

Metagenome Analysis of Premature Birth

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Overview

1 Introduction

2 Materials

3 Methods

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1. 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)

rRNA

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

Premature Birth (Preterm Birth; PTB)

PTB:

- ① PTB $<$ 37 GW (Gestational week)
- ② Normal \geq 37 GW

Detailed PTB:

- ① Early PTB $<$ 34 GW
- ② 34 GW \leq Late PTB $<$ 37 GW
- ③ Normal \geq 37 GW

(J. Tucker & McGuire, 2004; Voronkov, Solonovych, Liashenko, & Revenko, 2018)

2. 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 evolution.
- 16S rRNA is large enough for bioinformatics

Data Composition

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

Table: Sample Information

Data	Participants	Samples	Remarks
First	24	107	-
Second	35	288	-
Third	10	106	-
Stool	63	126	Stool

3. Methods

Qiime 2 Workflow

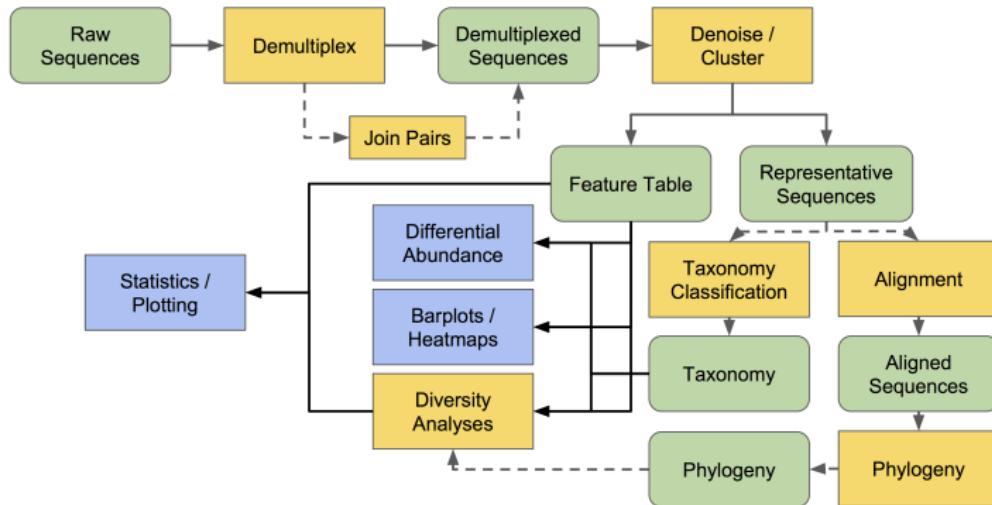


Figure: QIIME 2 workflow (Bolyen et al., 2019; Mandal, Van Treuren, White, Eggesbø, et al., 2015; McDonald et al., 2012)

4. Results

4. Results

4.1. Data Processing with Qiime

Filtering with Quality Score

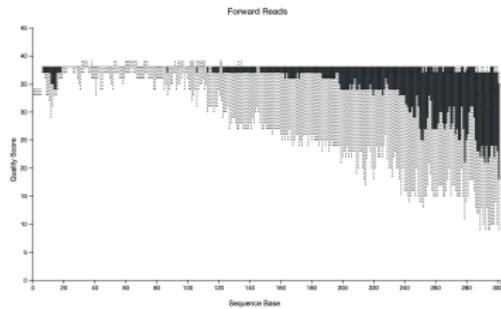
Drawback between:

- Longer sequence read
- Higher quality value

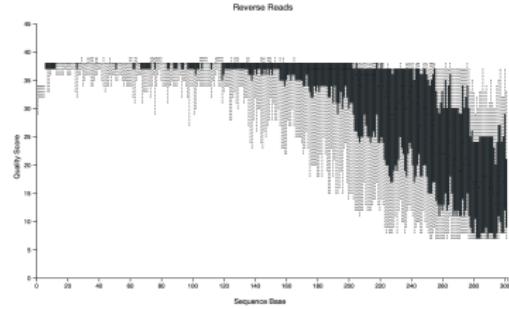
∴ Select the maximum length n where:

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

Quality Score from JBU/Helixco Data



(a) Forward



(b) Reverse

Figure: Quality Score Plot

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

Denoising Techniques

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

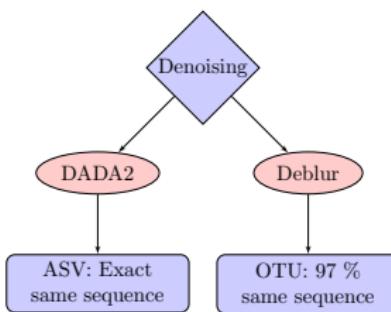


Figure: Denoising Algorithms

Taxonomy Classification

- Greengenes (GG) (DeSantis et al., 2006)
- SILVA (Pruesse et al., 2007; Quast et al., 2012)
- Human Oral Microbiome Database (HOMD) (Chen et al., 2010)

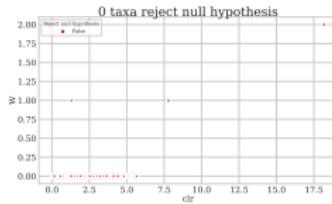
"A **higher** performance at taxonomic levels above *genus level*;
but performance appears to **drop** at *species level*" (Gihawi et al., 2019)

4. Results

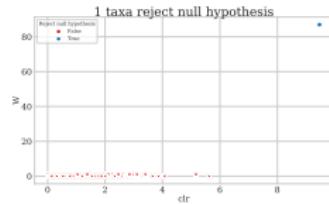
4.2. Abundance Test with ANCOM

- Analysis with 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

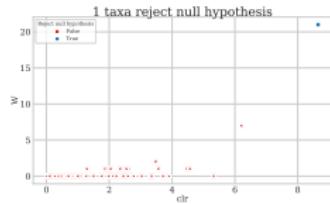
ANCOM with Detail PTB



(a) 1-day



(b) 3-day



(c) 5-day

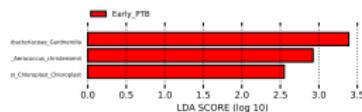
Figure: ANCOM for Detail PTB from Neonatal Mouth with DADA2+HOMD

4. Results

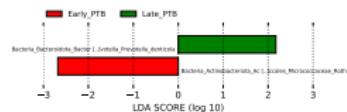
4.3. Abundance Test with LefSe

- Linear discriminant analysis Effect Size (Segata et al., 2011)
- LefSe finds the features likely to explicate differences between groups

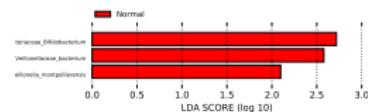
LefSe with Detail PTB



(a) Cervix



(b) Maternal Mouth



(c) Vagina

Figure: LefSe for Detail PTB with Deblur + Silva

4. Results

4.4. Batch effect removal

Abundance Distribution

t-SNE before & after

4. Results

4.5. Diversity Index

Diversity Indices

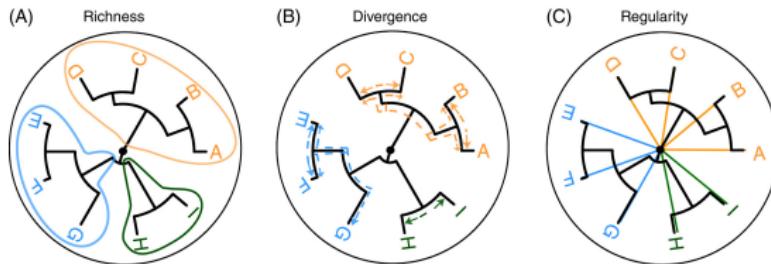
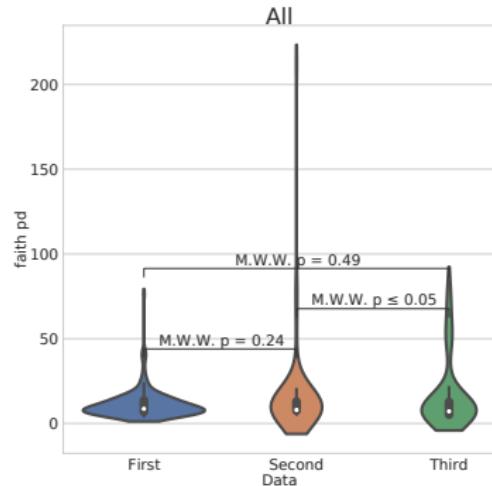


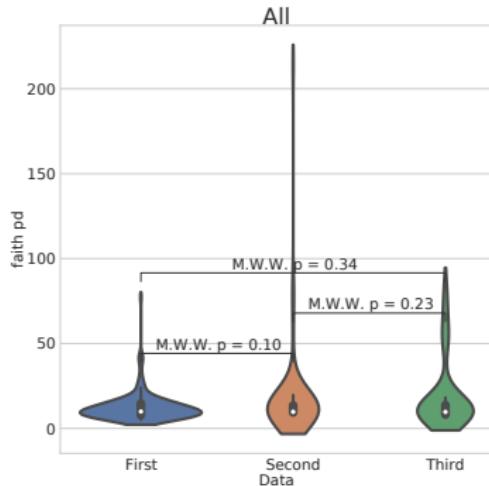
Figure: Three dimensions of phylogenetic information (C. M. Tucker et al., 2017)

- 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**

Violin Plot with Alpha diversity I



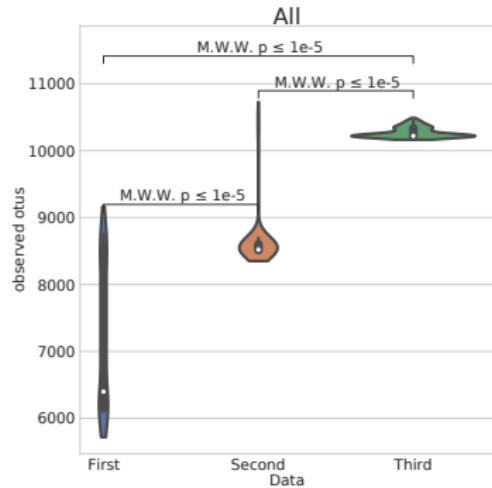
(a) Uncorrected



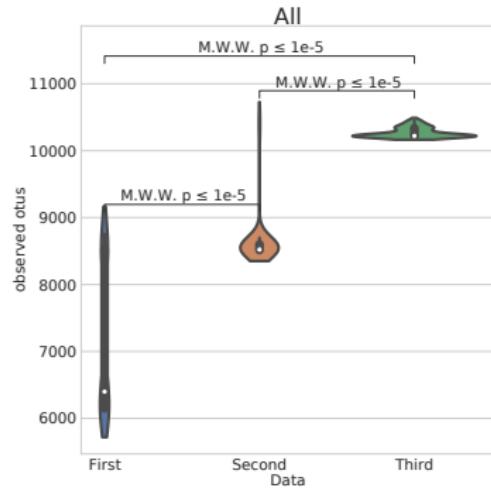
(b) Corrected

Figure: Data & Faith PD

Violin Plot with Alpha diversity II



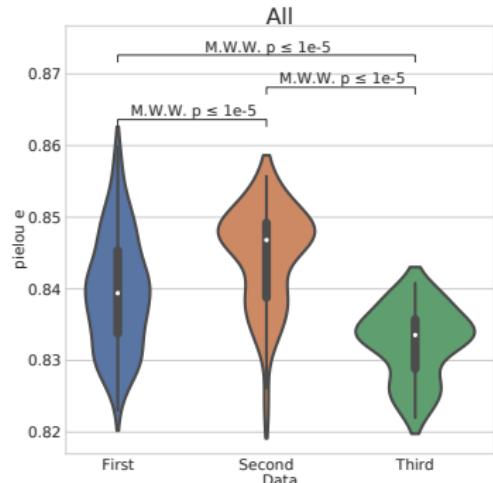
(a) Uncorrected



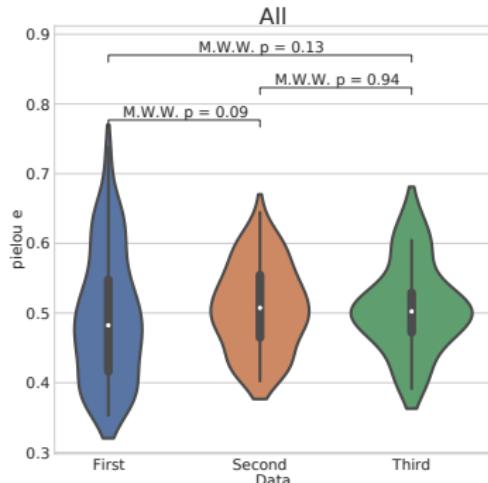
(b) Corrected

Figure: Data & Observed OTUs

Violin Plot with Alpha diversity III



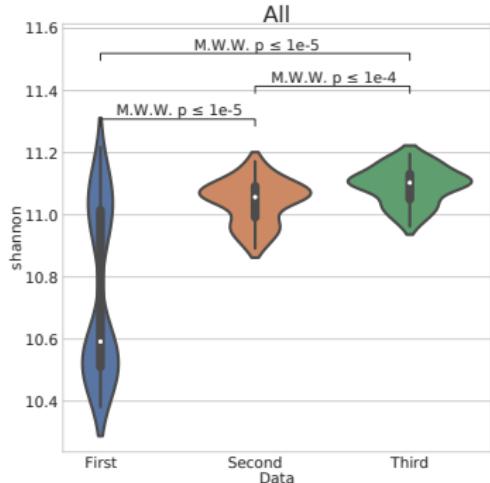
(a) Uncorrected



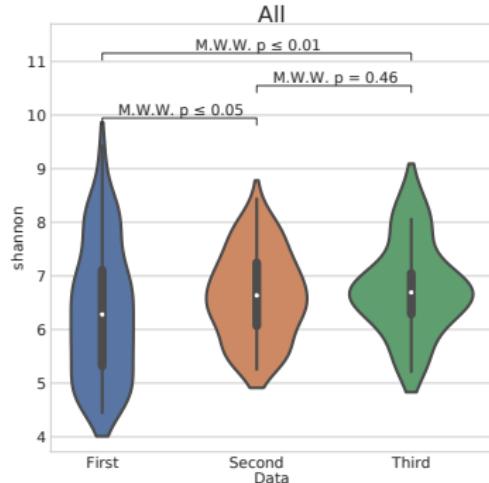
(b) Corrected

Figure: Data & Pielou Evenness

Violin Plot with Alpha diversity IV



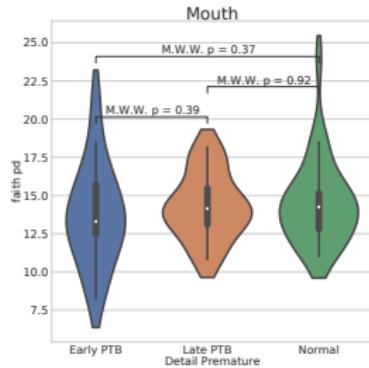
(a) Uncorrected



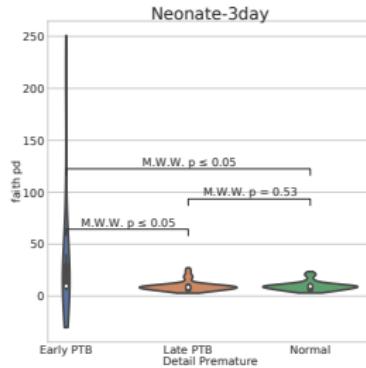
(b) Corrected

Figure: Data & Shannon Entropy

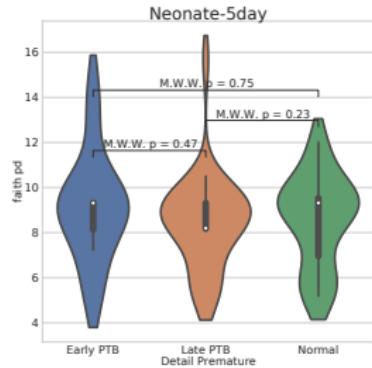
Violin Plot with Alpha diversity V



(a) Mother Mouth



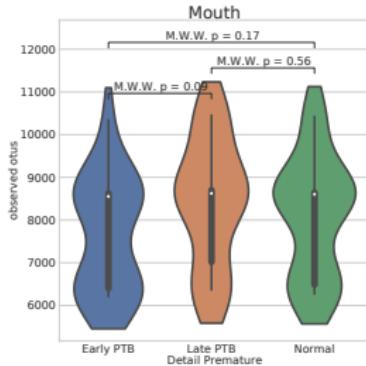
(b) Neonate 3-day



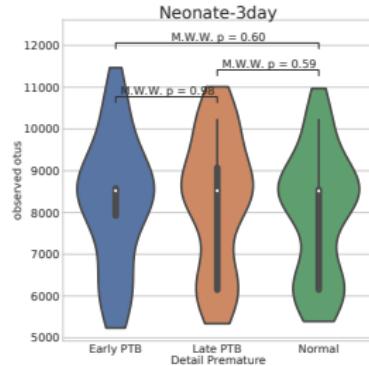
(c) Neonate 5-day

Figure: Detail premature & Faith's PD

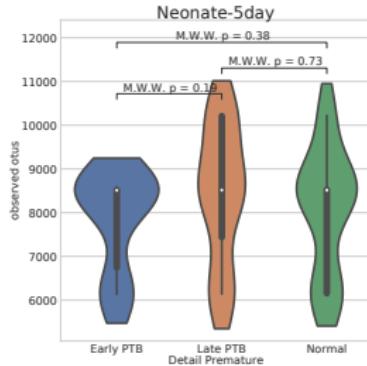
Violin Plot with Alpha diversity VI



(a) Mother Mouth



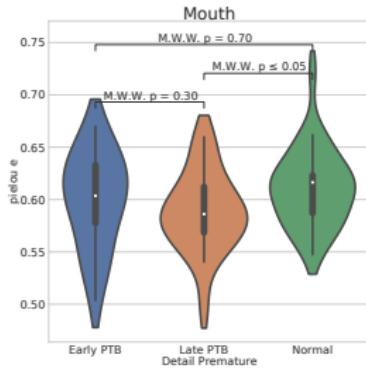
(b) Neonate 3-day



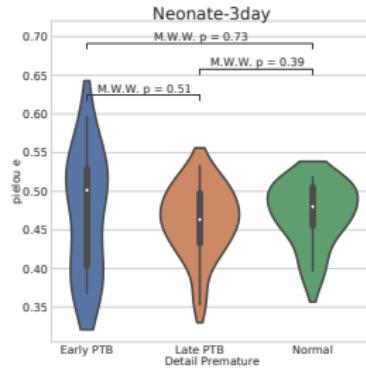
(c) Neonate 5-day

Figure: Detail premature & Observed OTUs

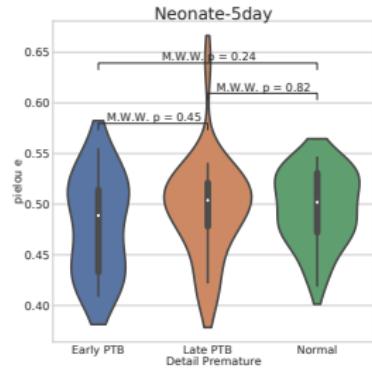
Violin Plot with Alpha diversity VII



(a) Mother Mouth



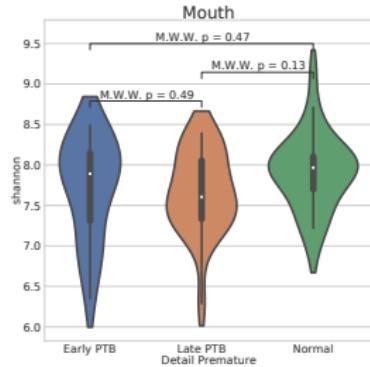
(b) Neonate 3-day



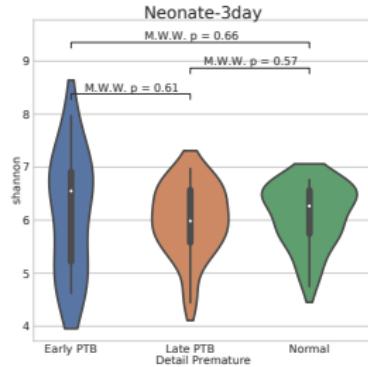
(c) Neonate 5-day

Figure: Detail premature & Pielou Evenness

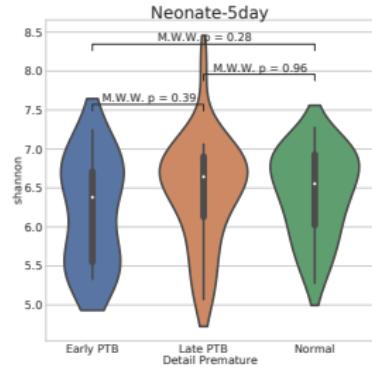
Violin Plot with Alpha diversity VIII



(a) Mother Mouth



(b) Neonate 3-day



(c) Neonate 5-day

Figure: Detail premature & Shannon Entropy

Cluster map with Beta diversity I

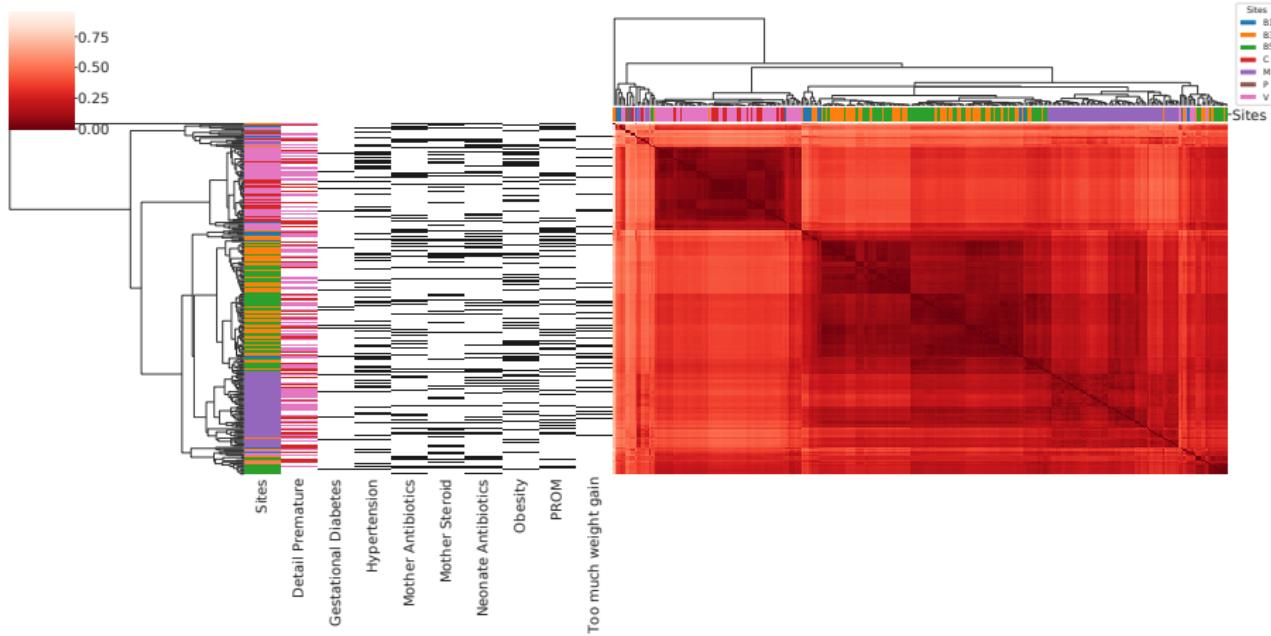


Figure: Cluster map with Weighted UniFrac distance index for DADA2

Cluster map with Beta diversity II

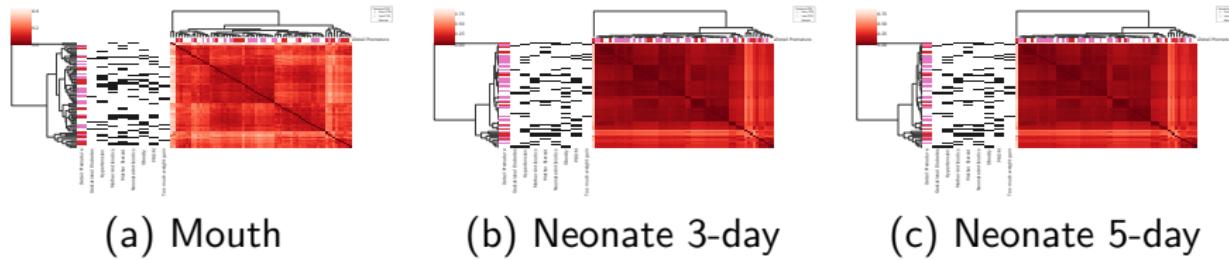


Figure: Clustermap with Site separation

4. Results

4.6. Taxonomy Analyses

Volcano plot

Shared Taxonomy with Neonates & Mothers

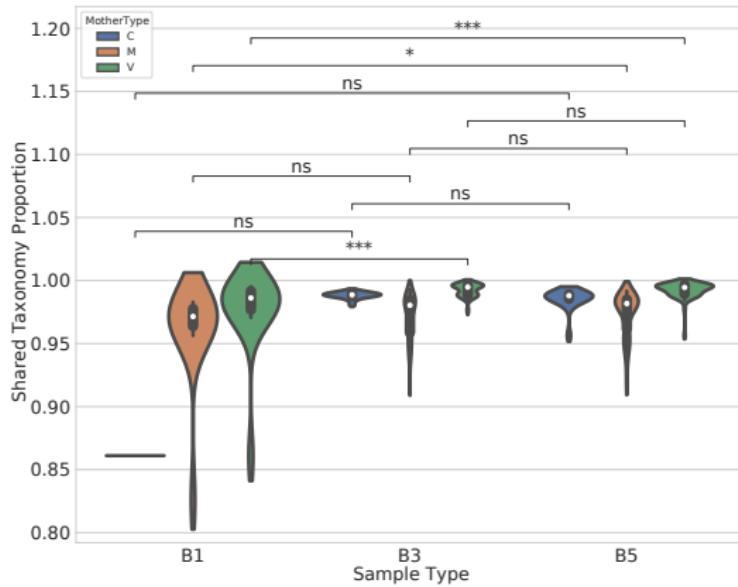


Figure: Shared Taxonomy with Neonates & Mothers from DADA2 & HOMD

Correlation between Taxonomy & Clinical data I

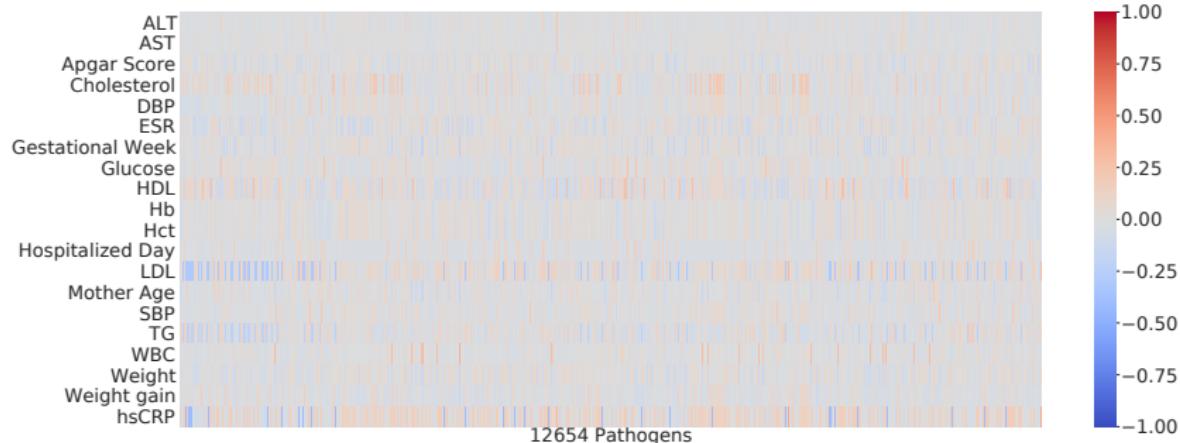


Figure: Pearson Correlation between taxonomy & clinical Data on DADA2 + HOMD

Correlation between Taxonomy & Clinical data II

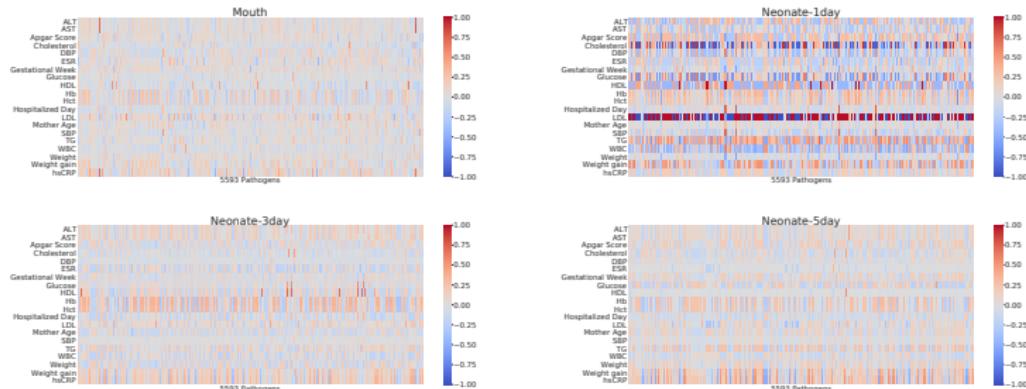


Figure: Person Correlation with Site separation

Correlation Plot

4. Results

4.7. Machine Learning

Random Forest with Detailed PTB I

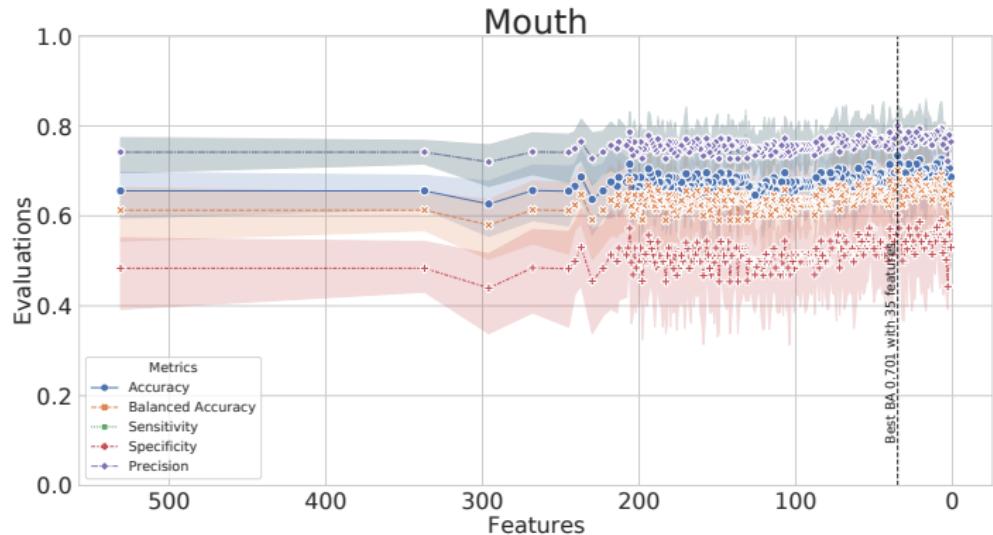


Figure: RF evaluations with feature counts

Random Forest with Detailed PTB II

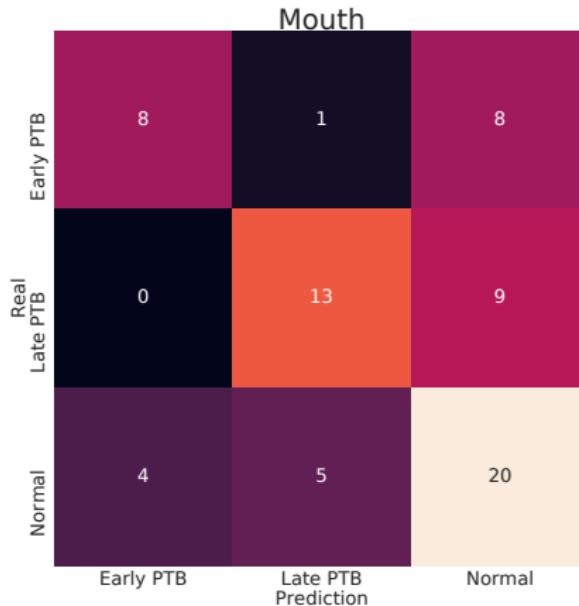


Figure: RF confusion matrix

Random Forest with Detailed PTB III

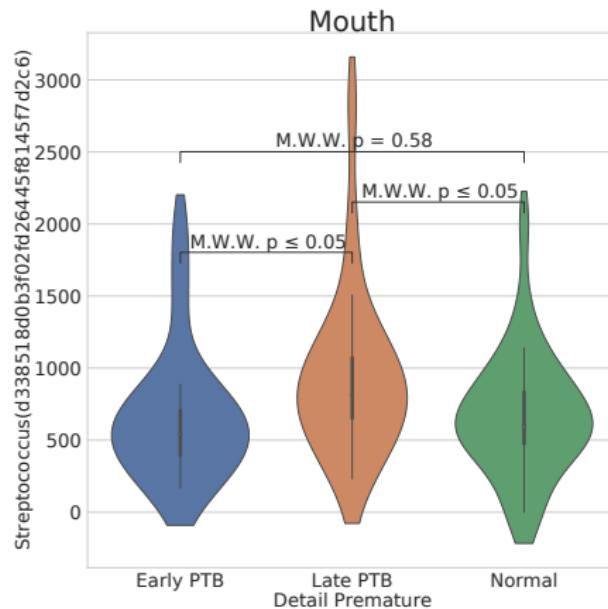


Figure: RF most important taxa

5. Discussion

6. References

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