Fig. 2.

Conclusions: We identified 2 intrinsic risk factors for meningitis after ventricular shunt, age <2 years and multiple surgical procedures, and 1 extrinsic risk factor, the preoperative length of hospital stay.
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Disclosures: None
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Presentation Type:
Poster Presentation
European Union One Health Country Visits as Driver to Combat on Antimicrobial Resistance
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Background: In 2016, the European Union adopted unanimously Council Conclusions on the next steps to combat antimicrobial resistance under a One Health approach. To implement some of the provisions laid down in the Council Conclusions, a European Joint Action on Antimicrobial Resistance (AMR) and Healthcare-Associated Infections (HCAI) or EU-JAMRAI was set up, gathering 44 partners. **Methods:** As part of EU-JAMRAI, 13 participating European countries set up a country-to-country peer review system to evaluate each other's national action plans (NAPs). This review system entailed a self-assessment, strengths–weaknesses–opportunities–threats (SWOT) analysis, and country visits. All steps were executed with representatives from both the human and the veterinary domains (One Health approach). Special attention was given to supervision and the way supervision can enhance the implementation of guidelines on AMR, both at the policy level and within healthcare institutions. **Results:** Despite differences in the stage of developing and implementing

NAPs, all 13 countries are working on NAPs. In this process, country visits function as a moment to exchange best practices and to provide an outsider's point of view. At the end of 2019, 13 country-to-country visits had taken place, resulting in tailor-made recommendations for each country. These recommendations were shared with the competent authority. An example is a country that used the recommendation to improve infection prevention as an immediate reason to get the topic on the agenda of the Ministry of Health. During the country visits, intersectoral participation was perceived as desirable, but in some cases it was challenging to arrange. For some highly relevant topics, it has been recognized that discussion should take place on a European level. Examples of such topics include supervision, infection prevention guidelines, funding, surveillance, and regular audits of antibiotic prescriptions for physicians including feedback loops. **Conclusions:** Peer review is a cooperative and friendly working method compared to common audits. The country visits function as an agenda setting tool to get or to keep AMR on the political agenda and presenting the most relevant topic(s) to address for each country.
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Presentation Type:
Poster Presentation
Evaluating Healthcare Worker Movements and Patient Interactions Within ICU Rooms
Karim Khader, University of Utah; Molly Leecaster, VA Salt Lake City Health Care System, University of Utah School of Medicine; William Ray, University of Utah School of Medicine; Candace Haroldsen, VA Salt Lake City Health Care System, University of Utah School of Medicine; Lindsay Keegan,

CrossMark

Table 1. Summary of Kinect data deployment.

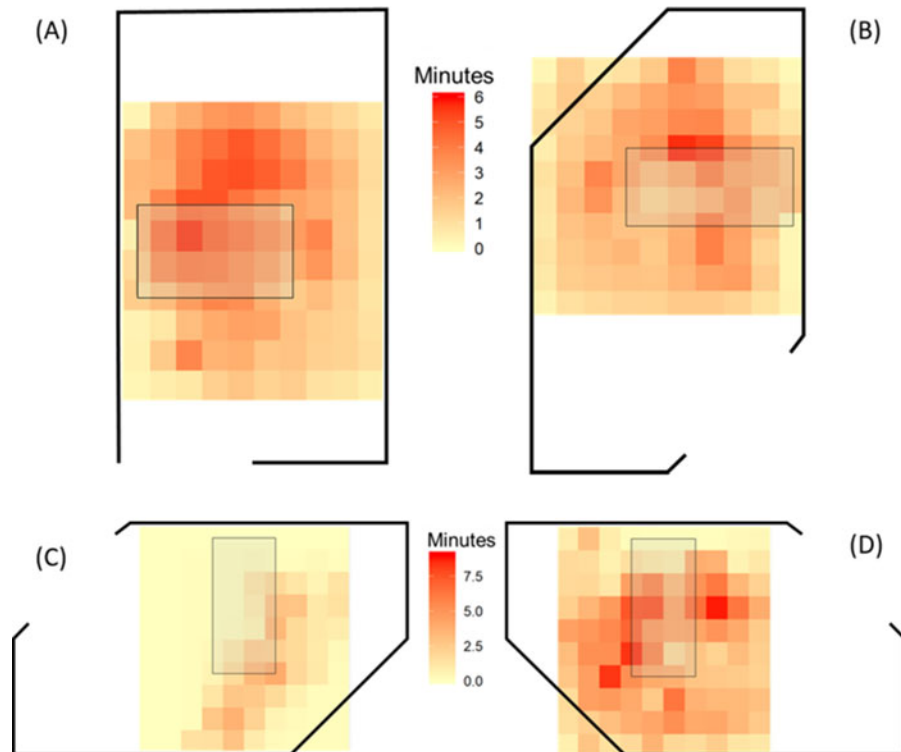|	Unit 1					Unit 2		
Room	1	2	3	4	5	1	2	3
# Days Kinect Deployed	48	26	15	19	15	36	36	21
Total Hours Deployed	609	368	168	260	210	494	660	256
% 1+ person ~3 ft. from bed	72%	71%	85%	59%	77%	95%	75%	66%
% 1+ person ~1 ft. from bed	30%	40%	45%	34%	43%	46%	40%	36%
Bed Touches / Hour ~3 ft. from bed	14.7	23.6	22.8	17.6	15.1	13.5	19.5	20.3

Figure 1. Kinect data with over-bed representing hand touches and other areas representing head location for a room in Unit 2 (A) and a room in unit 1 (B). Also, Kinect data representing both low (C) and high (D) room occupancy over one day.

Fig. 1.

University of Utah School of Medicine; Matthew Samore, University of Utah School of Medicine; Michael Rubin, University of Utah

Background: Contamination of healthcare workers and patient environments likely play a role in the spread of antibiotic-resistant organisms. The mechanisms that contribute to the distribution of organisms within and between patient rooms are not well understood, but they may include movement patterns and patient interactions of healthcare workers. We used an innovative technology for tracking healthcare worker movement and patient interactions in ICUs. **Methods:** The Kinect system, a device developed by Microsoft, was used to detect the location of a person's hands and head over time, each represented with 3-dimensional coordinates. The Kinects were deployed in 2 intensive care units (ICUs), at 2 different hospitals, and they collected data from 5 rooms in a high-acuity 20-bed cardiovascular ICU (unit 1) and 3 rooms in a 10-bed medical-surgical ICU (unit 2). The length of the Kinect deployment varied by room (range, 15–48 days). The Kinect data were processed to included date, time, and location of head and hands for all individuals. Based on the coordinates of the bed, we defined events indicating bed touch, distance ≤30 cm (1 foot) from the bed, and distance ≤1 m (3 feet) from the bed. The processed Kinect data were then used to generate heat maps showing density of person locations within a room and summarizing bed touches and time spent in different locations within the room. **Results:** The Kinect systems captured In total, 2,090 hours of room occupancy by at

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.

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.

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