

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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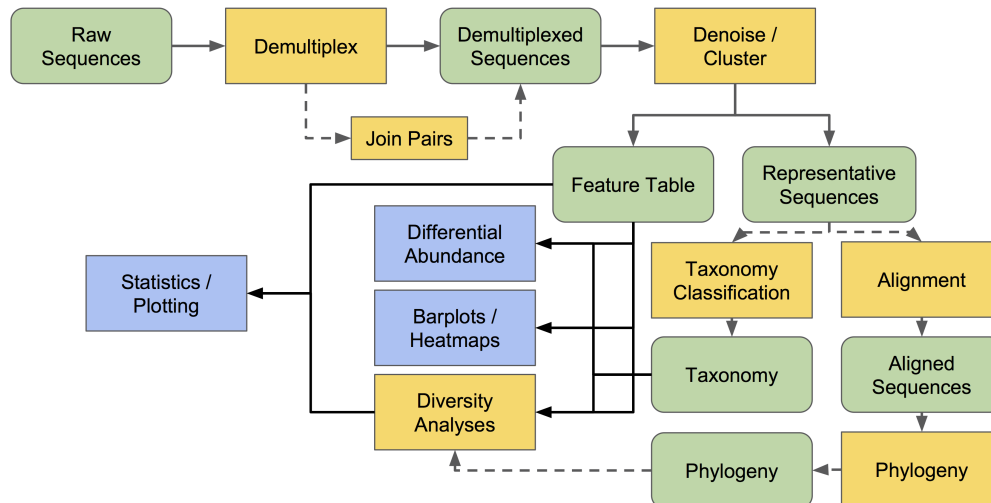


Figure 1: A Theoretic Overview of QIIME2 Workflow (Bolyen et al., 2019, 2018)

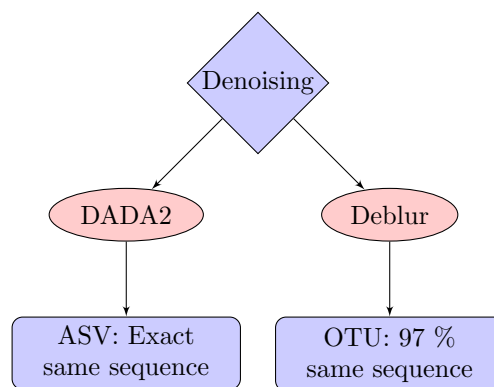


Figure 2: Denoising Techniques which provided by QIIME2

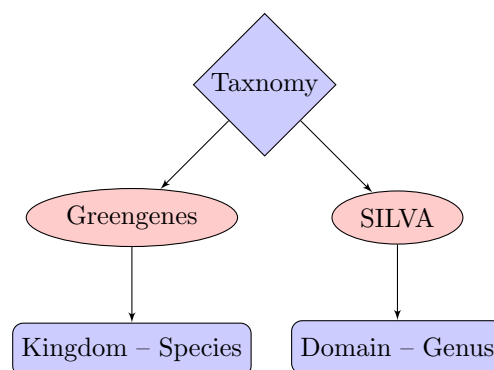


Figure 3: Taxonomy Classification which provided by QIIME2

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