

## Class Projects

1. *MutMapper* - Identify transposon, EMS, or UV induced mutations in a strain as compared to a reference genome. *Beth, Daniel*
2. *Transcriptomicon / RNAseq* - Develop a pipeline for processing raw RNAseq, assembling into transcripts, identifying ORFs, and extracting genes which have long UTRs, features. *Amanda, Mari, Madison, Tierney*
3. *Phylotrantrum / Gene Tree* - Build a pipeline to take a single gene sequence (protein) and identify homologs, align these, trim, and build gene trees. Refine tree or alignment to remove outliers and build a final gene alignment and Tree. *Laura, Luke, Sam, Stephanie*
4. *Selectable Gene Trees* - Selection identification by dN/dS analysis of paralogs/orthologs. *Kaleigh, Josh*
5. *INDELible* - Taking population genomic resequencing data, identify insertion/deletion patterns across a genome. Are there non random distributions of indel size across a chromosome? Generate reports/interactive view of indel sizes and sequence preferences. *Glen, Chris*
6. *Microbiomifcation\_16Ssss* - Process 16S data to ask questions about OTU picking and mapping to better custom databases *Hannah, Nicole, Nat, Julia*
7. *ProteinStatsClassify* - Protein statistics from protein. Can develop a classifier for outlier proteins and/or ecological adaptations (thermophilic vs halophilic). Using Bacteria and Fungal sequences. *Jesus*