



Chase J, Fouquier J, Zare M, Sonderegger D, Knight R, Kelley S, Siegel JA, Caporaso, JG. 2016. Geography and location are the primary drivers of office microbiome composition. *mSystems*, **1(2)**, e00022-16. DOI: [10.1128/mSystems.00022-16](https://doi.org/10.1128/mSystems.00022-16)

Abstract

In the United States, humans spend the majority of their time indoors, where they are exposed to the microbiome of the built environment (BE) they inhabit. Despite the ubiquity of microbes in BEs and their potential impacts on health and building materials, basic questions about the microbiology of these environments remain unanswered. We present a study on the impacts of geography, material type, human interaction, location in a room, seasonal variation, and indoor and microenvironmental parameters on bacterial communities in offices. Our data elucidate several important features of microbial communities in BEs. First, under normal office environmental conditions, bacterial communities do not differ on the basis of surface material (e.g., ceiling tile or carpet) but do differ on the basis of the location in a room (e.g., ceiling or floor), two features that are often conflated but that we are able to separate here. We suspect that previous work showing differences in bacterial composition with surface material was likely detecting differences based on different usage patterns. Next, we find that offices have city-specific bacterial communities, such that we can accurately predict which city an office microbiome sample is derived from, but office-specific bacterial communities are less apparent. This differs from previous work, which has suggested office-specific compositions of bacterial communities. We again suspect that the difference from prior work arises from different usage patterns. As has been previously shown, we observe that human skin contributes heavily to the composition of BE surfaces.

Importance

Our study highlights several points that should impact the design of future studies of the microbiology of Bes:

1. First, projects tracking changes in BE bacterial communities should focus **sampling efforts** on surveying **different locations** in offices and in different cities but not necessarily **different materials** or **different offices** in the same city.

2. Disturbance due to repeated sampling is small compared to that due to other variables
3. Studies requiring more samples than can be sequenced on a single sequencing run must control for run effects by including some of the same samples in all of the sequencing runs as technical replicates.
4. Finally, detailed tracking of indoor and material environment covariates is likely not essential for BE microbiome studies, as the normal range of indoor environmental conditions is likely not large enough to impact bacterial communities.

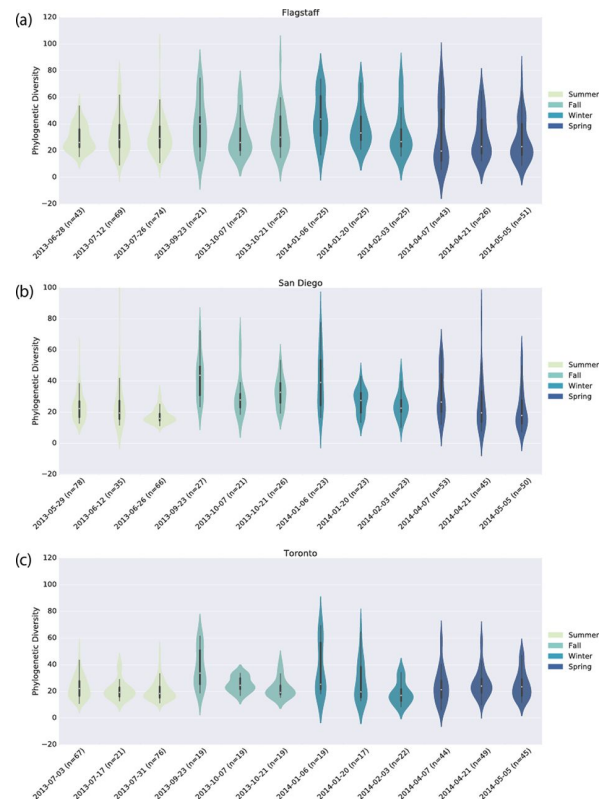


Figure 8 Longitudinal analysis of bacterial PD over 1 year in Flagstaff (a), San Diego (b), and Toronto (c). Each “violin” represents a 2-week period at the beginning, in the middle, or at the end of our four sampling periods.

