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

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Problem

Geography greatly influences the diversity of gut microbiota within a species.[1–3] An article published in *Molecular Ecology* in 2013 identified geography as a major determinant of mouse caecal microbial communities among eight sampling locations in Western Europe.[3] Interestingly, however, when their principal component analysis was unconstrained by coordinates, three distant locations all clustered together: Divonne les Bains (DB), Louan (LO), and Espelette (ES), all in France (Figure 1). Curiously, these regions showed far more similar caecal compositions than the comparatively close regions of Nancy, France (NA) and Schömberg/Langenbrand, Germany (SL) (Figure 1). The objective of my project is to 1) use orthogonal computational methods to replicate the results of the paper and 2) determine whether manmade networks for moving people and freight might explain why geographically distant mouse populations might have similar microbial communities.

Data

I will be using microbiome data from Linnenbrink et al 2013, available as study MGYS00000516 on MGnify.[3] These data contain caecal and mucosal microbiomes from 121 mice sampled from eight geographic locations. For my analysis, I will primarily use the caecal microbiomes, as the article showed these to be more influenced by geography than those from mucosa.

Both France and Germany have vast rail networks which are used primarily for passenger transport.[4,5] As such, I will use passenger timetables from SNCF (the French nationalized railway) and Deutsche Bahn (the German nationalized railway) to calculate relative distances between the sample sites in terms of train frequency. Freight in Europe primarily moves by the Trans-European Transport Network (TEN-T), a network of road, rail, and water transport.[6] To measure the influence of cargo transport, study sites will be ranked on their relative distance from one another and the TEN-T corridors.

Analyses

I will perform Principal Component Analysis on the microbiome data and calculate pairwise Euclidean distances as a measure of similarity. I will repeat the analyses in the original article to determine what proportion of the distances can be explained by geographic coordinates. I will then repeat these analyses using passenger train and freight relative distances to determine whether clusters of similar microbiomes are better explained by human transport networks than by raw geographic distance.

Citations

1. Suzuki, T. A. & Worobey, M. Geographical variation of human gut microbial composition. *Biol. Lett.* **10**, 20131037 (2014).

2. Gaulke, C. A. & Sharpton, T. J. The influence of ethnicity and geography on human gut microbiome composition. *Nat. Med.* **24**, 1495–1496 (2018).

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

4. Kuester, F. Is the German Rail Freight System broken? A portrait of DB Cargo | Combined Transport. *Combined Transport* https://combined-transport.eu/german-railway-system (2017).

5. Boudet, A. & Steinmann, L. The State once again supports rail freight | The echoes. *Les Echos* https://www.lesechos.fr/industrie-services/tourisme-transport/letat-une-enieme-fois-au-chevet-du-fret-ferroviaire-1226685 (2020).

6. The European Commission. Trans-European Transport Network (TEN-T). https://transport.ec.europa.eu/transport-themes/infrastructure-and-investment/trans-european-transport-network-ten-t_en.