Microbiome Premature

Jaewoong Lee 2020-09-07

Contents

1	Intr	oduction	3
	1.1	Microbiome	3
	1.2		3
	1.3	Premature	3
2	Mat	erials	3
-	2.1		3
3	Met	hods	3
	3.1		3
	3.2		3
			3
			3
	3.3		3
		·	3
		e	3
	3.4		4
	3.5	t-SNE	4
	3.6	Python Packages	4
		3.6.1 Pandas	4
		3.6.2 Scikit-Learn	4
		3.6.3 Matplotlib	4
		3.6.4 Seaborn	4
4	Resu	ults	4
5	Disc	eussion	4
Re	feren	nces	4
Li	ist of	f Tables	
Li	ist of	f Figures	
		W. 10 COVE FEE	_
	1 2		3 4

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 (Bolyen et al., 2019; Mandal et al., 2015; McDonald et al., 2012).

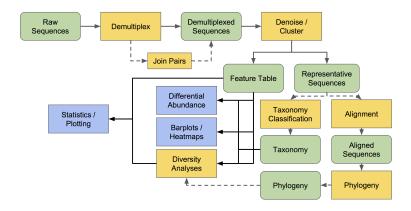


Figure 1: Workflow of QIIME2

3.2 Denoising Techniques

3.2.1 DADA2

DADA2 is an open-source software package for modeling and correcting Illumina-sequenced amplicon erros (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) visualizeds high-dimensional data by giving each datapoint a location in a two-dimensional map (Maaten & Hinton, 2008).

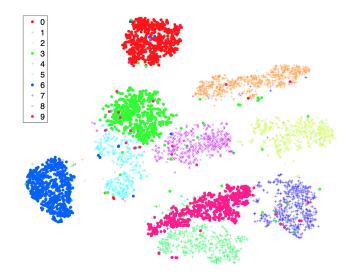


Figure 2: t-SNE Visualizations of handwritten digits from MNIST data (Maaten & Hinton, 2008)

3.6 Python Packages

3.6.1 Pandas

Pandas is a Python library of rich data structure and tools for working with structured data sets (McKinney et al., 2011).

3.6.2 Scikit-Learn

Scikit-learn is a Python module which integrating a wide range of state-of-the-art machine learning algorithms for medium-scale supervised and unsupervised problems (Pedregosa et al., 2011).

3.6.3 Matplotlib

Matplotlib is a two-dimensional graphics package used for Python for image generation (Hunter, 2007).

3.6.4 Seaborn

Seaborn is a Python data visualization library based on Matplotlib (Waskom et al., 2020).

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).

- Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., ... Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using qiime 2. *Nature Biotechnology*, 37(8), 852-857. Retrieved from https://doi.org/10.1038/s41587-019-0209-9 doi: 10.1038/s41587-019-0209-9
- 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 rrna gene database and workbench compatible with arb. *Applied and environmental microbiology*, 72(7), 5069–5072.
- Hunter, J. D. (2007). Matplotlib: A 2d graphics environment. *Computing in science & engineering*, 9(3), 90–95.
- Maaten, L. v. d., & Hinton, G. (2008). Visualizing data using t-sne. *Journal of machine learning research*, 9(Nov), 2579–2605.
- Mandal, S., Van Treuren, W., White, R. A., Eggesbø, M., Knight, R., & Peddada, S. D. (2015). Analysis of composition of microbiomes: a novel method for studying microbial composition. *Microbial ecology in health and disease*, 26(1), 27663. doi: 10.3402/mehd.v26.27663
- McDonald, D., Clemente, J. C., Kuczynski, J., Rideout, J. R., Stombaugh, J., Wendel, D., ... Caporaso, J. G. (2012). The biological observation matrix (biom) format or: how i learned to stop worrying and love the ome-ome. *GigaScience*, 1(1), 7. doi: 10.1186/2047-217X-1-7
- McKinney, W., et al. (2011). pandas: a foundational python library for data analysis and statistics. *Python for High Performance and Scientific Computing*, 14(9).
- Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., ... others (2011). Scikit-learn: Machine learning in python. *the Journal of machine Learning research*, 12, 2825–2830.
- 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
- Waskom, M., Botvinnik, O., Ostblom, J., Gelbart, M., Lukauskas, S., Hobson, P., ... Brian (2020, April). mwaskom/seaborn: v0.10.1 (april 2020). Zenodo. Retrieved from https://doi.org/10.5281/ zenodo.3767070 doi: 10.5281/zenodo.3767070