incidence can be explored using agent-based models (ABMs). ABMs can simulate complete systems (e.g., regional healthcare networks) comprised of discrete, unique agents (e.g., patients) which can be represented using a synthetic population, or model-generated representation of the population. We used an ABM of a North Carolina (NC) regional healthcare network to assess the impact of increasing antibiotic risk ratios (RRs) across locations on healthcare-associated (HA) and community-associated (CA) CDI incidence.

Methods. The ABM describes CDI acquisition and patient movement across 14 network locations (i.e., nodes) (11 short-term acute care hospitals, 1 long-term acute care hospital, 1 nursing home, and the community). We used a sample of 2 million synthetic NC residents as ABM microdata. We updated agent states (i.e., location, antibiotic exposure, C. difficile colonization, CDI status) daily. We applied antibiotic RRs of 1, 5, 8.9 (original model RR), 15, and 20 to agents across the network to simulate various risk corresponding to different antibiotic classes. We determined network HA-CDI and CA-CDI incidence and percent mean change for each RR.

Results. In this simulation study, HA-CDI incidence increased with increasing antibiotic risk, ranging from 11.3 to 81.4 HA-CDI cases/100,000 person-years for antibiotic RRs of 1 to 20, respectively. On average, the per unit increase in antibiotic RR was 33% for HA-CDI and 6% for CA-CDI (figure).

Conclusion. We used a geospatially explicit ABM to simulate increasing antibiotic risk, corresponding to different antibiotic classes, and to explore the impact on CDI incidence. The per unit increase in antibiotic risk was greater for HA-CDI than CA-CDI due to the higher probability of receiving antibiotics and higher concentration of agents with other CDI risk factors in the healthcare facilities of the ABM. These types of analyses, which capture the interconnectivity of network healthcare facilities and the associated community served by the network, might help inform targeted antibiotic stewardship efforts in certain network locations.

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2441. Automated, Rapid Detection of Potential Healthcare-Acquired Infection Clusters Using Microbial Genomics Data

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Background. Whole-genome sequencing (WGS) has shown promise in identifying transmissions of healthcare-associated infections (HAIs), but it may be costly to sequence all potential HAIs. By automatically identifying samples likely to be HAIs, WGS can be focused on specific samples. We describe an algorithm that quickly identifies potential HAI clusters by analyzing patient geotemporal and pathogen microbiology data. This approach systematizes triages potential HAI investigations to aid infection control professionals (ICPs) in their workflow.

Methods. This novel algorithm within Philips InteliSpace Epidemiology scores the potential of transmission for pairs of infections. Inputs include microbiology (MB) data (genus- or species-level identification and antimicrobial susceptibility test results) and geotemporal (GT) data (timing of sample collection and shared location stays). From the resulting pairwise scores, clusters of potential HAIs are identified. Leveraging 9 months (June, 2018 – March, 2019) of data from a 900-bed US hospital (i.e., 2835 samples, 1814 patients and 13 organisms—of which a subset of 404 samples had WGS performed concomitantly with MB studies), we evaluated the extent to which this algorithm captures genetically similar sample pairs.

Results. Pairwise scores enrich for genetically similar samples when considering MB data only (odds ratio: 17.3), GT only (odds ratio: 6.1) and a combination of both (odds ratio: 19.8), with highly significant P-values for all (P < 10^-9). Considering MB only, 91% of samples group together in potential transmission clusters. With MB and GT data, this fraction drops to 24.6% (604 samples) forming 177 possible clusters, 17 of which contain fewer than ten samples each. The 5 larger clusters contain 40–64 samples each and span multiple units in the hospital.

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2443. Impact of Antimicrobial Stewardship on the Incidence of Carbapenem-Resistant Pseudomonas aeruginosa: A Nonlinear Time-Series Analysis Approach to Identify Carbapenem Thresholds

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Background. Forming large cohorts to study prosthetic joint infections (PJIs) is a challenge without an existing surgical registry, as is the case in Canada. Administrative data are an option, yet PJI diagnostic codes are insensitive. There is a need to improve the detection of PJIs from within administrative databases.

Methods. Individuals who had a primary arthroplasty at four hospitals in Toronto, Canada from 2010 to 2016 were identified using Canadian Classification of Health Intervention codes (based on the International Classification of Disease, Tenth Revision). Each re-admission to the same hospital until December 31, 2016 was reviewed for the presence of a PJI. The performance characteristics (specificity, sensitivity and positive predictive value) of combinations of diagnostic and procedure codes were compared when adjusted with the gold standard of chart review were calculated. The primary outcome was the algorithm that maximized sensitivity and positive predictive value.

Results. 27,843 primary arthroplasties were performed with 8595 readmissions, of which 572 involved a PJI. Median follow-up was 1258 days (interquartile range (IQR) 614–1891 days), with median time to first re-admission of 352 days (IQR range 166–725 days). PJI codes exhibited a sensitivity of 0.86 (95% confidence interval (95% CI) 0.83–0.89) and positive predictive value (PPV) of 0.89 (95% CI 0.86–0.92). The best performing algorithm is a combination of a PJI code or joint spacer insertion procedure code or insertion of a peripherally inserted central catheter along with an arthroplasty code (sensitivity 0.90, 95% CI 0.88–0.93 and PPV 0.89, 95% CI 0.86–0.91). Using timing from primary arthroplasty, spacer insertion codes and presence of a subsequent arthroplasty procedure code identified 66% (71/105) of first stage and 74% (108/146) of debridement with joint retention procedures during the first re-admission for a PJI.

Conclusion. Combinations of diagnosis and procedure codes can reliably identify PJIs from administrative databases. Individual orthopaedic procedure codes and timing from primary arthroplasty can inform the surgical procedure performed. This PJI detection algorithm could be used for PJI surveillance and research.

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