Microbiome Premature

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Overview

Microbiome

Ribosomal RNA

Premature

16s rRNA Sequencing

Qiime 2

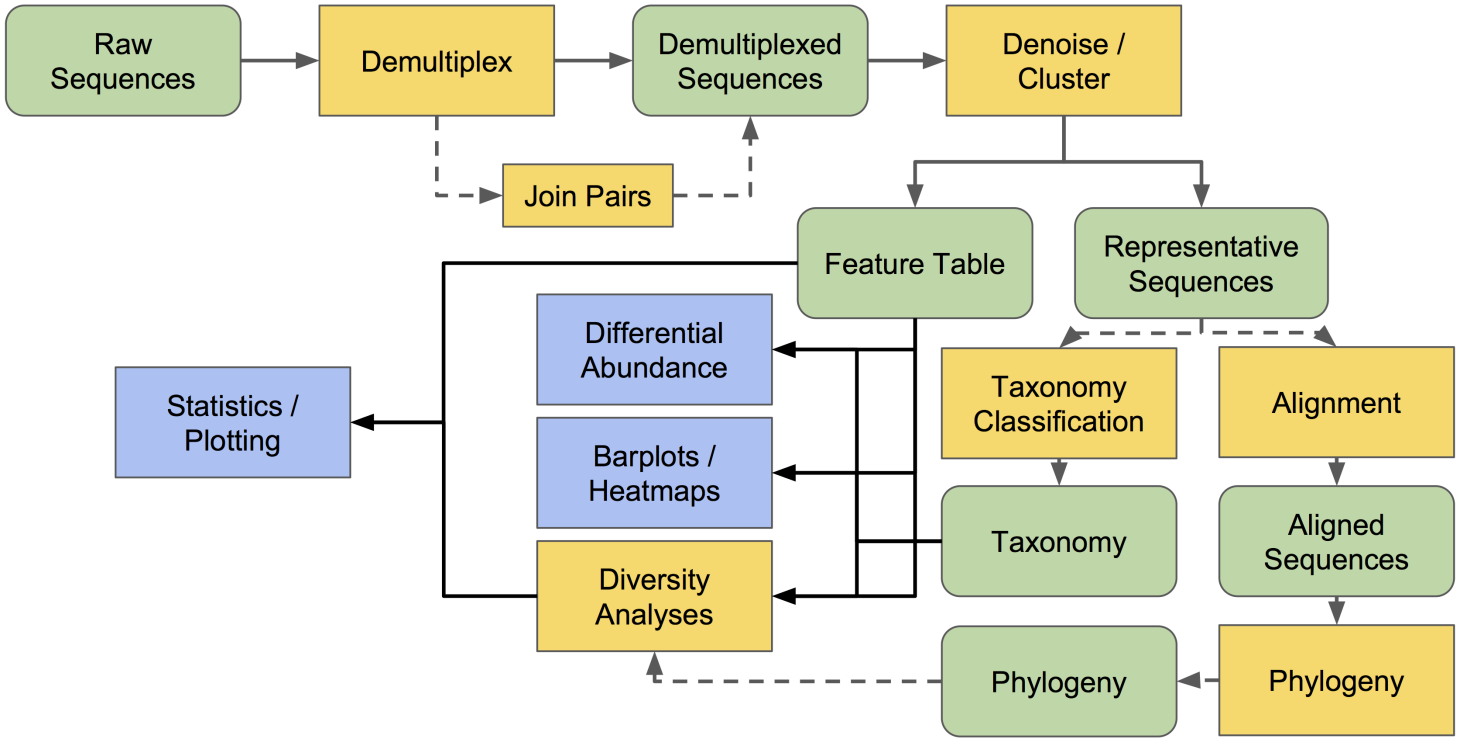


Figure: QIIME 2 workflow (Bolyen et al., 2019; Mandal et al., 2015; McDonald et al., 2012)

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)

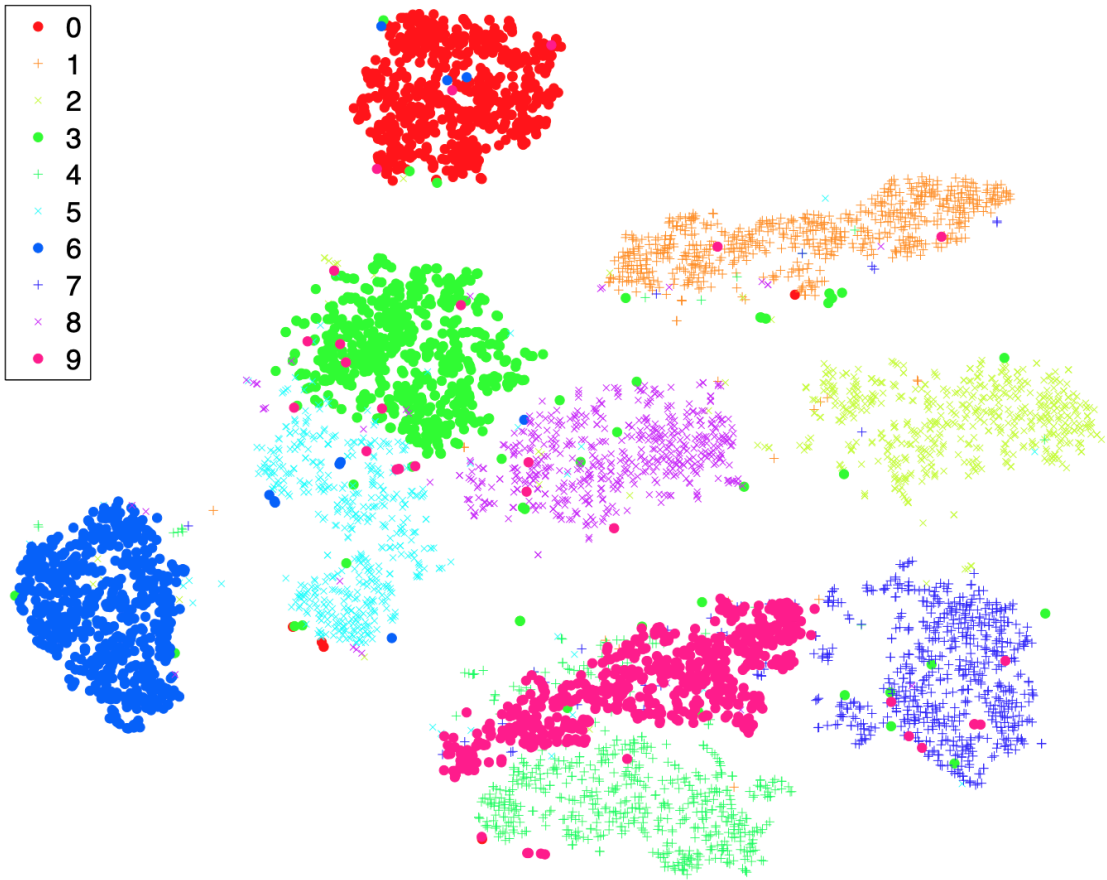
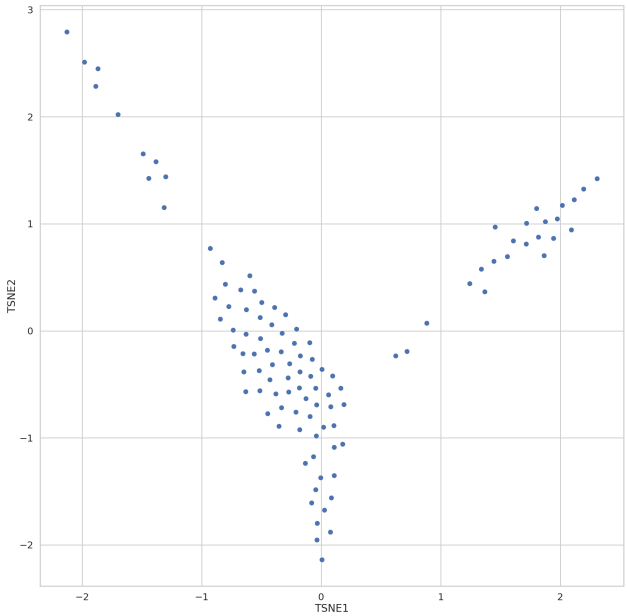


Figure: t-SNE with handwritten data (Maaten & Hinton, 2008)

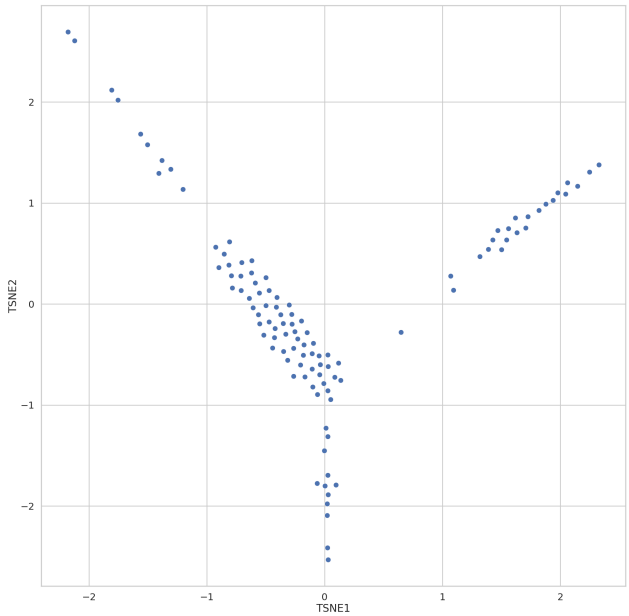
Python Packages

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

t-SNE for Brief Information



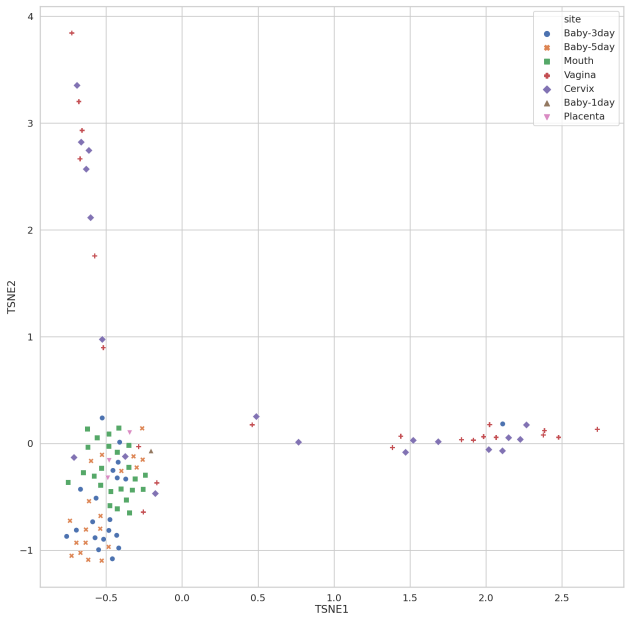
(a) DADA2



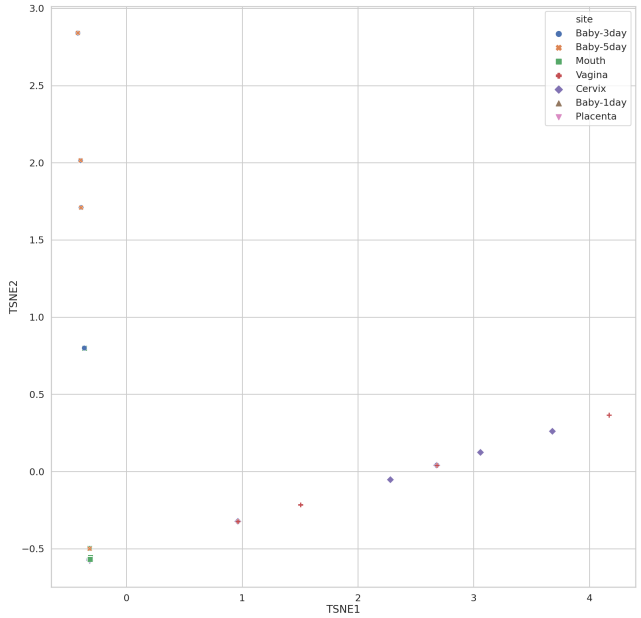
(b) Deblur

Figure: t-SNE for Brief Information

t-SNE with Site I

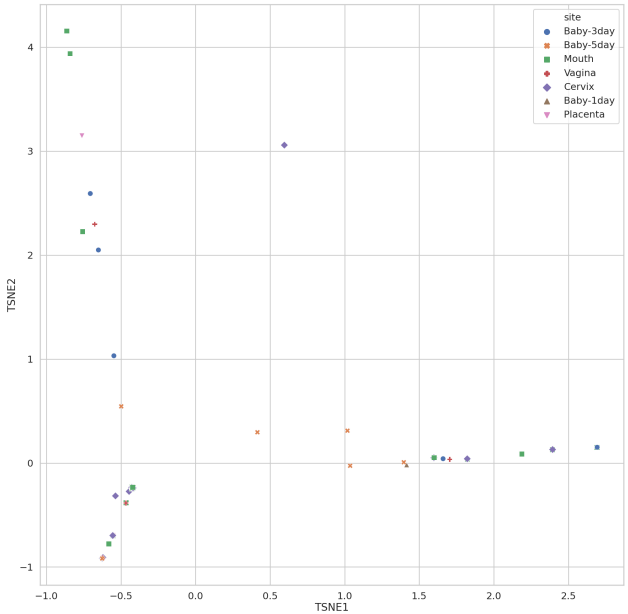


(a) DADA2 + GG

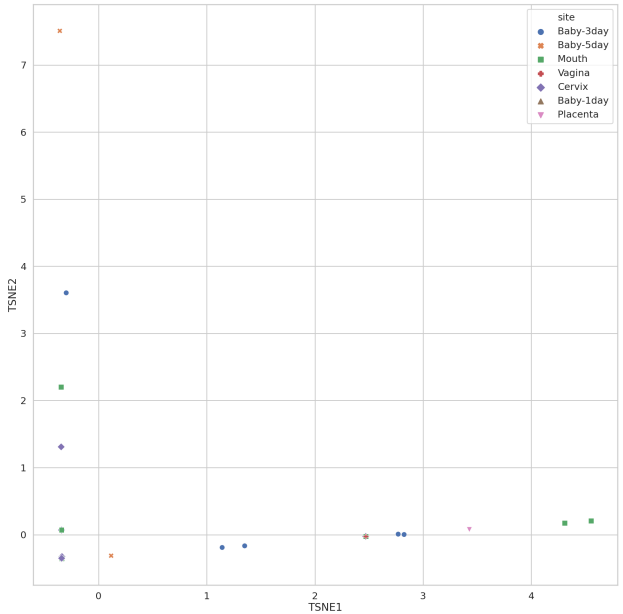


(b) DADA2 + SILVA

t-SNE with Site II



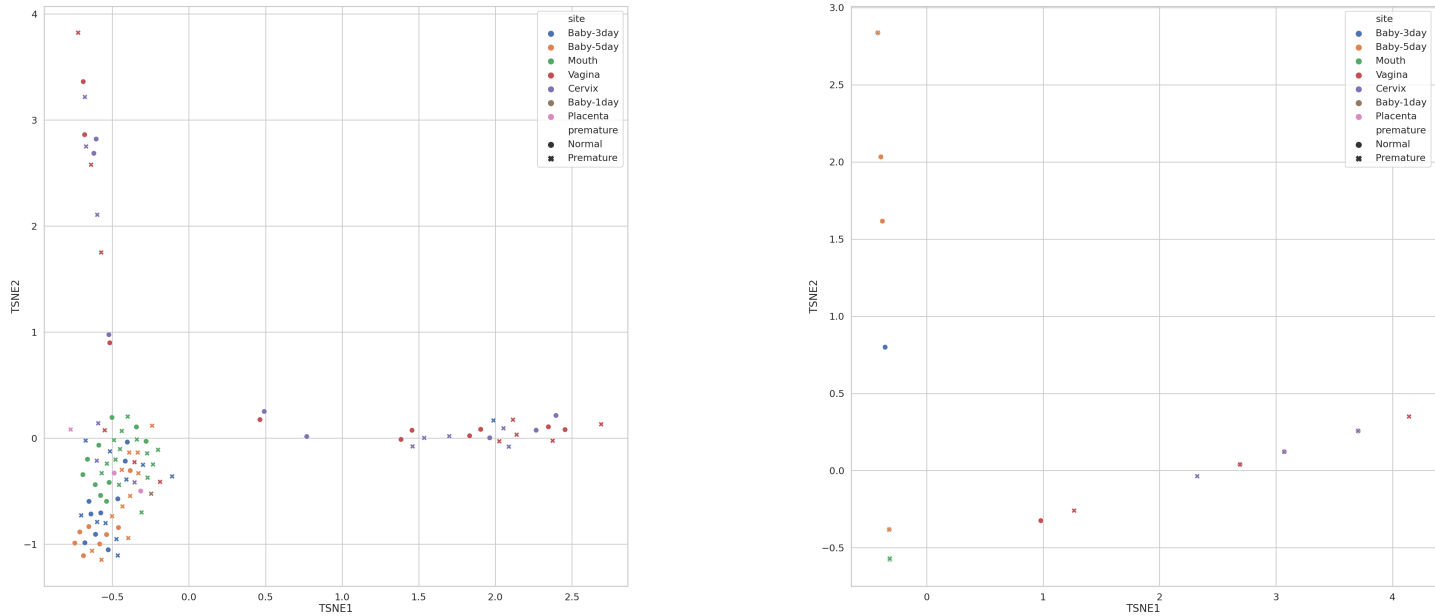
(c) Deblur + GG



(d) Deblur + SILVA

Figure: t-SNE with Site

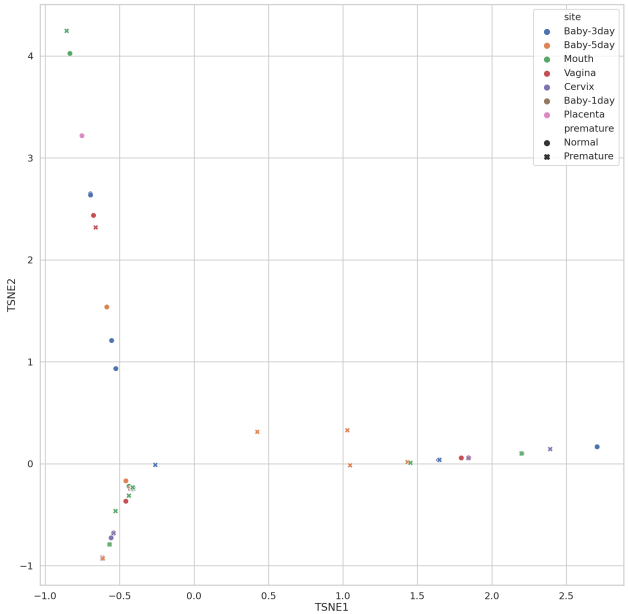
t-SNE with Site + Premature I



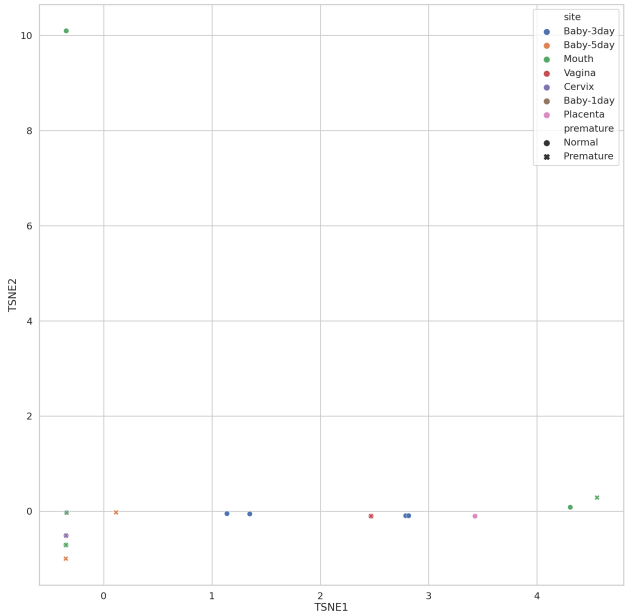
(a) DADA2 + GG (b) DADA2 + SILVA

Figure: t-SNE with Site

t-SNE with Site + Premature II



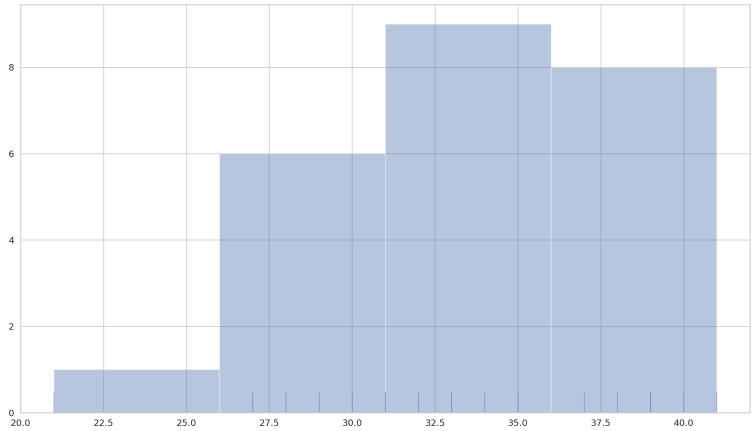
(c) Deblur + GG



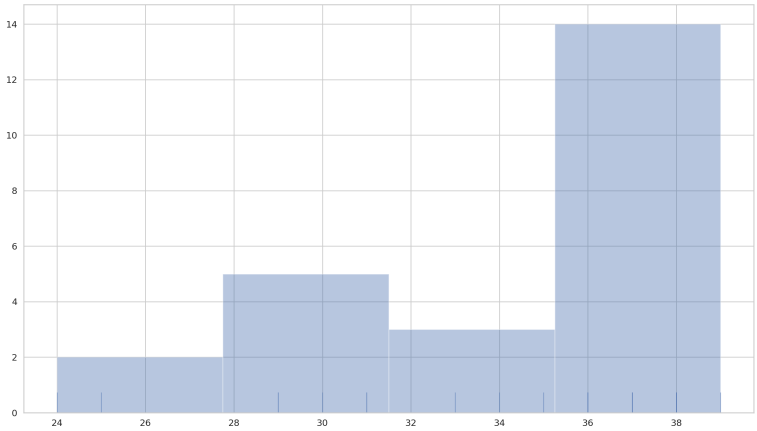
(d) Deblur + SILVA

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
- Have tried (but in vain)
  - ANCOM with premature/normal
  - Classification with raw TSV

Requirements I

- More data
- Mothur pipeline
- Classification

Expectations I

- Classifier result (Statistical values)

References I

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