

# Periodontitis

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# 1 Introduction

## 1.1 Periodontitis

## 1.2 Ribosomal RNA

# 2 Materials

## 2.1 16S rRNA Gene Sequencing

# 3 Methods

## 3.1 QIIME2 Workflow

QIIME2 is a capable, expandable and distributed microbiome analysis package with transparent analysis (Bolyen et al., 2019, 2018). A theoretic overview of QIIME2 workflow is shown as figure 1.

### 3.1.1 Denoising techniques

### 3.1.2 Taxonomy Classification

### 3.1.3 Rarefaction

### 3.1.4 Alpha-diversity

### 3.1.5 Beta-diversity

### 3.1.6 ANCOM

## 3.2 Python Packages

### 3.2.1 Pandas

Pandas is a Python package of rich data structures and tools for analyzing with structured data sets (McKinney et al., 2011).

### 3.2.2 Scikit-learn

Scikit-learn grants state-of-the-art implementation of many machine learning algorithms, while controlling an easy-to-use interface tightly integrated the Python code (Pedregosa et al., 2011).

### 3.2.3 Matplotlib

Matplotlib is a Python graphics package which used for application development, interactive scripting and publication quality image generation (Barrett, Hunter, Miller, Hsu, & Greenfield, 2005). Matplotlib, also, is designed to create simple plots with a few commands (Hunter, 2007).

### 3.2.4 Seaborn

Seaborn is a Python data visualization package which based on matplotlib, allows a high-level interface for displaying engaging and descriptive statistical graphics (Waskom & the seaborn development team, 2020).

# 4 Results

# 5 Discussion

# 6 References

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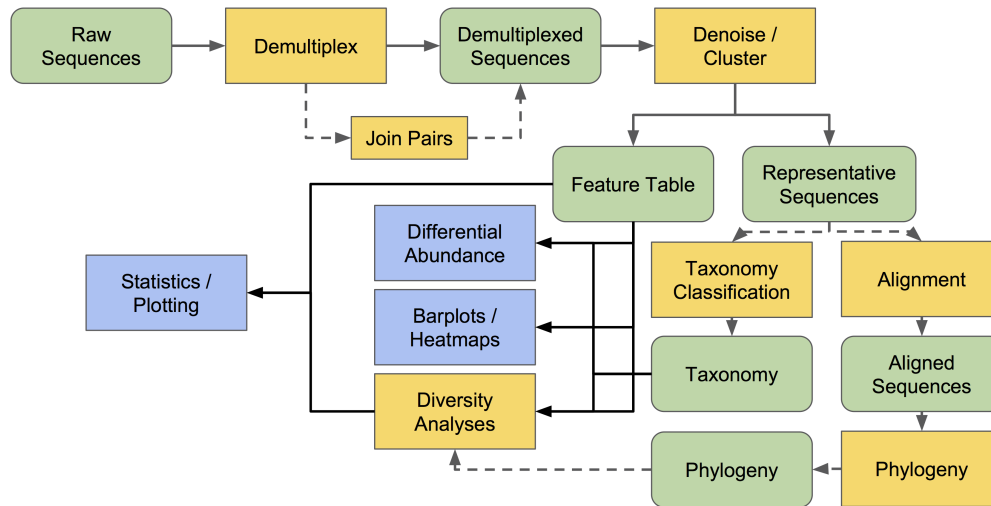
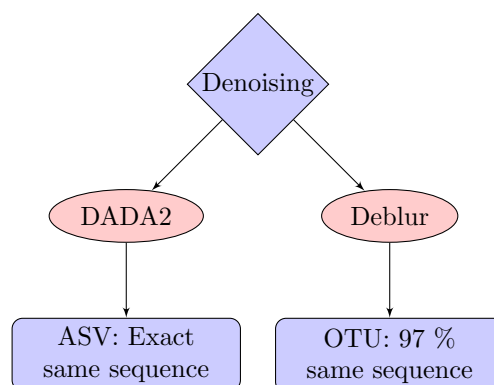


Figure 1: A Theoretic Overview of QIIME2 Workflow (Bolyen et al., 2019, 2018)



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