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Abstract.

1 Introduction

2 Data

Tp make microbiome analysis, we use both sequenced DNA samples of dental calculus as the experimental sample and the tooth root as a proxy for an environmental control [1]. The reads were obtained using sequencing machine Roche GS Junior (454). The data are demultiplexed. This data is part of the research about dental calculus metagenome [2].

3 Methods

First, we perform analysis of raw 16S data. Next, we use assembled genome and compare results.

For microbiome analysis, we use package QIIME2 [3]. This utilities are specialized for an analysis of raw DNA samples. The programme allows to obtain statistical results for sequence qualities. This is important for quality control and helps us to choose parameters during analysis. Using Quality plot, we can find suitable parameters to filter 16S amplicon samples from barcode, primer and artifact sequences.

DADA2 commande from QIIME2 package generates Matrix (Feature table), which contains measure the number of times each feature was observed in each sample. We can consider features as Operational taxonomic units (OTU). So, this is analogue of clustering OTU.

Next, we can find taxons which are contained in our metagenome samples. QIIME2 contains taxonomy classifiers based on Naive Bayes classifier. We use model pretrained on Greengenes Database [4]. Database consists of samples of full-length 16S rRNA genes.

After using taxonomic classifier, we get taxonomic composition which could be visualized as barplots for nice analysis. This is interesting for us as we can find bacterial groups such as Red complex, which is associated with periodontal disease.

Next, we perform analysis of whole genome. We use utilities MetaPhlAn for profiling the composition of microbe groups [5]. The approach is based on alignment our sequencing reads to the microbiota database. The MetaPhlAn tool allows to produce heatmap, which contains distances between samples using Bray–Curtis dissimilarity [6].

4 Results

References

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