Periodontitis

Seunghoon Kim   Jaewoong Lee   Semin Lee

2020-11-26

Contents

List of Tables

List of Figures

1 Introduction

1.1 Periodontitis

1.2 Ribosomal RNA

Ribosomal RNA (rRNA)

1.3 16S rRNA Gene Sequencing

2 Materials

2.1 16S rRNA Gene Sequencing

- 100 Healthy samples
- 50 Chronic Early Periodontitis Sample
- 50 Chronic Moderate Periodontitis Sample
- 50 Chronic Severe Periodontitis Sample

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

There are two denoising techniques provided by QIIME2: DADA2 (Callahan et al., 2016) and Deblur (Amir et al., 2017). Major difference between DADA2 and Deblur is a strategy, the strategy used to divide as different species.

3.1.2 Taxonomy Classification

There are two taxonomy classification databases which provided by QIIME2: Greengenes (GG) (DeSantis et al., 2006) and SILVA (Pruesse et al., 2007).

3.1.3 Rarefaction

3.1.4 Alpha-diversity

3.1.5 Beta-diversity

3.1.6 ANCOM

ANCOM (Analysis of composition of microbiomes) can be used for analyzing the composition of microbiome in multiple populations (Mandal et al., 2015).

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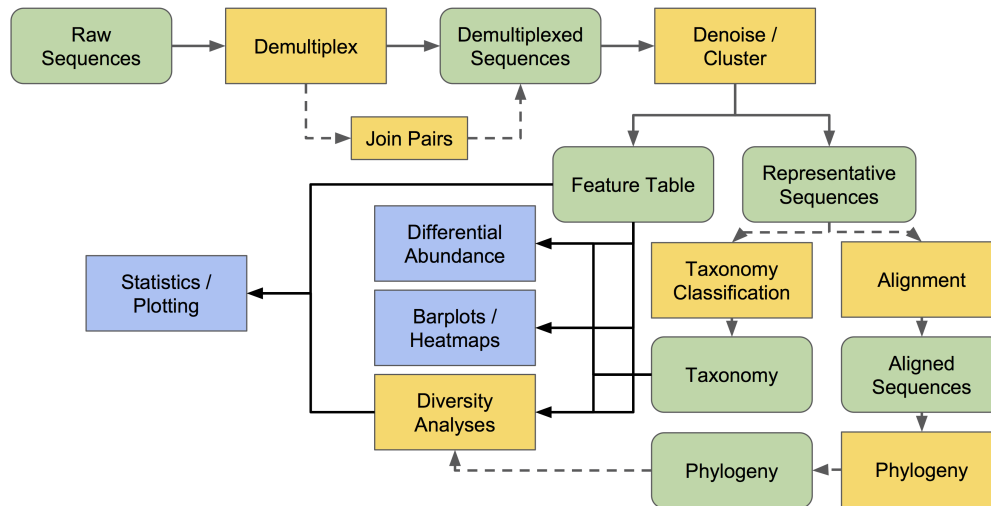
Figure 1: A Theoretic Overview of QIIME2 Workflow (Bolyen et al., 2019, 2018)
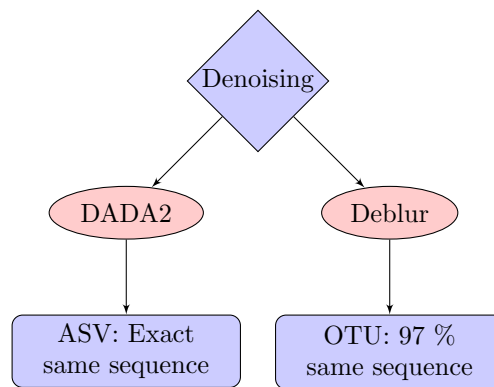

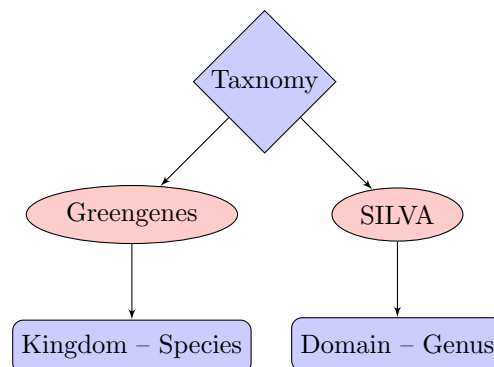Figure 2: Denoising Techniques which provided by QIIME2

Figure 3: Taxonomy Classification which provided by QIIME2

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

Amir, A., McDonald, D., Navas-Molina, J. A., Kopylova, E., Morton, J. T., Xu, Z. Z., . . . others (2017). Deblur rapidly resolves single-nucleotide community sequence patterns. *MSystems*, *2*(2).

Barrett, P., Hunter, J., Miller, J. T., Hsu, J.-C., & Greenfield, P. (2005). matplotlib–a portable python plotting package. In *Astronomical data analysis software and systems xiv* (Vol. 347, p. 91).

Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C., Al-Ghalith, G. A., . . . others (2018). *Qiime 2: Reproducible, interactive, scalable, and extensible microbiome data science* (Tech. Rep.). PeerJ Preprints.

Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., . . . others (2019). Reproducible, interactive, scalable and extensible microbiome data science using qiime 2. *Nature biotechnology*, *37*(8), 852–857.

Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., & Holmes, S. P. (2016). Dada2: high-resolution sample inference from illumina amplicon data. *Nature methods*, *13*(7), 581–583.

DeSantis, T. Z., Hugenholtz, P., Larsen, N., Rojas, M., Brodie, E. L., Keller, K., . . . Andersen, G. L. (2006). Greengenes, a chimera-checked 16s rrna gene database and workbench compatible with arb. *Applied and environmental microbiology*, *72*(7), 5069–5072.

Hunter, J. D. (2007). Matplotlib: A 2d graphics environment. *Computing in science & engineering*, *9*(3), 90–95.

Mandal, S., Van Treuren, W., White, R. A., Eggesbø, M., Knight, R., & Peddada, S. D. (2015). Analysis of composition of microbiomes: a novel method for studying microbial composition. *Microbial ecology in health and disease*, *26*(1), 27663.

McKinney, W., et al. (2011). pandas: a foundational python library for data analysis and statistics. *Python for High Performance and Scientific Computing*, *14*(9).

Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., . . . others (2011). Scikit-learn: Machine learning in python. *the Journal of machine Learning research*, *12*, 2825–2830.

Pruesse, E., Quast, C., Knittel, K., Fuchs, B. M., Ludwig, W., Peplies, J., & Glöckner, F. O. (2007). Silva: a comprehensive online resource for quality checked and aligned ribosomal rna sequence data compatible with arb. *Nucleic acids research*, *35*(21), 7188–7196.

Waskom, M., & the seaborn development team. (2020, September). *mwaskom/seaborn*. Zenodo. Retrieved from `https://doi.org/10.5281/zenodo.592845` doi: 10.5281/zenodo.592845
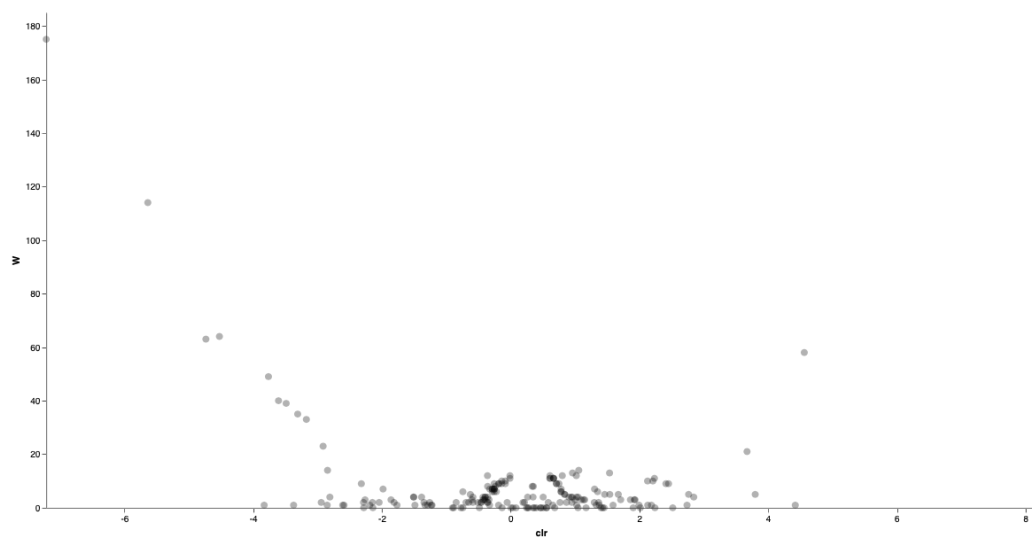
Figure 4: Example ANCOM Volcano Plot which Provided by QIIME2 (Bolyen et al., 2019, 2018)