

Microbiome Premature

Jaewoong Lee

Ulsan National Institute of Science and Technology

jwlee230@unist.ac.kr

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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)

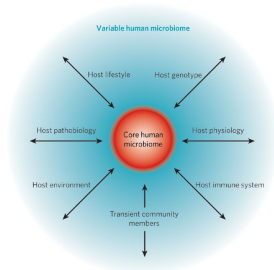


Figure: Concept of a core human microbiome (Turnbaugh et al., 2007)

- 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 I (Dominguez-Bello et al., 2016)

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

Literature Survey II (Fettweis et al., 2019)

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 Orendo¹,
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 Korlach¹⁹,
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*}

- Study Objectives
- Notable Methods/Results

Methods

Qiime 2

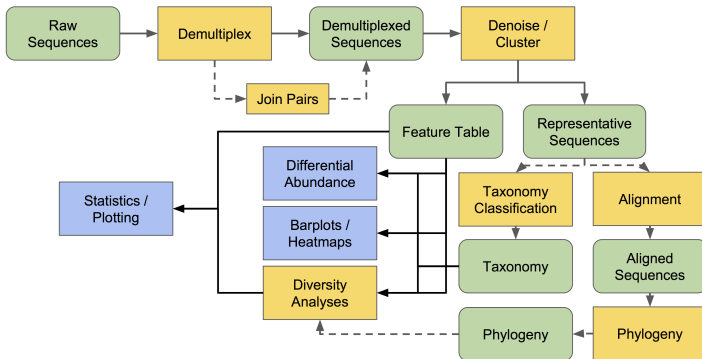


Figure: QIIME 2 workflow (Bolyen et al., 2019; Mandal et al., 2015; McDonald et al., 2012)

Filtering with Quality Score I

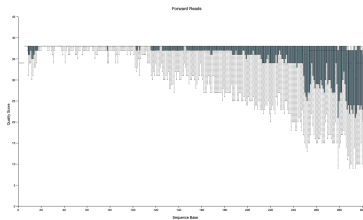
Drawback between:

- Longer sequence read
- Higher quality value

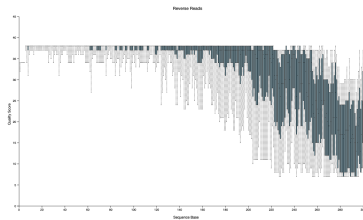
∴ I select the length n where:

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

Filtering with Quality Score II



(a) Forward



(b) Reverse

Figure: Sequence Quality Plot from Helixco Data

Maximum Length: 265

Filtering with Quality Score III

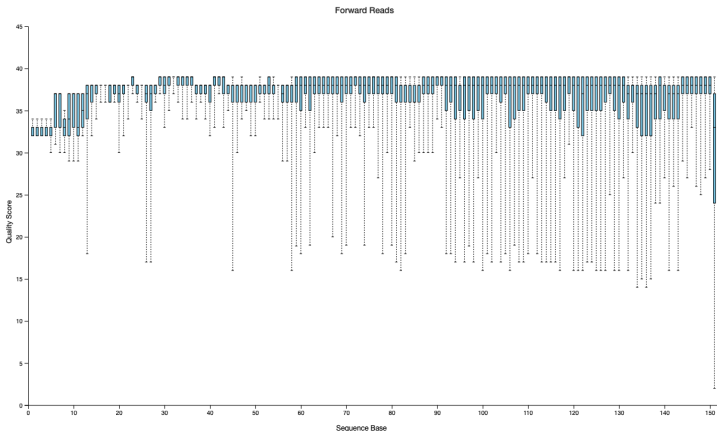
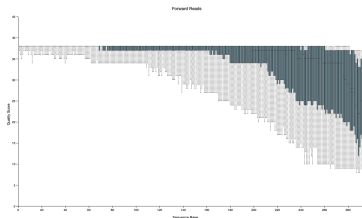


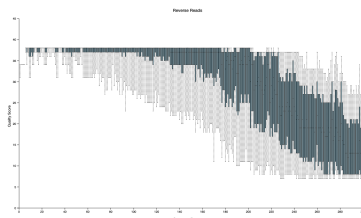
Figure: Sequence Quality Plot from EBI

Maximum Length: 150

Filtering with Quality Score IV



(a) Forward



(b) Reverse

Figure: Sequence Quality Plot from HMP Data

Maximum Length: 226

Denoising Techniques

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

Taxonomy Classification

- Greengenes (GG): Kingdom \leftrightarrow Species (DeSantis et al., 2006)
- SILVA: Domain \leftrightarrow Genus (Pruesse et al., 2007; Quast et al., 2012)

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



Figure: Mothur

Note: Still in progress

t-distributed Stochastic Neighbor Embedding (t-SNE)

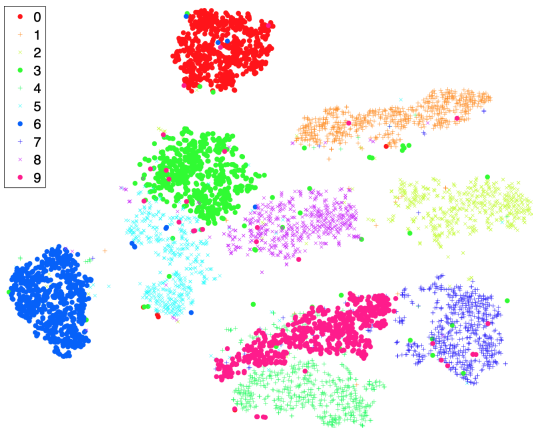
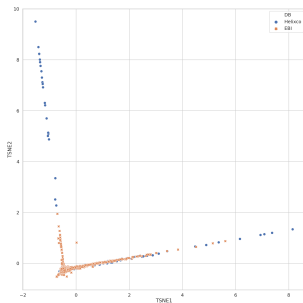


Figure: t-SNE with handwritten data (Maaten & Hinton, 2008)

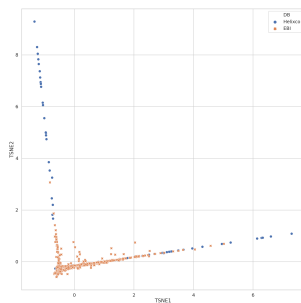
- Pandas (McKinney et al., 2011)
- Scikit-Learn (Pedregosa et al., 2011)
- SciPy (Virtanen et al., 2020)
- Matplotlib (Hunter, 2007)
- Seaborn (Waskom et al., 2020)

Results

t-SNE for Brief Information I



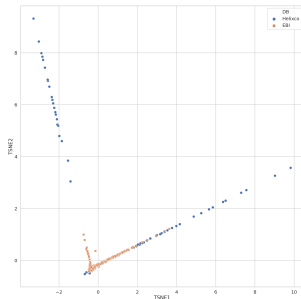
(a) DADA2 + GG



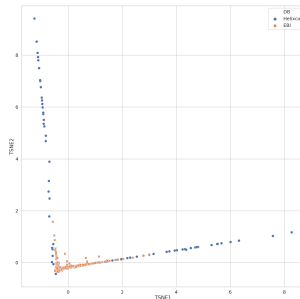
(b) DADA2 + SILVA

Figure: t-SNE for Brief Information

t-SNE for Brief Information II



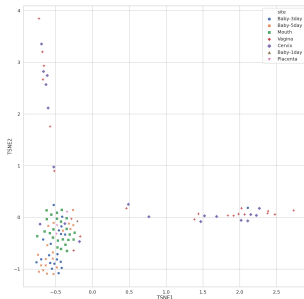
(c) Deblur + GG



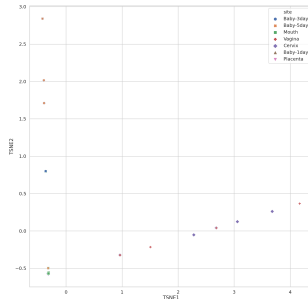
(d) Deblur + SILVA

Figure: t-SNE for Brief Information

t-SNE with Site I



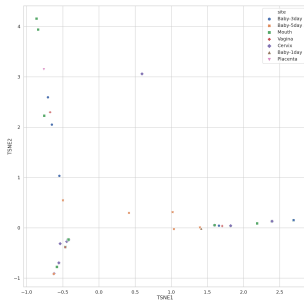
(a) DADA2 + GG



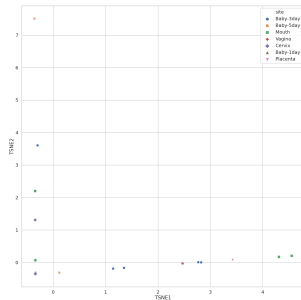
(b) DADA2 + SILVA

Figure: t-SNE with Site

t-SNE with Site II



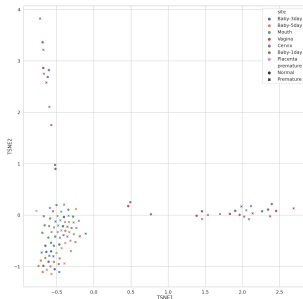
(c) Deblur + GG



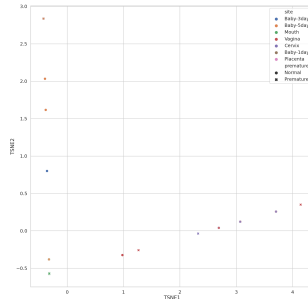
(d) Deblur + SILVA

Figure: t-SNE with Site

t-SNE with Site + Premature



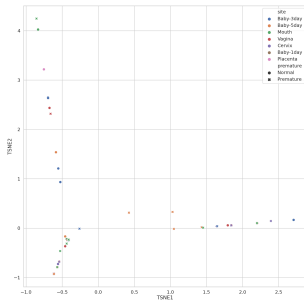
(a) DADA2 + GG



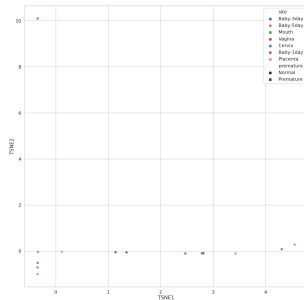
(b) DADA2 + SILVA

Figure: t-SNE with Site + Premature

t-SNE with Site + Premature II



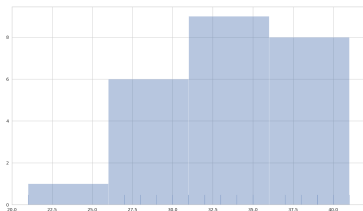
(c) Deblur + GG



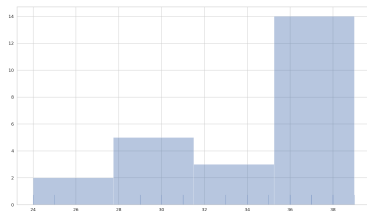
(d) Deblur + SILVA

Figure: t-SNE with Site + Premature

Histogram with Clinical Information



(a) Age



(b) Weeks

Figure: Histogram with Clinical Information

Random Forest Classifier I

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

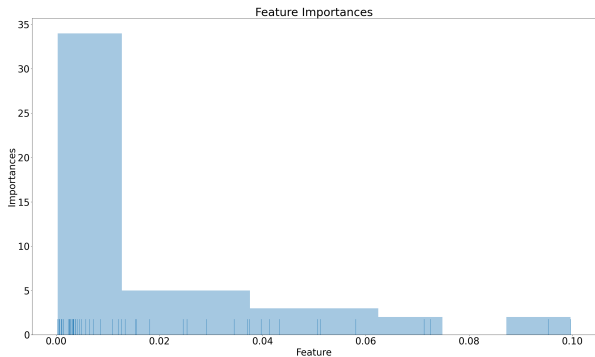


Figure: Feature Importance derived by Random Forest Classifier

Random Forest Classifier II

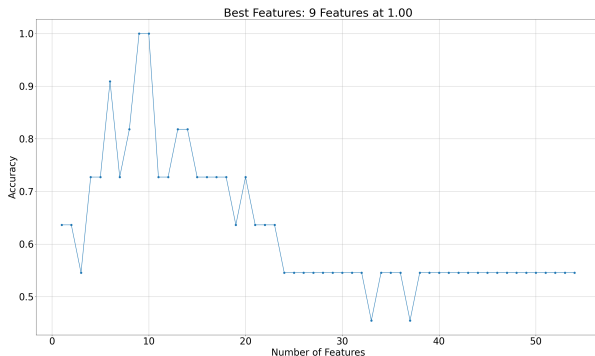


Figure: Number of Features vs. Accuracy

Random Forest Classifier III

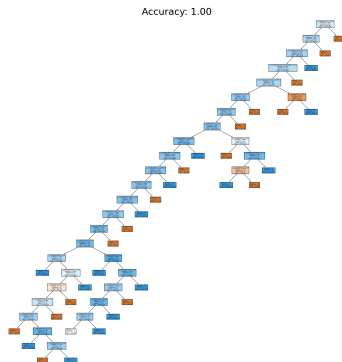


Figure: Random Forest Classifier

Random Forest Classifier IV

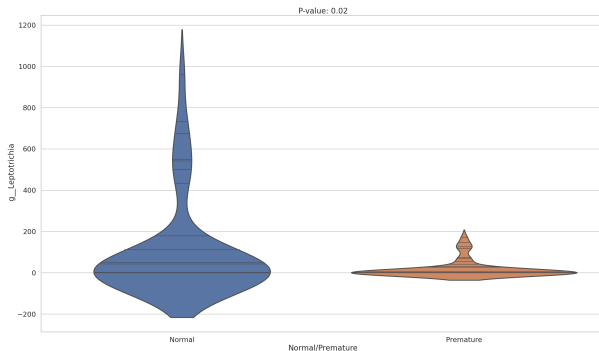


Figure: Violin Plot of *Leptotrichia*

Fusobacteriota Fusobacteriia Fusobacteriales Leptotrichiaceae Leptotrichia

Proceedings

- t-SNE with databases
- Random Forest Classifier

Requirements I

- More data
- Metadata for databases
- Mothur pipeline

- Classifier result (Statistical values)

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