

Project Title: GWAS tool: Implementation and Evaluating Genetic Visualization using Python

Group Members:

Elliott Ou A17370009

Lenny Lei A16727065

Audria Montalvo A16192284

Tool Description: Our tool will run GWAS for a dataset containing genotypes and phenotypes, and produce QQ plots and manhattan plots for visualization. We will compare the tools to the ones used in lab3. To create the results, we will utilize python scripts similar to how lab 3 is done.

Benchmarking: We will compare our results using the tool to results if we were to use the plink tool instead, similar to the steps in lab3. We will compare plots, clumps, and p values generated from our tools and plink to see if our tool performs as expected.

Dataset: We can use <https://www.internationalgenome.org/data-portal/sample> to get samples for genotype files. We will have to simulate our own phenotype files, since the phenotypes are not able to be found on 1000 genomes. We can also use the files from lab 3 to test efficiency and accuracy between our tool and the plink tool.