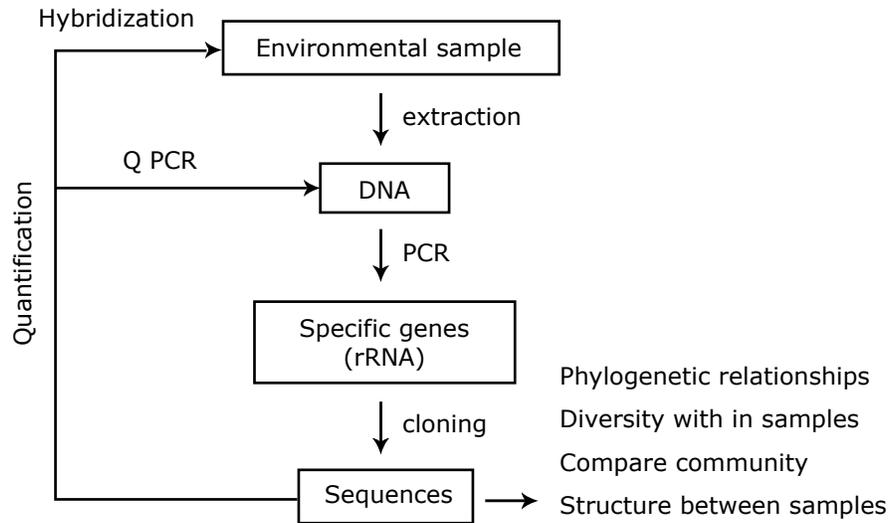


Recap

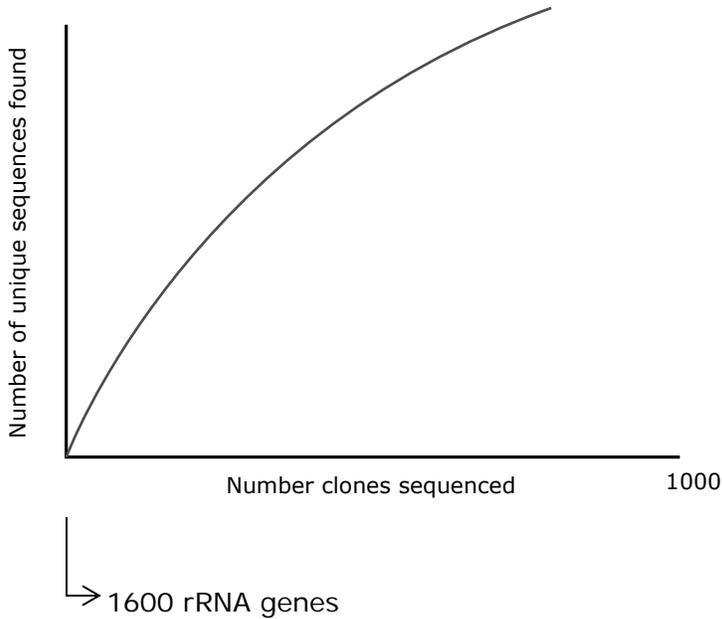


Overall

Major phylogenetic lineages have remained uncultured ⇒ existence only known from clone libraries

Estimation of Diversity

Example: coastal ocean bacterioplankton

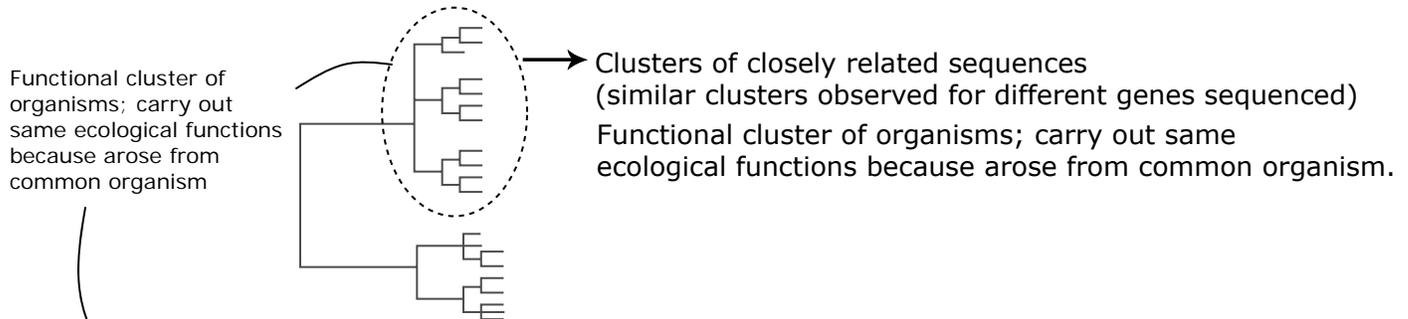
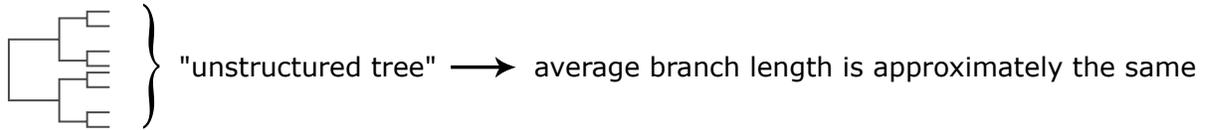


Statistical tools: chao 1 test

$$S = S_{obs} + \frac{a^2}{2b}$$

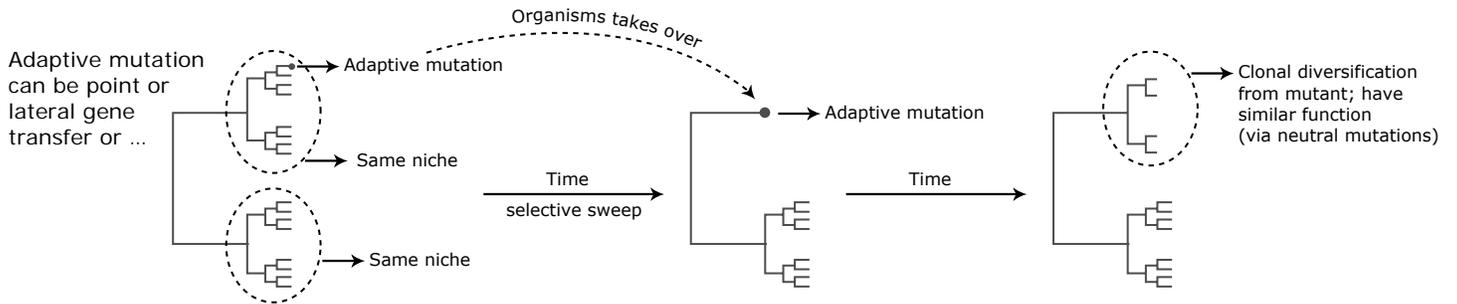
↓
Total number of sequences

a = number sequences found once
 b = number sequences found twice



see here

Question: How can such structures arise? What does it mean in an ecological context?



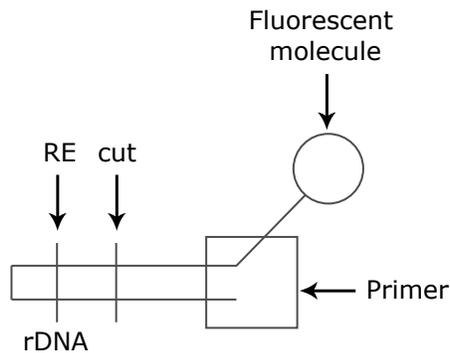
We can detect/quantify microbial diversity:

Community Fingerprinting: Only works on abundant organisms.

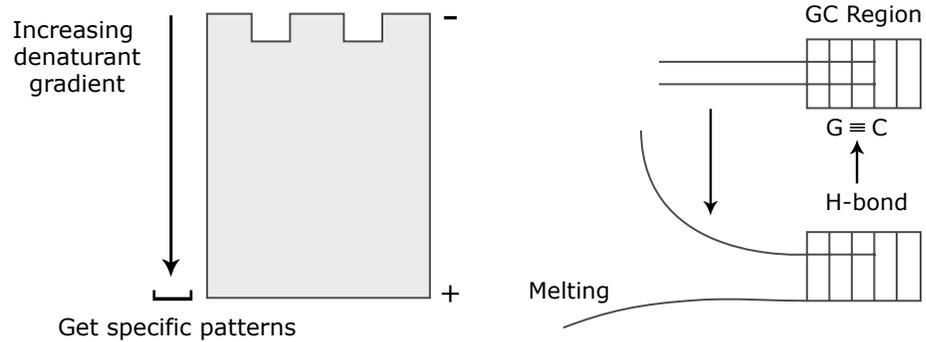
Techniques:

1. ARDRA (Restriction digestion of PCR amplified rDNA)
2. T-RF (introduce RE, cut at various places, specific patterns revealed on electropherograms)

Quick way of seeing if two communities contain the same types of organisms (temporal or spacial heterogeneity)



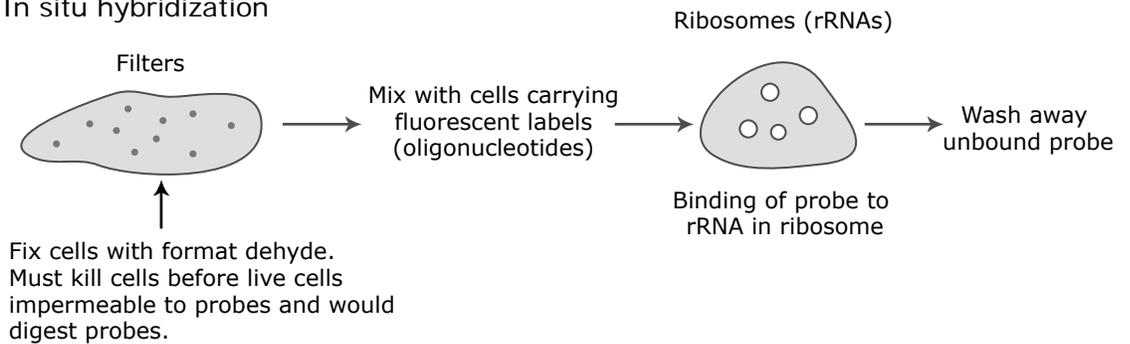
- DGGE (Denaturant Gradient Gel Electrophoresis) will not denature. Run on gel to get patterns that reveal ecologically significant patterns.



Detection/Quantification in Environment

Techniques:

- In situ hybridization



Count labeled cells

- QPCR (Quantitative PCR) see handout