

Microbial co-occurrences - microbial correlation Networks - Time Series - Human Gut - Survey genomic data 16S

Abstract

Bla bla bla

Introduction

Materials and Methods

Our aim is to identify a correlation between species withing ecological communities and their dynamics over time.

Counts and taxonomical assignment of OTU

OTU counts and their taxonomical classification from 244 unrelated individuals were obtained using "Mothur - Lotus" software (ref). Reads were classified using Silva 16S rRNA reference database.

-Output: OTU counts

Data treatment

The OTU counts are very sparse where zero values dominated most count values. We Assumed that nonsufficient sampling effort explains zero values, and that means zero values refer to unobserved values caused by the limited size of the sample. Under this assumption, we treated the zero values using the Bayesian-multiplicative approach (Pawlowsky-Glahn et. al. 2011-chap4).

$$r_{ij} = \begin{cases} (t_{ij}s_i)/(N_i + si) & \text{if } x_{ij} = 0 \\ x_{ij} & \text{if } x_{ij} = 0(1 - E) \end{cases}$$

Microbial correlation network

Owing to sequencing depth the total read counts across samples were different. Therefore, the OTU counts are normalized by the total number of counts. The resulting proportions fall into the category of compositional data which has its particular geometrical and statistical properties (Pawlowsky-Glahn et. al. 2011).

1. react
2. diffuse free particles
3. increment time by dt and go to 1

Results

Discussion

Supporting Information

References