Project topics suggestions

Team Microbiome

1. Develop analysis pipeline to process Microbiome data from a published study. Focus on existing clustered "OTUs" already not the first steps

2. Metagenome analyses. Take existing, published metagenomes and compare abundance of specific enzymes classes between the two.

Team Gene

1. Use a genome annotation of a set of species (plants, microbes might be best) to compare the differences in gene lengths, intron lengths, Untranslated lengths across the species. This is generating sumamry statistics about annotated genes.

Team Transcriptome

1. Identify a published RNAseq dataset for at least 2 conditions with replicate. Process the RNAseq to identify gene expression differences and identify if there are different functional classes of genes found in genes which are up or down regulated.

Team Proteins

1. Compare the protein content among sets of organisms. For example, Can develop a classifier for outlier proteins and/or ecological adaptations (thermophillic vs halophillic).

2. Examine the differences in Protein domain distribution between species.

Team Russian Doll

1. Many organisms have undetect symbionts of bacteria or viruses. Develop an analysis to look at sets of either assembled or unassembled bacteria to look for associated viruses (bacteria phage). Or develop a pipeline too look at assembled eukaryotic genomes and detect bacteria in the genome assemblies.