

Mark is working on the server, database, and containerization

Forest develops the client and defines the api requests

NCBI Server

SeqSim Server

SeqSim Server requests data from NCBI

NCBI responds to request with all genomes

Client requests data with get request

Server responds to with data structure for client

Client posts data from sample review

Server responds with static Krona plot and phylotree images

Client posts data from sample to execute analysis script

Server responds with data for review page, static Krona plot, and phylotree images

Server executes a script to transform data

Server executes script on post request to create genome and display static images as output

Server executes a script to generate static phylogenetic tree and krona plot for review

1: a) Define a data structure that will be used in the client
b) Transform raw NCBI data into a useable format
c) Connections between disparate tables can be defined in the database

2: We want to create static images for plots for the user to review until we have found a good way to develop custom dynamic krona plots in JS and D3.
· UI will be tricky because we want the user to change things like relative abundance and then be able to check these plots to ensure there sample is as expected. For now this process will require client/server communication, but this will be move to the client in the future.

3: We need to iterate on what the output is going to be. The last mockup described it as 4 things (Krona Plot, Error plot, Tree plot, and GC% Coverage Plot). These will all be static files until we have figured out how to combine D3 and JS on the front end.
· What inputs do we need to build a each plot?

Justin will develop the scripts here to support the client