Microbiome Premature

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3.1 QIIME 2

QIIME 2 is a next-generation microbiome bioinformatics platform which is extensible, free, open-source, and community developed.
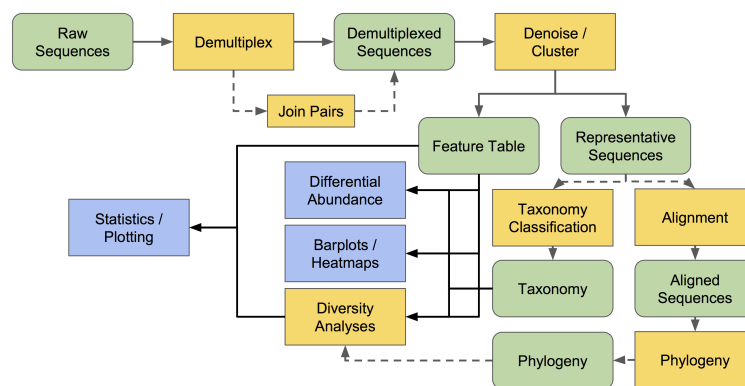

Figure 1: Workflow of Qiime2

3.2 Mothur

Mothur is an open-source software package for bioinformatics data processing, especially for the analysis of DNA from microbes (Schloss et al., 2009).

3.3 t-distributed Stochastic Neighbor Embedding

T-distributed stochastic neighbor embedding (t-SNE) visualizeds high-dimensional data by giving each data-point a location in a two-dimensional map (Maaten & Hinton, 2008).

4 Results

5 Discussion

References

Maaten, L. v. d., & Hinton, G. (2008). Visualizing data using t-sne. *Journal of machine learning research*, *9*(Nov), 2579–2605.

Schloss, P. D., Westcott, S. L., Ryabin, T., Hall, J. R., Hartmann, M., Hollister, E. B., . . . Weber, C. F. (2009). Introducing mothur: Open-source, platform-independent, community-supported software for describing and comparing microbial communities. *Applied and Environmental Microbiology*, *75*(23), 7537–7541. Retrieved from `https://aem.asm.org/content/75/23/7537` doi: 10.1128/AEM.01541-09
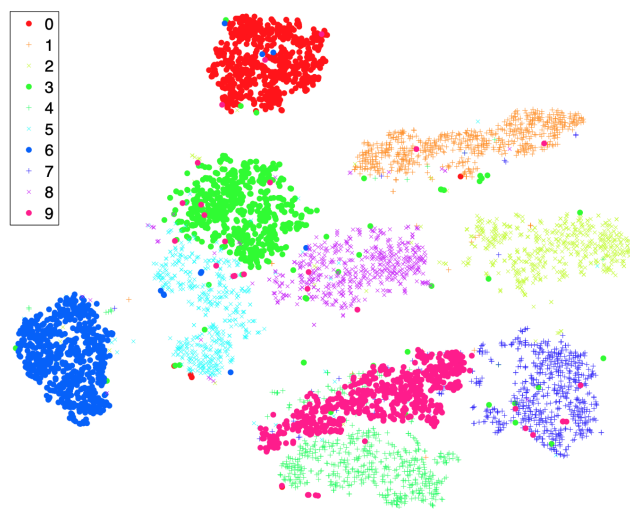
Figure 2: t-SNE Visualizations of handwritten digits from MNIST data (Maaten & Hinton, 2008)