

Microbiome Premature

Jaewoong Lee Semin Lee

Ulsan National Institute of Science and Technology

jwlee230@unist.ac.kr

2021-03-31

Overview

- 1 Introduction
- 2 Materials
- 3 Literature Survey
- 4 Methods
- 5 Results
- 6 Proceedings
References

Introduction

Microbiome

- Microbiota: the microorganisms which live inside & on humans (Turnbaugh et al., 2007)
- Microbiome: 10^{13} to 10^{14} microorganisms whose which collective genome (Gill et al., 2006)

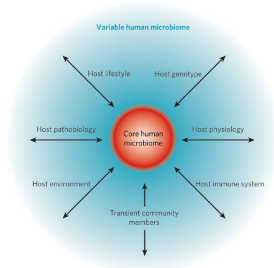


Figure: Concept of a core human microbiome (Turnbaugh et al., 2007)

- Ribosomal RNA
- Well-known as a key to phylogeny (Olsen & Woese, 1993)

Premature (Preterm Birth)

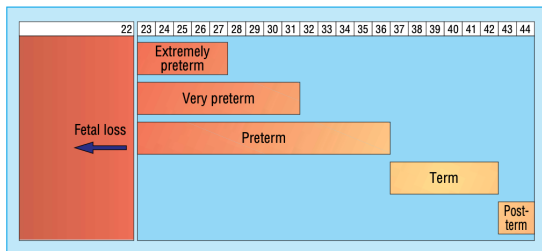


Figure: Definitions of Premature (Tucker & McGuire, 2004)

∴ Hence, in this study,

- Premature: < 37 weeks
- Normal: ≥ 37 weeks

Materials

16S rRNA Sequencing

16S rRNA sequencing is the *reference method* for bacterial taxonomy & identification (Mignard & Flandrois, 2006)

Reasons (Janda & Abbott, 2007):

- 16S rRNA exists in almost all bacteria
- Functions of the 16S rRNA has not changed over time
- 16S rRNA is large enough for bioinformatics

Train/Test Data vs. Validate Data

- Train/Test data
 - Helixco: Data collected by Helixco
- Validate data
 - EBI (European Bioinformatics Institute): Data collected by Dominguez-Bello et al., 2016
 - HMP (Human Microbiome Project): Data collected by Fettweis et al., 2019

Table: Metadata of Data

| Data | Participants | Samples | Remarks |
|---------|--------------|---------|----------------|
| Helixco | 24 | 107 | - |
| EBI | 18 | 1016 | Only Normal |
| HMP | 1572 | 9205 | Only Premature |

Literature Survey

BRIEF COMMUNICATIONS

nature.
medicine

Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer

Maria G Dominguez-Bello^{1,2}, Kassandra M De Jesus-Laboy², Nan Shen³, Laura M Cox¹, Amnon Amir⁴, Antonio Gonzalez⁴, Nicholas A Bokulich¹, Se Jin Song^{4,5}, Marina Hoashi^{1,6}, Juana I Rivera-Vinas⁷, Keimari Mendez⁷, Rob Knight^{4,8} & Jose C Clemente^{3,9}

estimated 15% of births that require C-section delivery to protect the health of the mother or baby¹¹.

Here we **exposed C-section-delivered infants to their maternal vaginal fluids** at birth and longitudinally **determined the composition of their microbiota** to assess whether it **developed more similarly to vaginally born babies** than to unexposed C-section-delivered infants. We collected samples from 18 infants and their mothers, including 7 born vaginally and 11 delivered by scheduled C-section, of which four were exposed to the maternal vaginal fluids at birth (**Supplementary Table 1**). Briefly, the **microbial restoration procedure**, or vaginal microbial transfer, consists of incubating sterile gauze in the vagina of moth-

- Study Objectives
 - ① Compare Vaginally vs. Cesarean-section (C-section)
 - ② Restore the microbiota of C-section
- Microbial restoration procedure
 - ① Measure maternal vaginal pH
 - ② Put sterile gauze with saline solution in vagina for 1 hour
 - ③ Swab the infant with the gauze
- Sample collection procedure
 - ① Sample at right after birth, day 3 and weekly for the first month
 - ② Sample from oral, forehead, arm, foot and anal
- Notable Methods/Results
 - ① Using distance methods: e.g. UniFrac distance, Hamming distance

ARTICLES

<https://doi.org/10.1038/s41591-019-0450-2>

nature
medicine

OPEN

The vaginal microbiome and preterm birth

Jennifer M. Fettweis^{1,2,3}, Myrna G. Serrano^{1,3}, J. Paul Brooks^{3,4}, David J. Edwards^{3,5},
Philippe H. Girerd^{2,3}, Hardik I. Parikh¹, Bernice Huang¹, Tom J. Arodz^{3,6}, Laahirie Edupuganti^{1,3},
Abigail L. Glascock⁷, Jie Xu^{3,8,9}, Nicole R. Jimenez^{1,3}, Stephany C. Vivadellj^{1,3}, Stephen S. Fong^{3,10},
Nihar U. Sheth¹¹, Sophonie Jean¹, Vladimir Lee^{1,3}, Yahya A. Bokhari⁶, Ana M. Lara¹, Shreni D. Mistry¹,
Robert A. Duckworth III¹, Steven P. Bradley¹, Vishal N. Koparde¹¹, X. Valentine Orendo¹¹,
Sarah H. Milton², Sarah K. Rozycki¹², Andrey V. Matveyev¹, Michelle L. Wright^{13,14,15},
Snehalata V. Huzurbazar¹⁶, Eugenie M. Jackson¹⁶, Ekaterina Smirnova^{17,18}, Jonas Korfach¹⁹,
Yu-Chih Tsai¹⁹, Molly R. Dickinson¹, Jamie L. Brooks¹, Jennifer I. Drake¹, Donald O. Chaffin²⁰,
Amber L. Sexton²⁰, Michael G. Gravett^{20,21}, Craig E. Rubens²⁰, N. Romesh Wijesooriya⁹,
Karen D. Hendricks-Muñoz^{3,8,9}, Kimberly K. Jefferson^{1,3}, Jerome F. Strauss III^{2,3} and Gregory A. Buck^{1,3,6*}

HMP Data (Fettweis et al., 2019) II

- Study Objectives
 - ① Predicting & Preventing premature
 - ② Report community resources
 - ③ Provide an analysis of the longitudinal, comprehensive, multi-omic profiling of vaginal samples
- Sample collection Procedure
 - ① Premature birth vs. Matched normal birth
 - ② Ethnically diverse cohort
- Notable Methods/Results
 - ① Imitate figures

HMP Data (Fettweis et al., 2019) III

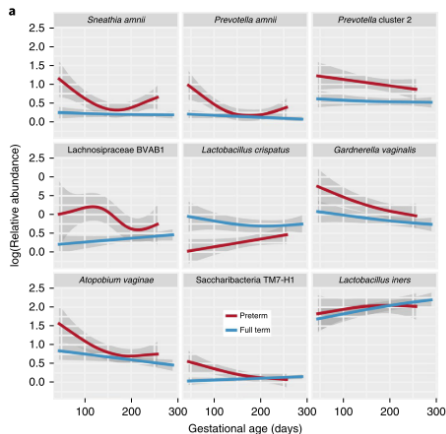


Figure: Microbiome Composition during Pregnancy

Methods

Qiime 2 Workflow

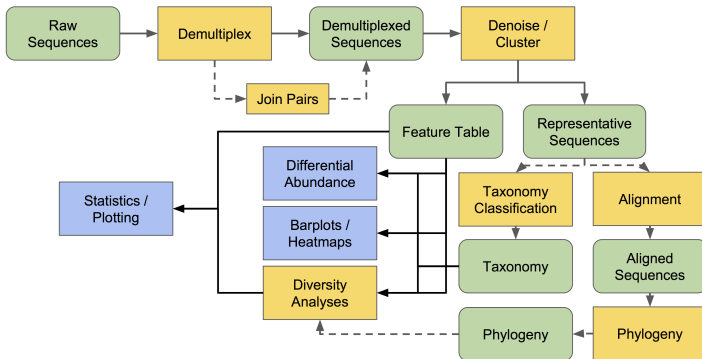


Figure: QIIME 2 workflow (Bolyen et al., 2019; Mandal et al., 2015; McDonald et al., 2012)

Filtering with Quality Score I

Drawback between:

- Longer sequence read
- Higher quality value

∴ Select the maximum length n where:

$$\begin{aligned} \forall n_i \in \{n_k | \text{MedianQualityScore} \geq 30\} \\ \exists! n \in \{n_i\} : n \geq n_i \end{aligned} \quad (1)$$

Denoising Techniques

- DADA2: Amplicon Sequence Variants (ASVs) (Callahan et al., 2016)
- Deblur: Operational Taxonomic Units (OTUs) (Amir et al., 2017)

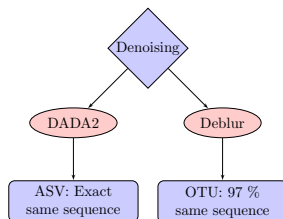


Figure: Denoising Algorithms

Taxonomy Classification

- Greengenes (GG) (DeSantis et al., 2006)
- SILVA (Pruesse et al., 2007; Quast et al., 2012)

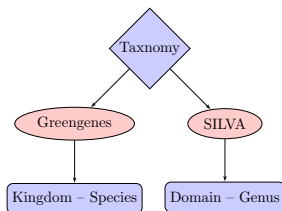


Figure: Taxonomy Classifications

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

Merging Denoising/Taxonomy

Merging multiple IDs (ASV or OTU) into one, which have

- Different IDs
- Identified as same taxonomy

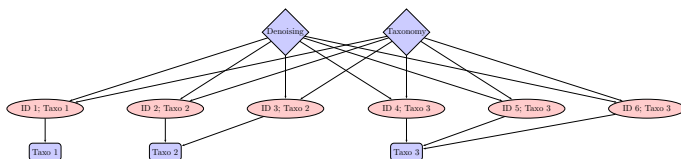


Figure: Example Diagram for Merging Denoising/Taxonomy



Figure: Mothur

Note: Still in progress

t-distributed Stochastic Neighbor Embedding (t-SNE)

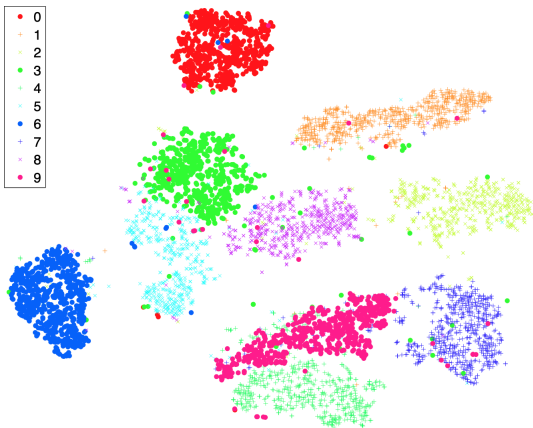
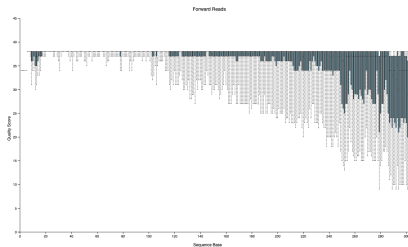


Figure: t-SNE with handwritten data (Maaten & Hinton, 2008)

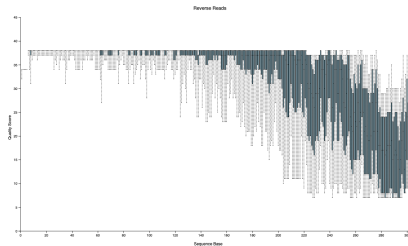
- Pandas (McKinney et al., 2011)
- Scikit-Learn (Pedregosa et al., 2011)
- SciPy (Virtanen et al., 2020)
- Matplotlib (Hunter, 2007)
- Seaborn (Waskom et al., 2020)

Results

Filtering with Quality Score I



(a) Forward



(b) Reverse

Figure: Sequence Quality Plot from Helixco Data

Maximum Length: $n_{forward} = 300$, $n_{Reverse} = 265$

Filtering with Quality Score II

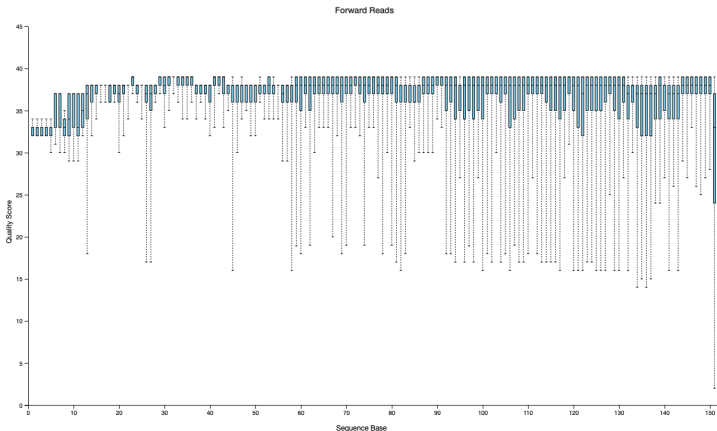
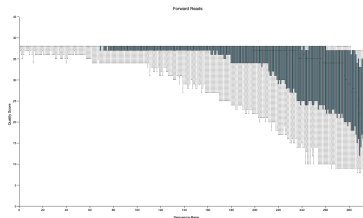


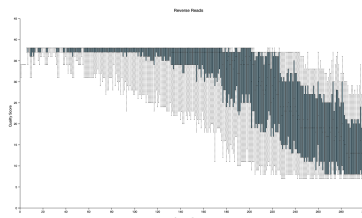
Figure: Sequence Quality Plot from EBI Data

Maximum Length: 150

Filtering with Quality Score III



(a) Forward

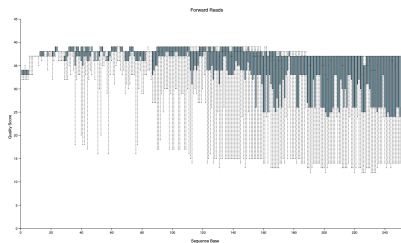


(b) Reverse

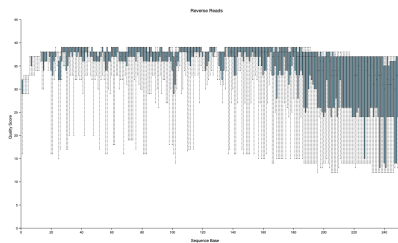
Figure: Sequence Quality Plot from HMP Data

Maximum Length: $n_{forward} = 278$, $n_{Reverse} = 226$

Filtering with Quality Score IV



(a) Forward



(b) Reverse

Figure: Sequence Quality Plot from Stool Data

Maximum Length: $n_{forward} = 250$, $n_{Reverse} = 251$

t-SNE for Comparing Databases I

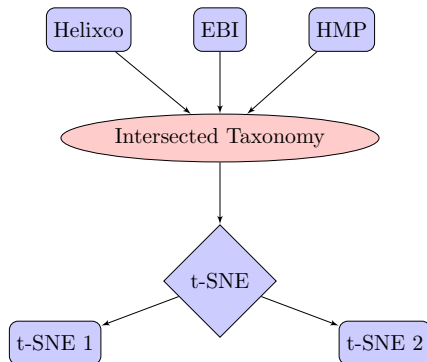


Figure: Workflow of t-SNE for Brief Information

t-SNE for Comparing Databases II



(a) DADA2 + GG



(b) DADA2 + SILVA



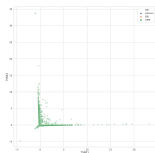
(c) Deblur + GG



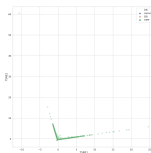
(d) Deblur + SILVA

Figure: Intersected Taxa Information

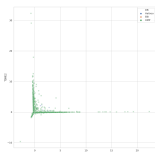
t-SNE for Comparing Databases III



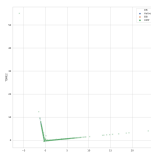
(a) DADA2 + GG



(b) DADA2 + SILVA



(c) Deblur + GG



(d) Deblur + SILVA

Figure: t-SNE for Brief Information

t-SNE with Site/Premature Information I

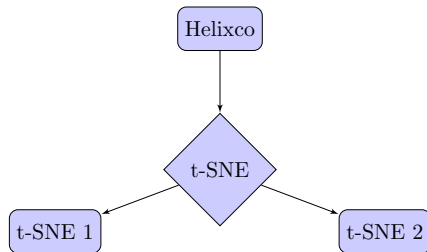
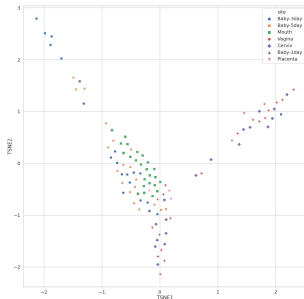
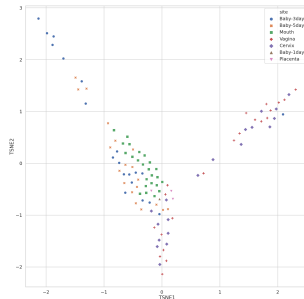


Figure: Workflow of t-SNE for Site/Premature Information

t-SNE with Site/Premature Information II



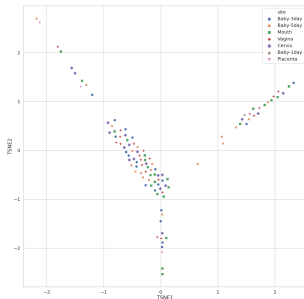
(a) DADA2 + GG



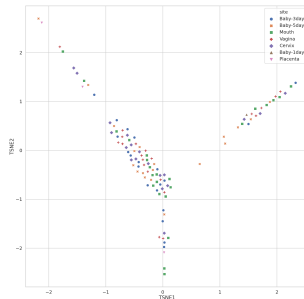
(b) DADA2 + SILVA

Figure: t-SNE with Site

t-SNE with Site/Premature Information III



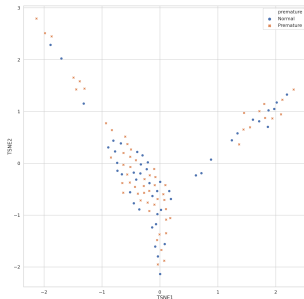
(c) Deblur + GG



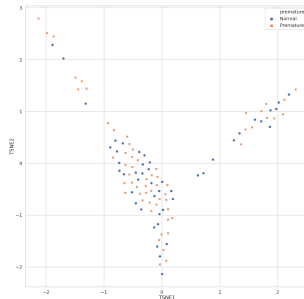
(d) Deblur + SILVA

Figure: t-SNE with Site

t-SNE with Site/Premature Information IV



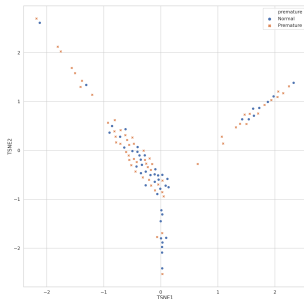
(a) DADA2 + GG



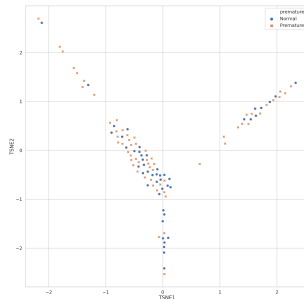
(b) DADA2 + SILVA

Figure: t-SNE with Site + Premature

t-SNE with Site/Premature Information V



(c) Deblur + GG



(d) Deblur + SILVA

Figure: t-SNE with Site + Premature

Bacterial Abundance I

Alpha-Diversity I

Beta-Diversity I

Classification I

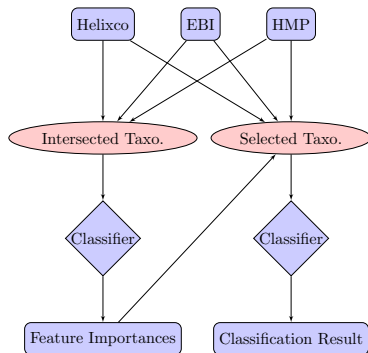


Figure: Workflow with Classification

Random Forest Classifier I

Input Data was treated with **Deblur** and **SILVA**.

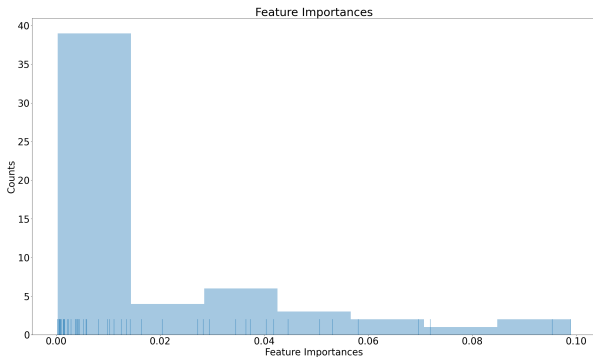


Figure: Feature Importance derived by Random Forest Classifier

Random Forest Classifier II

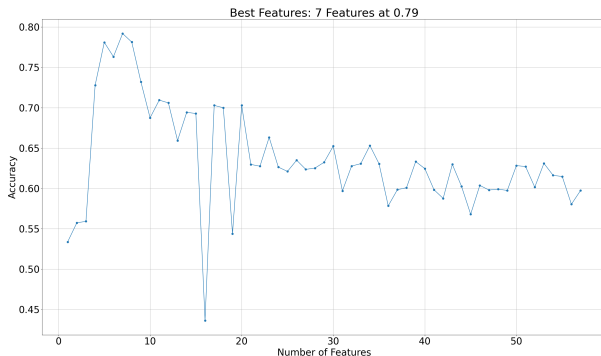


Figure: Number of Features vs. Accuracy

Random Forest Classifier III

- ① *Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Lactobacillus Lactobacillus iners*
- ② *Bacteria Fusobacteriota Fusobacteriia Fusobacteriales Leptotrichiaceae Leptotrichia*
- ③ *Bacteria Actinobacteriota Actinobacteria*
- ④ *Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Lactobacillus*
- ⑤ *Bacteria Firmicutes Clostridia Peptostreptococcales-Tissierellales Peptostreptococcaceae Romboutsia*
- ⑥ *Bacteria Firmicutes Bacilli Mycoplasmatales Mycoplasmataceae Ureaplasma*
- ⑦ *Bacteria Actinobacteriota Actinobacteria Corynebacteriales Corynebacteriaceae Corynebacterium Corynebacterium matruchotii*

Random Forest Classifier IV

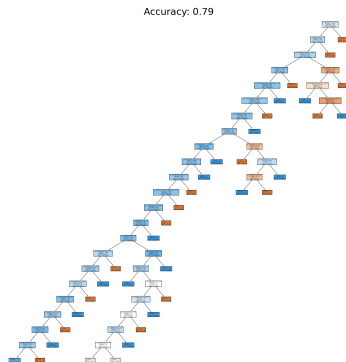
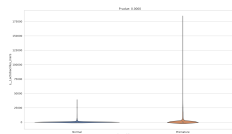
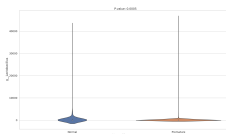


Figure: Random Forest Classifier

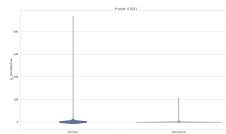
Random Forest Classifier V



(a) *Lactobacillus iners*



(b) *Lactobacillus*



(c) *Romboutsia*

Figure: Violin Plot of Taxonomy

- a *Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Lactobacillus Lactobacillus iners*
- b *Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Lactobacillus*
- c *Bacteria Firmicutes Clostridia Peptostreptococcales-Tissierellales Peptostreptococcaceae Romboutsia*

Lactobacillus (Lb.)

- Vaginal *Lb.* may be clinically useful tools at PTB under 33 weeks. (Usui et al., 2002)
- Presence of *Lb.* sp (odds ratio 0.2) was negatively associated. (MARTIUS et al., 1988)
- *Lb. crispatus/gasseri* could decrease the risk of PTB. (Stafford et al., 2017)
- *Lb.* were associated with decreased risk of PTB. (Tabatabaei et al., 2019)

Proceedings

- Add validation data
- t-SNE with databases
- Random Forest Classifier

Requirements

- Metadata for databases
- Mothur pipeline

Expectations

- Alpha-diversity
- Beta-diversity

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).
- Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., ... Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using qiime 2. *Nature Biotechnology*, 37(8), 852-857. Retrieved from <https://doi.org/10.1038/s41587-019-0209-9> doi: 10.1038/s41587-019-0209-9
- 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.
- Dominguez-Bello, M. G., De Jesus-Laboy, K. M., Shen, N., Cox, L. M., Amir, A., Gonzalez, A., ... others (2016). Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. *Nature medicine*, 22(3), 250.
- Fettweis, J. M., Serrano, M. G., Brooks, J. P., Edwards, D. J., Girerd, P. H., Parikh, H. I., ... others (2019). The vaginal microbiome and preterm birth. *Nature medicine*, 25(6), 1012–1021.

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.
- Janda, J. M., & Abbott, S. L. (2007). 16s rrna gene sequencing for bacterial identification in the diagnostic laboratory: pluses, perils, and pitfalls. *Journal of clinical microbiology*, 45(9), 2761–2764.
- 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. doi: 10.3402/mehd.v26.27663
- MARTIUS, J., KROHN, M. A., HILLIER, S. L., STAMM, W. E., HOLMES, K. K., & ESCHENBACH, D. A. (1988). Relationships of vaginal lactobacillus species, cervical chlamydia trachomatis, and bacterial vaginosis to preterm birth. *Obstetrics & Gynecology*, 71(1), 89–95.
- McDonald, D., Clemente, J. C., Kuczynski, J., Rideout, J. R., Stombaugh, J., Wendel, D., ... Caporaso, J. G. (2012). The biological observation matrix (biom) format or: how i learned to stop worrying and love the ome-ome. *GigaScience*, 1(1), 7. doi: 10.1186/2047-217X-1-7

- McKinney, W., et al. (2011). pandas: a foundational python library for data analysis and statistics. *Python for High Performance and Scientific Computing*, 14(9).
- Mignard, S., & Flandrois, J.-P. (2006). 16s rrna sequencing in routine bacterial identification: a 30-month experiment. *Journal of microbiological methods*, 67(3), 574–581.
- 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.
- 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.

- Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., ... Glöckner, F. O. (2012). The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. *Nucleic acids research*, 41(D1), D590–D596.
- Stafford, G. P., Parker, J. L., Amabebe, E., Kistler, J., Reynolds, S., Stern, V., ... Anumba, D. O. (2017). Spontaneous preterm birth is associated with differential expression of vaginal metabolites by lactobacilli-dominated microflora. *Frontiers in physiology*, 8, 615.
- Tabatabaei, N., Eren, A., Barreiro, L., Yotova, V., Dumaine, A., Allard, C., & Fraser, W. (2019). Vaginal microbiome in early pregnancy and subsequent risk of spontaneous preterm birth: a case-control study. *BJOG: An International Journal of Obstetrics & Gynaecology*, 126(3), 349–358.
- Tucker, J., & McGuire, W. (2004). Epidemiology of preterm birth. *Bmj*, 329(7467), 675–678.

References VII

- 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.
- Usui, R., Ohkuchi, A., Matsubara, S., Izumi, A., Watanabe, T., Suzuki, M., & Minakami, H. (2002). Vaginal lactobacilli and preterm birth. *Journal of perinatal medicine*, 30(6), 458–466.
- Virtanen, P., Gommers, R., Oliphant, T. E., Haberland, M., Reddy, T., Cournapeau, D., ... others (2020). Scipy 1.0: fundamental algorithms for scientific computing in python. *Nature methods*, 17(3), 261–272.
- Waskom, M., Botvinnik, O., Ostblom, J., Gelbart, M., Lukauskas, S., Hobson, P., ... Brian (2020, April). *mwaskom/seaborn: v0.10.1 (april 2020)*. Zenodo. Retrieved from <https://doi.org/10.5281/zenodo.3767070> doi: 10.5281/zenodo.3767070