Empirical signatures of compositional stability in the gut microbiome
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Method
One way to investigate stability of communities is to ask: "Does the abundance of one OTU affect the composition of the remaining community in reproducible and predictable way?"

Data - Analyses are performed on 4 longitudinal datasets and one cross-sectional dataset.

Regression - Removing Y from OTU table and re-normalizing removes compositional effects in remaining community. Regressing Y on re-normalized OTU table captures predictable relationships between Y's abundance and the composition of the remaining community.

Stable communities within donors have predictable interactions
Longitudinal data from individual donors yields better predictions than cross-sectional samples.

Specific interactions between bacteria vary across donors
The correlation between an OTU and its other community members is not conserved across individuals.

Analysis - Correlation between estimated and real values of Y indicates the strength of Y's impact on the community. Further examining the correlation of each OTU in X with Y provides insight into specific interactions.

Some interactions are unique to each donor's community state
Some interactions are present in only a subset of individuals.

Further analyses could probe features of stable communities

Validation
Gold standard statistical method to serve as a "positive control"?

Investigation
Why does donorB perform worse?
How does variance of an OTU affect its predictability?

Exploration
What is the most interesting next thing to do?

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