

# Periodontitis

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# Overview

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# Introduction

# Microbiome

- Microbiota: the micro-organisms which live inside & on humans (Turnbaugh et al., 2007)
- Microbiome: about  $10^{13}$  micro-organisms whose which collective genome (Gill et al., 2006)



**Figure:** Concept of a core human microbiome (Turnbaugh et al., 2007)

- Ribosomal RNA
- Well-known as a key to phylogeny (Olsen & Woese, 1993)

# Periodontitis (Periodontal disease)

- CAL (Clinical Attachment Loss) & BL (Bone Loss) (Flemmig, 1999)
- Risk Factors (Van Dyke & Dave, 2005)
  - ① Smoking
  - ② Diabetes
  - ③ Genetic factor
  - ④ Host response

# Materials

# 16S rRNA Sequencing

- 100 Healthy people
- 50 Chronic periodontitis – Early
- 50 Chronic periodontitis – Moderate
- 50 Chronic periodontitis – Severe



# Methods

# Qiime2 Workflow

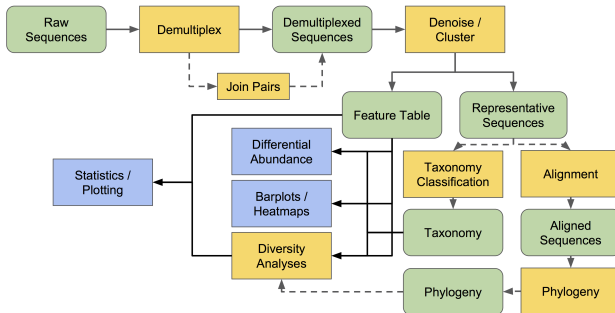


Figure: Qiime2 Workflow (Bolyen et al., 2019, 2018)

# Denoising techniques

- DADA2: Amplicon Sequence Variants (ASVs) (Callahan et al., 2016)
- Deblur: Operational Taxonomic Units (OTUs) (Amir et al., 2017)

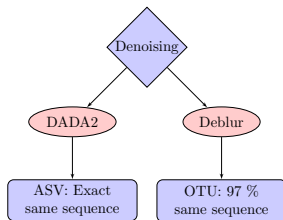


Figure: Denoising Techniques

# Taxonomy Classification

- Greengenes (GG) (DeSantis et al., 2006)
- SILVA (Pruesse et al., 2007)



Figure: Taxonomy Classification

“A **higher** performance at taxonomic levels above *genus* level; but performance appears to drop at *species* level” (Gihawi et al., 2019)

- a statistical method of estimating the number of species expected in a random sample which taken from a collection (James & Rathbun, 1981)
- allows comparisons of the species richness among communities
- a good choice for normalization (Weiss et al., 2017)

# Alpha- & Beta-diversity

- alpha-diversity: the richness of taxa at a single community
- beta-diversity: the taxonomic differentiation between communities

- Shannon's diversity index: a quantitative measure of community richness
- Observed Features: a quantitative measure of community richness
- Faith's Phylogenetic Diversity: a qualitative measure of community richness which incorporates phylogenetic relationship between the features
- Evenness: a measure of community evenness

(Bolyen et al., 2019, 2018)

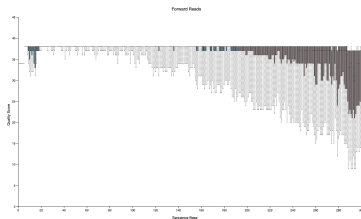
- Jaccard distance: a qualitative measure of community dissimilarity
- Bray-Curtis distance: a quantitative measure of community dissimilarity
- unweighted UniFrac distance: a qualitative measure of community dissimilarity which incorporates phylogenetic relationships between the features
- weighted UniFrac distance: a quantitative measure of community dissimilarity which incorporates phylogenetic relationship between the features

(Bolyen et al., 2019, 2018)

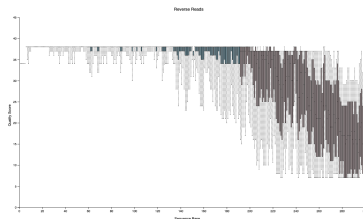


## Results

# Quality Filter



(a) Forward Reads

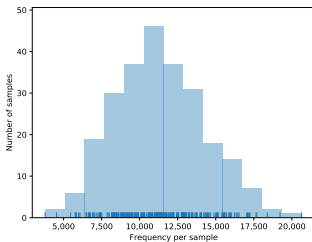


(b) Reverse Reads

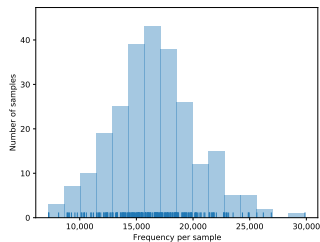
Figure: Sequence Quality Plot

- ∴ Maximum Sequence Length  $n_{forward} = 300$ ,  $n_{reverse} = 265$
- ∴ The longest length which has sequence quality  $\geq 30$  at middle.

# Rarefaction



(a) DADA2

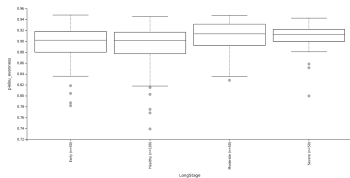


(b) Deblur

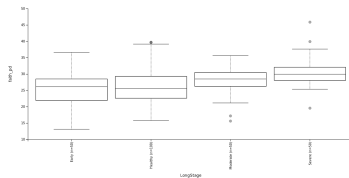
Figure: Frequency per sample

$\therefore$  p-sampling-depth  $n_{DADA2} = 3786$  and  $n_{Deblur} = 7253$

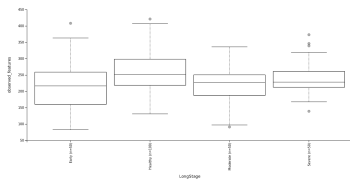
# Alpha-diversity I



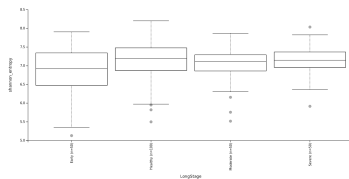
(a) Evenness ( $p < 0.01$ )



(b) Faith PD ( $p < 10^{-6}$ )



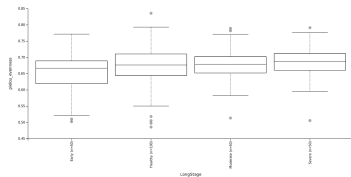
(c) Observed features ( $p < 10^{-3}$ )



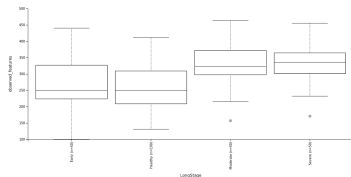
(d) Shannon ( $p > 0.05$ )

Figure: Alpha Diversity from DADA2 with Kruskal-Wallis among All Groups

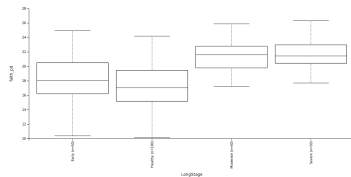
# Alpha-diversity II



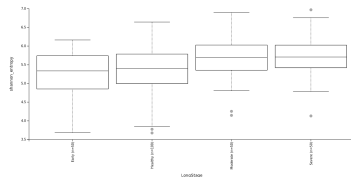
(a) Evenness ( $p < 0.05$ )



(c) Observed features ( $p < 10^{-12}$ )



(b) Faith PD ( $p < 10^{-18}$ )



(d) Shannon ( $p < 10^{-4}$ )

**Figure:** Alpha Diversity from Deblur with Kruskal-Wallis among All Groups

# Beta-diversity I

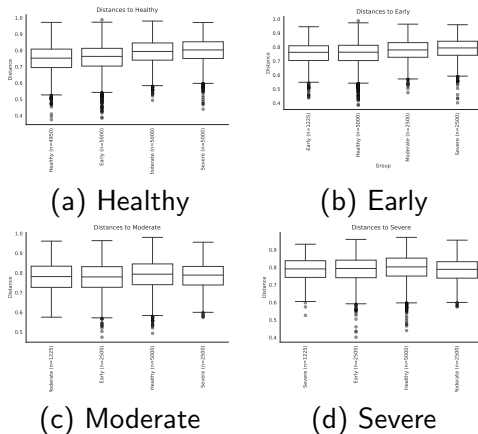


Figure: Bray-Curtis Distance with DADA2 ( $p < 0.001$ )

# Beta-diversity II

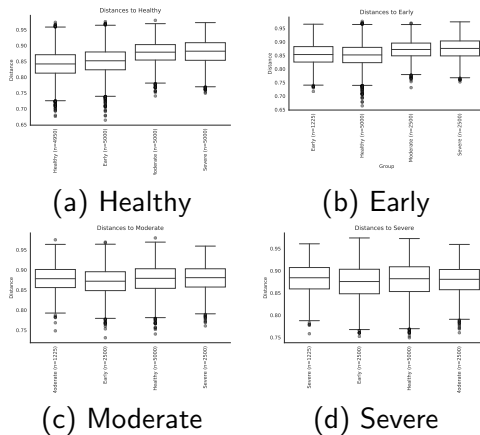


Figure: Jaccard Distance with DADA2 ( $p < 0.001$ )

## Discussion



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