# Data Analysis of 16S/18S/ITS Amplicon Sequencing Results

16S/18S/ITS Amplicon Sequencing provides a rapid, easy and effective access to the exploration of microbial identification, diversity and classifications in complex communities, considering the majority of natural microorganisms can not be isolated and cultured clonally. The genetic materials are easy to recover from environmental samples, and the NGS technology greatly advances and perfects the metagenomics studies.

We provide multiple customized bioinformatics analyses:

1. Species annotation

Tags assembly, OTUs clustering, taxonomy profiling histogram, abundance heatmap and phylogenetic tree, etc.
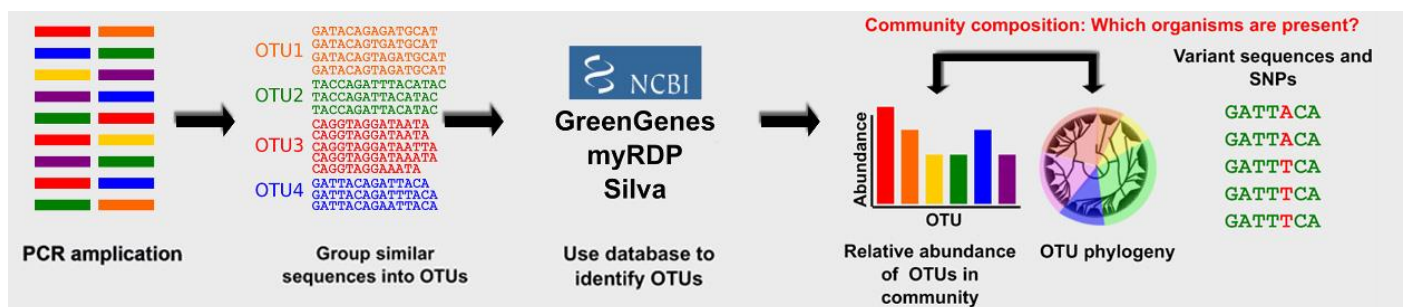

2. Diversity analysis: alpha diversity, beta diversity, meta-analysis, multivariate statistical analysis

While the alpha diversity analysis acts like a summary statistics of a single population, the beta diversity measure acts like a similarity score between populations. Meta-analysis is the process of performing comparative studies of abundant features between datasets, which is greatly enhanced by the combination of metagenomics data and metadata. Multivariate analysis is based on the statistical principle of multivariate statistics, which involves observation and analysis of more than one statistical outcome variables at a time, including ANOVA analysis, Wilcoxon test and ternary plot.
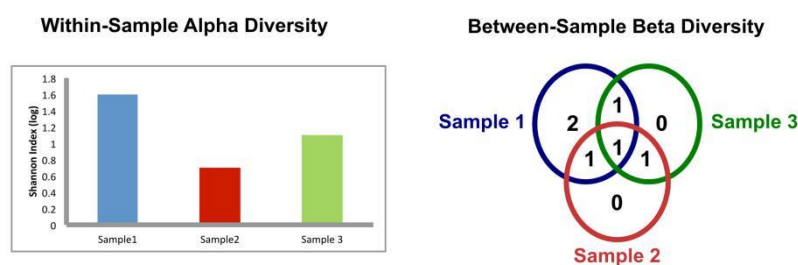

3. PICRUSt

A computational approach to predict the functional composition of a metagenome using marker gene data, such as the 16S rRNA gene, and a database of reference genomes. The abundance of KEGG and COG functional pathways can be calculated based on the 16S copy number.
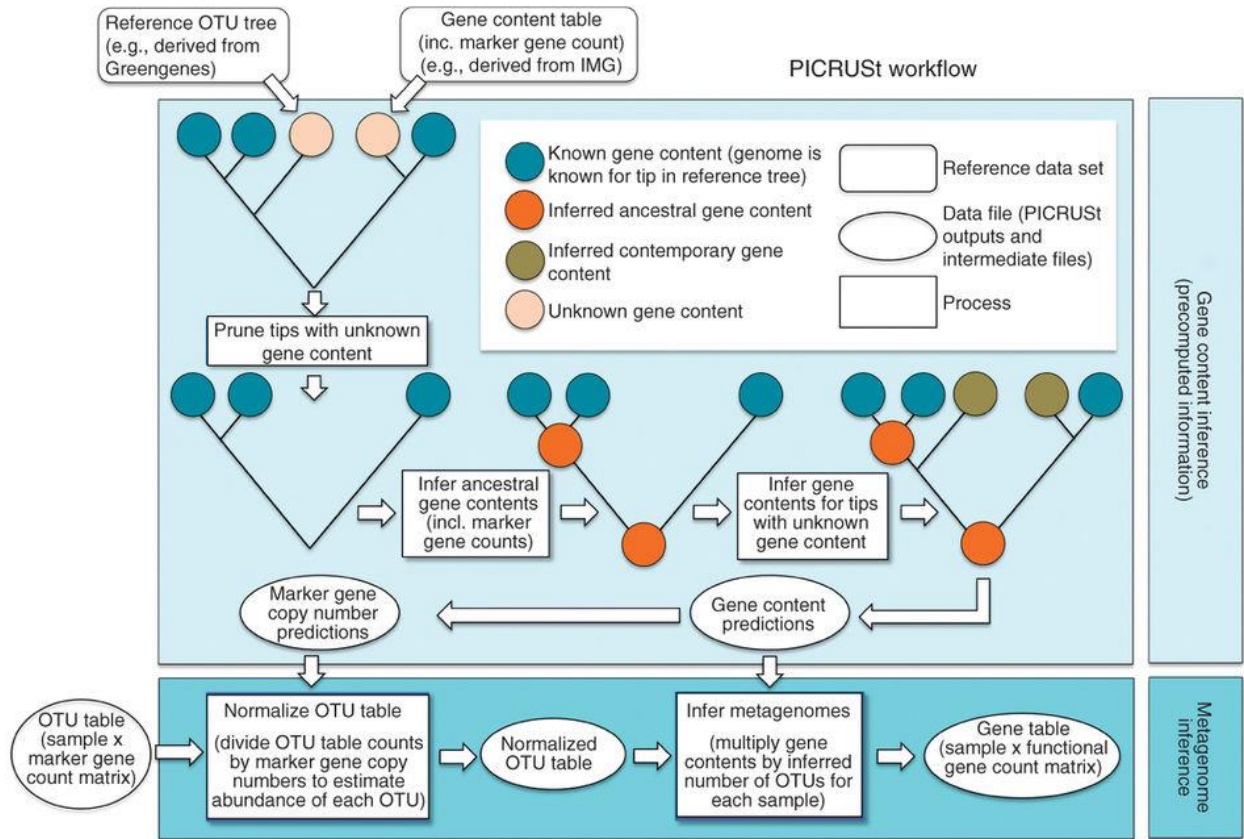
PICRUSt workflow

4. Enterotypes analysis

Enterotypes, closely associated with long-term diet, represent the classification of living organism on the basis of a bacteriological ecosystem in the gut. The enterotypes analysis contributes to the investigations of illness-related intestinal bacteria, and disease prediction and treatment based on 16S rRNA or metagenomics sequencing data.
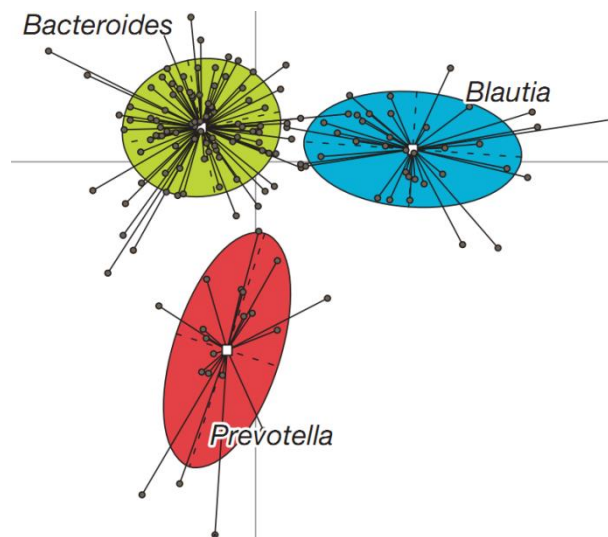
PCA analysis based on 154 16S sequences.

··· (more upon request)

Take the sequencing data by PCR-based method for example
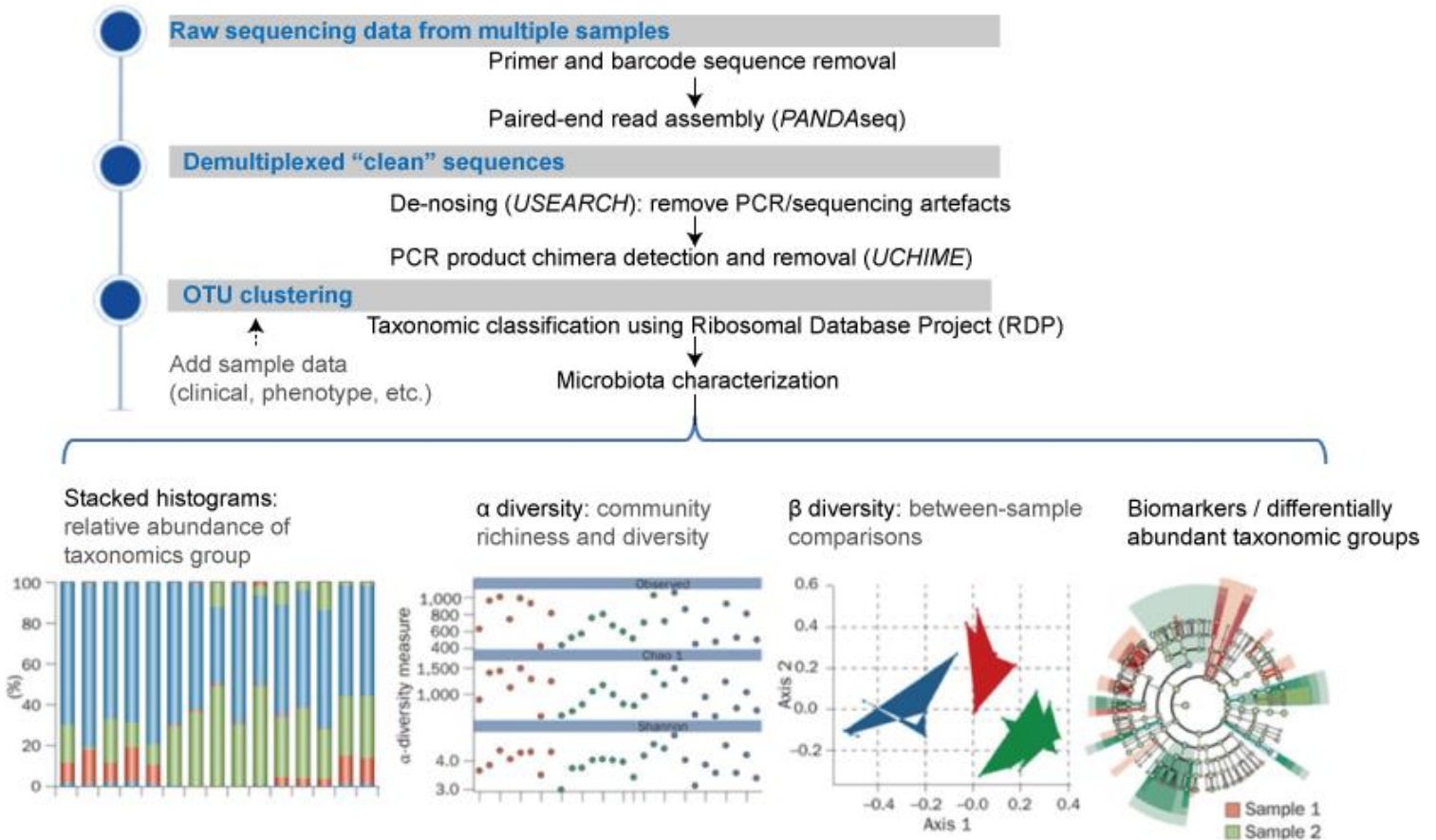
References

1. Langille *et al*. Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. *Nature biotechnology*. 2013, 31.9: 814-821.

2. Gilbert J. Metagenomics, metadata, and meta-analysis. *Encyclopedia of Metagenomics: Genes, Genomes and Metagenomes: Basics, Methods, Databases and Tools.* 2015: 439-442.

3. Arumugam M., *et al*. Enterotypes of the human gut microbiome. *Nature*. 2011, 473.7346: 174.

CD Genomics
The Genomics Services Company

Contact CD Genomics for more inspiration and service content.