

# Metagenome Analysis of Premature Birth

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# Overview

1 Introduction

2 Materials

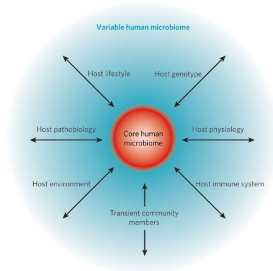
3 Methods

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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 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 Birth (Preterm Birth)



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

∴ Hence, in this study,

- Premature:  $< 37$  weeks
- Normal:  $\geq 37$  weeks

# Materials

# 16S rRNA Sequencing

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

Three main 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

- JBNU/Helixco data
  - First data
  - Second data
  - Stool data

Table: Sample Information

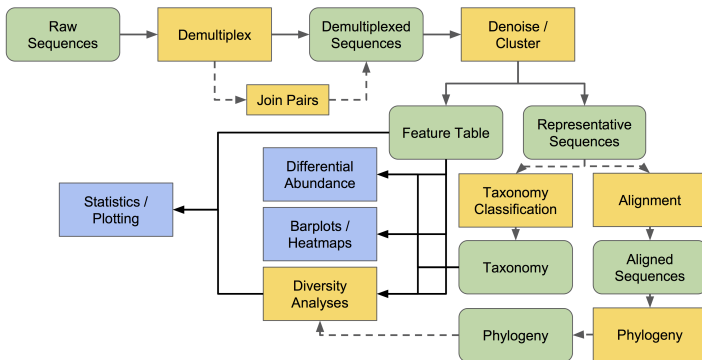
Data	Participants	Samples	Remarks
First	24	107	-
Second	35	288	-
Stool	63	126	Stool

# Methods

# Methods

## Qiime 2 Workflow

# QIIME 2 Workflow



**Figure:** QIIME 2 workflow (Bolyen et al., 2019; Mandal, Van Treuren, White, Eggesbø, et al., 2015; McDonald et al., 2012)

# Filtering with Quality Score

Drawback between:

- Longer sequence read
- Higher quality value

∴ Select the maximum length  $n$  where:

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

# 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)

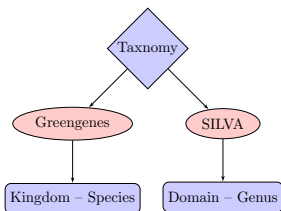


Figure: Taxonomy Classifications

“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 (ASVs or OTUs) into one, which have

- Different IDs
- Identified as same taxonomy

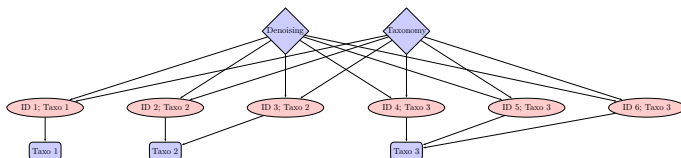


Figure: Example Diagram for Merging Denoising/Taxonomy



# Methods

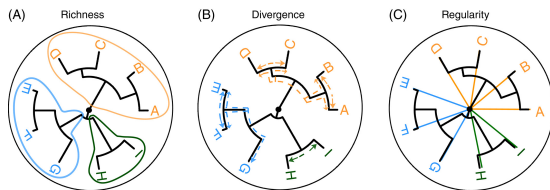
## Abundance Test

- Analysis of composition of microbiome (Mandal, Van Treuren, White, Eggesbø, et al., 2015)
- ANCOM detects significantly abundant taxa, while maintain high statistical power
- Find taxa that can divide each classes

# Methods

## Diversity Indices

# Diversity Indices



**Figure:** Three dimensions of phylogenetic information (C. M. Tucker et al., 2017)

- A quantitative measure that shows richness, divergence, and regularity (C. M. Tucker et al., 2017)
- Alpha diversity indices: the richness of taxa **at a single community**
- Beta diversity indices: the taxonomic differentiation **between communities**

# Alpha Diversity Indices

- Evenness index
- Faith's Phylogenetic Diversity (Faith PD) index
- Oberseved Features index
- Shannon's Diversity index

# Beta Diversity Indices

- Bray-Curtis distance index
- Jaccard distance index
- Unweighted UniFrac distance index
- Weighted UniFrac distance index

Methods

Miscellaneous

# t-distributed Stochastic Neighbor Embedding (t-SNE)



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



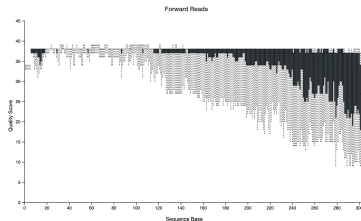
- Pandas (McKinney et al., 2011)
- Scikit-Learn (Pedregosa et al., 2011)
- SciPy (Virtanen et al., 2020)
- Matplotlib (Hunter, 2007)
- Seaborn (Waskom et al., 2020)
- Statannot

## Results

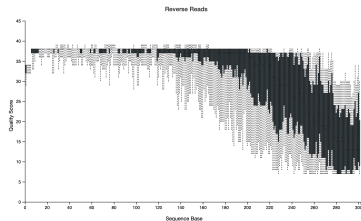
# Results

## Filtering Results

# Quality Score from JBNU/Helixco Data



(a) Forward



(b) Reverse

Figure: Quality Score Plot

- $\ell_{Forward} = 300$
- $\ell_{Reverse} = 245$

# Results

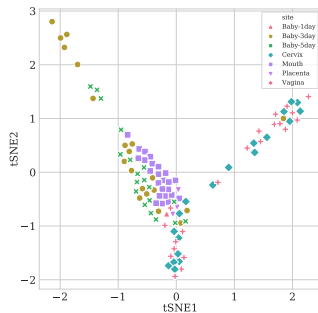
t-SNE with Site/Premature Information

# Workflow for t-SNE with Site/Premature Information

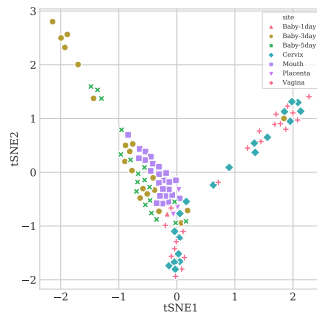


Figure: Workflow of t-SNE for Site/Premature Information

# t-SNE with Site Information I



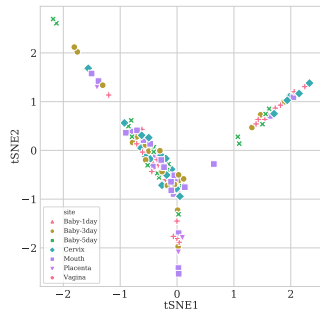
(a) DADA2 + GG



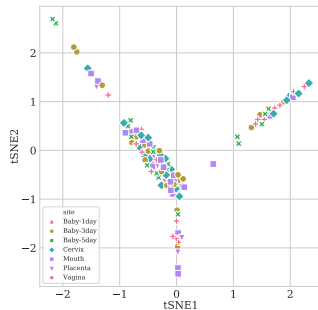
(b) DADA2 + SILVA

Figure: t-SNE with Site by DADA2

# t-SNE with Site Information II



(c) Deblur + GG

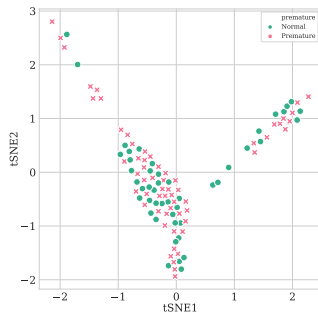


(d) Deblur + SILVA

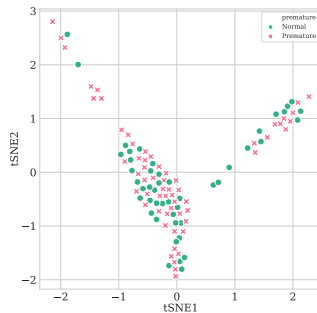
Figure: t-SNE with Site by Deblur



# t-SNE with Premature Information I



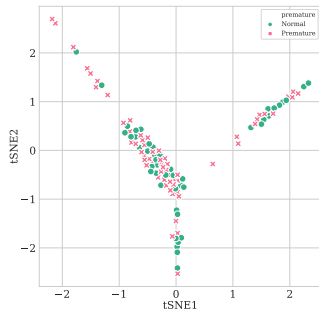
(a) DADA2 + GG



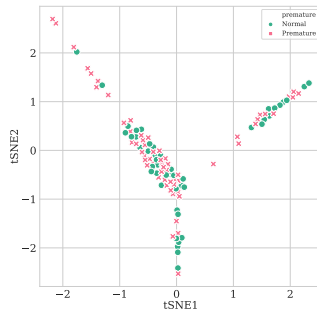
(b) DADA2 + SILVA

Figure: t-SNE with Premature by DADA2

# t-SNE with Premature Information II



(c) Deblur + GG



(d) Deblur + SILVA

Figure: t-SNE with Premature by Deblur

# Results

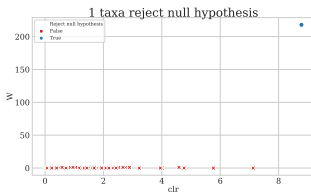
## Bacterial Abundance Test with ANCOM

# ANCOM?

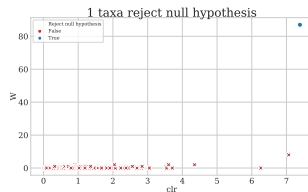
- Analysis of composition of microbiomes
- ANCOM can be used for analyzing the composition of microbiomes in multiple populations (Mandal, Van Treuren, White, Eggesbø, et al., 2015)
- Differential abundance testing
- ① clr: Centered log(*Ratio*)
- ② W: a count of the number of sub-hypothesis which have passed for given species

- Site where get the microbiome
- Premature – Before 37 weeks and After 37 weeks
- Detailed Premature – Before 34 weeks, After 37 weeks, and the other
- C-section
- PROM – Premature rupture of membranes
- Using Steroid?
- Using anti-biotic?

# ANCOM with Detailed Premature



(a) DADA2 + GG

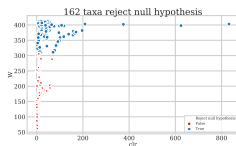


(b) Deblur + GG

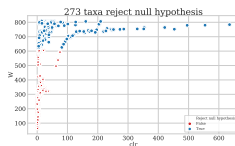
Figure: ANCOM results with Detailed Premature

- *Ureaplasma* genus
- *Aerococcus* genus

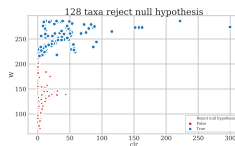
# ANCOM with Site



(a) DADA2 + GG



(b) DADA2 + Silva



(c) Deblur + GG

Figure: ANCOM results with Site

# ANCOM with PROM

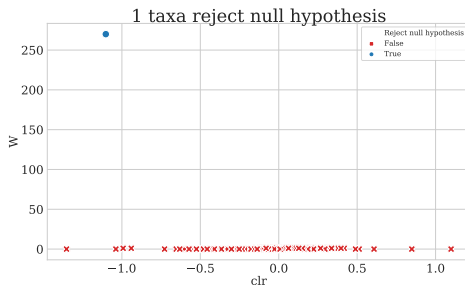
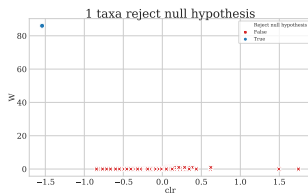


Figure: ANCOM result with PROM (DADA2 + GG)

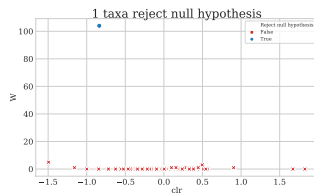
- *Campylobacteraceae* genus *Campylobacter* species



# ANCOM with Using Steroid



(a) DADA2 + GG



(b) Deblur + GG

Figure: ANCOM results with Using Steroid

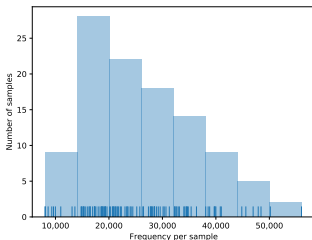
- *Ureaplasma* genus
- *Aerococcus* genus

## Results

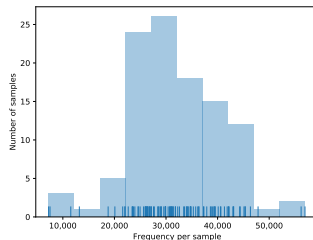
### Rarefaction

# Rarefaction?

# Rarefaction from First Data



(a) DADA2



(b) Deblur

Figure: Rarefaction from the First Data

- DADA2: 8062
- Deblur: 7239

# Results

## Alpha-Diversity

# Alpha-Diversity

# Results

## Beta-Diversity

# Beta-Diversity



# Results

## Classification

# Workflow for Classification

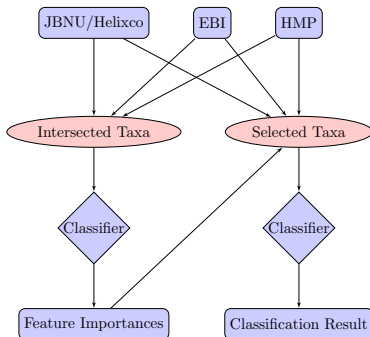


Figure: Workflow with Classification

# Random Forest Classifier I

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