

Project Ideas for Class projects

1. *MutMapper* - Identify transposon, EMS, or UV induced mutations in a strain as compared to a reference genome.
2. *Transcriptomicon* - Develop a pipeline for processing raw RNAseq, assembling into transcripts, identifying ORFs, and extracting genes which have long UTRs, features.
3. *Phylotantrum* - 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.
4. *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.