Helixco Cavity

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1 Introduction

1.1 Dental Cavity

Dental cavity is one of the most common bacterial infections in humans. *Streptococcus mutans* in the acquired enamel pellicle have a main role in human dental cavity (Loesche, 1986; Alaluusua & Renkonen, 1983).

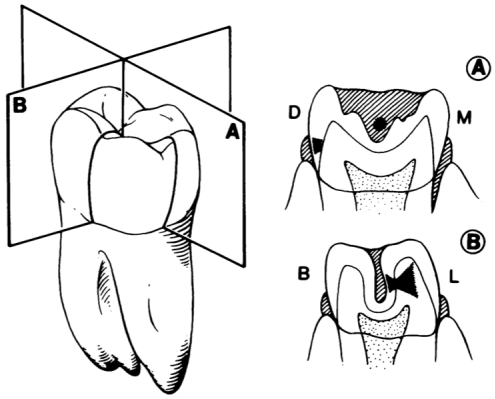


Figure 1: Saggital and cross-sectional sections through a permanent molar (Loesche, 1986)

1.2 Microbiome

Microbiome refers the genome of microbal symbionts which live inside and on human (Turnbaugh et al., 2007). Microbiome is highly personalized, and gives effects to human health.

2 Materials

2.1 16S rRNA Analysis

3 Methods

3.1 t-SNE

t-SNE is one of the dimension reduction algorithm which visualizes high-dimensional data by giving each data-point a location in a two-dimensional map. (Maaten & Hinton, 2008)

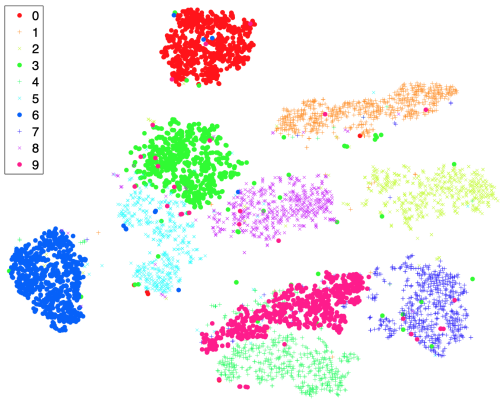


Figure 2: Visualizations of handwritten digits from the MNIST data set (Maaten & Hinton, 2008)

3.2 Programming Methods

3.2.1 Docker

Docker is light-weight linux containers for consistent development and deployment (Merkel, 2014).

3.2.2 QIIME 2

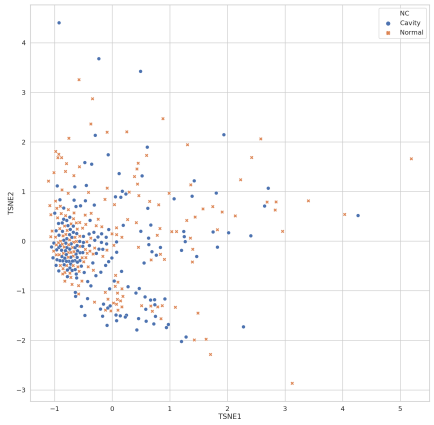
QIIME 2 is a powerful, extensible, and decentralized microbiome analysis package with a focus on data and analysis transparency.

3.2.3 Scikit-learn

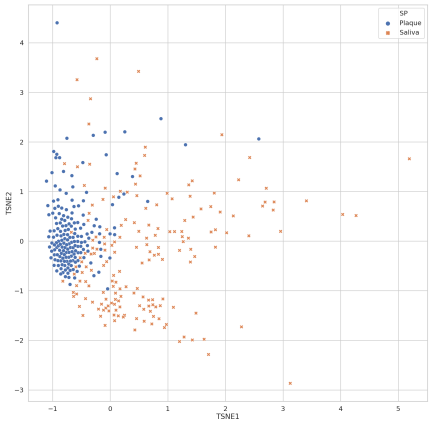
Scikit-learn is a simple and efficient tools for predictive data analysis (Pedregosa et al., 2011; Buitinck et al., 2013).

4 Results

4.1 t-SNE with Every Bacterium



(a) Normal vs. Cavity



(b) Saliva vs. Plaque

5 Discussion

References

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