Knowledge about how changes in gene expression are encoded by expression quantitative trait loci (eQTLs) is a key to construct the genotype-phenotype map for complex traits or diseases. Traditional eQTL mapping is to associate one transcript with a single marker at a time, thereby limiting our inference about a complete picture of the genetic architecture of gene expression. Here, I present innovative applications of variable selection approaches to systematically detect main effects and interaction effects among all possible loci on differentiation and function of gene expression and other phenotypes of interest. Forward-selection-based procedures were particularly implemented to tackle complex covariance structures of gene-gene interactions. Simulation studies were performed on each of the models to assess the computational properties of each model. Applications of the models were also performed on real datasets. The first was a reanalysis of a published genetic and genomic dataset collected in a mapping population of Caenorhabditis elegans, gaining new discoveries on the genetic origin of gene expression differentiation, which could not be detected by a traditional one-locus/one-transcript analysis approach. The next dataset was of Mei Tree growth, analyzing the genetic control of the height and diameter during the developmental process. The underlying genotypes and epistasis that impact the process of these developments were considered as candidates for the selection of the procedure.

\documentclass{article}

\usepackage[utf8]{inputenc}

\usepackage[english]{babel}

\pagenumbering{roman}

\begin{document}

\tableofcontents

\section{First section}

\setcounter{page}{11}

\section{Second section}

\section{Heading on Level 1 (section)}

\pagenumbering{arabic}

Chapter 03

\*\*Shoot-Root Manuscript\*\*

Following Sun et al.’s \cite{sun2014model} developmental model, we calculated and chose four key heterochronic parameters, asymptotic growth (a), relative growth rate (r), the timing of inflection point (TI), and the duration of linear growth (L), as phenotypic values to perform QTL mapping. A great variability was observed for growth curve parameters of both phenotypic traits (Table 1). Compared with taproot length, shoot length has a greater rate of growth and reaches the maximum growth rate at an earlier

Chapter 04

Advantages

* Computationally efficient algorithm for static phenotypes
* Includes epistatic interactions in a meaningful/biologically relevant manner
* Incorporates functional component
  + Parsimonious able to fit growth parameters during the fitting of

Areas of concern

* Many areas of estimation error
* Overfitting because of flexibility
* Need for lab verification
  + Used as screening tool

complex and many moving parts to the selection procedure. Very flexible but this could have it be prone to over fitting at times if not well controlled.

With the complexity and expense that comes with genetic mapping, espically with a functional trait that needs repeated measures

Used as a screening tool for initial findings and exploratory data analysis to aid and guide future research. Needs to be then be lab validated. Especially with something as intricate as epistatic effects between gene markers.

Further investigations are needed to confirm or modify our findings by QTL mapping in natural populations.