient Safety: The SIPPS Trial (AHRQ grant no. R18: 1R18HS026418 to Columbia University)
Doi:10.1017/ice.2020.1110

Presentation Type:
Poster Presentation

Democratizing Sequencing for Infection Control: A Scalable, Automated Pipeline for WGS Analysis for Outbreak Detection

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Background: Whole-genome sequencing (WGS) is well established as a high-resolution method for measuring bacterial relatedness to better understand infection transmission in cases of healthcare-associated infections (HAIs). However, sequencing is still rarely used in HAI investigations due to a lack of access to computational analysis platforms with actionable turnaround times. Single-nucleotide polymorphism (SNP) analysis is typically used to determine bacterial relatedness. However, SNP-based methods often require a suite of bioinformatics tools that can be difficult to use and interpret without the expertise of a trained computational biologist. These obstacles become more significant in the case of prospective, real-time surveillance of HAIs, which can require the analysis of a large number of isolates. To enable the use of WGS for proactive determination of infection outbreaks, a rapid, automated method that can scale to large data sets is needed. Methods: Here, we demonstrate the capabilities of *ksim*, a novel automated algorithm to determine the clonality of bacterial samples using WGS. *ksim* measures the number of shared *k*mers (genomic subsequences of length *k*) between bacterial samples to determine their relatedness. *ksim* also filters out accessory genomic regions, such as plasmids, that can confound genetic relatedness estimates. We benchmarked the accuracy and speed of *ksim* relative to an SNP-based pipeline on simulated data sets (with sequencing reads generated in silico) and on 9 clinical-cluster data sets (6 publicly available and 3 real-time data sets from Massachusetts General Hospital [MGH]). We also used *ksim* to determine the relatedness of >5,000 historical clinical bacterial isolates from MGH, collected between 2015 and 2019. Results: *ksim* first preprocesses raw sequencing data to generate a common data structure, after which it computes the genomic distance between bacterial samples in ~0.2 seconds in simple cases and in ~4 seconds in complex cases when accessory genome filtering is required. In simulations across 5 species, *ksim* determined clonality (defined as <40 SNPs) with high accuracy (sensitivity, 99.7% and specificity, 99.6%). *ksim* performance on 9