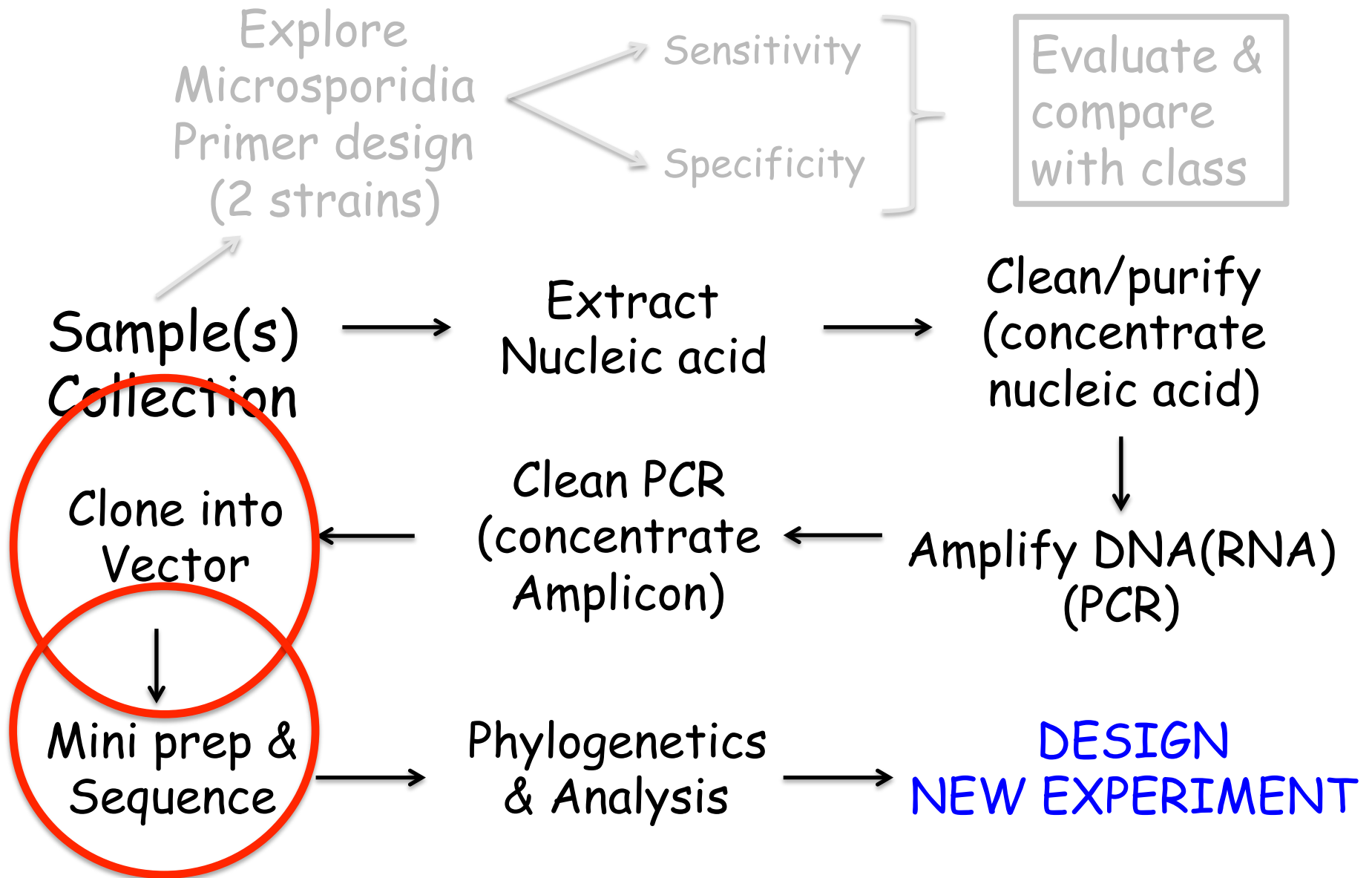


20.109
Laboratory Fundamentals in
Biological Engineering

Module 1
Nucleic Acid Engineering
Lecture 5

Office hours: by appt.

Module 1



Sequence analysis

UniFrac?

1) Alpha and beta diversity

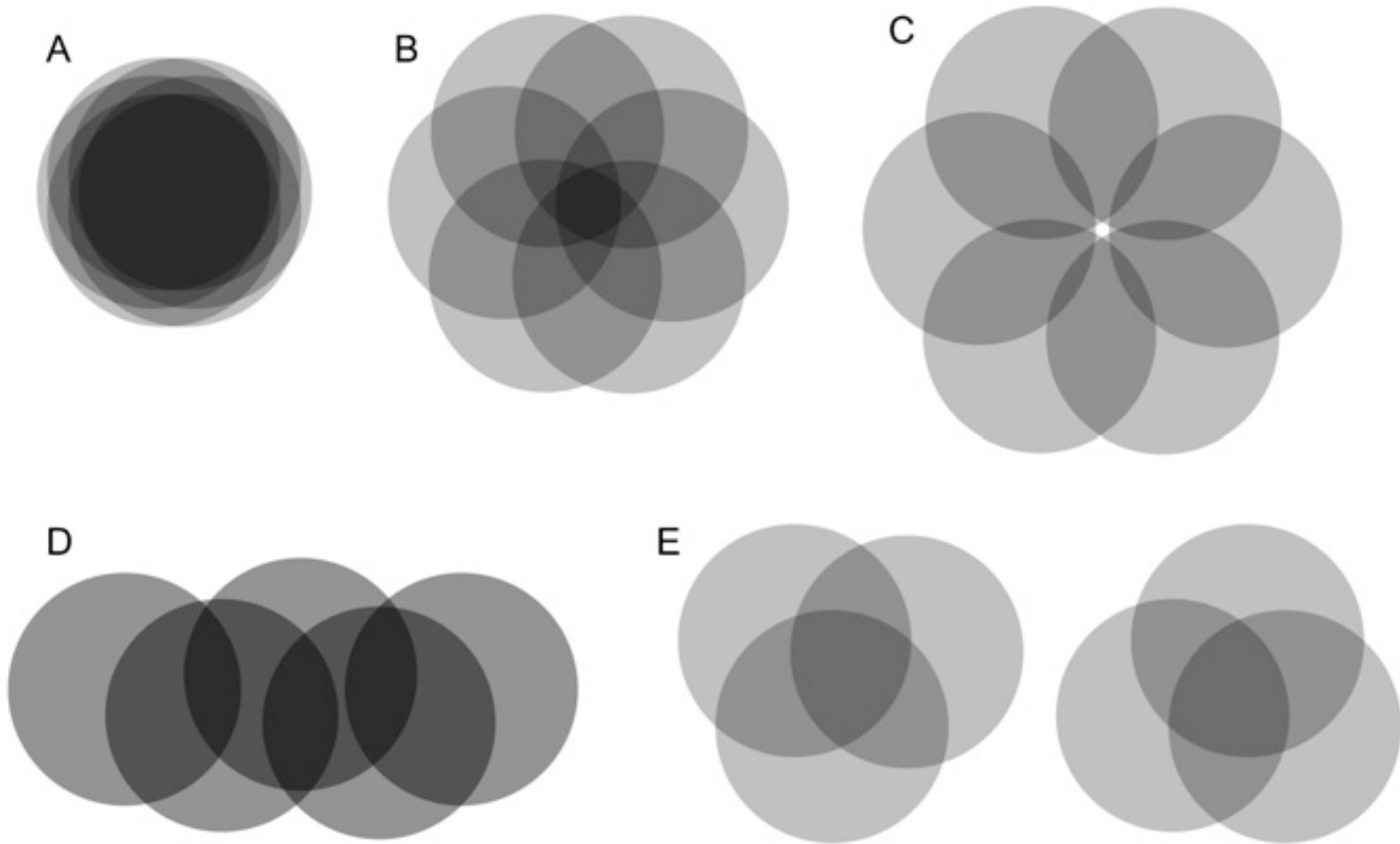
2) Qualitative or quantitative ?
unweighted or weighted

3) Phylogeny or taxon based

Back to the core questions

- What is the basic structure and behavior of host associated communities?
 - Measure → model
- How might we possibly fix/engineer it?
 - Manipulate → make

Models of a core microbiome



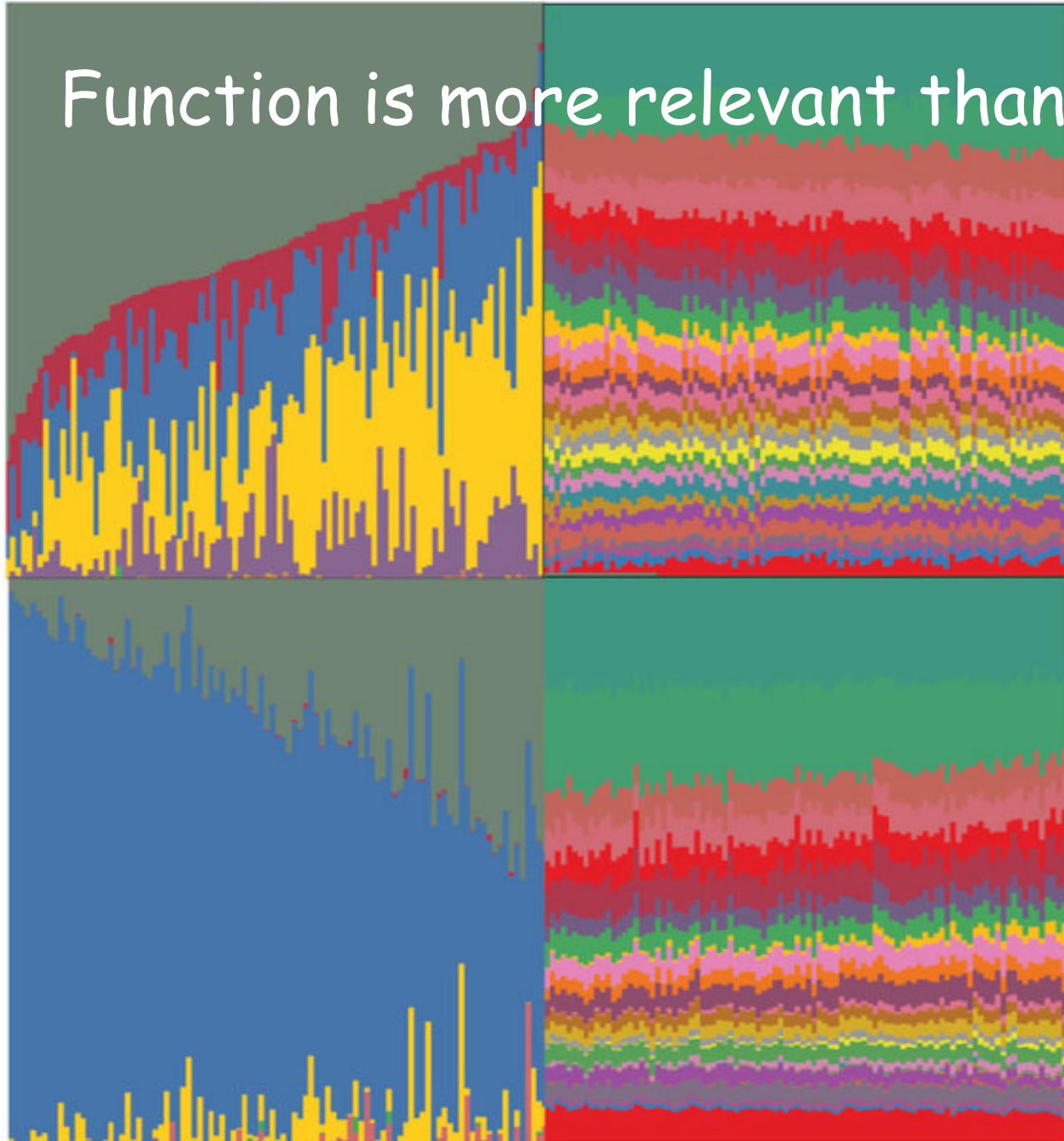
If taxonomy is not conserved,
what does that mean for
function?

- Functional core?
- Interchangeable parts?

Phylum

Function

Function is more relevant than taxonomy



Nature 486 (2012)

How do you examine structure/ function?

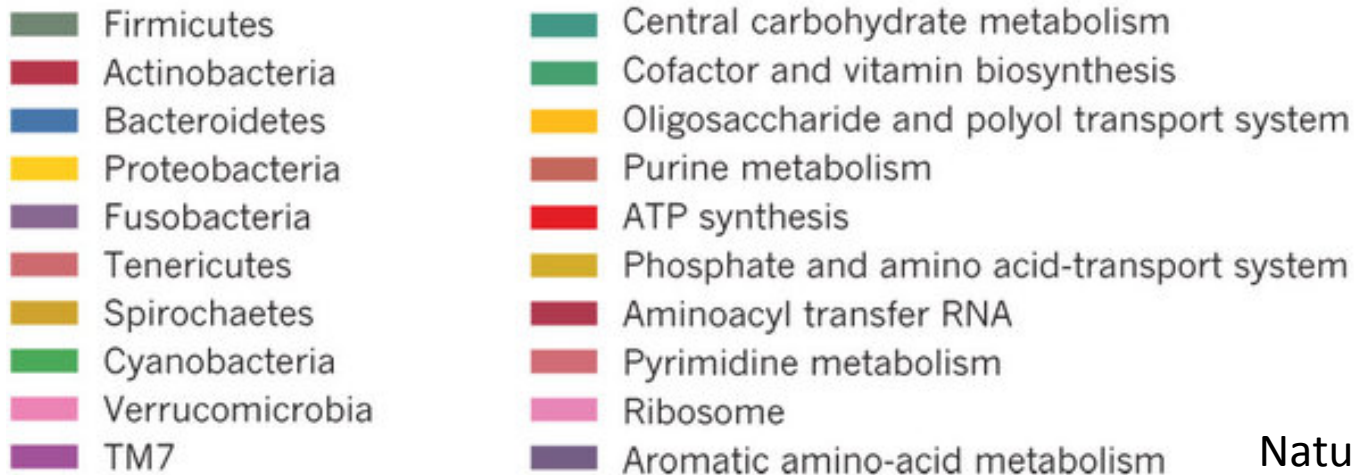
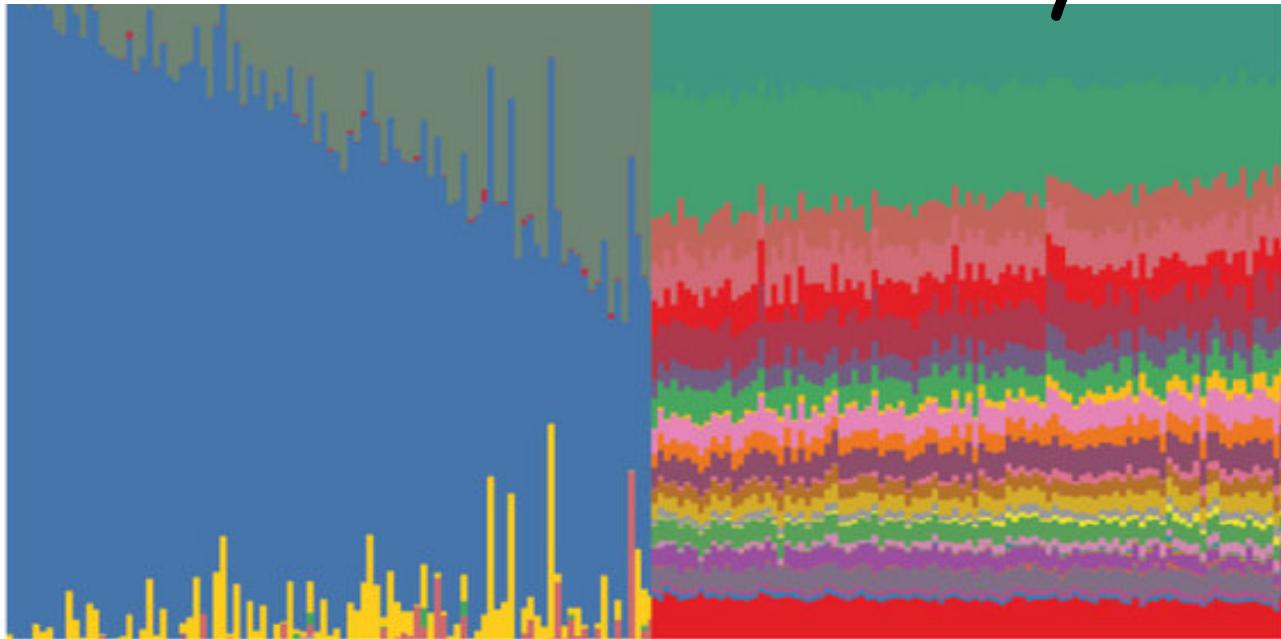
- data cleanup
- derivative data sets (pathways, OTUs, reference alignments, etc...)
- Trees and relationships of communities (abundance curves, biodiversity plots, variant identification, etc...)

Exploring function through collective databases

National Center for
Biotechnology Information

Kegg pathway database

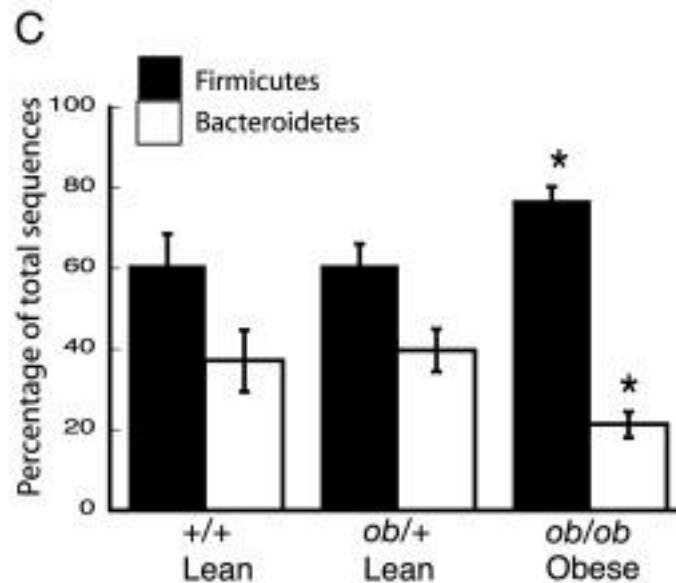
Function is more relevant than taxonomy



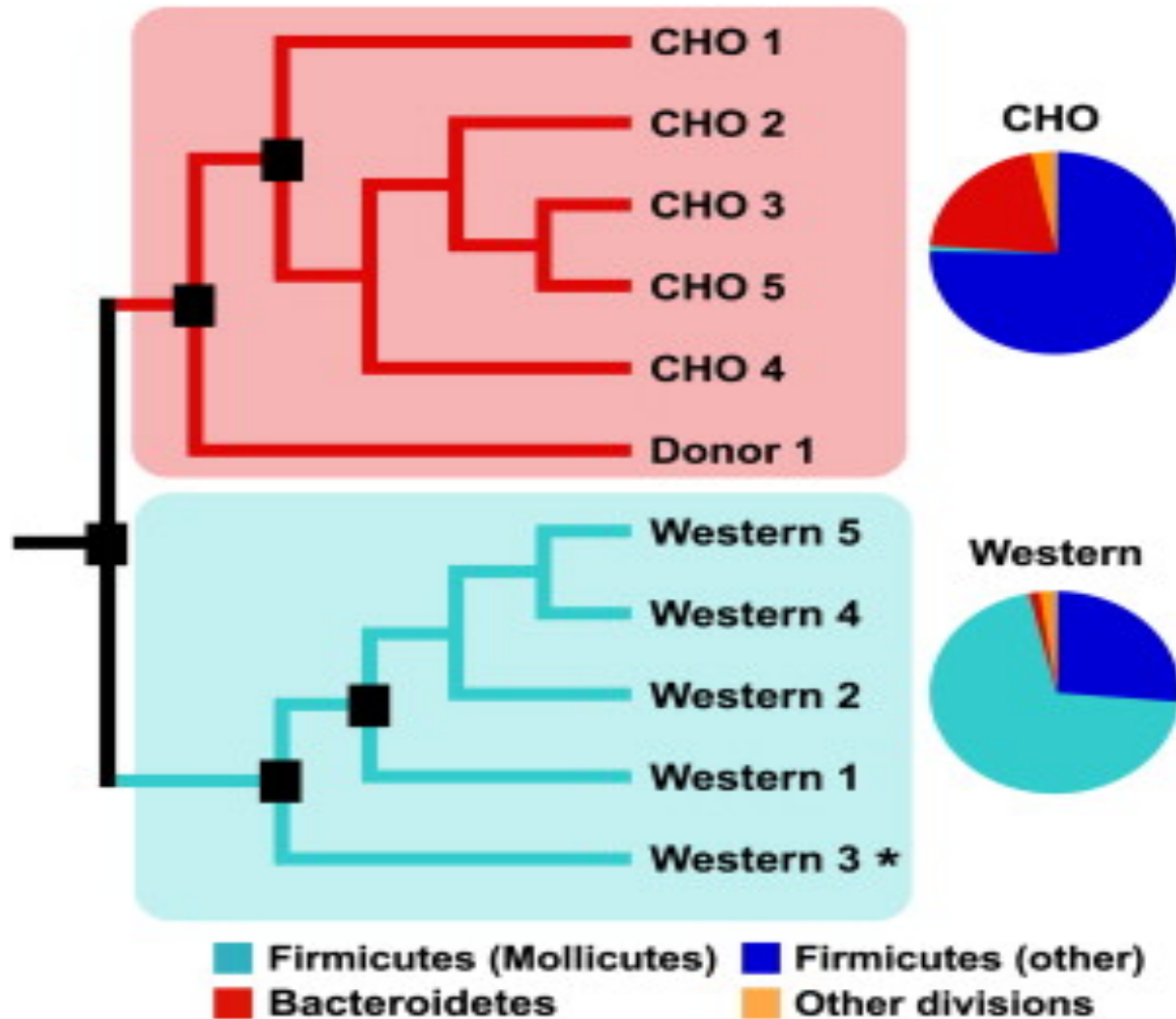
Nature 486 (2012)

Does diet affect microbial composition?

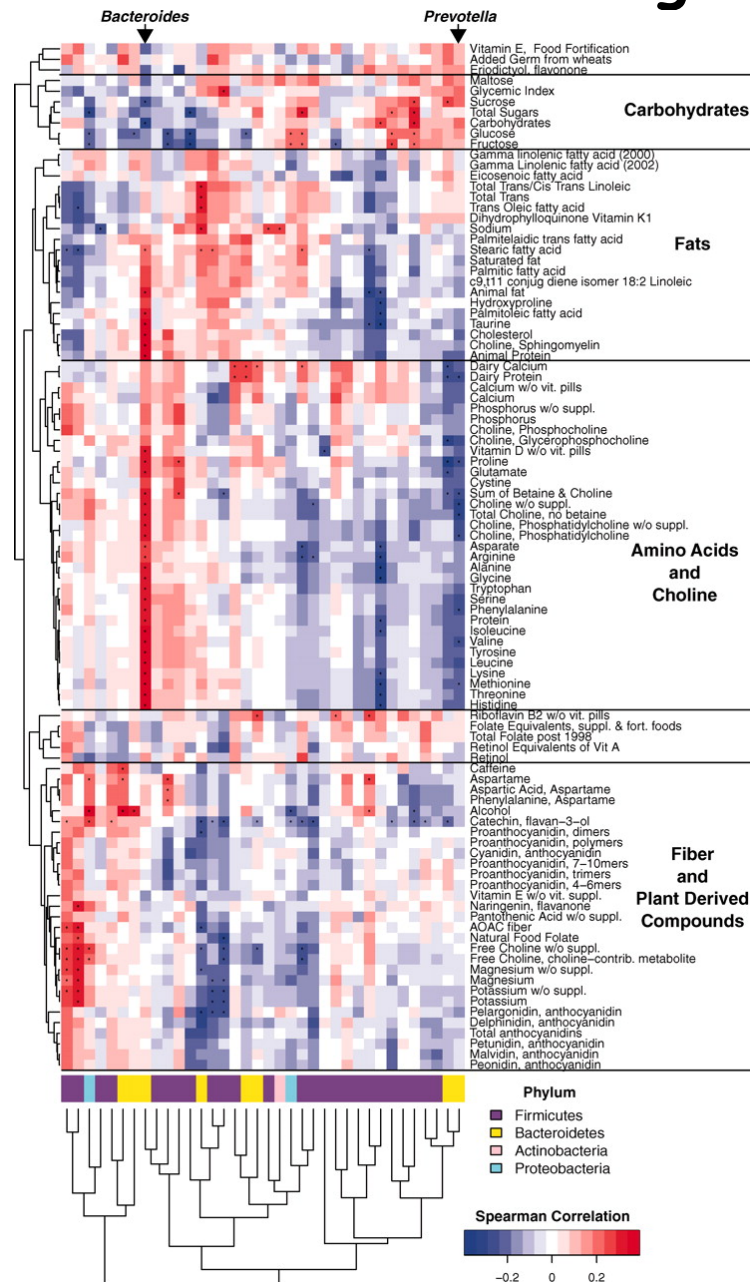
- Genetically Obese mice harbor a significantly different community than lean conventional mice



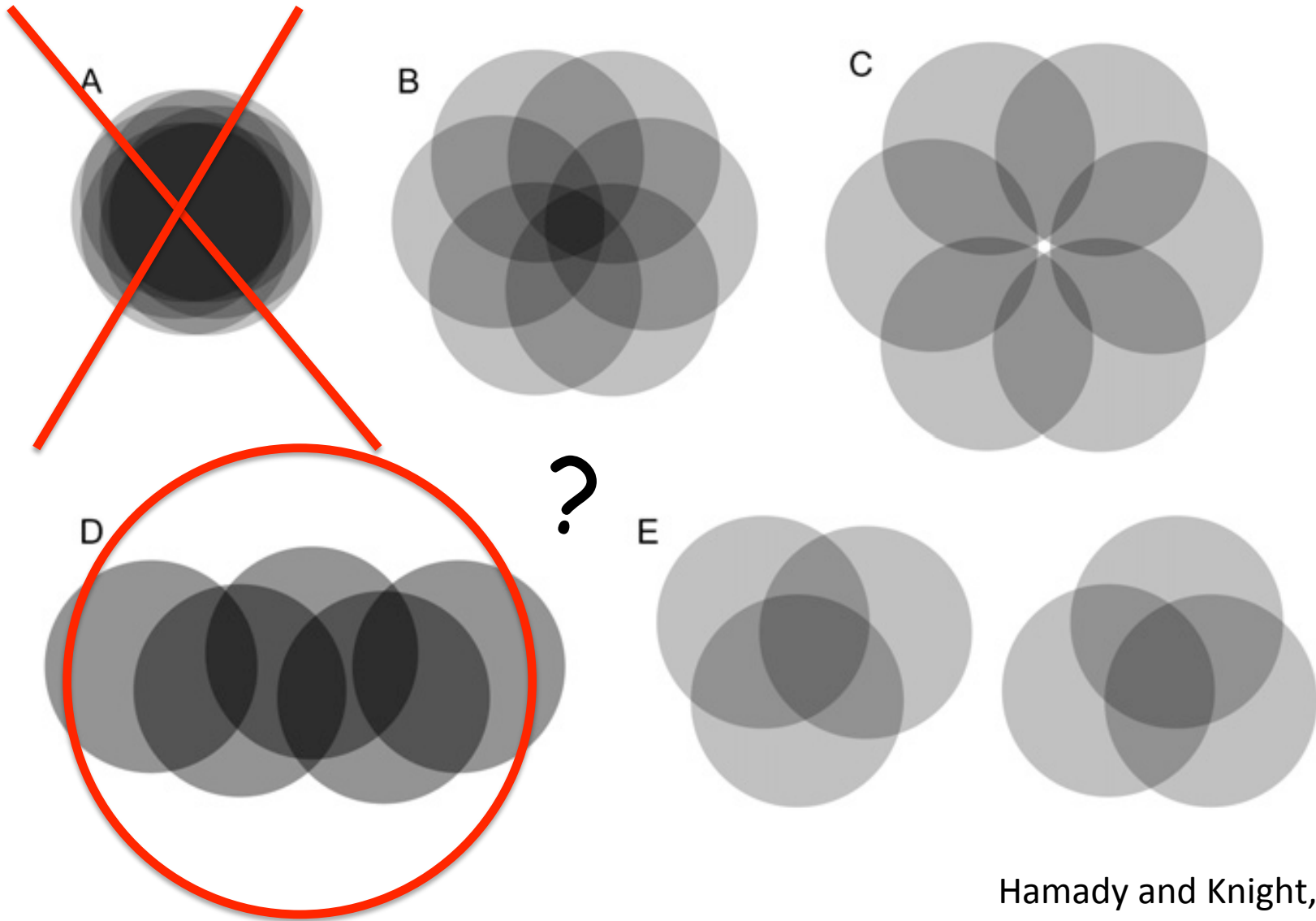
Diet affects microbial composition



Correlation of diet and gut microbial taxa

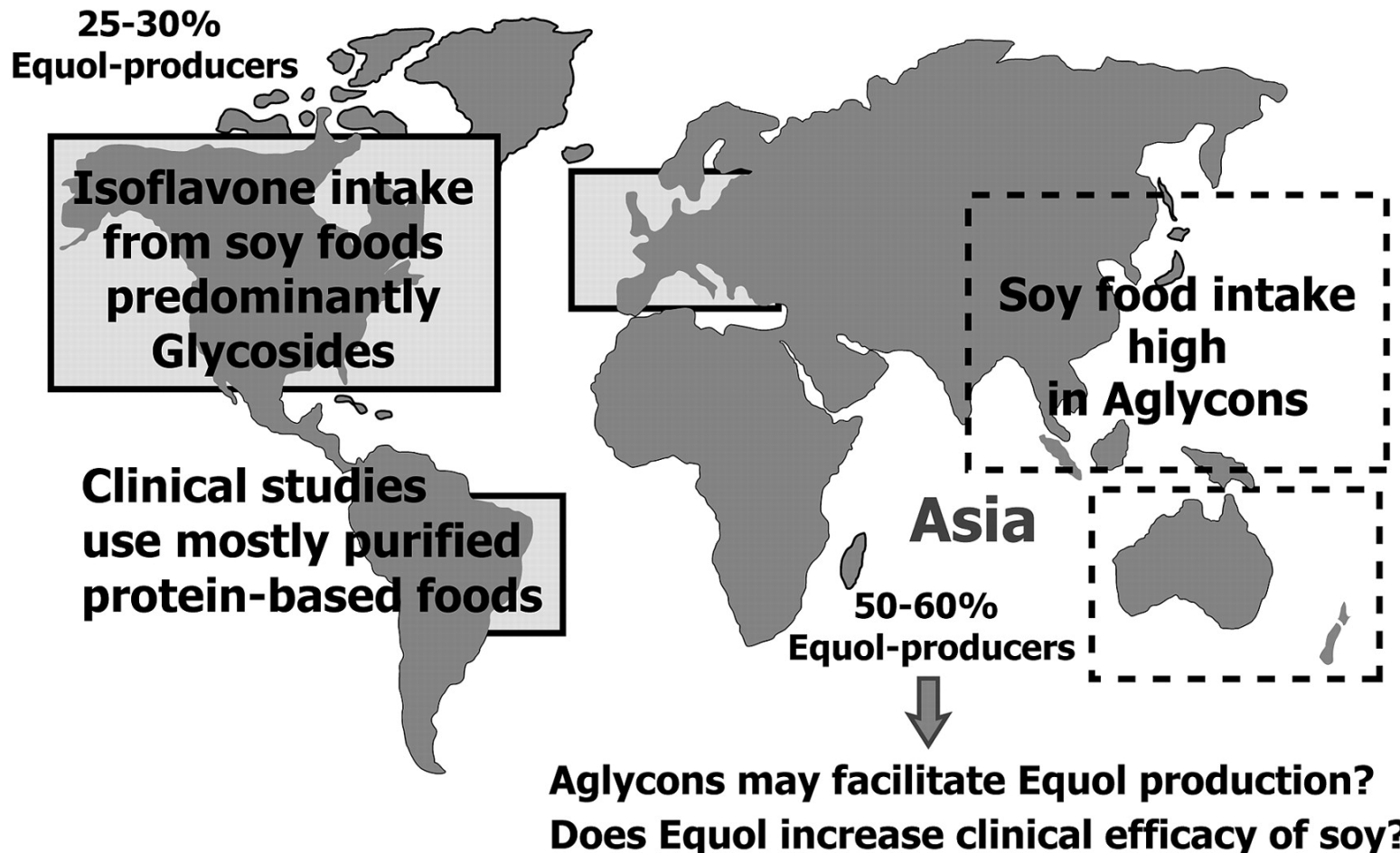


Models of a core microbiome

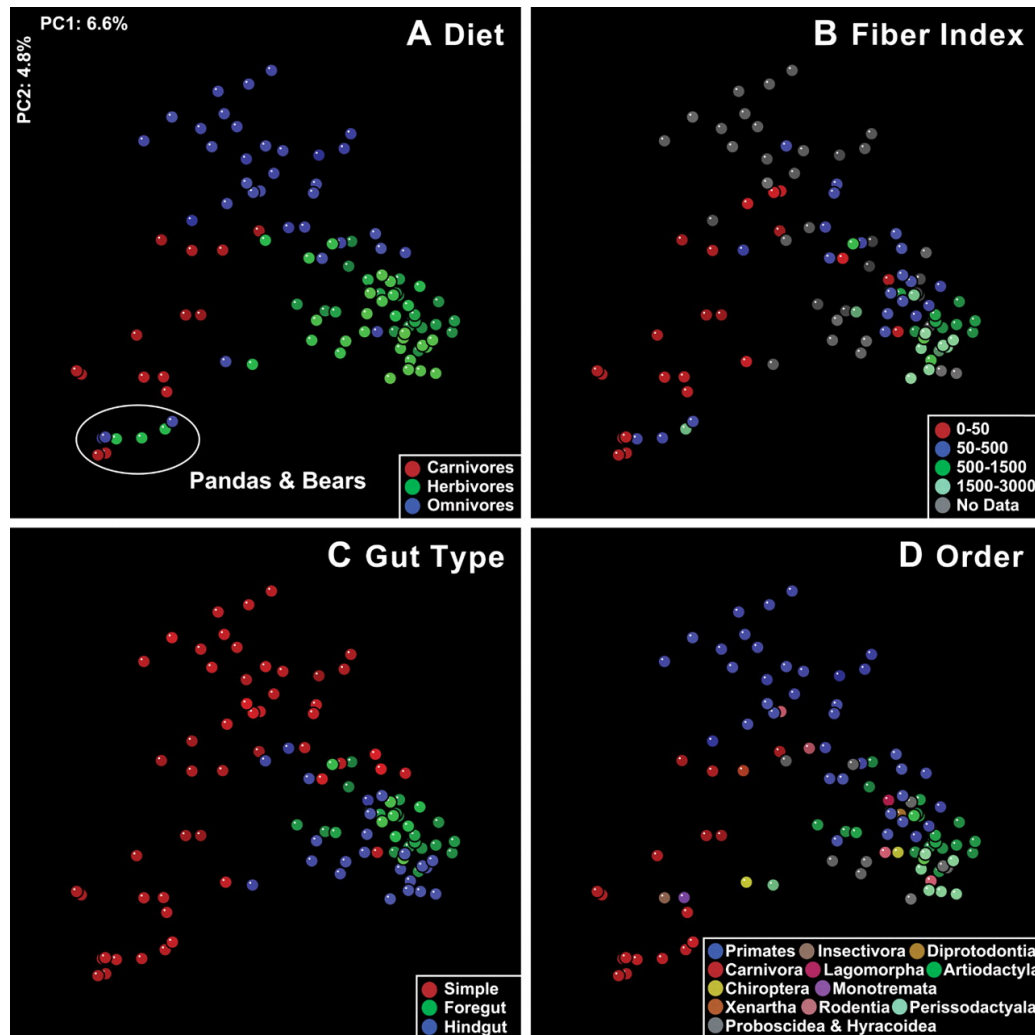


The type of food consumed may account for microbiome function

Western World



Mammalian fecal bacterial communities clustered using PCoA



Other factors affecting microbiota structure

- Antibiotic treatment or other drugs
- Physiological state (pregnancy, age, gender, etc...)
- Population (genetics?) - ethnicity
- Disease
- Other?

Cause or effect?

Evaluation of a diagnostic test

- Sensitivity
- Specificity

Module 1

