

Bi270a Update: The influence of human transport networks on mouse microbiomes

Drew Honson
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Background

Linnenbrink et al examined the role of geography on microbial communities in mice in their 2013 paper *The role of biogeography in shaping diversity of the intestinal microbiota in house mice*.¹ Their conclusion was that physical distance between two locations explained more of the microbial variance (11-16%) than genetic distance (6%).¹

Interestingly, however, some more distant sampling sites appeared to have more similar microbial content than sites that were closer together. I hypothesized that the mice might move between these locations on human transport networks, particularly commuter rail. This could make the likelihood of mice travelling between distant locations higher than geographic distance would suggest. In turn, more communication between these physically distant mouse communities could make their microbial content more similar.

Progress

To calculate physical distance between the study sites, I used the Haversine formula with the coordinates given for each site in the paper. To scrape public transportation data I used Google Maps API. This allowed me to gather the number of legs of the journey, the mode of transportation used for each leg, the number of stops for heavy rail legs, and the distance for bus, subway, or automobile legs. I then decided on penalties for each of these parameters. These penalties are detailed in the notebook. In retrospect, I think this strategy is overly complex and unintuitive. I plan to alter it such that pairs of locations are made “closer” based on the percentage of the distance between them that is serviced by heavy rail.

I have also begun to replicate the analyses of the original paper. More details of that are in the “Problems” section.

Problems

In addition to the work described in “Progress,” I have independently analyzed the microbial data. So far, I have used LAPACK Single Value Decomposition as distributed in sci-kit learn for PCA, as well as Bray-Curtis distance as described in the original paper. Neither seems to show any obvious correlation between microbial content and geographic distance as reported in the paper. In particular, the range of Bray-Curtis distances between samples within a single site is indistinguishable from the range of values between samples taken hundreds of kilometers apart. I still need to replicate the remaining analyses in the paper, but I am concerned that either my analysis is incorrect or that the original conclusions of the paper were overstated. Either scenario would make it difficult to meaningfully compare the roles of geographic and human transit adjusted distances on microbial content.

References

1. Linnenbrink, M. *et al.* The role of biogeography in shaping diversity of the intestinal microbiota in house mice. *Mol. Ecol.* **22**, 1904–1916 (2013).