

Metagenome Analysis of Preterm Birth

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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)

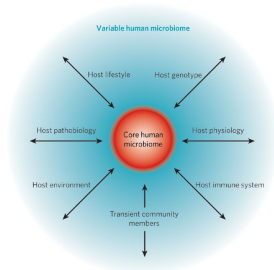


Figure: Concept of a core human microbiome (Turnbaugh et al., 2007)

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

Preterm Birth (PTB)

PTB:

- 1 PTB < 37 GW (Gestational week)
- 2 Normal ≥ 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 I

Data composition

59 pregnant women & 55 newborns

PTB

- Mother \Rightarrow PTB: 30 & Normal: 29
- Newborn \Rightarrow PTB: 25 & Normal: 30

Table: Clinical characteristics of mothers

Clinical	<37 GW (n=30)	≥37 GW (n=29)	p-value	Remarks
Cholesterol	289.6±72.6	269.6±50.6	0.496	
DBP	83.1±17.5	80.7±9.8	0.887	
Glucose	97.3±27.7	83.1±14.3	0.034	*
HDL	83.7±17.6	82.4±30.8	0.374	
Hb	11.6±1.4	12.2±1.6	0.095	
Hct	34.7±3.5	36.2±3.9	0.115	
LDL	151.3±32.6	157.3±26.4	0.779	
Mother Age	31.8±5.1	33.7±4.4	0.142	
SBP	142.0±28.0	129.3±15.7	0.079	
Weight gain	9.0±5.8	11.6±4.0	0.022	*
Advanced maternal age	8 (26.7%)	10 (34.5%)	0.580	
C-section	20 (66.7%)	24 (82.8%)	0.233	
Gestational Diabetes	0 (0.0%)	3 (10.3%)	0.112	
Hypertension	10 (33.3%)	5 (17.2%)	0.233	
Mother Antibiotics	13 (43.3%)	4 (13.8%)	0.020	*
Mother Steroid	18 (60.0%)	0 (0.0%)	0.000	*
Obesity	8 (26.7%)	7 (24.1%)	1.000	
PROM	12 (40.0%)	1 (3.4%)	0.001	*
Preterm Labor	13 (43.3%)	1 (3.4%)	0.000	*
Too much weight gain	4 (13.3%)	4 (13.8%)	1.000	

Table: Clinical characteristics of newborns

Clinical	<37 GW (n=25)	≥37 GW (n=30)	p-value	Remarks
Apgar Score	8.4±1.2	9.7±0.7	0.000	*
Gestational Week	33.3±2.5	38.0±1.0	0.000	*
Hospitalized Day	20.6±19.5	8.3±6.2	0.002	*
Weight	2150.7±587.1	3267.9±397.8	0.000	*
CPAP	9 (36.0%)	2 (6.7%)	0.015	*
Dyspnea	11 (44.0%)	2 (6.7%)	0.002	*
Gender	12 (48.0%)	13 (43.3%)	0.790	
Neonate Antibiotics	7 (28.0%)	6 (20.0%)	0.537	
PROM	9 (36.0%)	1 (3.3%)	0.003	*
Respirator	6 (24.0%)	1 (3.3%)	0.039	*
Sepsis	6 (24.0%)	5 (16.7%)	0.521	

Statistical tests

- Continuous: M.W.W. test
- Categorical: Fisher exact test

3. Methods

Qiime 2 Workflow

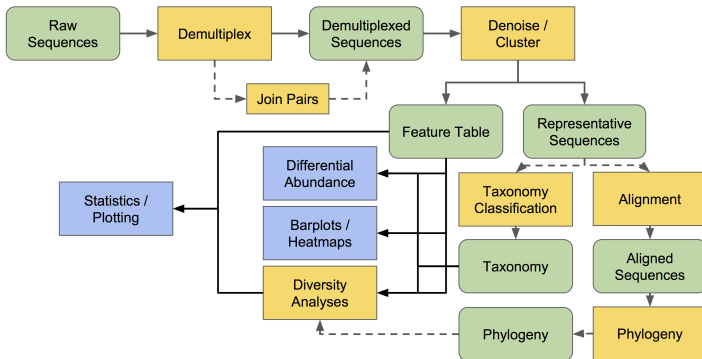


Figure: QIIME 2 workflow (Bolyen et al., 2019; Mandal et al., 2015; McDonald et al., 2012)

4. Results

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4.1. Taxonomy Overview

Microbial community with Proportion I

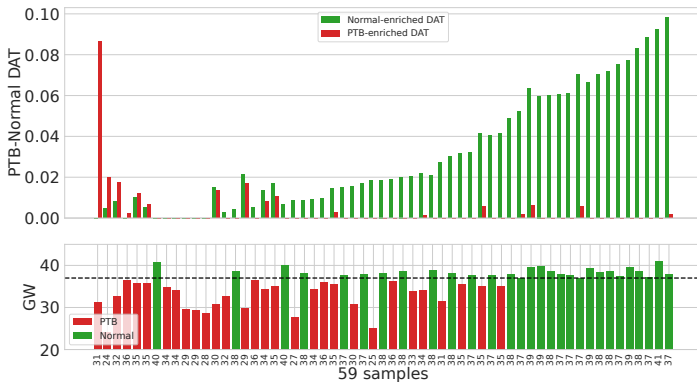


Figure: Microbial community with Proportion

Microbial community with Proportion II

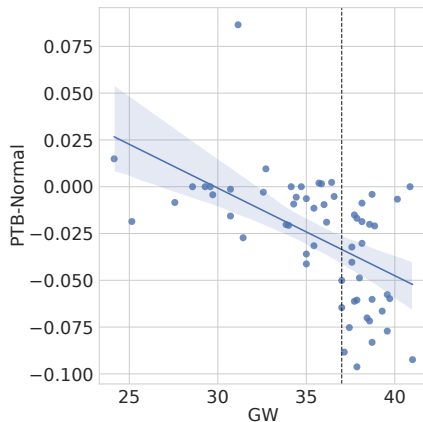


Figure: Microbial community with Proportion

4. Results

4.2. Diversity Index

Diversity Index

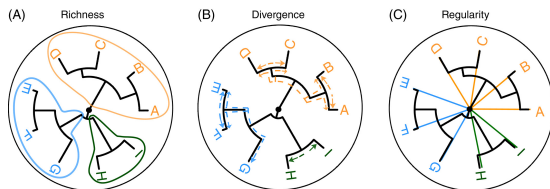


Figure: Three dimensions of phylogenetic information (C. M. Tucker et al., 2017)

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

4. Results

4.2. Diversity Index

4.2.1. Alpha-diversity

Violin Plot with Alpha-diversity

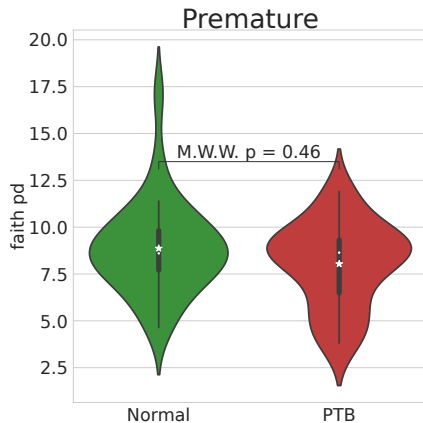


Figure: Premature & Faith's PD

4. Results

4.2. Diversity Index

4.2.2. Beta-diversity

Beta-diversity t-SNE plots I

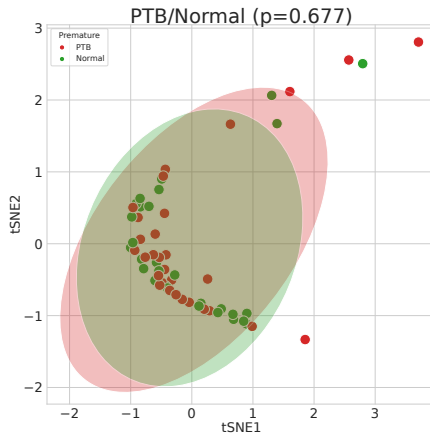


Figure: Hamming distance index t-SNE plot

4. Results

4.3. Taxonomy Analyses

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4.3. Taxonomy Analyses

4.3.1. Differentially Abundant Taxa

Volcano plots

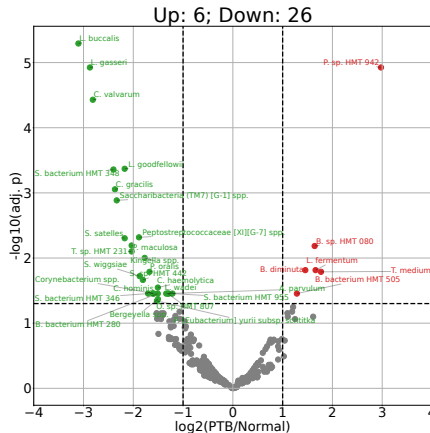


Figure: DAT in Mouth

Box plots

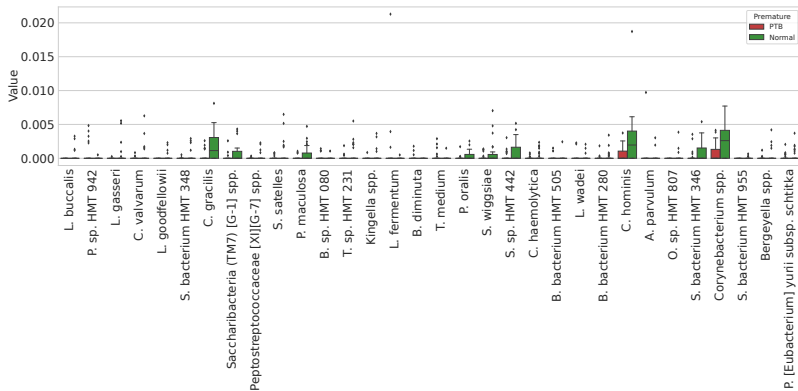


Figure: DAT box plots

4. Results

4.4. Machine Learning

ML algorithm comparison

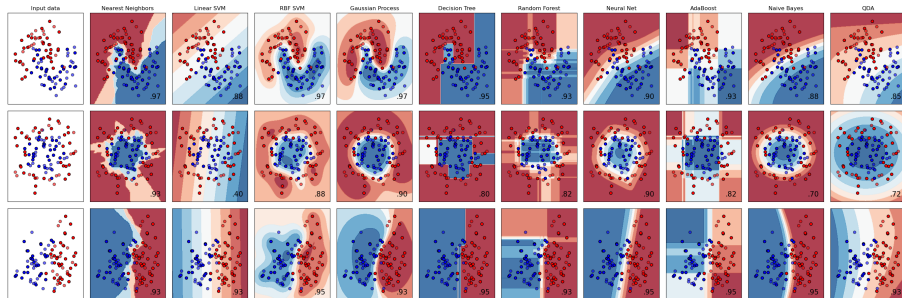


Figure: Classification Comparison (Pedregosa et al., 2011)

4. Results

4.4. Machine Learning

4.4.1. Random Forest Classifier on Proportion

Random Forest with (PTB vs. Normal) I

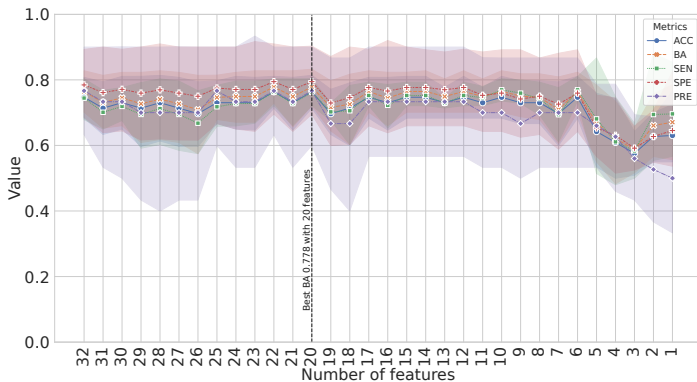


Figure: RF evaluations with feature counts

Random Forest with (PTB vs. Normal) II

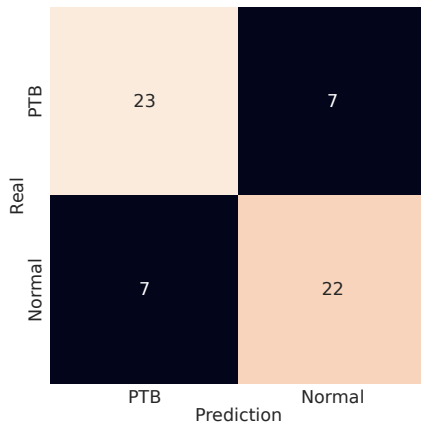


Figure: RF confusion matrix

Random Forest with (PTB vs. Normal) III

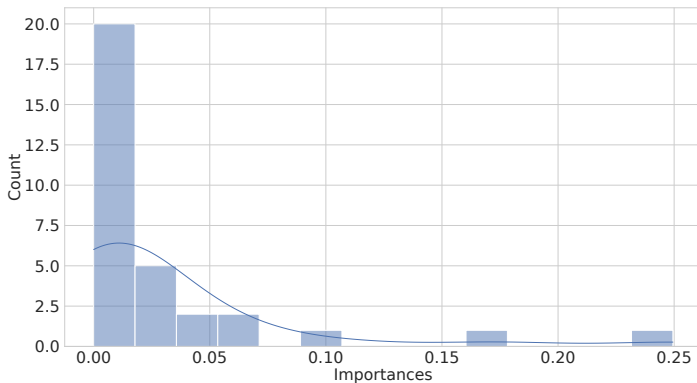


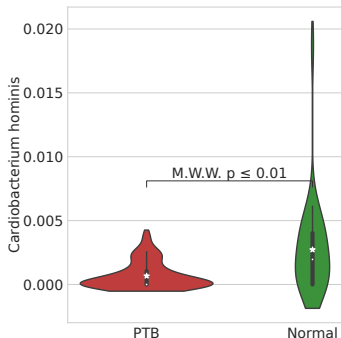
Figure: RF importances

Random Forest with (PTB vs. Normal) IV

Highest Importances

- 1 *Cardiobacterium hominis*
- 2 *Campylobacter gracilis*
- 3 *Corynebacterium* spp.
- 4 *Selenomonas* sp. HMT 442

Random Forest with (PTB vs. Normal) V

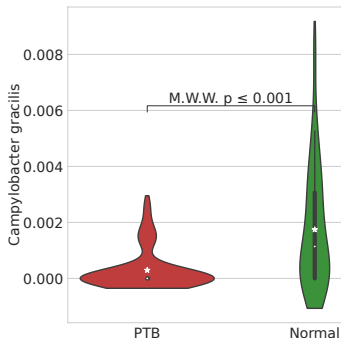


Cardiobacterium hominis

- *C. hominis* causes endocarditis (Malani, Aronoff, Bradley, & Kauffman, 2006).

Figure: *C. hominis*

Random Forest with (PTB vs. Normal) VI

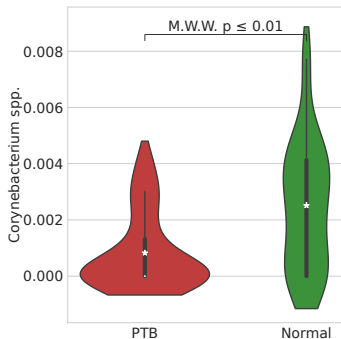


Campylobacter gracilis

- Odontogenic brain abscess with *C. gracilis* (Jang, Elliott, Herman, & Booher, 2021).

Figure: *C. gracilis*

Random Forest with (PTB vs. Normal) VII

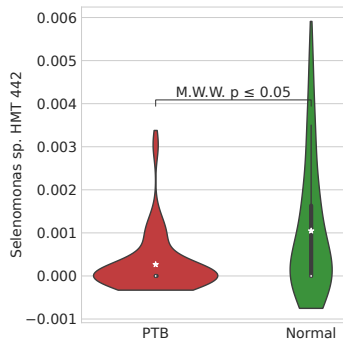


Corynebacterium spp.

- *C. sp.* HMSC078H07 associated with PTB (Huo, Jiang, & Zhao, 2022) enriched in PTB ?

Figure: *Corynebacterium* spp.

Random Forest with (PTB vs. Normal) VIII



Selenomonas sp. HMT 442

- *S. sp. HMT 442* associated with dental caries (da Costa Rosa et al., 2021).

Figure: *S. sp. HMT 442*

5. Discussion

6. References

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