

Periodontitis

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Overview

1 Introduction

2 Materials

3 Methods

4 Results

5 Discussion

Introduction

Microbiome

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



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

rRNA

- 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

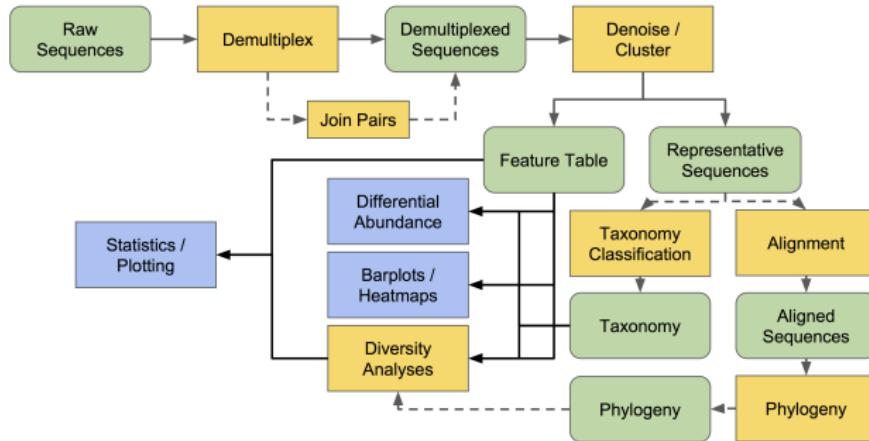


Figure: QIIME2 Workflow (Bolyen et al., 2019, 2018)

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)

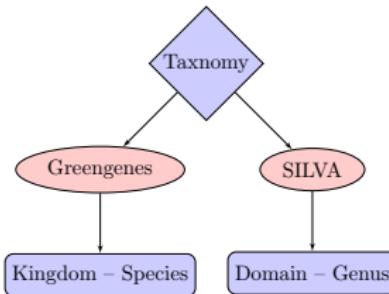


Figure: Taxonomy Classification

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

Merging Denosing and Taxonomy Classification

Merging multiple IDs (ASVs and OTUs) into one, which have:

- Different IDs.
- Identified as same taxonomy.

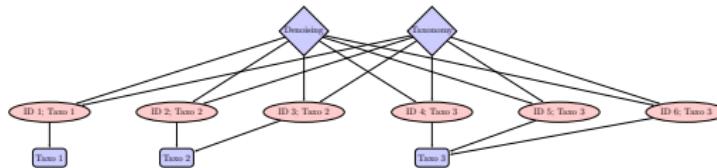


Figure: Example Diagram for Merging Denosing and Taxonomy Classification

Rarefaction

- 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

Alpha-diversity

- Shannon's diversity index: a quantitative measure of community richness
- Observed Features: a qualitative 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)

Beta-diversity

- Bray-Curtis distance: a quantitative measure of community dissimilarity
- Jaccard distance: a qualitative 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)

ANCOM

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

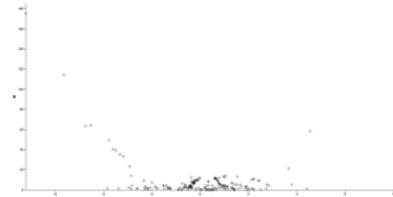


Figure: Example ANCOM Volcano Plot (Bolyen et al., 2019, 2018)

- clr: Centered log Ratio
- W: a count of the number of sub-hypothesis which have passed for given species

Python Packages

- Pandas (McKinney et al., 2011)
- Scikit-learn (Pedregosa et al., 2011)
- Matplotlib (Hunter, 2007; Barrett, Hunter, Miller, Hsu, & Greenfield, 2005)
- Seaborn (Waskom & the seaborn development team, 2020)

t-SNE

- t-distributed stochastic neighbor embedding
- reveals high-dimensional data a location in two-dimensional map
(Maaten & Hinton, 2008)

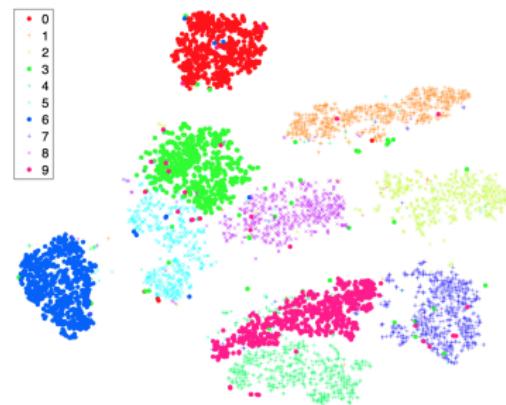


Figure: Visualization by t-SNE (Maaten & Hinton, 2008)

Classification I



Figure: Workflow of Classification

Classification Metrics:

- Accuracy
- Balanced Accuracy
- Sensitivity
- Specificity
- Precision

Classification II

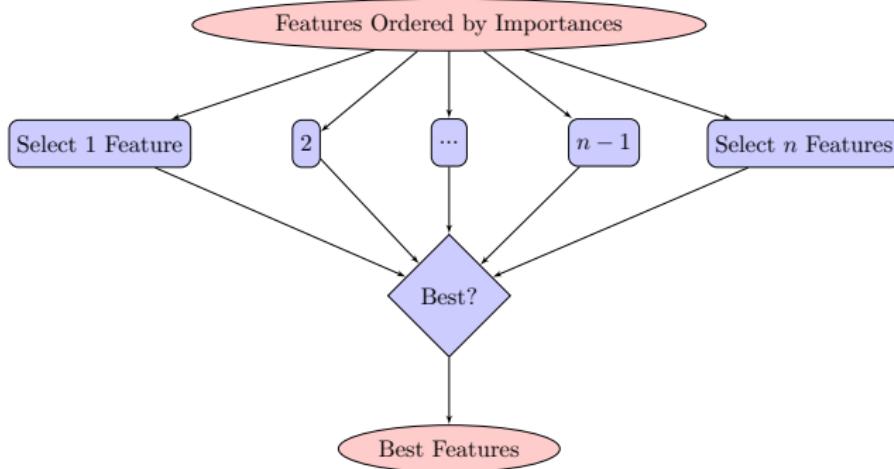
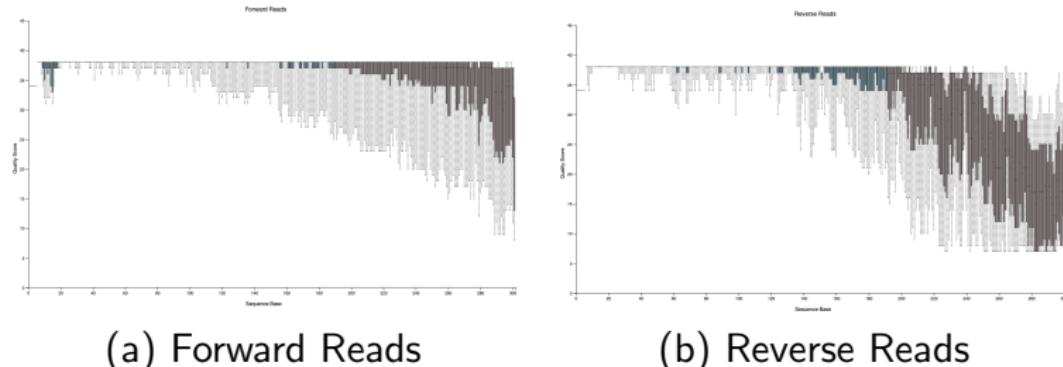


Figure: Deciding the Best Features

Results

Quality Filter



(a) Forward Reads

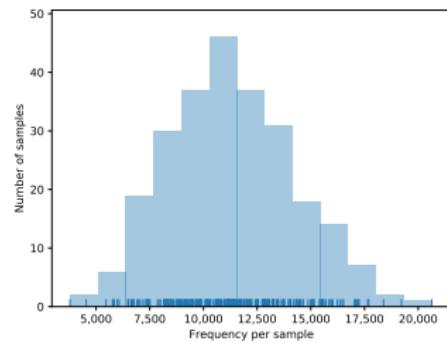
(b) Reverse Reads

Figure: Sequence Quality Plot

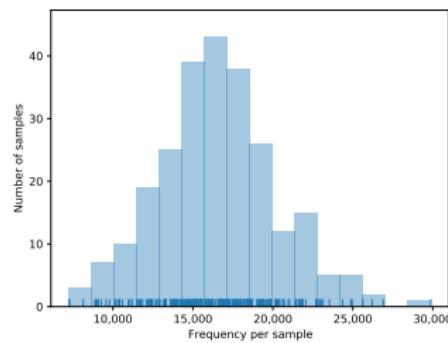
∴ Maximum Sequence Length $n_{forward} = 300$, $n_{reverse} = 265$

∴ The longest length which has sequence quality ≥ 30 at middle.

Rarefaction



(a) DADA2

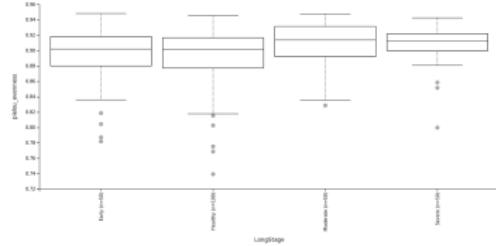


(b) Deblur

Figure: Frequency per sample

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

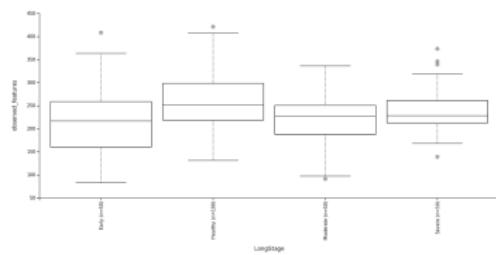
Alpha-diversity I



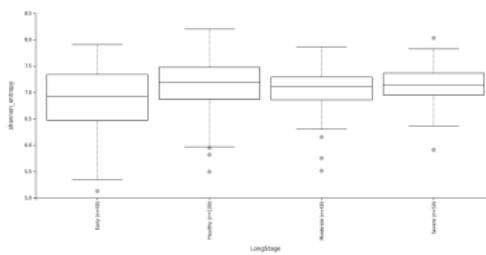
(a) Evenness ($p < 0.01$)



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



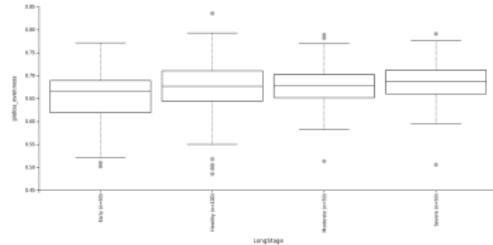
(c) Observed features ($p < 10^{-3}$)



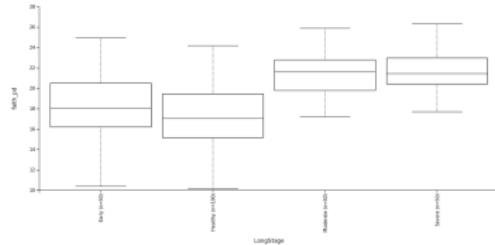
(d) Shannon's diversity ($p > 0.05$)

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

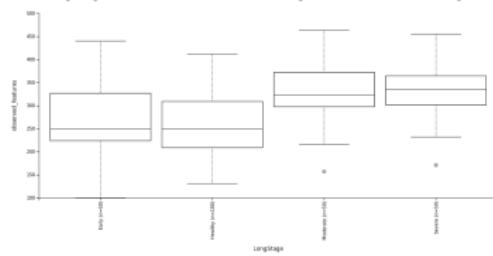
Alpha-diversity II



(a) Evenness ($p < 0.05$)



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



(c) Observed features ($p < 10^{-12}$) (d) Shannon's diversity ($p < 10^{-4}$)

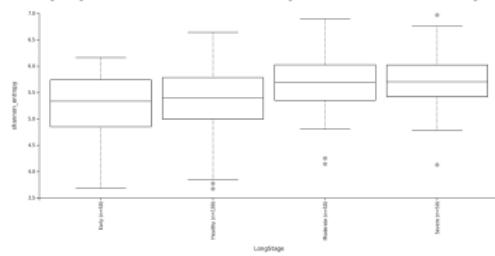


Figure: Alpha Diversity from Deblur with Kruskal-Wallis among All Groups

Beta-diversity I

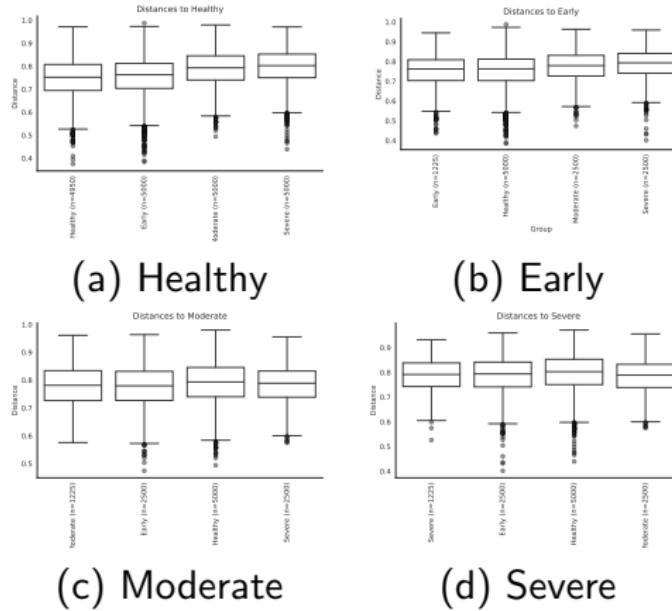


Figure: Bray-Curtis Distance with DADA2

Beta-diversity II

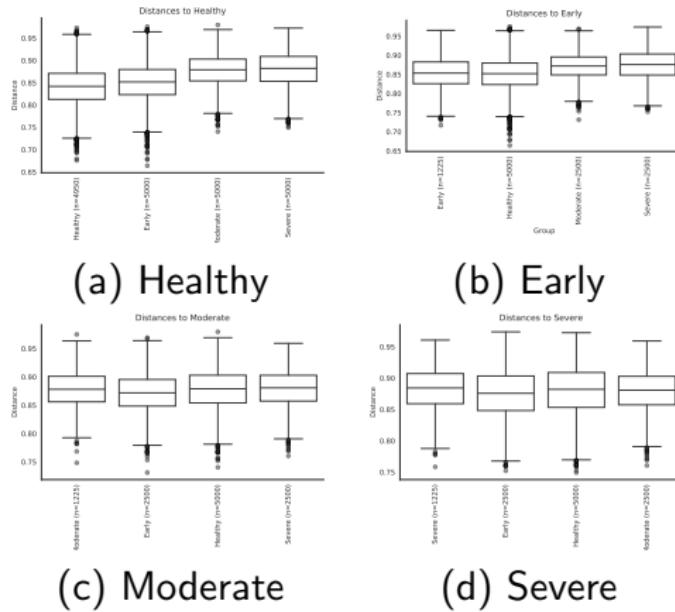
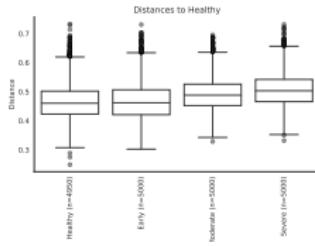
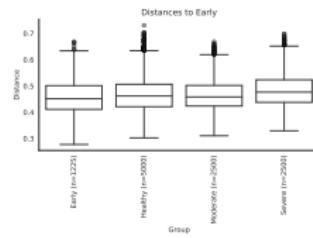


Figure: Jaccard Distance with DADA2

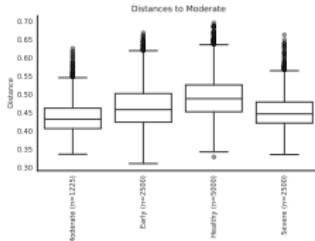
Beta-diversity III



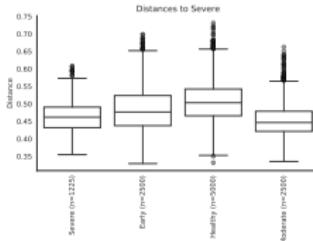
(a) Healthy



(b) Early



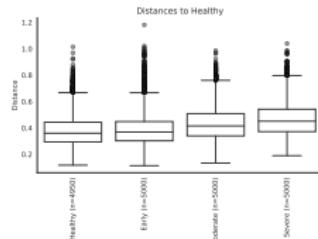
(c) Moderate



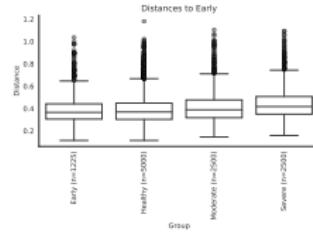
(d) Severe

Figure: Unweighted Unifrac Distance with DADA2

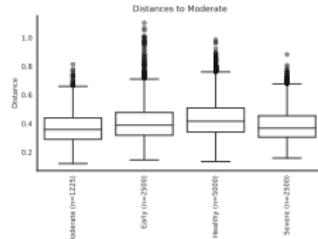
Beta-diversity IV



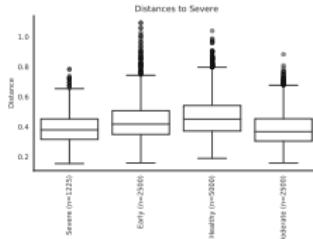
(a) Healthy



(b) Early



(c) Moderate



(d) Severe

Figure: Weighted Unifrac Distance with DADA2

Beta-diversity V

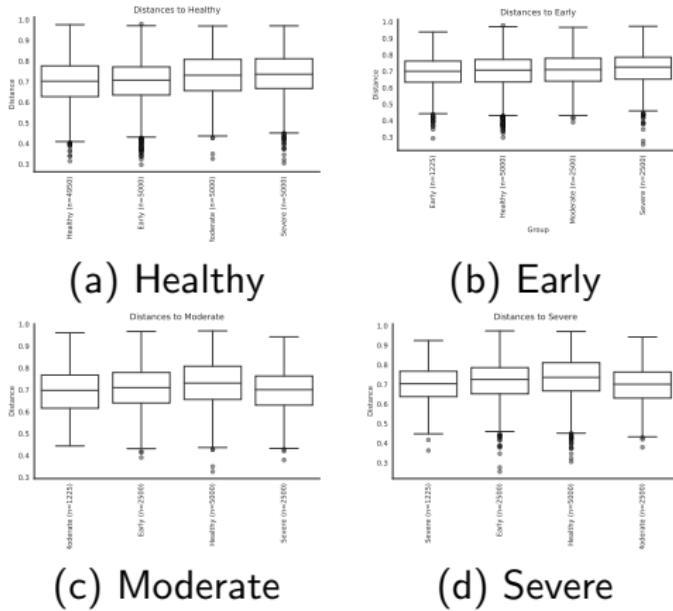


Figure: Bray-Curtis Distance with Deblur

Beta-diversity VI

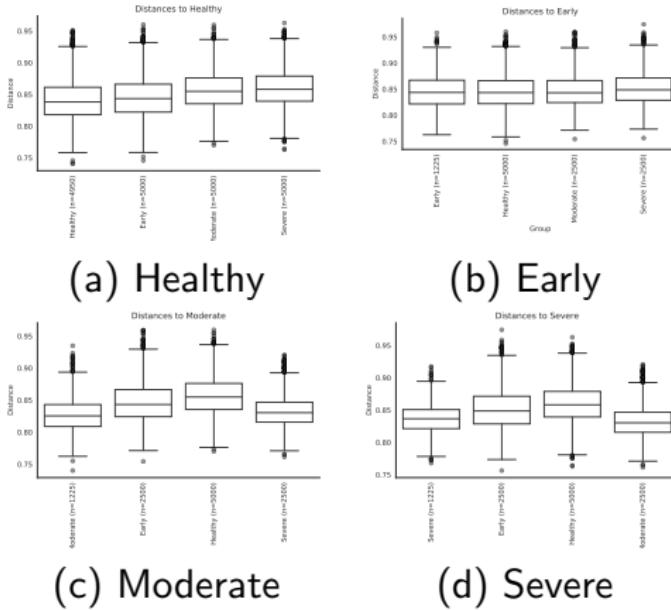


Figure: Jaccard Distance with Deblur

Beta-diversity VII

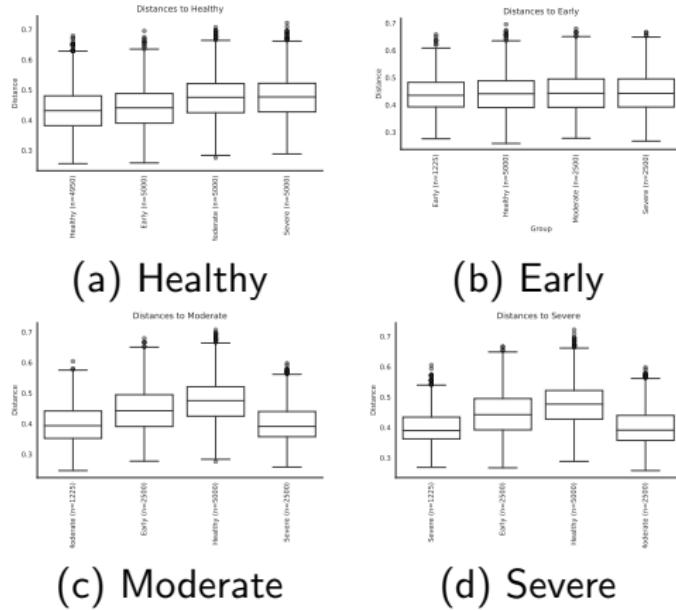


Figure: Unweighted Unifrac Distance with Deblur

Beta-diversity VIII

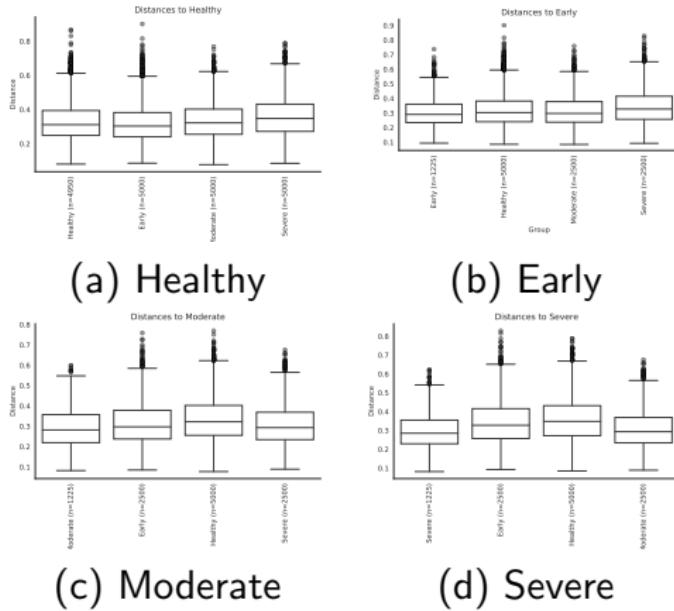
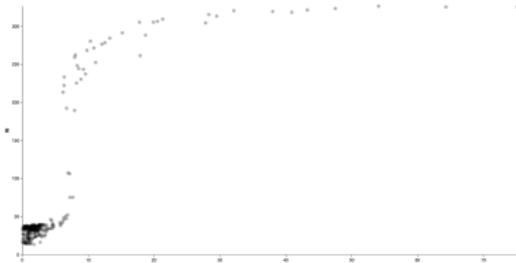
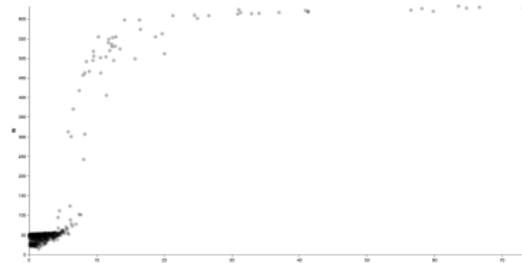


Figure: Weighted Unifrac Distance with Deblur

ANCOM I



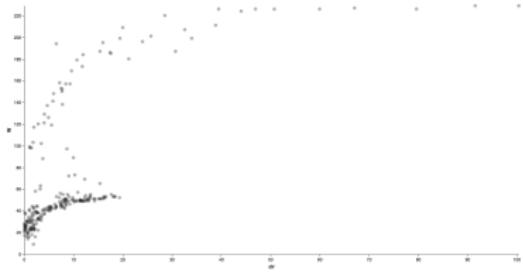
(a) Greengenes



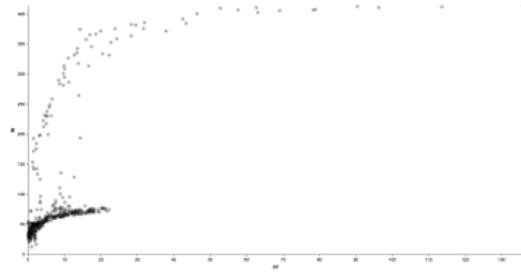
(b) SILVA

Figure: ANCOM Volcano Plot with DADA2

ANCOM II



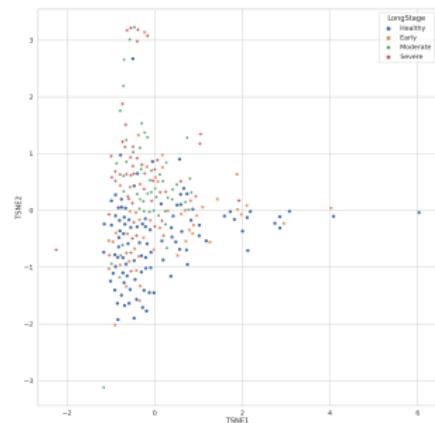
(a) Greengenes



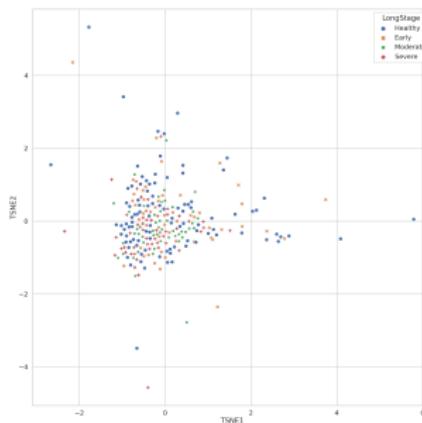
(b) SILVA

Figure: ANCOM Volcano Plot with Deblur

t-SNE with Whole Microbiome I



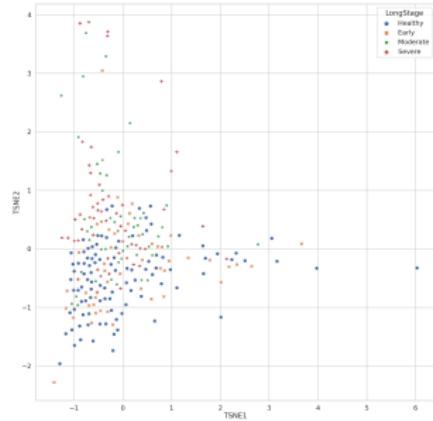
(a) Greengenes (328 Taxa)



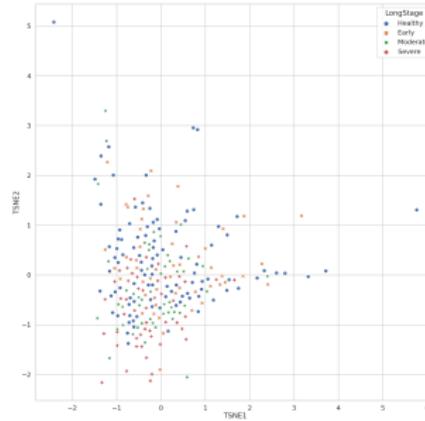
(b) SILVA (633 Taxa)

Figure: t-SNE Plot with Whole Microbiome from DADA2

t-SNE with Whole Microbiome II



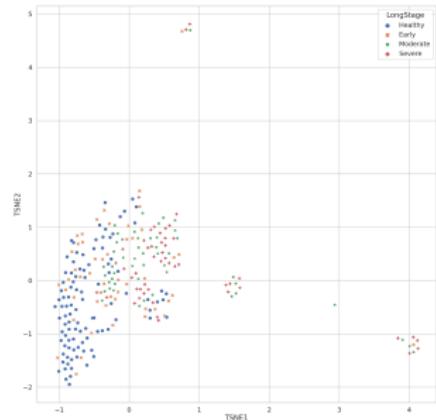
(a) Greengenes (232 Taxa)



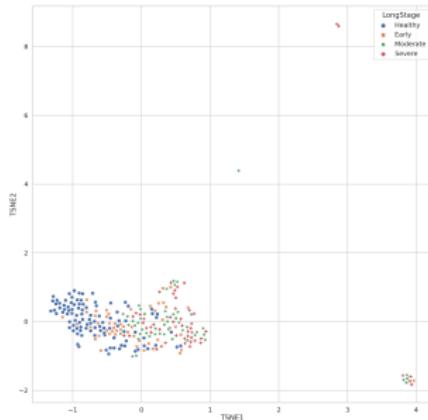
(b) SILVA (414 Taxa)

Figure: t-SNE Plot with Whole Microbiome from Deblur

t-SNE with ANCOM Selected I



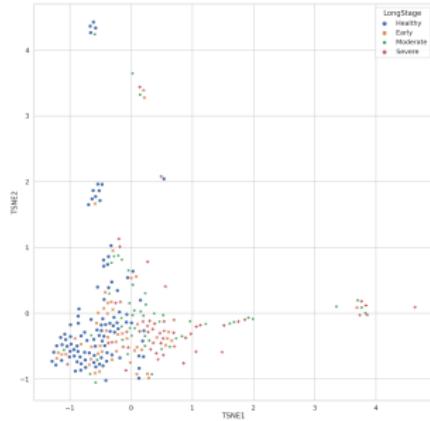
(a) Greengenes (15 Taxa)



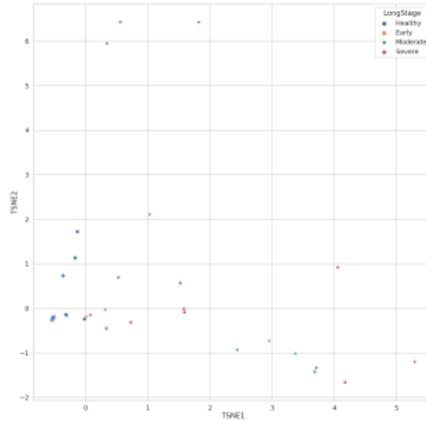
(b) SILVA (23 Taxa)

Figure: t-SNE Plot with ANCOM Selected from DADA2

t-SNE with ANCOM Selected II



(a) Greengenes (27 Taxa)



(b) SILVA (20 Taxa)

Figure: t-SNE Plot with ANCOM Selected from Deblur

Random Forest Classifier I

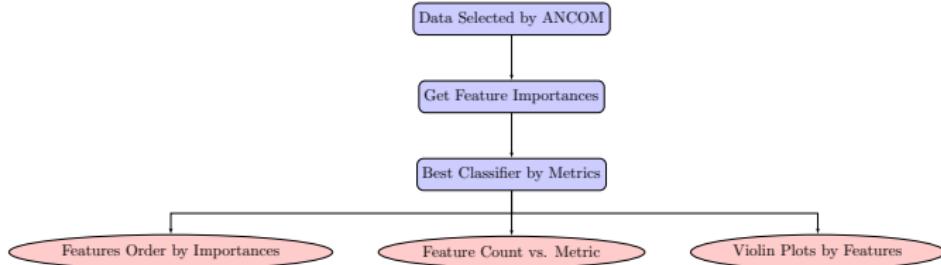


Figure: Random Forest Classifier Workflow

DADA2 + SILVA gives the best result with balanced accuracy.

Random Forest Classifier II

Table: Features Order by Importances

Order	Taxonomy (Genus [Species])
0	<i>Actinomyces</i>
1	<i>Actinomyces Schaalia-odontolytica</i>
2	<i>Prevotella Prevotella-intermedia</i>
3	<i>Filifactor Filifactor-alocis</i>
4	<i>Oribacterium</i>
5	<i>Tannerella Tannerella-forsythia</i>

Random Forest Classifier III

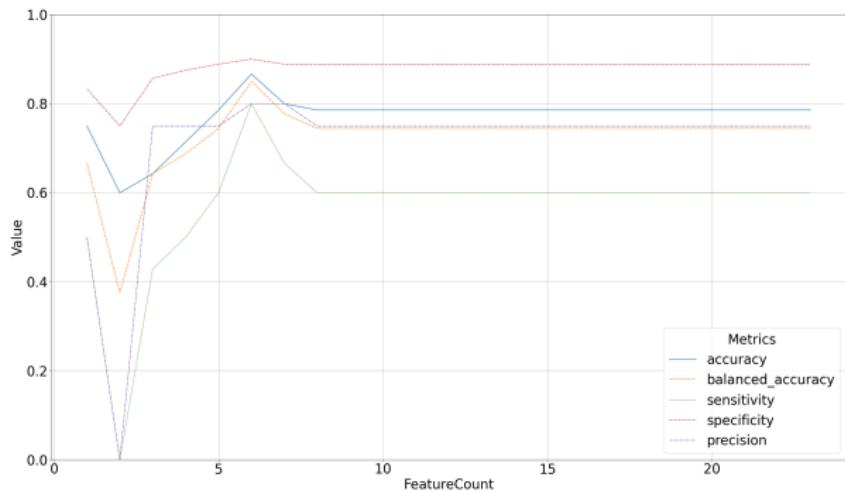


Figure: Metrics by Feature Count

Random Forest Classifier IV

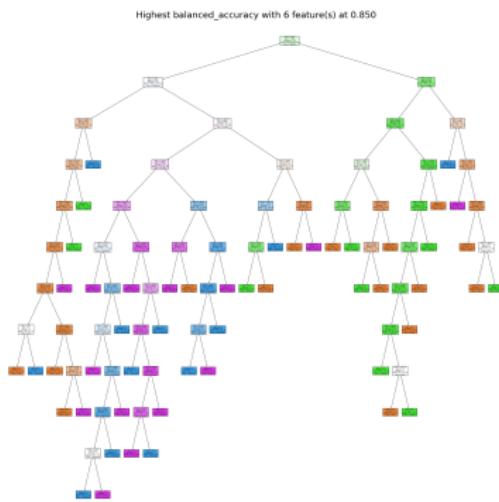
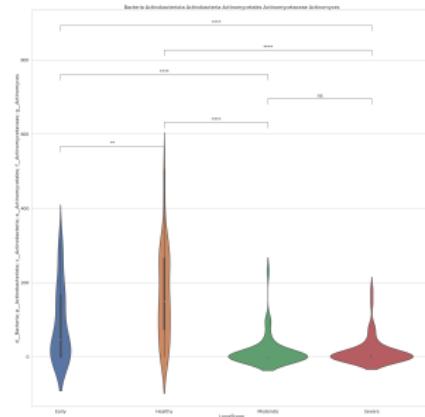
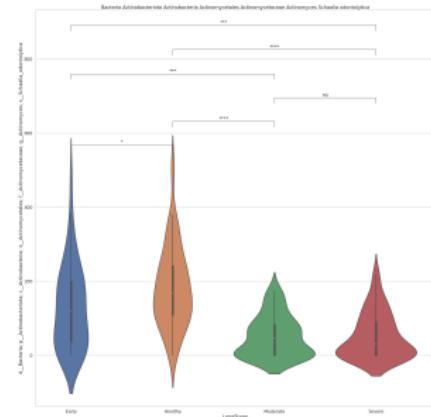


Figure: Random Forest Tree Plot

Random Forest Classifier V



(a) *Actinomyces*



(b) *Actinomyces Schaalia-odontolytica*

Figure: Violin Plot by Features

Random Forest Classifier – Merge (Healthy+Early) I

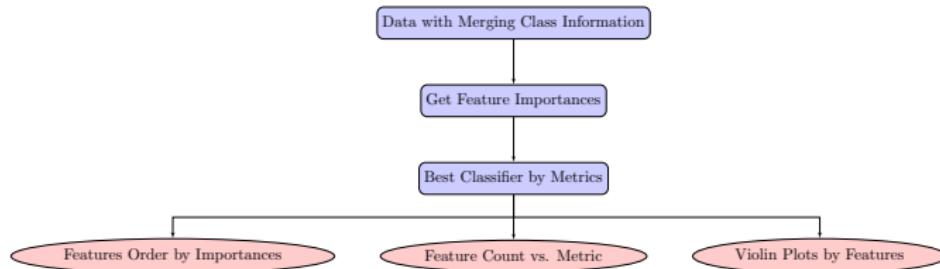


Figure: Random Forest Classifier with Merging Workflow

DADA2 + GG gives the best result with balanced accuracy.

Random Forest Classifier – Merge (Healthy+Early) II

Table: Features Order by Importances

Order	Taxonomy (Genus [Species])
0	<i>Actinomyces</i>
1	<i>Filifactor</i>
2	<i>Prevotella intermedia</i>

Random Forest Classifier – Merge (Healthy+Early) III

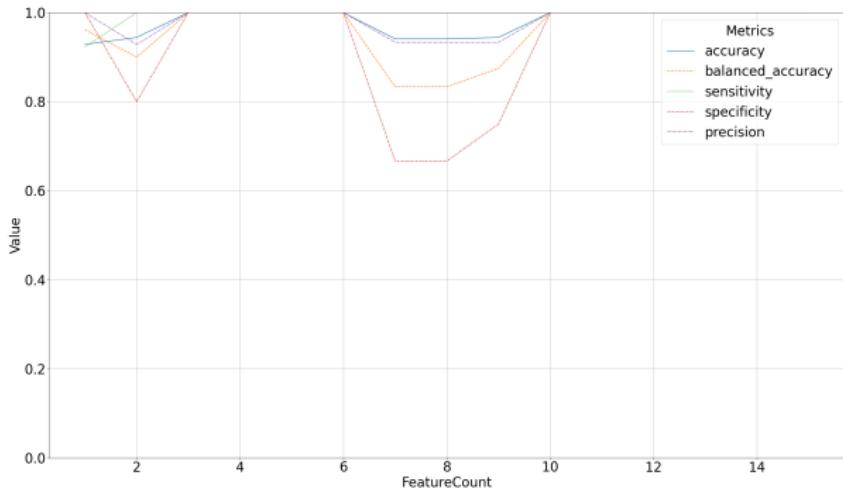


Figure: Metrics by Feature Count

Random Forest Classifier – Merge (Healthy+Early) IV

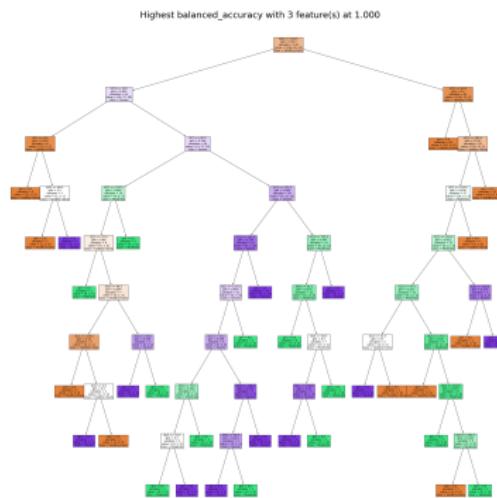
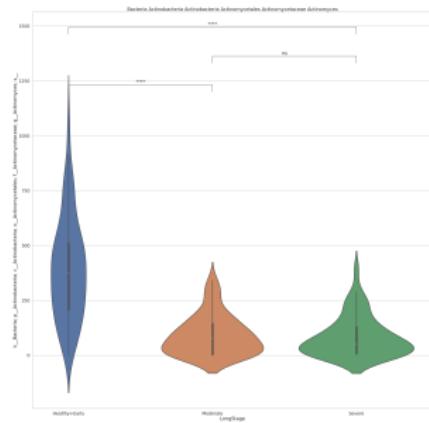
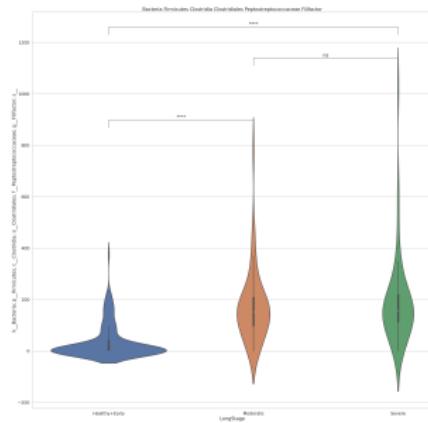


Figure: Random Forest Tree Plot

Random Forest Classifier – Merge (Healthy+Early) V



(a) *Actinomyces*



(b) *Filifactor*

Figure: Violin Plot by Features

Random Forest Classifier – Merge (Moderate + Severe) I

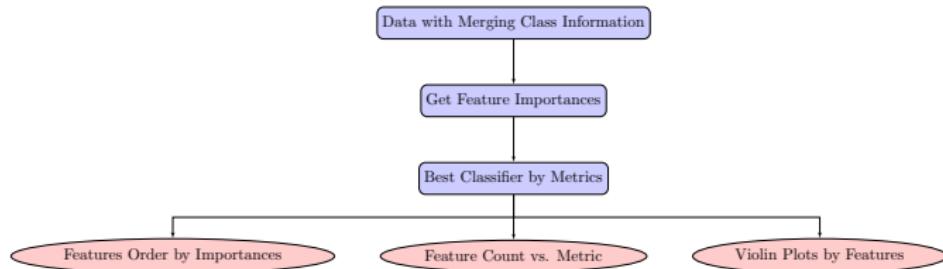


Figure: Random Forest Classifier with Merging Workflow

DADA2 + GG gives the best result with balanced accuracy.

Random Forest Classifier – Merge (Moderate + Severe) II

Table: Features Order by Importances

Order	Taxonomy (Genus [Species])
0	<i>Actinomyces</i>
1	<i>Filifactor</i>
2	<i>Prevotella intermedia</i>

Random Forest Classifier – Merge (Moderate + Severe) III

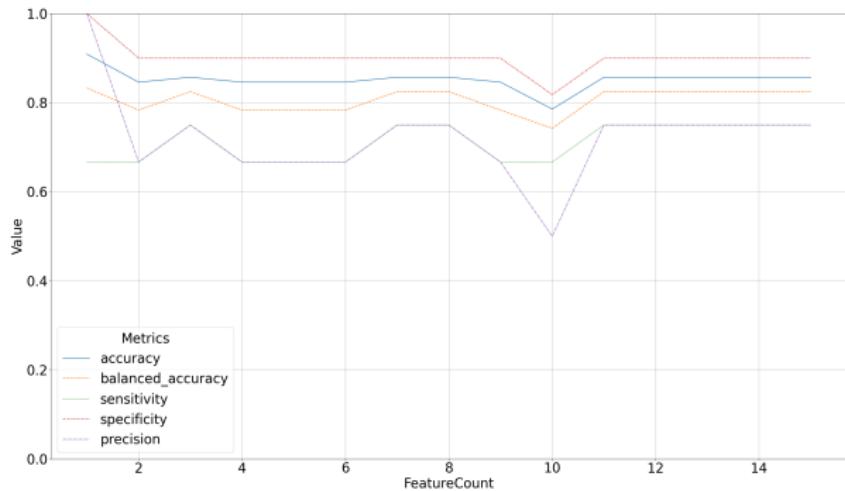


Figure: Metrics by Feature Count

Random Forest Classifier – Merge (Moderate + Severe) IV

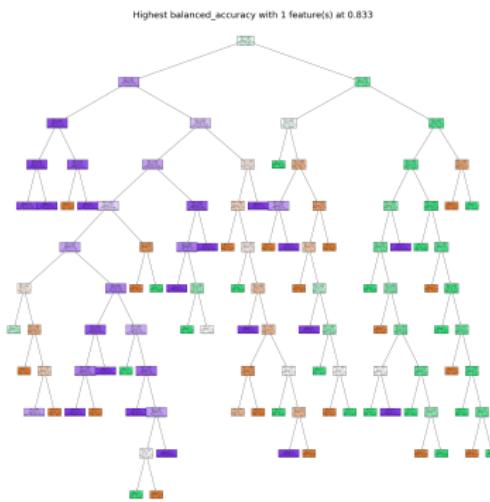
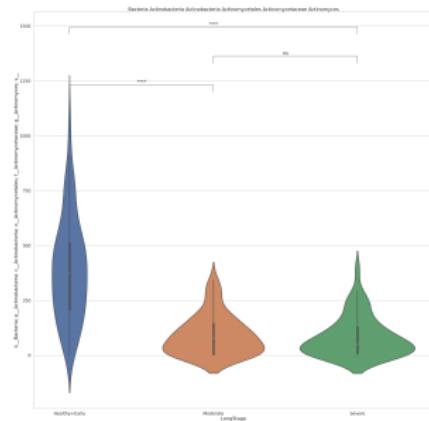
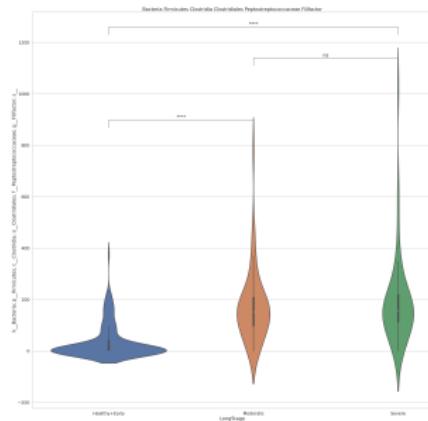


Figure: Random Forest Tree Plot

Random Forest Classifier – Merge (Moderate + Severe) V



(a) *Actinomyces*



(b) *Filifactor*

Figure: Violin Plot by Features

Discussion

Actinomyces Genus

- *Actinomyces*: a deceptive infection of oral cavity (Thukral, Srivastav, Mathur, Barodiya, & Srivastav, 2017)
- Prevalence of *Actinomyces* spp. in patients with chronic periodontitis (Vielkind, Jentsch, Eschrich, Rodloff, & Stingu, 2015)

Filifactor Genus

- *Filifactor alocis* – a new emerging periodontal pathogen (Aruni et al., 2015)
- *In Situ* Anabolic Activity of Periodontal Pathogens *Porphyromonas gingivalis* and *Filifactor alocis* in Chronic Periodontitis (Spooner et al., 2016)

References I

- 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).
- Aruni, A. W., Mishra, A., Dou, Y., Chioma, O., Hamilton, B. N., & Fletcher, H. M. (2015). Filifactor alocis—a new emerging periodontal pathogen. *Microbes and Infection*, 17(7), 517–530.
- 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.

References II

- 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.
- Flemmig, T. F. (1999). Periodontitis. *Annals of Periodontology*, 4(1), 32–37.

References III

- Gihawi, A., Rallapalli, G., Hurst, R., Cooper, C. S., Leggett, R. M., & Brewer, D. S. (2019). Sepath: benchmarking the search for pathogens in human tissue whole genome sequence data leads to template pipelines. *Genome biology*, 20(1), 1–15.
- Gill, S. R., Pop, M., DeBoy, R. T., Eckburg, P. B., Turnbaugh, P. J., Samuel, B. S., ... Nelson, K. E. (2006). Metagenomic analysis of the human distal gut microbiome. *science*, 312(5778), 1355–1359.
- Hunter, J. D. (2007). Matplotlib: A 2d graphics environment. *Computing in science & engineering*, 9(3), 90–95.
- James, F. C., & Rathbun, S. (1981). Rarefaction, relative abundance, and diversity of avian communities. *The Auk*, 98(4), 785–800.
- Maaten, L. v. d., & Hinton, G. (2008). Visualizing data using t-sne. *Journal of machine learning research*, 9(Nov), 2579–2605.

References IV

- 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).
- Olsen, G. J., & Woese, C. R. (1993). Ribosomal rna: a key to phylogeny. *The FASEB journal*, 7(1), 113–123.
- 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.

References V

- 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.
- Spooner, R., Weigel, K. M., Harrison, P. L., Lee, K., Cangelosi, G. A., & Yilmaz, Ö. (2016). In situ anabolic activity of periodontal pathogens *porphyromonas gingivalis* and *filifactor alocis* in chronic periodontitis. *Scientific reports*, 6(1), 1–8.
- Thukral, R., Srivastav, K., Mathur, V., Barodiya, A., & Srivastav, S. (2017). Actinomyces: a deceptive infection of oral cavity. *Journal of the Korean Association of Oral and Maxillofacial Surgeons*, 43(4), 282–285.
- Turnbaugh, P. J., Ley, R. E., Hamady, M., Fraser-Liggett, C. M., Knight, R., & Gordon, J. I. (2007). The human microbiome project. *Nature*, 449(7164), 804–810.

References VI

- Van Dyke, T. E., & Dave, S. (2005). Risk factors for periodontitis. *Journal of the International Academy of Periodontology*, 7(1), 3.
- Vielkind, P., Jentsch, H., Eschrich, K., Rodloff, A. C., & Stingu, C.-S. (2015). Prevalence of actinomyces spp. in patients with chronic periodontitis. *International Journal of Medical Microbiology*, 305(7), 682–688.
- 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
- Weiss, S., Xu, Z. Z., Peddada, S., Amir, A., Bittinger, K., Gonzalez, A., ... others (2017). Normalization and microbial differential abundance strategies depend upon data characteristics. *Microbiome*, 5(1), 27.