least 1 person within ~1 m of the bed (Table 1). Approximately half of the time spent within ~1 m from the bed was at the bedside (within ~30 cm). The estimated number of bed touches per hour when within ~1 m was 13–23. Patients spent more time on one side of the bed, which varied by room and facility (Fig. 1A, 1B). Additionally, we observed temporal variation in intensity measured by person time in the room (Fig. 1C, 1D). **Conclusions:** High occupancy tends to be on the far side (away from the door) of the patient bed where the computers are, and the bed touch rate is relatively high. These results can be used to help us understand the potential for room contamination, which can contribute to both transmission and infection, and they highlight critical times and locations in the room, with a potential for focused deep cleaning.

Presentation Type:
Poster Presentation
Evaluating Metagenomic Analysis for Pathogen Transmission in Healthcare Settings

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Background: The prevalence of healthcare-acquired infections (HAIs) and rising levels of antimicrobial resistance place a significant burden on modern healthcare systems. Cultures are typically used to track HAIs; however, culture methods provide limited information and are not applicable to all pathogens. Next-generation sequencing (NGS) can detect and characterize pathogens present within a sample, but few research studies have explored how NGS could be used to detect pathogen transmission events under HAI-relevant scenarios. The objective of this CDC-funded project was to evaluate and correlate sequencing approaches for pathogen transmission with standard culture-based analysis. **Methods:** We modeled pathogen transfer via hand contact using synthetic skin. These skin coupons were seeded with a community of commensal organisms to mimic the human skin microbiome. Pathogens were added at physiologically relevant "high" or "low" levels prior to "skin-to-skin" contact. The ESKAPE pathogens: *E. faecium, S. aureus, K. pneumoniae, A. baumannii, P. aeruginosa,* and *Enterobacter* spp plus *C. difficile* were employed because they are the most common antibiotic resistant HAIs. Pathogen transfer between skin coupons was measured following direct skin contact and fomite surface transmission. The effects of handwashing or fomite decontamination were also evaluated. Transferred pathogens were enumerated via culture to establish a robust data set against which DNA and RNA sequence analyses of the same samples could be compared. These data also provide a quantitative assessment of individual ESKAPE+C pathogen transfer rates in skin contact scenarios. **Results:** Metagenomic and metatranscriptomic analysis using custom analysis pipelines and reference databases successfully identified the commensal and pathogenic organisms present in each sample at the species level. This analysis also identified antibiotic resistance genes and plasmids.

Metatranscriptomic analysis permitted not only gene identification but also confirmation of gene expression, a critical factor in the evaluation of antibiotic resistance. DNA analysis does not require cell viability, a key differentiator between sequencing and culturing reflected in simulated handwashing data. Sensitivity remains a key limitation of metagenomic analysis, as shown by the poor species identification and gene content characterization of pathogens present at low abundance within the simulated microbial community. Species level identification typically failed as ratios fell below 1:1,000 pathogen CFU:total community CFU. **Conclusions:** These findings demonstrate the strengths and weaknesses of NGS for molecular epidemiology. The data sets produced for this study are publicly available so they can be employed for future metagenomic benchmarking studies.

Presentation Type:
Poster Presentation
Evaluating the Cost-Effectiveness of Proposed Algorithms for *C. difficile* Infection in Different Pretest Probability Settings

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Background: The use of real-time polymerase chain reaction (RT-PCR) as a first-line test for the diagnosis of *Clostridioides difficile* may result in overdiagnosis and overtreatment because the test is not capable of distinguishing infection from carriage. Toxin EIA assays have impeditive low sensitivity. Some algorithms using enzyme immunoassay for glutamate dehydrogenase (GDH) antigen and toxins A and B as the first step have been proposed to increase diagnostic performance. However, cost-effectiveness of different diagnostic algorithms would depend on the cost of each test and on the pretest probability in different settings. The objective of the present study was to evaluate the cost-effectiveness of 2 algorithms proposed by current guidelines to diagnose *C. difficile* infection by developing a mathematical model that would take into account the epidemiology and costs in our hospital. **Methods:** The study was conducted in a 480-bed tertiary-care teaching hospital in São Paulo, Brazil. All suspected *C. difficile* infection cases from January to December of 2017 were evaluated for pretest probability analysis. All stools collected from patients with a requested PCR test for suspected *C. difficile* infection were selected for additional testing to measure the specificity and sensitivity of each different test: *C. diff* GDH/Toxin A/B combined test, Toxin A/B Microplate Assay, GDH, and PCR. Toxigenic stool culture for *C. difficile* was considered the gold standard. A mathematical model was developed and simulations were done. The outcomes evaluated were: final annual costs with diagnostic tests in US dollars and number of patients receiving a false-positive or a false-negative diagnosis in a year simulation. **Results:** In total, 1,441 stool samples were tested by PCR for *C. difficile* in our institution from January 2017 to December 2017. Overall, 206 had a positive result, with a pretest probability of 14.3%. In our simulations, the PCR-based algorithm had an annual cost of US$279,914.25, with 4 false-negative results and 8 false-positive results. The implementation of a GDH/Toxin/PCR stepwise algorithm would have reduced the annual cost to US$160,488.75, with 6 false-negative results and 1 false-positive