Comparing two metagenomic sample sets:

1. How many sequences were uploaded for each of the datasets?
2. What type of sequencing chemistry/technology was used to produce this data?
3. What types of sequencing platforms were used during the [global ocean sampling expedition](http://metagenomics.anl.gov/mgmain.html?mgpage=project&project=mgp27" \t "_blank)?
4. How many other metagenomes are available based on the sequencing technologies for the “[global ocean sampling expedition](http://metagenomics.anl.gov/mgmain.html?mgpage=project&project=mgp27" \t "_blank)”?
5. How many eukayotic phyla are present among the sequences in each dataset do you observe at the e -10 and e -20 significance levels?
6. Why do you find differences in results at e -10 and e -20 significance levels?
7. Look at the rarefaction curves, for each of the sample, which of the phyla would you consider to be rare?

Comparing multiple metagenomic sample sets:

1. How many sequences were uploaded for each of the datasets?
2. What type of sequencing chemistry/technology was used to produce this data?
3. At the phylum level, how many Actinobacteria and Bacteriodetes sequences do you observe in each dataset?
4. Can you find a reason for such high levels of Bacteriodetes?
5. What do you observe when you vary the taxa level of the heatmap for this dataset?