**Analyze your gtdb-tk output in groups**

**A) Look inside your *gtdbtk.log* file. Has it run until it was done, still running or encountered an issue?**

It ran until it was done

**B) *Look inside your gtdbtk.\*.summary.tsv* files. How many bacterial and archaeal genomes did your group have?**

We have the two files:

1. gtdbtk.ar53.summary.tsv
2. gtdbtk.bac120.summary.tsv

In the ar53 output we see that there is identified archeal genomes for two bins from samples 8020 and 9020. In the bac120 we see that gtdb have identified 69 bacterial genomes from the 4 different samples.

**C) Do you have any MAGs where GTDB-tk couldn’t assign the species, there are no warnings suggesting contamination, and the msa\_percent (i.e. completeness) is above 50%?**

No, all the MAGs where gtdb couldn’t assign a species we see a red\_value indication indicating unusual characteristics. If we had such a MAG it could be a new species.

**D) How many different families of bacteria did your group have according to GTDB-tk?**

27 families

**E) Try to open your Newick tree files in e.g. FigTree and determine out how to color the genomes from a specific farm**