

Microbiome Premature

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1 Introduction

1.1 Microbiome

1.2 Ribosomal RNA

1.3 Premature

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.

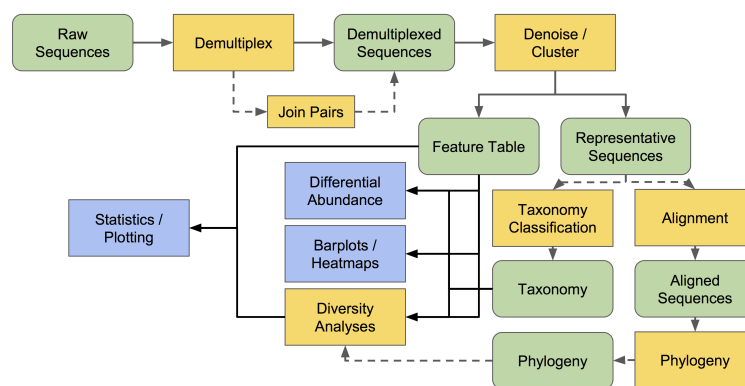


Figure 1: Workflow of Qiime2

3.2 Denoising Techniques

3.2.1 DADA2

DADA2 is an open-source software package for modeling and correcting Illumina-sequenced amplicon errors (Callahan et al., 2016).

3.2.2 Deblur

Deblur is a software packages which uses error profiles to obtain putative error-free sequences from Illumina MiSeq and HiSeq sequencing platforms (Amir et al., 2017).

3.3 Taxonomy Classification

3.3.1 Greengenes

Greengenes is a chimera-checked 16S rRNA gene database (DeSantis et al., 2006).

3.3.2 SILVA

SILVA is a comprehensive web resource for up-to-date, quality-controlled databases of aligned rRNA gene sequences from the Bacteria domains (Pruesse et al., 2007; Quast et al., 2012).

3.4 Mothur

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

3.5 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).

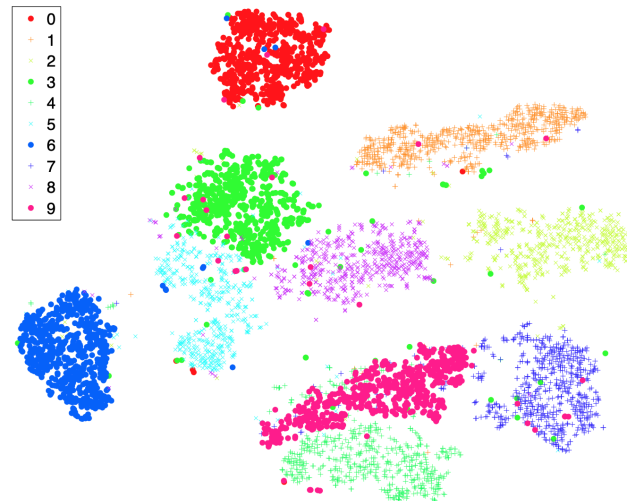


Figure 2: t-SNE Visualizations of handwritten digits from MNIST data (Maaten & Hinton, 2008)

4 Results

5 Discussion

References

- Amir, A., McDonald, D., Navas-Molina, J. A., Kopylova, E., Morton, J. T., Xu, Z. Z., . . . others (2017). Deblur rapidly resolves single-nucleotide community sequence patterns. *MSystems*, 2(2).
- Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., & Holmes, S. P. (2016). Dada2: high-resolution sample inference from illumina amplicon data. *Nature methods*, 13(7), 581–583.
- DeSantis, T. Z., Hugenholtz, P., Larsen, N., Rojas, M., Brodie, E. L., Keller, K., . . . Andersen, G. L. (2006). Greengenes, a chimera-checked 16s rna gene database and workbench compatible with arb. *Applied and environmental microbiology*, 72(7), 5069–5072.
- Maaten, L. v. d., & Hinton, G. (2008). Visualizing data using t-sne. *Journal of machine learning research*, 9(Nov), 2579–2605.
- Pruesse, E., Quast, C., Knittel, K., Fuchs, B. M., Ludwig, W., Peplies, J., & Glöckner, F. O. (2007). Silva: a comprehensive online resource for quality checked and aligned ribosomal rna sequence data compatible with arb. *Nucleic acids research*, 35(21), 7188–7196.
- Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., . . . Glöckner, F. O. (2012). The silva ribosomal rna gene database project: improved data processing and web-based tools. *Nucleic acids research*, 41(D1), D590–D596.
- 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