# 20.109 Laboratory Fundamentals in Biological Engineering

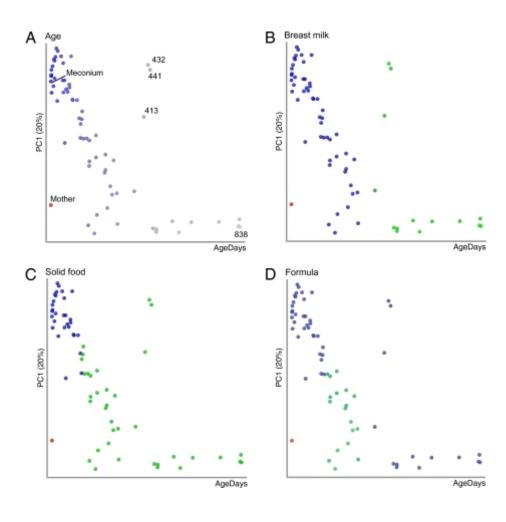
Module 1
Nucleic Acid Engineering
Lecture 7

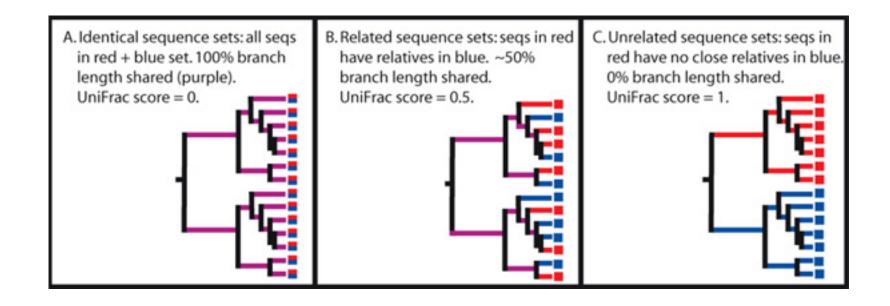
### How do you compare the composition of two microbial communities?

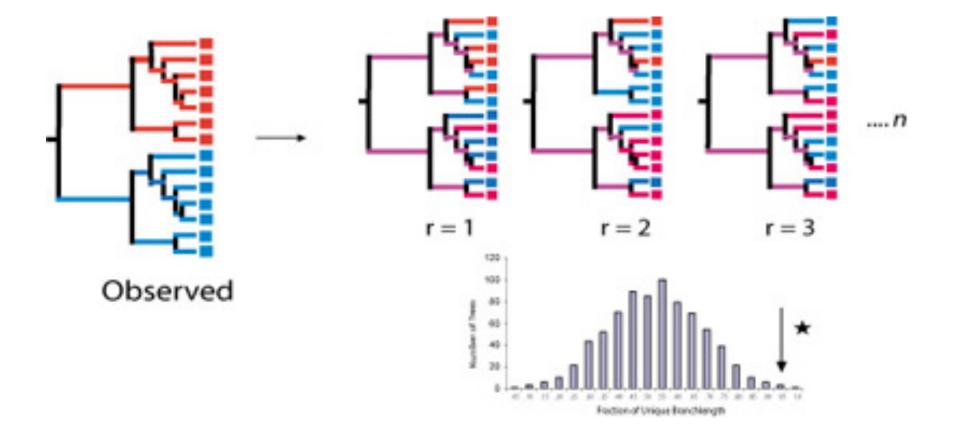
#### Diversity

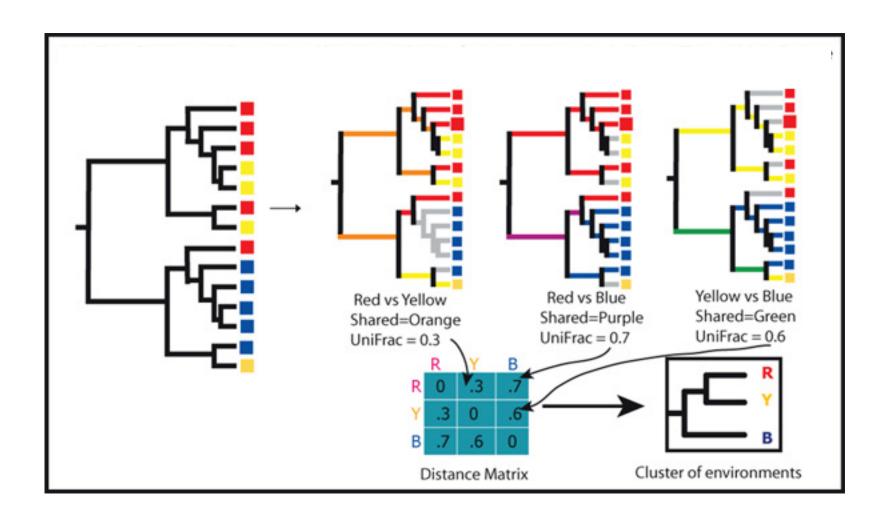
- $-\alpha$  diversity: taxa within a sample
- B diversity: between sample comparisons

#### UniFrac

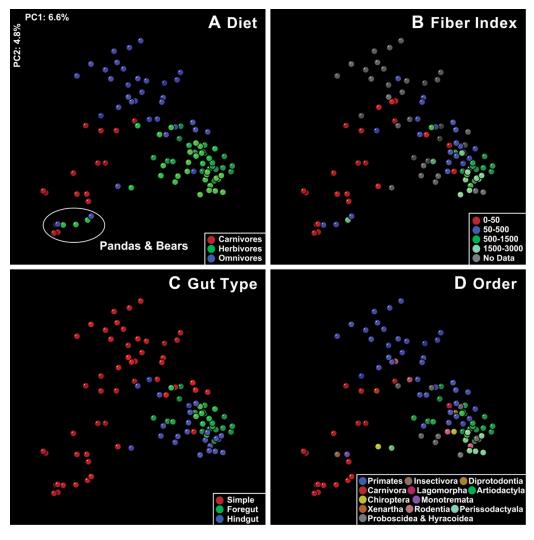








# Mammalian fecal bacterial communities clustered using PCoA



#### UniFrac



#### How to build a phylogenetic tree

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Collect data i.e. DNA

Retrieve homologous sequences

Multiple sequence alignment

Model selection

Assessing confidence in topology

#### Model selection

- Scoring a matrix can't tell you which traits are derived and which are ancestral
- Need trees to infer evolutionary relationships
- Choose the simplest or most likely tree corresponding to the matrix

Parsimony Neighborjoining Maximum Bayesian likelihood inference

#### Simplest vs most likely

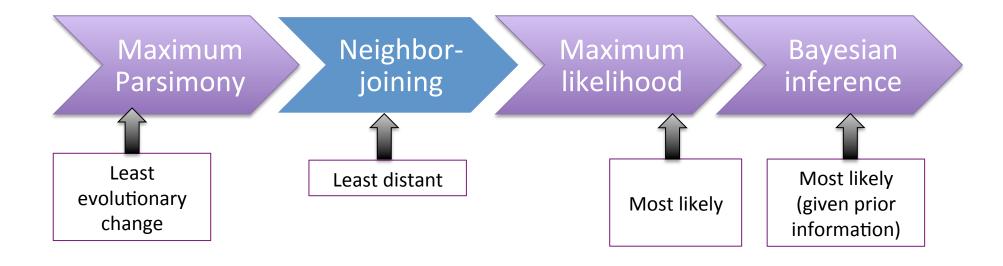
- We need a metric to decide which trees are better and which trees are worse
- Optimality criterion = a metric of quality (i.e. tree length, parsimony or likelihood) used to assess the optimal tree

Which methods use an optimality criteria to decide on best tree?

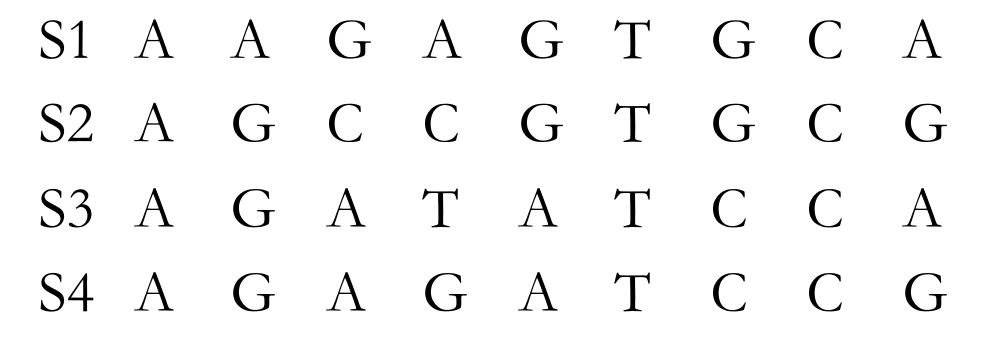
Maximum Parsimony

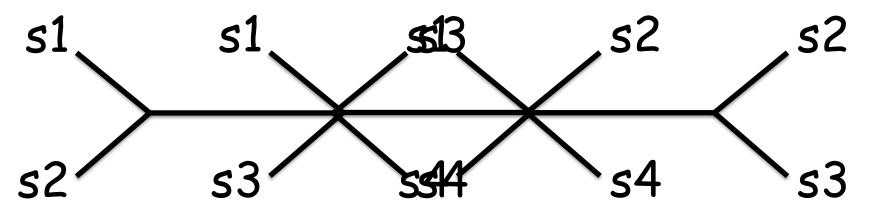
Neighborjoining Maximum likelihood

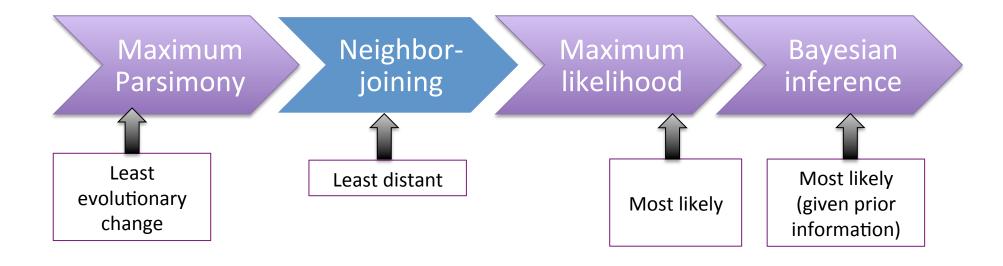
Bayesian inference



#### Parsimony







## NJ

