



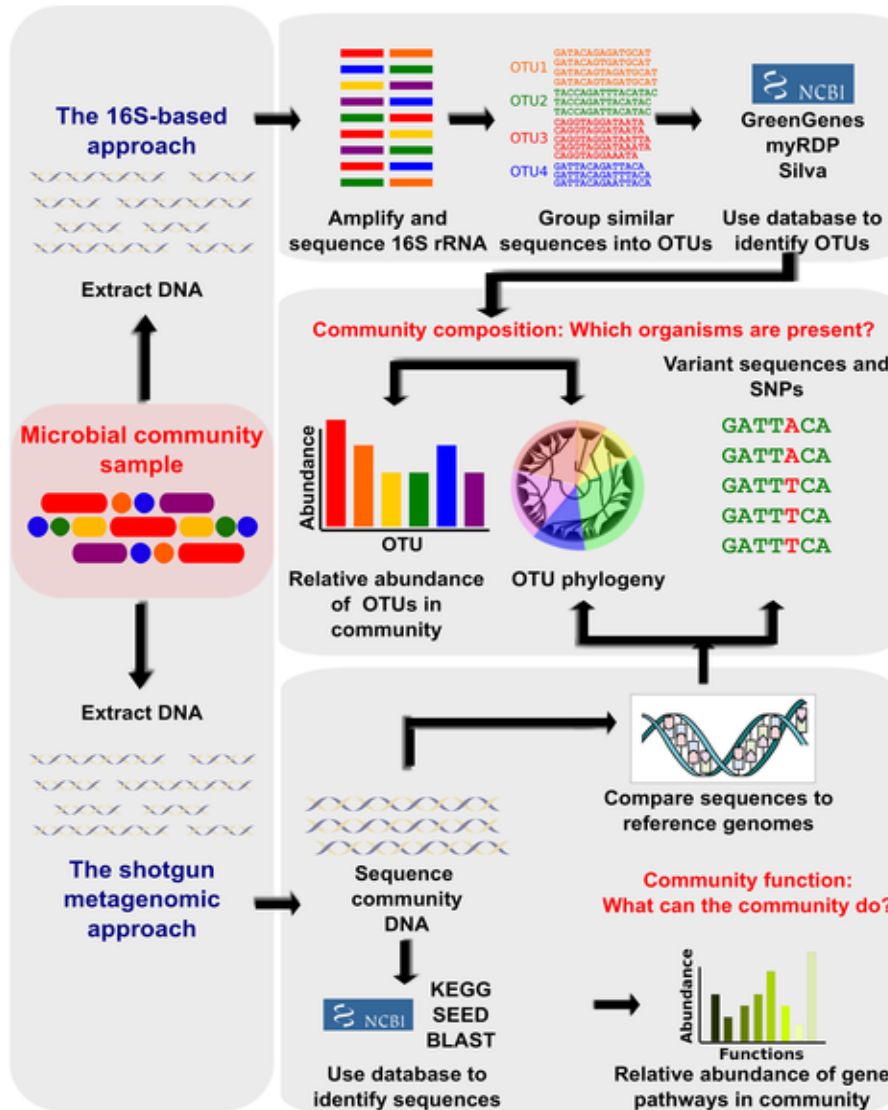
Microbiome analysis based on 16S rDNA

-An introduction

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Methodology: taxonomical and functional profiling



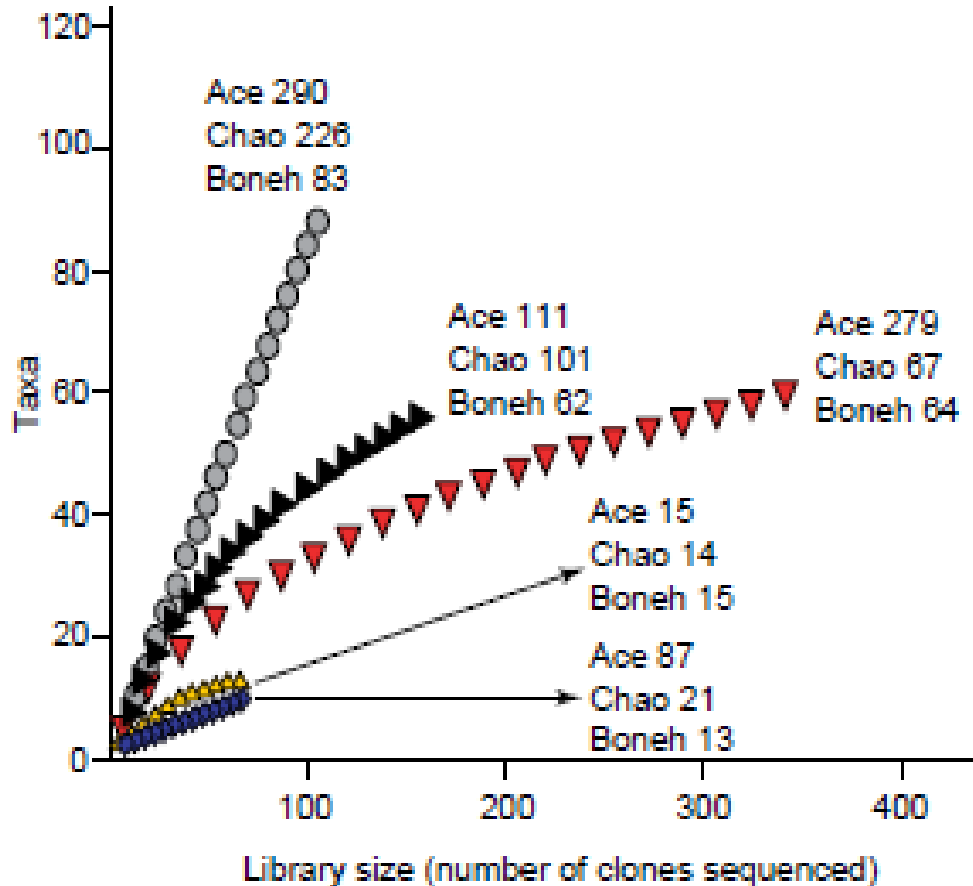
--16S rRNA profiling of gut microbial communities (for this workshop)

--Shotgun metagenomics for functional profiling (Illumina Hiseq)

--Alpha-diversity: the richness of bacterial taxa within a community (i.e. how complex a community is)

--Beta-diversity: the shared and unique bacterial taxa between communities (i.e. how different communities are)

Alfa-diversity: observed vs hidden



Sampling procedure are rarely exhaustive/comprehensive

Observed number of taxa: dependent on sampling depth

Richness/Diversity: extrapolate on rarefaction curve

Evenness: relative proportion of each other

“Biodiversity on one dimension”

Margalef index

$$D_m = (s - 1) / \sqrt{\log N}$$

Shannon-wiener

$$H = \sum_{i=1}^s p_i * \log p_i$$

Simpson

$$D = \sum_{i=1}^s p_i^2$$

Community comparison

Hill's index

$$N_0 = S$$

$$N_1 = \exp(H')$$

$$N_2 = 1/D$$

$$N_\infty = 1/p_1$$

$$N_{10}, N_{10'}, N_{21}, N_{21}'$$

Easy to define, hard to compare

Etc.

Beta-diversity: paired community comparison

- Bary-Curtis

$$D_{ij} = 100 \left(1 - \frac{\sum |x_{ik} - x_{jk}|}{\sum x_{ik} + \sum x_{jk}} \right)$$

x_{ik} = abundance of species k in sample i

x_{jk} = abundance of species k in sample j

Or jaccard (based on presence/absence)

$$J_{\mu}(A, B) = \frac{\mu(A \cap B)}{\mu(A \cup B)}$$