

# Empirical signatures of compositional stability in the gut microbiome

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## Method

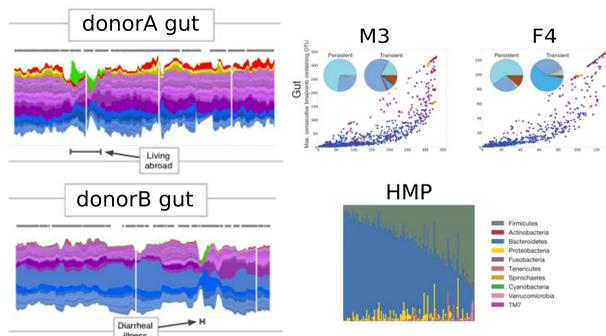
One way to investigate stability of communities is to ask: "Does the abundance of one OTU affect the composition of the remaining community in reproducible and predictable way?"

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

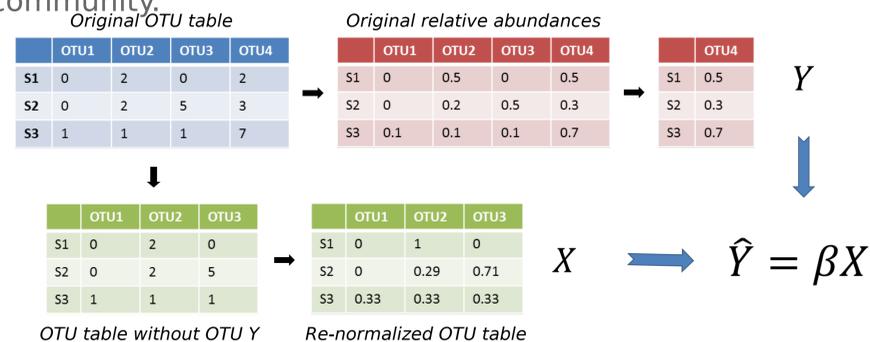
David, Alm, et al. *Genome Biology* 2014

Caporaso, Knight, et al. *Genome Biology* 2011

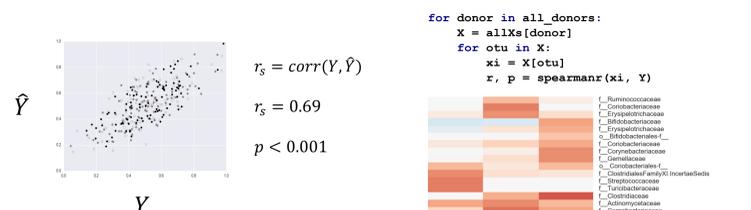
HMP Consortium *Nature* 2012



**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.

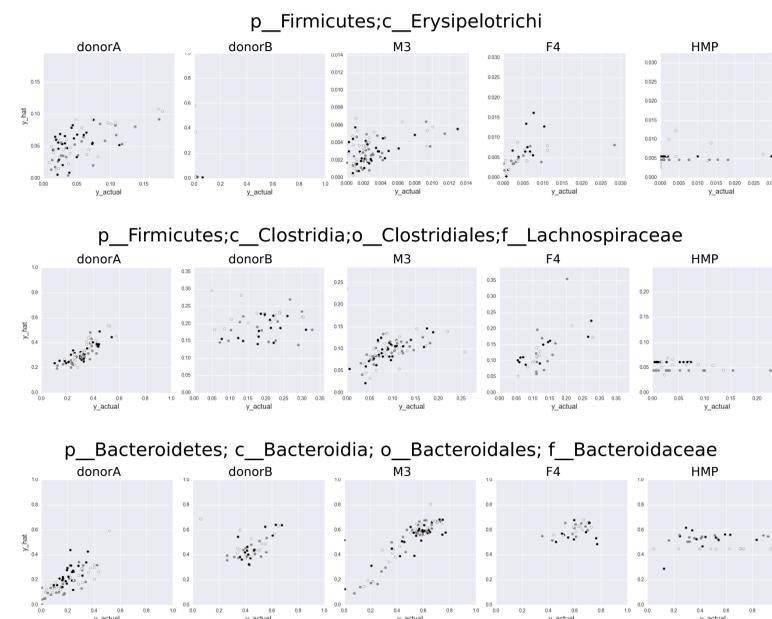


**Analysis** - Correlation between estimated and real values of Y indicates the strength of Y's impact on the community. Further examining the correlation of each OTU in X with Y provides insight into specific interactions.



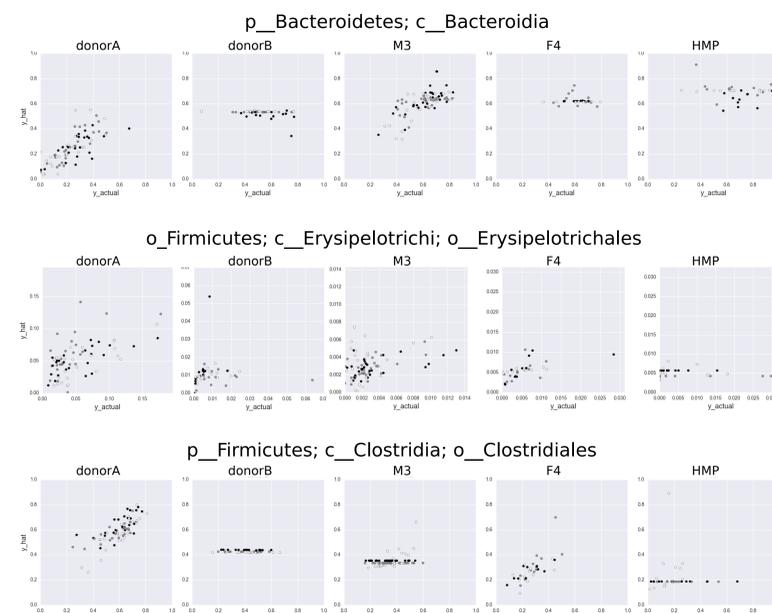
## Stable communities within donors have predictable interactions

Longitudinal data from individual donors yields better predictions than cross-sectional samples.



## Some interactions are unique to each donor's community state

Some interactions are present in only a subset of individuals.

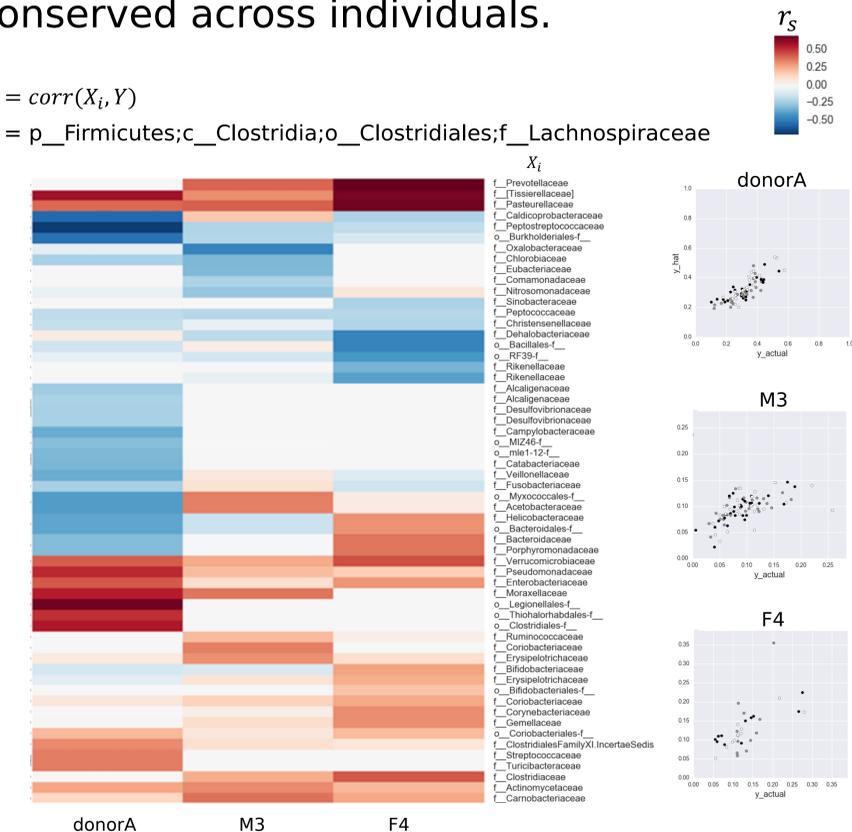


## Specific interactions between bacteria vary across donors

The correlation between an OTU and its other community members is not conserved across individuals.

$$r_s = corr(X_i, Y)$$

$$Y = p\_Firmicutes;c\_Clostridia;o\_Clostridiales;f\_Lachnospiraceae$$



## 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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