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

*pictures are from internet
“Biodiversity on one dimension”

Margalef index

\[ D_m = \frac{(s - 1)}{\sqrt{\log N}} \]

Shannon-Wiener

\[ H = \sum_{i=1}^{s} p_i \cdot \log p_i \]

Simpson

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

Community comparison

Hill’s index

N0 = S

N1 = \exp (H')

N2 = 1/D

N\infty = 1/p1

N10, N10', N21, N21'

Easy to define, hard to compare

Etc.

*pictures are from internet*
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)

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