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MDSC 679: Machine Learning Project 1

Abstract

Introduction

*Arabadopsis thaliana* is an important model organism which has a relatively short life cycle, small genome with 135 megabase pairs (Mbp) and community curated . *A. thaliana* is useful for studying multifactorial traits such as flowering time (FT) that are potentially regulated by the interaction of multiple genes on various chromosomes and stimulus from the environment.

The goal of this particular study is to find the relationship of genotype to phenotype for the flowering time (FT) trait. Leveraging this knowledge I hope to. Since this is a

In this study only homozygous genotypes were observed. Making it quite difficult to use the fischer exact test for Hardy-Weinberg Equilibrium (HWE) for each Single Nucleotide Polymorphism (SNP) variant because of the significant derivations to HWE.

Methods

In order to study the genetic causation of flowering time (FT), a phenotype to genotype mapping study was conducted to assess the underlying mechanism of the trait. A genome wide association study (GWAS) was conducted using 251 individuals. A panel of 214553 variant SNPs were genotyped and analyzed using a custom pipeline implemented in the python and the R programming languages. The pipeline workflow is captured in the following figure x. In the first step, the quality control workflow was developed in python for filtering the data for further analysis. The quality\_control.py script performs the following tasks. Flowering time phenotypes are filtered for “NA” values, which indicated that those genotypes had missing data and were removed. A total of 238 phenotypes were retained for further processing of individual genotypes. Genotypes were first filtered for biallelic SNPs. Genotypes with flowering time phenotype data were assessed for minor and major allele frequency. Alleles of each variant were observed and counted, and minor and major alleles were determined. After filtering by phenotypes and biallelic SNPs, the Minor Allele Frequency (MAF) of each variant was calculated. Variants with a MAF of greater than or equal to 0.01 were retained and considered for further analysis. A total of 230 genotypes and a total of 214219 variants were retained before association testing SNP sets. All variants were subjected to blank tests (paper) to assess the population for genotyping quality, population stratification and as test of association of using a blank model. Variants with a P-value of less than or equal to α = 10-4 were retained for further processing as this indicated that they were significant with a False Discovery Rate of 5%. A total of xxx individual genotypes and XXX variants were retained. The type I error rate was assessed using a Quantile-Quantile Plot (QQ-Plot) shown in figure x. The plot indicates that the type I error rate is under control and further analysis can be performed. A Manhattan plot (−log10(P) genome-wide association plot)

was generated to visualize significant SNP variants across the entire genome in the locations that were genotyped. Genotypes at each SNP variant that passed the filtering procedure were encoded 0 for the major allele and 1 for the minor allele. Genotypes and corresponding phenotypes were written to a file for input into the machine learning models.

The second step of the workflow executes the machine learning models, artificial neural network (paper), Support Vector Machine (SVM) (blank), and Random Forest (blank).

The dataset criteria for input into the three models were the following. Genotypes were filtered using MAF >= 0.01, adjusted p-value (q-value blank) alpha<=0.05 for an FDR of 5%, and the major allele (reference) was encoded as 0 and the minor allele (alternative) was encoded as 1 and Phenotypes were filtered by missing values in the quality control step. There were 230 genotyped individuals and xxx SNP variants used as input for each of the three models. All machine learning models were implemented in the python scikit-learn package version x (blank). The encoded genotype files were parsed using the python pandas version x (blank) and loaded into a numpy array using the python numpy package version x (blank) for each model. Then a cross-validation approach ( which one ) was used in order to validate the hyperparameter (look up more information). Then a test set was used for prediction.

## Need to structure the artificial neural network (paper), Support Vector Machine (SVM) (blank), and Random Forest (blank) methods. Then talk about it in the results/discussion.

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A search for *Arabadopsis thaliana* genes known to be associated with flowering time was conducted using the TAIR website (<https://www.arabidopsis.org/>). A total of 79 genes were found using the search term “flowering time” and the accession numbers were downloaded. The 79 genes found in the TAIR database were compared to the genes with variants to assess whether or not these “flowering time” associated

genotypes.csv

Annotations (gene\_model.gff)

References:

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