Group work Wednesday

1. Introduce yourself (in case you have not met)
2. OTUs versus ASVs – what is the difference (if there are any)?
3. What are potential negative effects of rarefying your data down to a certain number of sequences per sample?
4. How might the removal of “singletons” affect your results? And what should be the threshold for a “singleton” (one sequence, two, etc.)?
5. Is any transformation of your final data matrix appropriate – and why?
6. If you have sequences in your negative controls – what will you do and why?
7. If you have additional sequences in your mock community (of other species) – what will you do?
8. If you have used technical replicates in your setup (e.g. introduced at the extraction or PCR level) and they differs widely – what will you do?