# Background

Bacteria have different numbers of 16S rRNA genes and different amounts of variability across them. Furthermore, the specific 16S rRNA genes are often shared among bacteria.

# Problem

16S rRNA gene sequencing is often used for quantification of bacterial diversity and for bacterial identification. Here, different copy number, different variability of the 16S rRNA gene and the sharing of 16S rRNA genes can lead to inaccurate results.

Therefore, it is important to better understand the factors which affect the 16S rRNA genes multiplicity and diversity.

# Hypothesis

We hypothesize that ecological factors influence 16S rRNA gene diversity in bacteria.

# Aim

The aim of this project is to establish correlations between the variability and abundance of 16S rRNA genes and ecological factors. This will be done through datamining both databases and bacterial genomes for 16s rRNA gene information and ecological information.