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**Abstract**

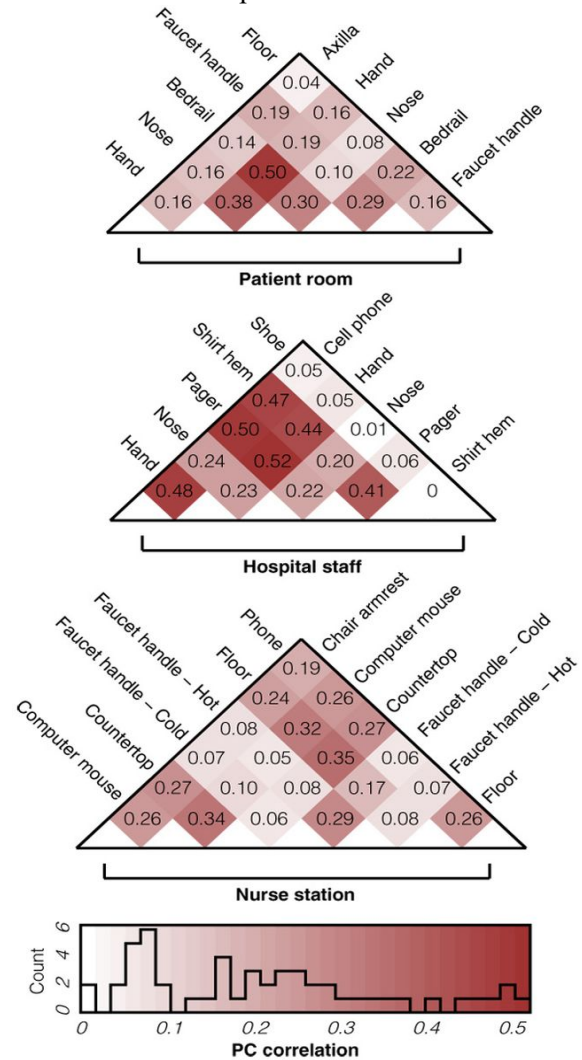
The microorganisms that inhabit hospitals may influence patient recovery and outcome, although the complexity and diversity of these bacterial communities can confound our ability to focus on potential pathogens in isolation. To develop a community-level understanding of how microorganisms colonize and move through the hospital environment, we characterized the bacterial dynamics among hospital surfaces, patients, and staff over the course of 1 year as a new hospital became operational. The bacteria in patient rooms, particularly on bedrails, consistently resembled the skin microbiota of the patient occupying the room. Bacterial communities on patients and room surfaces became increasingly similar over the course of a patient’s stay. Temporal correlations in community structure demonstrated that patients initially acquired room-associated taxa that predated their stay but that their own microbial signatures began to influence the room community structure over time. The  $\alpha$ - and  $\beta$ -diversity of patient skin samples were only weakly or nonsignificantly associated with clinical factors such as chemotherapy, antibiotic usage, and surgical recovery, and no factor except for ambulatory status affected microbial similarity between the microbiotas of a patient and their room. Metagenomic analyses revealed that genes conferring antimicrobial resistance were consistently more abundant on room surfaces than on the skin of the patients inhabiting those rooms. In addition, persistent unique genotypes of *Staphylococcus* and *Propionibacterium* were identified. Dynamic Bayesian network analysis suggested that hospital staff were more likely to be a source of bacteria on the skin of patients than the reverse but that there were no universal patterns of transmission across patient rooms.

**A New Hospital Teems with Life...**

This yearlong survey of the bacterial diversity associated with the patients, staff, and built surfaces in a newly opened hospital. We found that the bacterial communities on patient skin strongly resembled those found in their rooms. We demonstrated that the patient skin microbial

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communities were shaped by a diversity of clinical and environmental factors during hospitalization. We found little effect of intravenous or oral antibiotic treatment on the skin microbiota of patients.



**Figure 4** Heat map of principal coordinate space correlations between sample types. Values represent the average correlation between samples taken from the same location and date along the first 10 axes (eigenvectors) of the PCoA plot of all samples, weighted by the variance captured by each axis’ eigenvalues. PCoA = principle component analysis.



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