Task list for development of genTB in order of priority:

1. Familiarilize yourself with website, gain access to orchestra
2. Make a list of improvements/tasks to streamline work flow
3. Complete Predict Pipeline
4. Allow download of predict pipeline intermediary files (vcf and var files)
5. Convert Maps from R to python and add the following features:
   1. Maps to allow graphing the pooled country data
   2. Maps to allow two by two table or bar chart of mutation vs drug resistance data.
6. Implement two parallel predict pipelines one that extracts snps from fastq for those not interested in intermediary files, and the one that we currently have
7. Implement a pipeline that allows bacterial lineage calls from WGS using Tom Ioerger or Taane Clark’s method
8. Develop a new page to allow for power calculations based on R code
9. Develop a new page to allow for data analysis based on R, perl and bash code for genomic data analysis (GWAS)