Microbiome Premature

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Overview

Microbiome
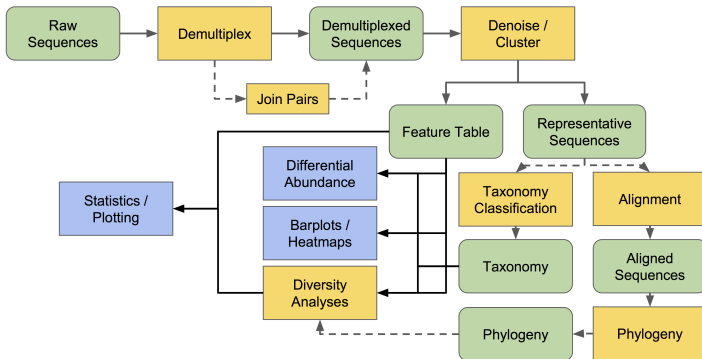
Ribosomal RNA

Premature

16s rRNA Sequencing

Qiime 2

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

Denoising Techniques

- DADA2 (Callahan et al., 2016)
- Deblur (Amir et al., 2017)

Taxonomy Classification

- Greengenes (GG): Kingdom - Species (DeSantis et al., 2006)
- SILVA: Domain - 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)
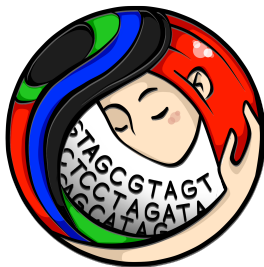
Mothur

Figure: Mothur

Note: Still in progress
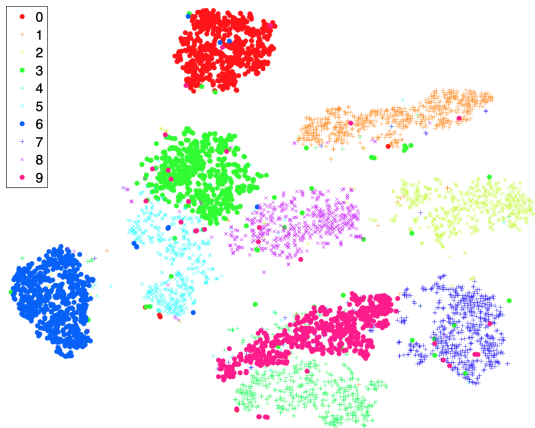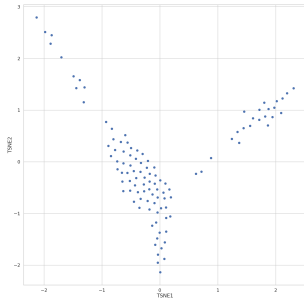
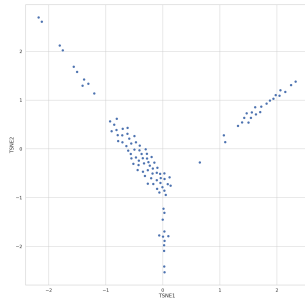# t-distributed Stochastic Neighbor Embedding (t-SNE)

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

Python Packages

- Pandas (McKinney et al., 2011)
- Scikit-Learn (Pedregosa et al., 2011)
- Matplotlib (Hunter, 2007)
- Seaborn (Waskom et al., 2020)
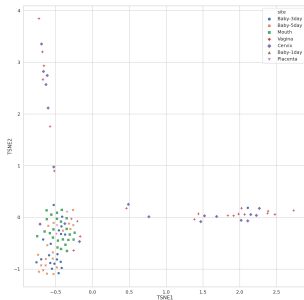
t-SNE for Brief Information

(a) DADA2   (b) Deblur
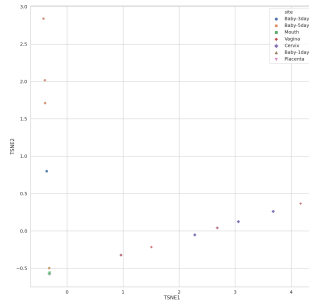
Figure: t-SNE for Brief Information
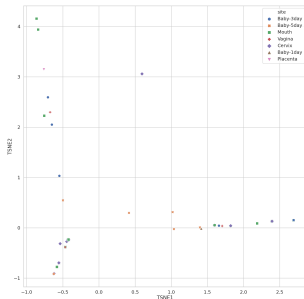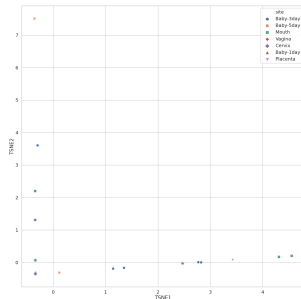
(a) DADA2 + GG

(b) DADA2 + SILVA
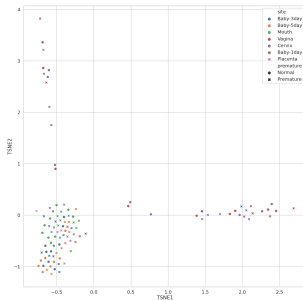
(c) Deblur + GG   (d) Deblur + SILVA
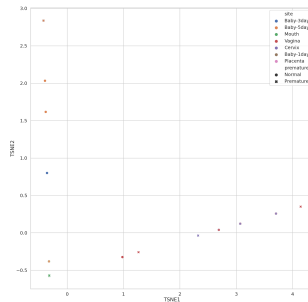
Figure: t-SNE with Site

(a) DADA2 + GG   (b) DADA2 + SILVA
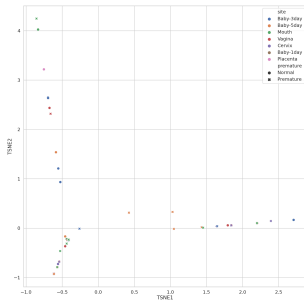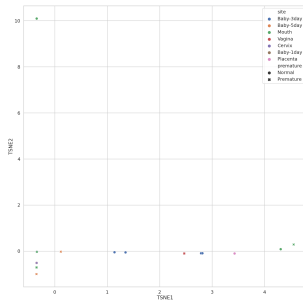
(c) Deblur + GG (d) Deblur + SILVA

Figure: t-SNE with Site

Histogram with Clinical Information
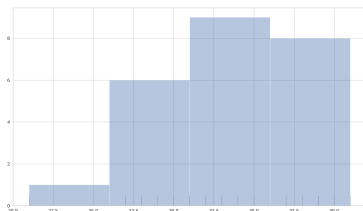
(a) Age
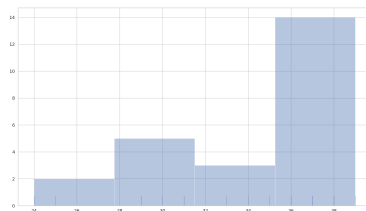
(b) Weeks

Figure: Histogram with Clinical Information

Yields I

- t-SNE plots
    - in Brief
    - by Site
    - by Site + Premature
- Histogram
    - by Age
    - by Weeks

Requirements I

- More data
- Mothur pipeline
- Classification

Expectations I

- Classifier result (Statistical values)

References I

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