

Periodontitis

Seunghoon Kim Jaewoong Lee Semin Lee

Ulsan National Institute of Science and Technology

jwlee230@unist.ac.kr

2021-03-09

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)

- Clinical Attachment Loss & 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

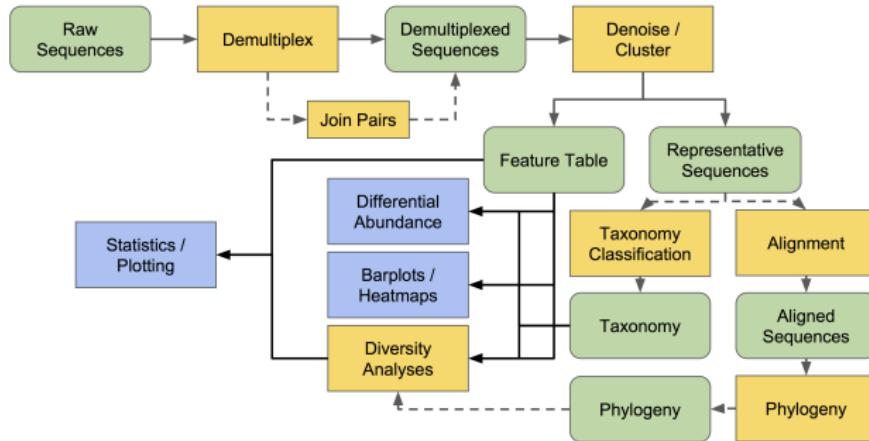


Figure: QIIME2 Workflow (Bolyen et al., 2019, 2018)

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)
- Human Oral Microbiome Database (HOMD) (Chen et al., 2010)

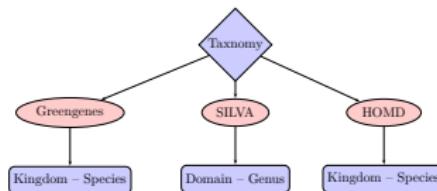


Figure: Taxonomy Classification

"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.

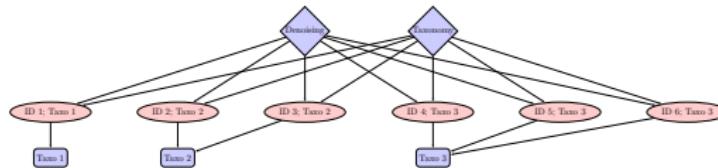


Figure: Example Diagram for Merging Denosing and Taxonomy Classification

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**

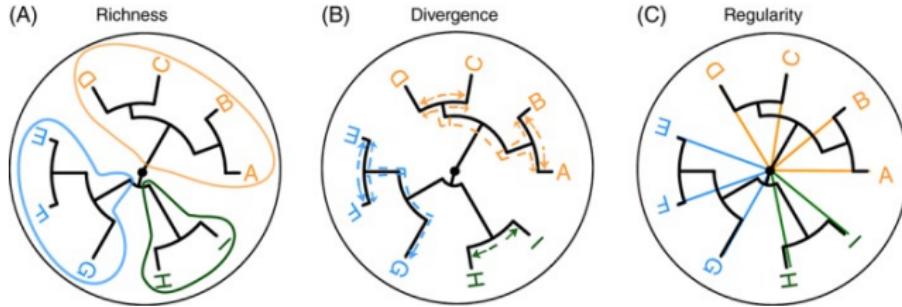


Figure: Three Dimensions of Phylogenetic Information (Tucker et al., 2017)

Alpha-diversity

- Evenness: a measurement of diversity in different type at community (Pielou, 1966)
- Faith's Phylogenetic Diversity: a qualitative measurement of community richness which prioritizes species conservation, incorporates with taxic diversity (Faith, 1992)
- Observed Features: a number of observed taxa
- Shannon's diversity index: a significant aspect of community richness (Shannon, 1948)

Beta-diversity

- Bray-Curtis distance: a quantitative measurement of dissimilarity among communities (Sørensen, 1948)
- Jaccard distance: a measurement of local distribution among communities (Jaccard, 1912)
- Unweighted UniFrac distance: a qualitative measurement of phylogenetic distances (McDonald et al., 2018)
- Weighted UniFrac distance: a quantitative measurement of phylogenetic distances (McDonald et al., 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)

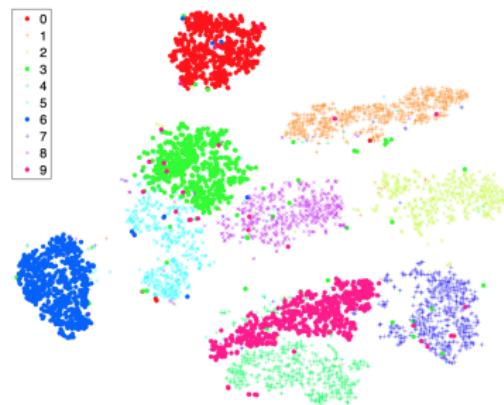


Figure: Visualization by t-SNE (Maaten & Hinton, 2008)

Classification I

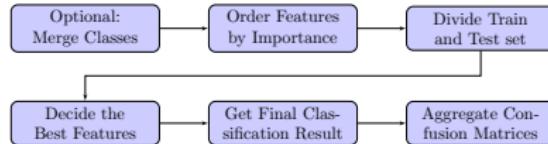


Figure: Workflow of Classification

Classification Metrics:

- Accuracy
- Balanced Accuracy
- Sensitivity
- Specificity
- Precision

Classification II

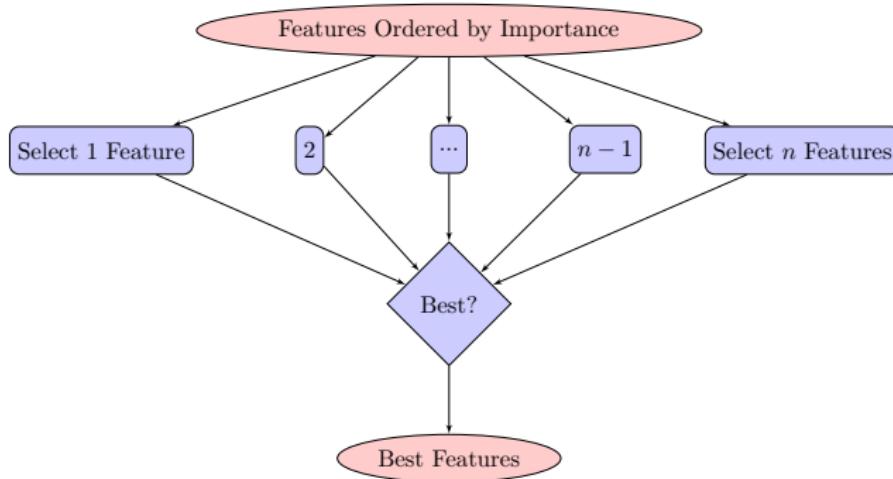
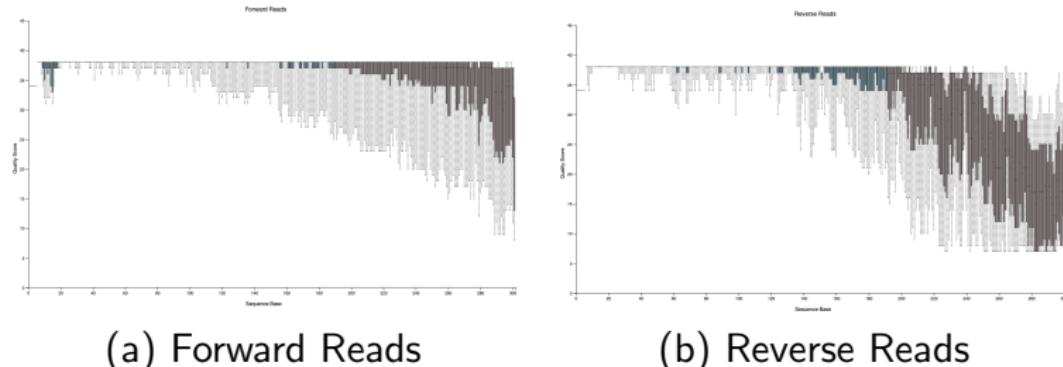


Figure: Deciding the Best Features

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

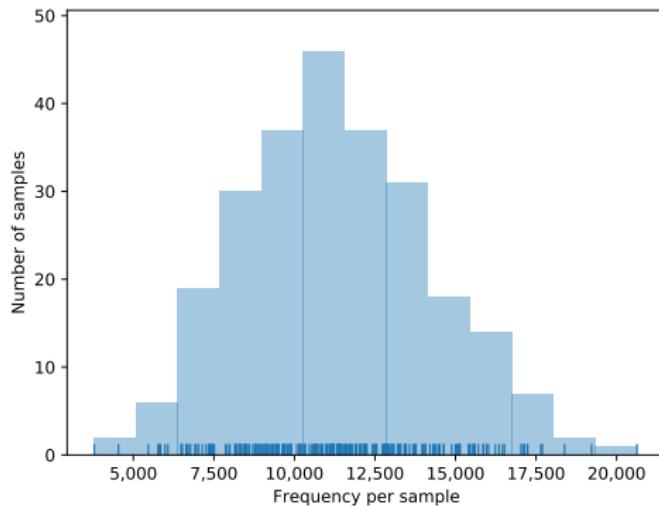
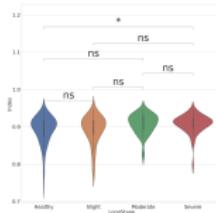


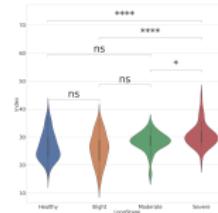
Figure: Frequency per sample

∴ p-sampling-depth $n_{DADA2} = 3786$.

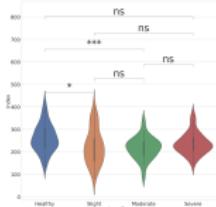
Alpha-diversity



(a) Evenness ($p < 0.01$)



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



(c) Observed features ($p < 10^{-3}$) (d) Shannon's diversity ($p > 0.05$)

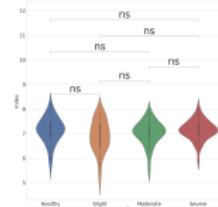
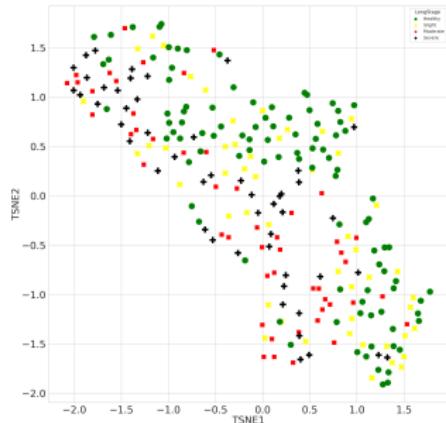
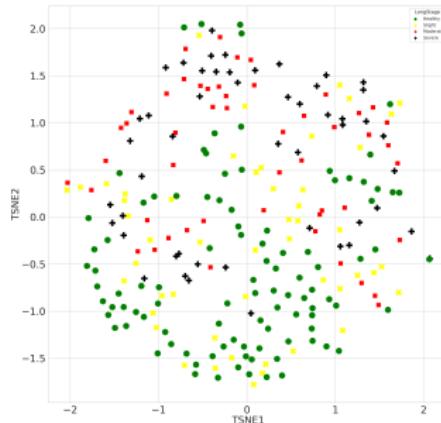


Figure: Alpha Diversity from DADA2 with Kruskal-Wallis among All Groups

Beta-diversity I



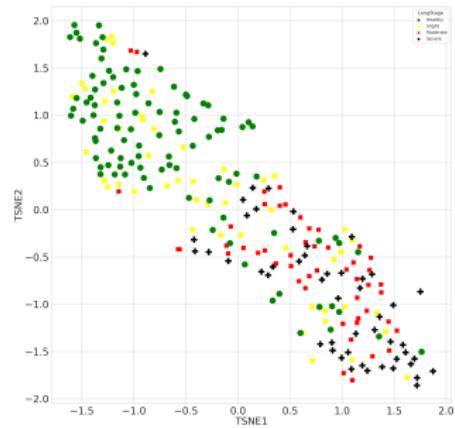
(a) Bray-Curtis



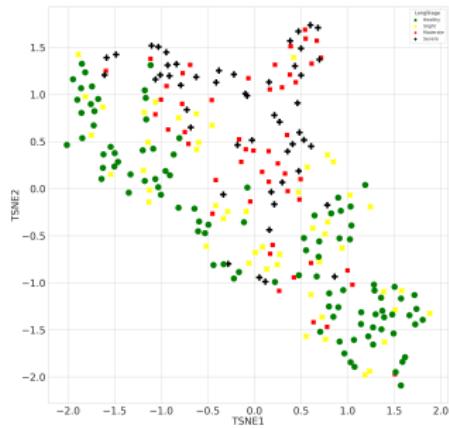
(b) Jaccard

Figure: Beta-diversity with DADA2

Beta-diversity II



(a) Unweighted UniFrac



(b) Weighted UniFrac

Figure: Beta-diversity with DADA2

ANCOM

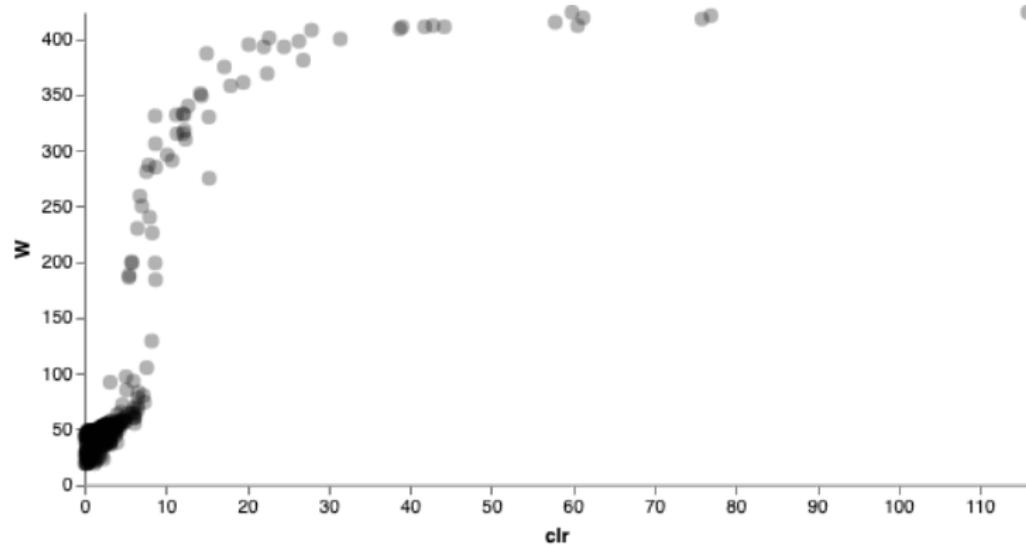


Figure: ANCOM Volcano Plot with DADA2 & HOMD

t-SNE with Whole Microbiome

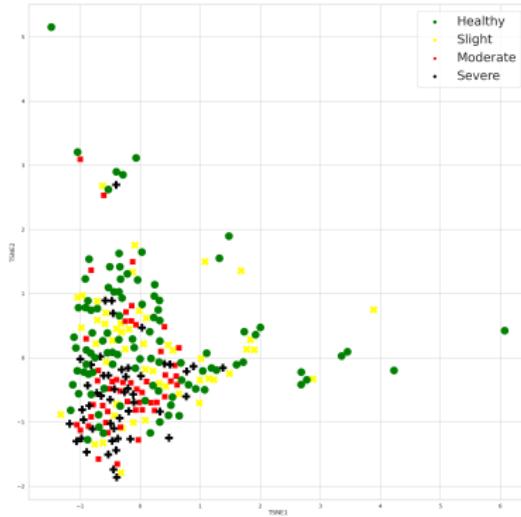


Figure: t-SNE Plot with Whole Microbiome from DADA2 & HOMD

t-SNE with ANCOM Selected

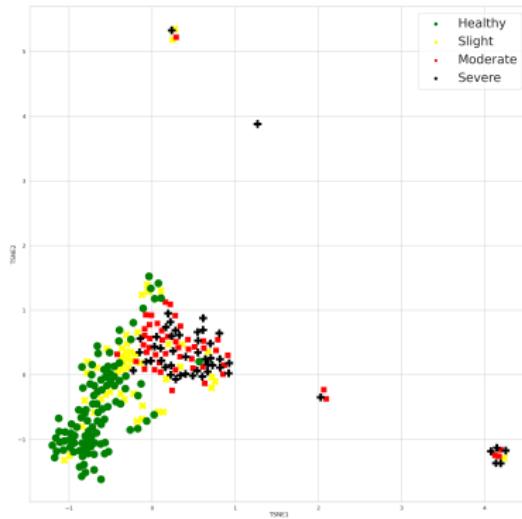


Figure: t-SNE Plot with ANCOM Selected from DADA2 & HOMD

Random Forest Classifier with Every Class I

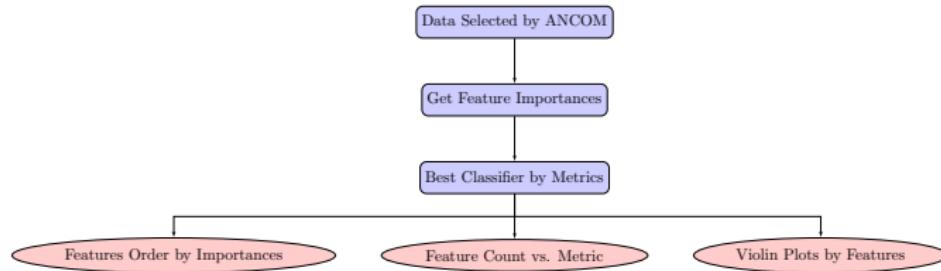


Figure: Random Forest Classifier Workflow

The best result is at **0.765** with 9 features.

Random Forest Classifier with Every Class II

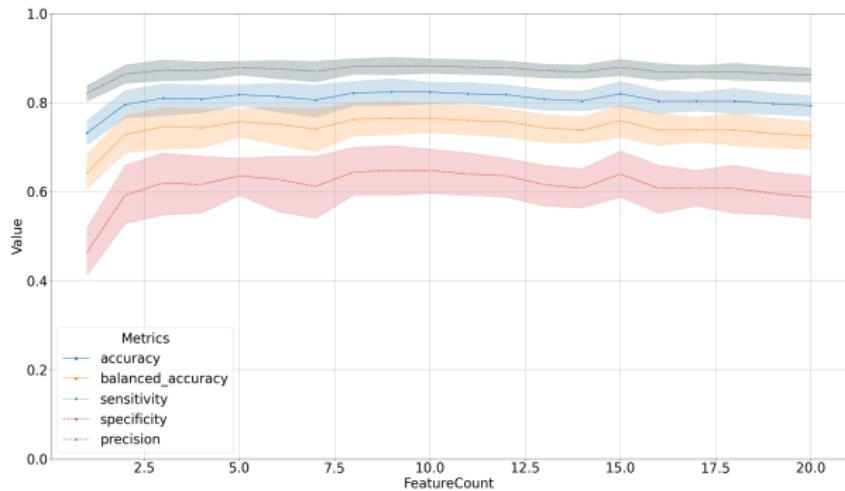
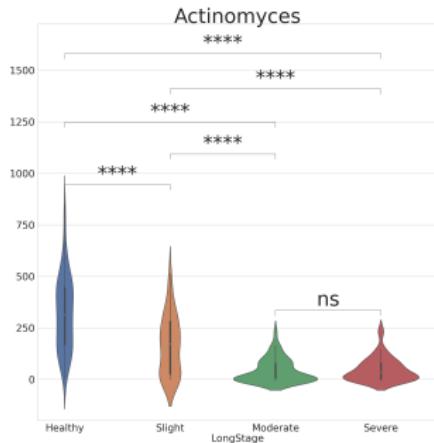
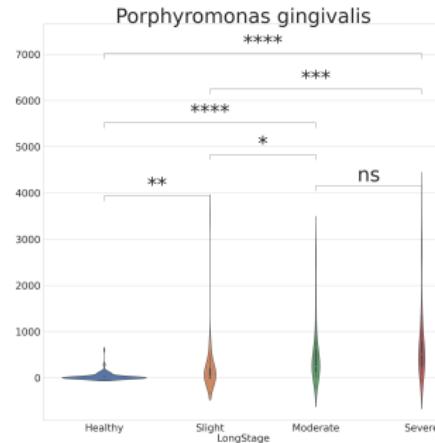


Figure: Metrics by Feature Count

Random Forest Classifier with Every Class III



(a) *Actinomyces*



(b) *Porphyromonas gingivalis*

Figure: Most Important Two Features

Random Forest Classifier with (M+S) Classes I

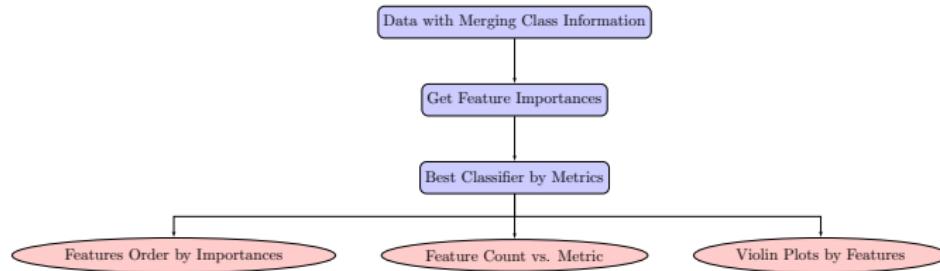


Figure: Random Forest Classifier Workflow

The best result is at **0.841** with 10 features.

Random Forest Classifier with (M+S) Classes II

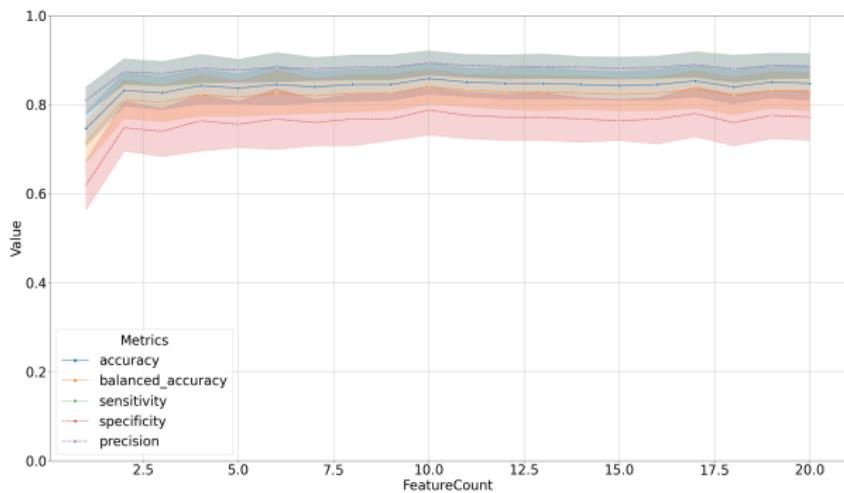
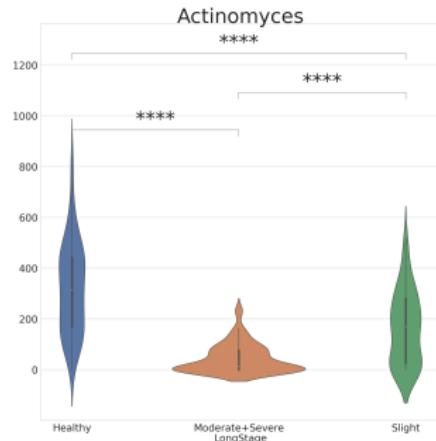
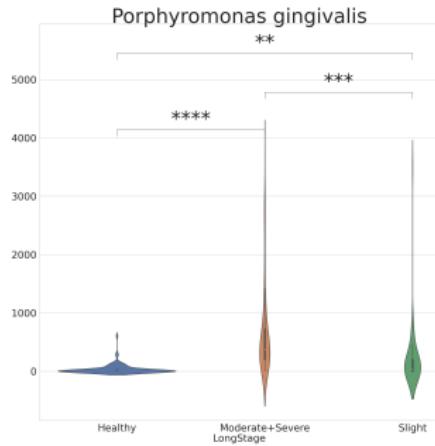


Figure: Metrics by Feature Count

Random Forest Classifier with (M+S) Classes III



(a) *Actinomyces*



(b) *Porphyromonas gingivalis*

Figure: Most Important Two Features

Random Forest Classifier with (H & E) Classes I

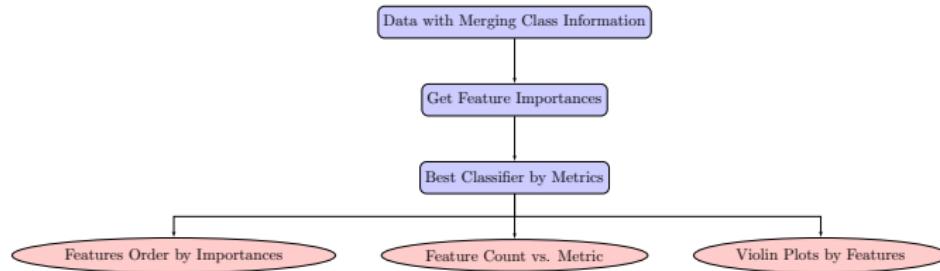


Figure: Random Forest Classifier Workflow

The best result is at **0.768** with 4 features.

Random Forest Classifier with (H & E) Classes II

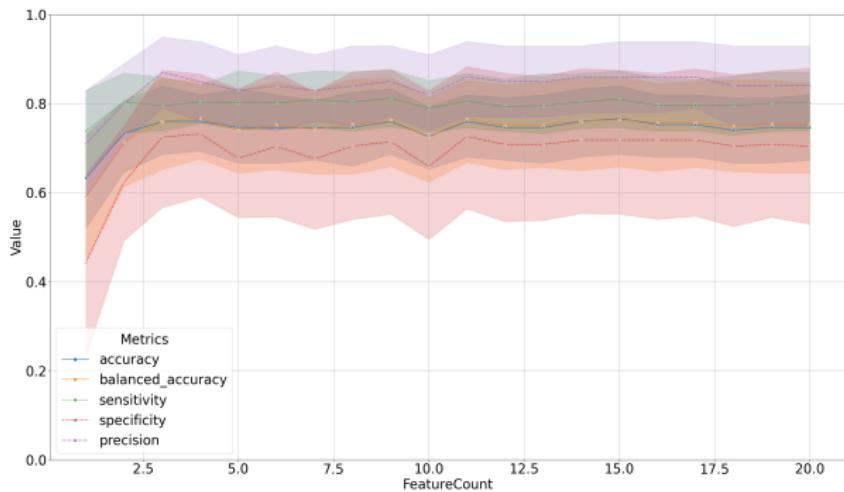
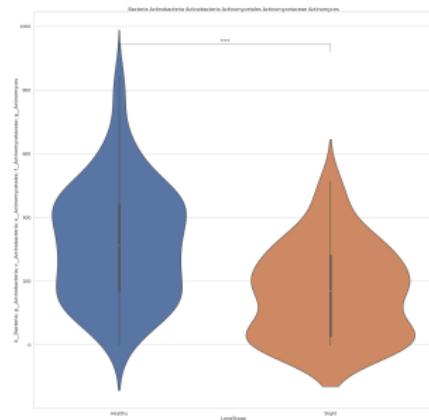
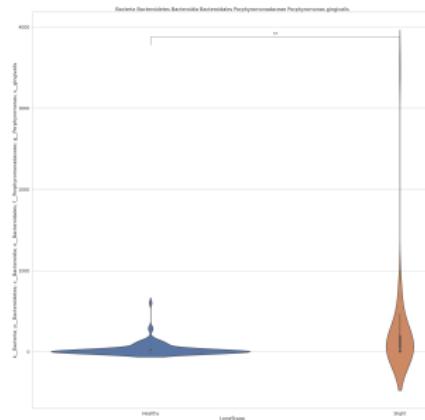


Figure: Metrics by Feature Count

Random Forest Classifier with (H & E) Classes III



(a) *Actinomyces*



(b) *Porphyromonas gingivalis*

Figure: Most Important Two Features

2D plot with Act. & Pg.

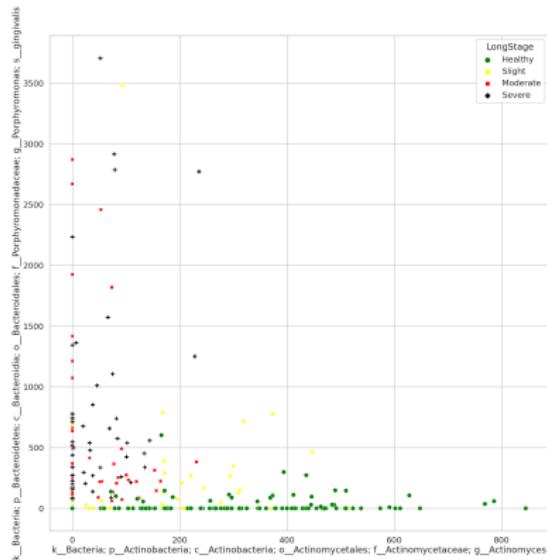


Figure: 2D Plot with Act. & Pg.

Discussion

Actinomyces Genus

Porphyromonas gingivalis

Actinomyces graevenitzii

Filifactor alocis

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).
- 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.

References II

- 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.
- Chen, T., Yu, W.-H., Izard, J., Baranova, O. V., Lakshmanan, A., & Dewhirst, F. E. (2010). The human oral microbiome database: a web accessible resource for investigating oral microbe taxonomic and genomic information. *Database*, 2010.
- 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.
- Faith, D. P. (1992). Conservation evaluation and phylogenetic diversity. *Biological conservation*, 61(1), 1–10.

References III

- Flemmig, T. F. (1999). Periodontitis. *Annals of Periodontology*, 4(1), 32–37.
- 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.
- Jaccard, P. (1912). The distribution of the flora in the alpine zone. 1. *New phytologist*, 11(2), 37–50.
- James, F. C., & Rathbun, S. (1981). Rarefaction, relative abundance, and diversity of avian communities. *The Auk*, 98(4), 785–800.

References IV

- Maaten, L. v. d., & Hinton, G. (2008). Visualizing data using t-sne. *Journal of machine learning research*, 9(Nov), 2579–2605.
- 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.
- McDonald, D., Vázquez-Baeza, Y., Koslicki, D., McClelland, J., Reeve, N., Xu, Z., ... Knight, R. (2018). Striped unifrac: enabling microbiome analysis at unprecedented scale. *Nature methods*, 15(11), 847–848.
- 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.

References V

- 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.
- Pielou, E. C. (1966). The measurement of diversity in different types of biological collections. *Journal of theoretical biology*, 13, 131–144.
- 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.
- Shannon, C. E. (1948). A mathematical theory of communication. *The Bell system technical journal*, 27(3), 379–423.
- Sørensen, T. (1948). A method of establishing groups of equal amplitude in plant sociology based on similarity of species and its application to analyses of the vegetation on danish commons. *Biol. Skr.*, 5, 1–34.

References VI

- Tucker, C. M., Cadotte, M. W., Carvalho, S. B., Davies, T. J., Ferrier, S., Fritz, S. A., ... others (2017). A guide to phylogenetic metrics for conservation, community ecology and macroecology. *Biological Reviews*, 92(2), 698–715.
- 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.
- Van Dyke, T. E., & Dave, S. (2005). Risk factors for periodontitis. *Journal of the International Academy of Periodontology*, 7(1), 3.
- 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

References VII

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.