

# Microbiome Premature

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# 1 Introduction

## 1.1 Microbiome

# 2 Materials

## 2.1 16S rRNA Sequencing

# 3 Methods

## 3.1 QIIME 2

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

## 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) visualizes high-dimensional data by giving each data-point a location in a two-dimensional map (Maaten & Hinton, 2008).

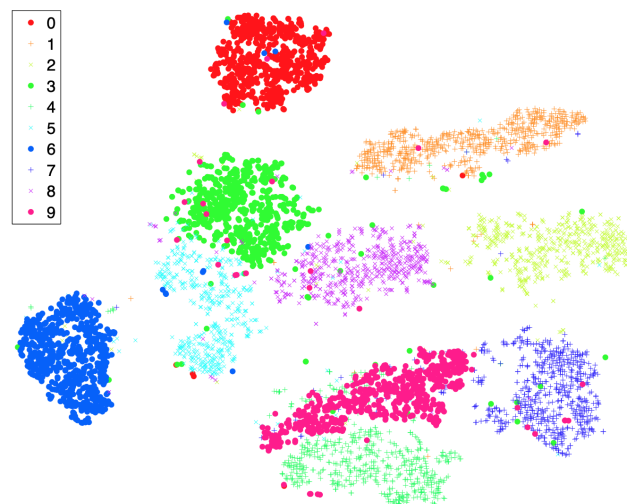


Figure 1: t-SNE Visualizations of handwritten digits from MNIST data (Maaten & Hinton, 2008)

# 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