

The Pennsylvania State University

The Graduate School

College of Medicine Public Health Sciences

**STATISTICAL MODELS FOR HIGH DIMENSIONAL SCREENING OF
GENETIC AND EPIGENETIC EFFECTS**

A Dissertation in

Biostatistics

by

Kirk Gosik

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The dissertation of Kirk Gosik was reviewed and approved* by the following:

Rongling Wu

Distinguished Professor of Public Health Sciences and Statistics

Thesis Advisor, Chair of Committee

Vernon Chinchilli

Distinguished Professor and Chair of Public Health Sciences

Lan Kong

Associate Professor of Public Health Sciences

James Broach

Distinguished Professor and Chair of Biochemistry and Molecular Biology

Abstract

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.

Contents

List of Tables	1
List of Figures	1
1 Introduction	1
1.1 Background	1
1.2 Some Existing Methods	3
1.3 Chapter Overview	5
2 High Dimensional eQTL	11
2.1 Motivation	11
2.2 Methods	14
2.3 Application	20
2.4 Discussion	28
3 High-order Epistatic Networks	33
3.1 Motivation	33
3.2 Methods	35
3.3 Application	42

3.4	Discussion	54
4	iForm Functional Mapping (A computational method)	57
4.1	Motivation	57
4.2	Methods	60
4.3	Application	67
4.4	Discussion	71
5	Conclusions	73
5.1	Summary	73
5.2	Discussion	75
5.3	Future Steps	76
5.4	Aim 2	77
6	Appendix	81
	Bibliography	81

List of Tables

1.1	Here is a nice table!	9
2.1	Simulation 1 Table (sigma=1)	22
2.2	Simulation 2 Table (sigma=2)	22
2.3	Simulation 3 Table (sigma=3)	23
2.4	iFORM Single Marker Analysis	26
2.5	Distribution of cisQTLs	28
3.1	Table 1 Simulation results when the truth obeys strong heredity	45
3.2	Table 2 Simulation results when the truth obeys weak heredity	45
3.3	Table 3 Simulation results when the truth is anti-heredity	46
3.4	Table 4 Simulation results when the truth is constructed of pure interactions	46
3.5	Table 5 The detection of epistasis for the relative growth rate (r) of shoot length in the full-sib family of mei tree by a low-order epistatic model	49
3.6	Table 6 The detection of epistasis for the relative growth rate (r) of shoot length in the full-sib family of mei tree by a high-order epistatic model	51

List of Figures

1.1	SNP Picture	2
1.2	Systems Map	8
1.3	Here is a nice figure!	8
2.1	SNP Picture	24
2.2	SNP Picture	25
3.1	Growth Curve Comparison	51
3.2	Epistasis Comparison	53
4.1	First 10 Legendre Polynomials	64
4.2	Example Growth Curve	68
4.3	Example Data with Growth Cruve	68
4.4	Additional Legendre Fit to Data	69

Chapter 1

Introduction

1.1 Background

There are several techniques used for studying genetics and mapping the results. Some of the more popular techniques include cross-breeding experiments or, in the case of humans, the examination of family histories, known as pedigrees. More recently, CRISPR/Cas9 can be used to mimic mitotic recombination to help map out genes as well. (?)

Construction of genetic maps are a variety of techniques used to show relative positions between genes or other sequence features of the genome and the phenotype that is controlled by such sequences. Genes are very useful markers but they are by no means ideal. One problem, especially with larger genomes such as those of vertebrates and flowering plants, is that a map based entirely on genes is not very detailed.(?) Genes have long areas of non-coding regions between them and therefore result in large gaps from gene to gene. This is further complicated because not every gene has allelic forms that can be easily or conveniently distinguished. With these considerations in

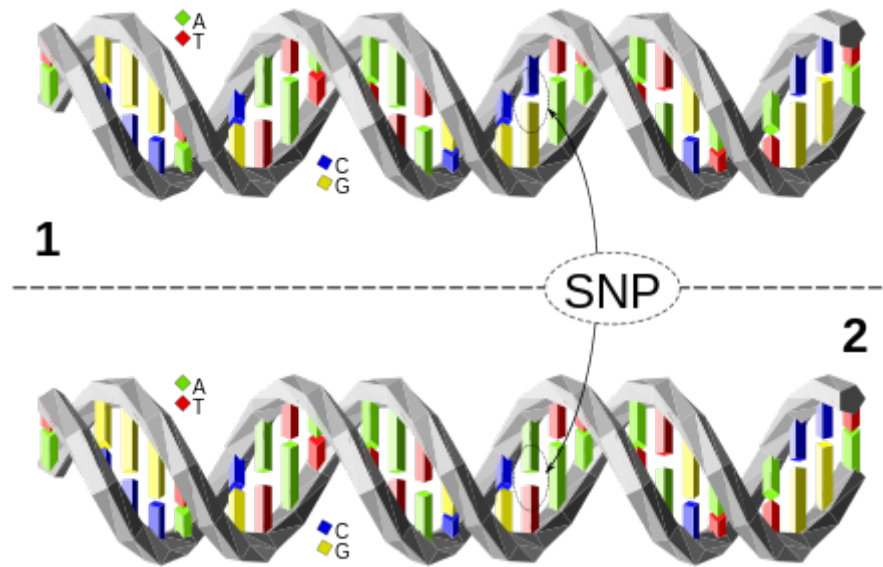


Figure 1.1: SNP Picture

mind gene maps may not be comprehensive enough and other markers may be needed.

According to brown, mapped features that are not genes are called DNA markers. As with gene markers, a DNA marker must have at least two alleles to be useful. There are three types of DNA sequence feature that satisfy this requirement: restriction fragment length polymorphisms (RFLPs), simple sequence length polymorphisms (SSLPs), and single nucleotide polymorphisms (SNPs). (?) The genetic markers that have been emphasised in this work are single nucleotide polymorphisms. Attempting to be at the highest levels of resolution for identifying quantitative traits, using SNPs are the most specific case. This will give exact location of the nucleotide that may be impacting the genetic control over the phenotype.

There are several goals to genetic mapping and association studies that identify certain regions of the genome that contain genes involved in specifying a quantitative trait, referred to as quantitative trait loci (QTLs). One main goal is to estimate the genetic effects of these loci. The relationship between the genetic effects of QTLs and the phenotypic value of quantitative traits can be described

by a linear model (1, 2). Typically, because of the high throughput nature of the data there are a large number of markers across the whole genome, and most of the markers may have very little or next no effect on the phenotype under study. The models can be very sparse, with most cases, the number of genetic markers or variables is bigger than the sample size, especially when interactions among markers are considered. This makes a model is oversaturated and further model selection techniques may be required to capture the necessary information. 3

1.2 Some Existing Methods

Numerous methods exist and are being developed to measure and find quantitative trait loci (QTL) effects. These methods can broadly fall into three main categories. These categories are Least-Square methods, maximum likelihood and Bayesian approaches. (4) Each method has advantages and considerations that you would need to be aware before conducting analyses to find QTL effects from the given markers. A brief discussions on a few of the methods are given to highlight some areas of consideration and how the methods proposed can handle such considerations.

Marker Regression would fall in the category of Least Squares approaches. If looking at one marker analysis general t-test and ANOVA procedures can be used to analyze the relationship. It is not recommended however for use in general practice because you do not know how dense the markers are measured. QTL interval mapping would be preferred in such an analysis because the methods take account for missing genotype data that may not have been measured. When estimating a QTL position through maximum likelihood methods, like interval mapping, positions of other possible QTLs could affect the detection of the true position. Neighboring QTLs could possibly flatten the likelihood in instances where there are multiple QTLs on the same chromosome. This would make

an effect look less significant at a given location than it actually is. Another possibility is that in the search over the interval you may find an area where the likelihood could reach a peak but could be a “ghost” QTL. This is where an effect is observed because a neighboring QTL is skewing the results at the particular position you are looking in and the result is a false discovery of the position. Marker Regression has been shown to improve interval mapping, which is call Composite Interval Mapping. This is where the QTL position found is also combined in a linear regression where the covariates are the other markers in the dataset. By including the markers as covariates the other position in the chromosome are accounted for in the analysis and false discovery is reduced.

The analysis of interval mapping and single marker analyses has shown to be effective but it limits our inference to one marker at a time as a possible loci that controls a trait. Using Marker Regression however you can incorporate multiple markers in a single analysis to test for possible QTL for a given trait. It is cautioned that running such an analysis is only an approximate test because the null hypothesis is there is no difference between the marker levels and therefore a non-mixture distribution but the alternative is a mixture of distributions. The assumptions regression would make of the errors within the marker type to be normally distributed may not be entirely met if the QTL’s fall between the marker regions. However ? have shown that a direct regression of phenotypes on marker types, provides the same information about location of QTL-effects without having to step to all positions on the interval. With this information using the entire marker set in a regression analysis would provide a nice, computationally efficient way to map out the genetic architecture of a trait.

1.3 Chapter Overview

The main goal of this paper is to propose an improved selection procedures which use regression techniques to approach high scale variable selection problems such as the ones arising in epistatic analysis

The variable selection procedure for QTLs mapping can be seen as one of deciding which subset of variables have effects on phenotypes, and identifying out all possible effects of those markers.

1.3.1 HighDeQTL

In this chapter we introduce the iform procedure, originally proposed by (hao and zhang 2014). This includes the algorithm and how it compares to forward selection. From there it is adapted to use for a genetic mapping studies. The properties of this will be explored in detail. Simulation studies were conducted to assess the properties. These were also compared to other models to get a sense of the utility and advantages that come with the new selection procedure. After the comparisons and simulations a real world application is performed. In the application a data set using C Elegans

The model performed well but feedback was given on... consider weak heredity

Needs more flexibility

a lot of important genetic variance and heritability were discovered by the inclusion epistatic effects. These effects boost the overall variance explained and predictive power of the final model selected.

1.3.2 Higher Order Epistasis

Higher order epistasis is important but under studied because of practical limitations not because of biological limitations

from chapter 03 The theoretical models of high-order epistasis have well been established by mathematical biologists (??). These models provided a foundation to interpret high-order epistasis from a biological standpoint. A few statistical models have been derived to estimate and test high-order epistasis in case-control designs (?) and population-based mapping settings

By extending the order of interaction effects the properties would still need to be studied. The theoretical properties that held for the iForm procedure were inspected again. Simulation studies were performed to assess practical applications. Several scenarios and comparison models were considered to extensively look at what properties were being met and which were not. Then an application to Mei tree growth was conducted in order to see the real world application of such a selection procedure. Different growth parameters were previously fit and these were used as the phenotype. Interesting and more predictive implications came out of the model when considering higher order epistasis throughout the selection procedure.

The static growth parameters were interesting but using the entire growth curve would be more beneficial to capture all relevant information.

1.3.3 iForm Funcional Mapping

In order to use all relevant information of the repeated measure data would take additional computation burden to the selection and the modeling but it would also give more power and

flexibility to the modeling that would not be present otherwise. It is important to use all relevant information in order to make the most accurate prediction about the data.

Using a growth curve model to assist in fitting the data would help ease some of the computational burden. The selection of genetic effects however would be very simplistic as some additive shift to the curve. This simplistic view may not be the most accurate and therefore more complicated structures could produce better results. As we have seen in Chapter 03, the genetic effects over time seem to vary among different genotypes and the interaction effects follow more of a non-linear pattern. In order to allow for more flexible, non-linear modeling without expending too much computation burden, Legendre Orthogonal Polynomials were considered to model the genetic effects. These polynomials have various forms and would allow for the genetic effect to follow different patterns but also not induce unnecessary correlation between predictors included in the model.

These benefits do come at a computational cost but by including the repeated measures portion of the data it enabled for the use of more data and therefore increase the power of the modeling.

You can label chapter and section titles using `{#label}` after them, e.g., we can reference Chapter 1. If you do not manually label them, there will be automatic labels anyway, e.g., Chapter 2.2.

Figures and tables with captions will be placed in `figure` and `table` environments, respectively.

```
par(mar = c(4, 4, .1, .1))  
plot(pressure, type = 'b', pch = 19)
```

Reference a figure by its code chunk label with the `fig:` prefix, e.g., see Figure 1.3. Similarly, you can reference tables generated from `knitr::kable()`, e.g., see Table 1.1.

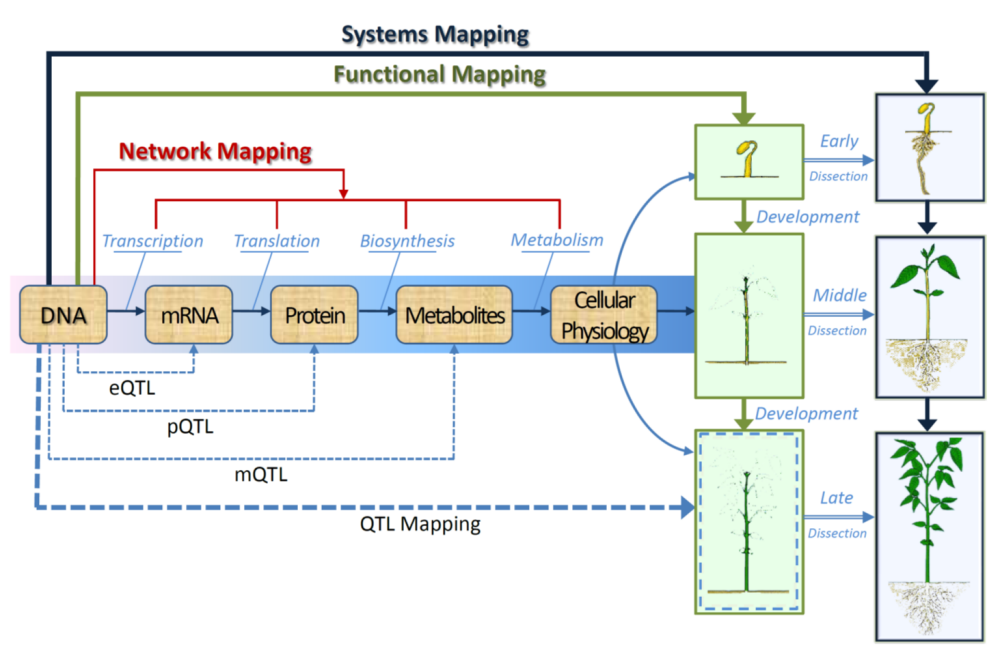


Figure 1.2: Systems Map

Figure 1.3: Here is a nice figure!

```
knitr::kable(
  head(iris, 20), caption = 'Here is a nice table!',
  booktabs = TRUE
)
```

You can write citations, too. For example, we are using the **bookdown** package (?) in this sample book, which was built on top of R Markdown and **knitr** (?).

Table 1.1: Here is a nice table!

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa
4.6	3.4	1.4	0.3	setosa
5.0	3.4	1.5	0.2	setosa
4.4	2.9	1.4	0.2	setosa
4.9	3.1	1.5	0.1	setosa
5.4	3.7	1.5	0.2	setosa
4.8	3.4	1.6	0.2	setosa
4.8	3.0	1.4	0.1	setosa
4.3	3.0	1.1	0.1	setosa
5.8	4.0	1.2	0.2	setosa
5.7	4.4	1.5	0.4	setosa
5.4	3.9	1.3	0.4	setosa
5.1	3.5	1.4	0.3	setosa
5.7	3.8	1.7	0.3	setosa
5.1	3.8	1.5	0.3	setosa

Chapter 2

High Dimensional eQTL

2.1 Motivation

Since activation or inhibition of gene expression causes change in phenotypic formation, the identification of expression quantitative trait loci (eQTLs) that regulate the pattern of gene expression is essential for constructing a precise genotype-phenotype map (1; 2; 3). With the advent and development of various biotechnologies, it has become possible that genome-scale marker and expression data can be generated, providing an important fuel to systematically study the biological function of any types of cellular components in an organism (4; 5; 6). Several genome-wide association studies (GWAS) have been initiated to map a complete set of eQTLs for the abundance of genome-wide transcripts whose expression levels are related to biological or clinical traits (7; 8; 9). Statistical analysis and modeling are playing an increasing role in mapping and identifying the underlying eQTLs from massive amounts of observed data (10; 11; 12; 13).

A typical eQTL mapping approach is to associate a gene transcript with a single marker such as

single nucleotide polymorphism (SNP). By analyzing the significance of all these markers one by one adjusted for multiple testing, one can count significant loci that contribute to variation of expression by the gene. This marginal approach based on a simple regression model has been instrumental for the identification of eQTLs in a variety of organisms (??). However, there are two major limitations for the results by such a marginal analysis: First, it does not take into account the dependence of different markers, thus a significant association detected by one marker may be due to the other markers that are linked with it. The marginal marker analysis cannot separate the confounding effect of eQTLs due to marker-marker dependence or linkage (?). Second, an eQTL may act through its interaction with other eQTLs and environmental factors. Because of their paramount importance in affecting complex diseases and traits, gene-gene interactions, or epistatic effects, and gene-environment interactions have been studied intensively in modern biological and medical research (???)

These two limitations can be overcome by analyzing all markers and their pairwise interactions simultaneously through formulating a high-dimensional regression model. Although it can infer a complete picture of the genetic architecture of gene expression, this endeavor is highly challenged by the curse of dimensionality, i.e., the number of predictors far exceeds the number of observations. The past decade has witnessed the tremendous development of variable selection models for high-dimensional data analysis, such as LASSO (?), SCAD (?), Dantzig selector (?), elastic net (?), minimax concave penalty (MCP) (?) among others. Many methods possess favorable theoretical properties such as model selection consistency (?) and oracle properties (Fan and Lv 2011). When the number of predictors is much larger than the number of observation, sure screening is a more realistic goal to achieve than oracle properties or selection consistency (??). Sure screening assures that all important variables are identified with a probability tending to one, hence achieving effective dimension reduction without information loss and providing a reasonable starting point for

low-dimensional methods to be applied.

More recently, Hao and Zhang (?) extended variable selection approaches to jointly model main and interaction effects from high-dimensional data. Based on a greedy forward approach, their model can identify all possible interaction effects through two algorithms iFORT and iFORM which have been proved to possess sure screening property in an ultrahigh-dimensional setting. In this article, we implement and reform Hao and Zhang’s model to map the genetic architecture of eQTL actions and interactions for gene expression profiles. This model is modified to accommodate to the feature of a genetic mapping or GWAS design in which molecular markers as genetic predictors are discrete although some additional continuous predictors can also be considered. We expand Hao and Zhang’s regression model to include discrete components. Also, for an F2 or a natural population with three genotypes at each locus, we need to estimate a total of eight genetic effects for a pair of markers, which are additive and dominant effects at each locus, and additive-additive, additive-dominant, dominant-additive and dominant-dominant effects between the two loci (?). Thus, if the number of markers is p , a total number of predictors including all main and two-way interaction terms is $2p^2$. For a typical moderate-sized mapping study, in which several thousands of markers are genotyped on a few hundred individuals, consideration of pair-wise genetic interactions will quickly make the dimension of predictors an ultrahigh one.

By modeling all markers jointly at one time under an organizing framework, the modified model can detect all possible significant eQTLs and their epistasis. An eQTL can be either a cis-QTL, coming from the same physical location as the gene expression, or a trans-QTL, coming from other areas of the genome. Our model can more precisely discern these two different types of eQTLs and their interactions than traditional marginal analysis. By reanalyzing a published data collected in a mapping population of *C. elegans* (?), the new model has validated previous results by the

marginal approach, meanwhile obtained new discoveries on the genetic origin of gene expression differentiation, which could not be detected in a traditional way.

2.2 Methods

2.2.1 Experimental design

Consider an experimental population for genetic studies of complex traits, such as the backcross and F2 initiated from two inbred lines, full-sib family derived from two outcrossing parents, or random samples drawn from a natural population. These types of populations are used specifically for different species. Although they have different levels of complexities for statistical modeling, the genetic dissection of different populations underlies a similar principle. For the purpose of simplicity, we consider a backcross design in which there are only two genotypes at each marker.

Suppose the backcross contains n progeny, each of which is genotyped by p markers, such as single nucleotide polymorphisms (SNPs), distributed over different chromosomes. The number of SNPs p should be large enough to completely cover the entire genome at an adequate depth so that we can possibly capture all possible genetic variants. An increasing body of evidence suggests that significant SNPs associated with complex traits or diseases are more likely to be eQTLs (?). Hence the identification of eQTLs is an important first step toward the genetic dissection of end-point phenotypes. For this reason, we assume that genome-wide gene transcripts have been available for the assumed study population. Assume that all progeny are recorded for the same organ by microarray, leading to expression abundance data of m gene transcripts. We purport to identify all possible genetic variants including main effects and interaction effects of SNPs that contribute to

each gene transcript.

2.2.2 Adaptation of iFORM procedure

Hao and Zhang ? formulated an interaction forward selecting procedure under the marginality principle (iFORM). The marker and gene transcript data of the study population can be denoted as $(X_i, Y_i)(i = 1, \dots, n)$ which are independent and identically distributed copies of (X, Y) , where $X = (X_1, \dots, X_p)^T$ is a p -dimensional predictor vector and Y is the response, expressed by a linear regression model:

$$Y = \beta_0 + \beta_1 X_1 + \dots + \beta_p X_p + \epsilon \quad (2.1)$$

The β 's are the coefficients for the genetic effects of each marker. Like most genome-wide datasets, the number of markers here grossly outnumbers the number of observations, $p \gg n$. Therefore, selection procedures would need to be implemented in order to fit a linear regression model such as (3.1). We are already at the point of high-dimensional data but if we want to include epistatic effects between different markers as predictors as well it would increase the amount of predictors by $(p^2 + p)/2$. The resulting linear model would grow to be,

$$Y = \beta_0 + \beta_1 X_1 + \dots + \beta_p X_p + \gamma_{11} X_1^2 + \gamma_{12} X_1 X_2 + \dots + \gamma_{pp} X_p^2 + \epsilon \quad (2.2)$$

where γ 's are the coefficients for the epistatic effects for all the quadratic and two-way interactions between the markers. For convenience we will assume that the markers and the transcripts are

standardized before running the selection procedure. Therefore, $E(X_{ij}) = 0$, $Var(X_{ij}) = 1$, $E(Y_i) = 0$ and $Var(Y_i) = 1$ for $i = 1, \dots, n$; $j = 1, \dots, p$. Also, the quadratic and two-way interaction effects will be centered which we will write as $Z_i = (\dots, X_{ik}X_{il} - E(X_{ik}X_{il}), \dots)^T$. By doing so we would eliminate the need for an intercept in regression model (2.2). This would reduce the model to the form,

$$Y = X^T\beta + Z^T\gamma \quad (2.3)$$

Some notations that will be used to define the elements of ? iFORM procedure are as follows.

$P_1 = 1, 2, \dots, p$ $P_2 = (k, l) : 1 \leq k \leq l \leq p$. which are the index sets for the linear and two-way interactions terms, respectively. The significant main effects for the markers and their interaction effects are $T_1 = j : \beta_j \neq 0, j \in P_1, T_2 = (j, k) : \beta_{jk} \neq 0, (j, k) \in P_2$. For any model M, |M| will be used to denote the number of predictors contained in the model. The true model size would be indicated by $|T_1| = p_0$ and $|T_2| = q_0$ or together would be $|T|=d_0=p_0+q_0$. For the procedure, three sets will be used throughout. The sets are M for the model set, C for the candidate set of predictors and S for the solution set of predictors currently selected in the model.

There are two principles that are used in the selection procedure when considering interactions as candidates for selection into the final model. The first is considering the principle of marginality. The principle states that it is inappropriate to model interaction terms when the main effects contributing to the interaction have either not been included in the model or are deleted because their effects become marginal by the inclusion of the interaction effect. The second principle important to the procedure is the heredity principle. The strong case of the principle states that an interaction effect should not be considered unless both the contributing main effects are in the model (?). This would

translate to $\gamma_{jk} = 0$ only if $\beta_j, \beta_k \neq 0 \forall j, k$ for model ((2.2)). By including both principles during the selection process it allows for dynamically including both main effects and interactions effects. The interaction effects can only be considered between the main effects currently selected into the solution set of the model according the discussed principles. A more formal description of the procedure is given below.

2.2.3 iFORM

? formulated an interaction forward selecting procedure under the marginality principle (iFORM). The procedure's initial step starts with the empty set for both the solution set and the model set, $S_0 = \emptyset$ and $M_0 = \emptyset$. The candidate set contains all main effects at the beginning, $C_0 = P_1$, for each of the markers as a possible eQTL. Typical forward selection procedures are carried out to start the selection. Each marker is tested individually using a marker regression. The marker that results in the lowest residual sum of squares is the marker selected from the candidate set into the solution set as an eQTL. This is then iterated again for a selection of another marker into the model set. Once there are at least two main effects selected into the solution set, using the strong heredity principle, the quadratic and two-way interactions are then created and placed into the candidate set as possible eQTLs for selection in the next step. This process continues selecting main effects or the newly created interaction effects into the solution set. If another main effect is selected into the solution set, then the candidate set grows with the creation of all possible two-way interactions of the main effects that are currently in the solution set. This is continued until a designated stopping value, say d . For the number of predictors placed into the model set from the solution set the Bayesian information Criterion was used, $BIC_2(\hat{M}) = \log(\hat{\sigma}^2 \hat{M}) + n^{-1} |\hat{M}| \star (\log(n) + 2 \star \log(d^*))$, where $\sigma^2 \hat{M}$ is the sample variance for the given model, $|\hat{M}|$ is the size of the model or the number

of predictors selected into the given model, and n is the sample size. The d^* term is the number of predictors in the full model. This was proposed as BIC_2 by ? which they derived to help control the false discovery rate in high dimensional data situations. They also showed that it was selection consistent if $d^* = O(n^\xi)$ for some $\xi > 0$. The only difference between the traditional BIC calculation and the BIC_2 is the additional term involving $2\log(d^*)$. Ignoring the BIC , the most the number of steps in the solution path is of size n . The parameter d controls the overall length of the solution path. In practice, the exact number of predictors to include, say d_0 , in the true model is unknown. We want to make d large enough to include d_0 but not so large as to fit the model to the point where it becomes over saturated. Using the BIC_2 should help avoid such a matter as well. It is reasonable to assume that d_0 is much smaller than n in high dimensional sparse regression problems (?). Since this is the case, for the purposes of our model, d was set to be no larger than $n/\log(n)$. Generally, the BIC_2 should reach minimum, indicating the optimal stopping point, before the designated stopping value, is reached.

2.2.4 Some considerations

There were some considerations and pre-processing steps taken before the iFORM procedure was implemented. The first consideration was to see if there were any exact duplicate markers in the dataset. One drawback that could arise with marker datasets when attempting to run multiple linear regression is the possibility of duplicate markers in the dataset. If two different markers would happen to have exactly the same genotypes for each subject it would show up as an exact linear combination of each other if both markers were to be placed in the linear model. Including redundant markers in a linear model would not add any additional information and therefore should not be included in the candidate set during the selection procedure. This also reduces the dimension

slightly when there are duplicate markers in the dataset.

Another consideration made is the type of coding used for the genotypes. At any given eQTL, the j th eQTL, say, there are two possible genotypes: $Q_j Q_j$ and $Q_j q_j$, making the total number of possible QTL genotypes in the population 2^m . The goal of a genetic model is to relate the 2^m possible genotypic values to a set of genetic parameters, such that these parameters are interpretable in terms of main and epistatic effects of the m eQTL. A genetic model is to use orthogonal contrast scales because it is consistent in the sense that the effect of a eQTL is consistently defined whether the genetic model includes one, two, three, or more eQTL (?). The orthogonal contrasts for the genetic model can be expressed by

$$x_{ij} = \left[\frac{-1}{2} \text{if homozygote } Q_j Q_j, \frac{-1}{2} \text{if heterozygote } Q_j q_j \right]$$

Typically in an inbred line backcross population a given genotype is coded with a 0 and 1. However there are two draws backs to this coding when considering the selection procedures discussed above. The first issue comes with not including an intercept in model ((2.2)). If this is the case each of the predictors would need to be centered making the coding to $-\frac{1}{2}$ and $\frac{1}{2}$ instead of 0 and 1. Besides meeting the assumptions of the model that the predictors are centered, it is also beneficial for the interaction effects as well. If the coding would remain at 0's and 1's, the interaction coding would also consist of 0's and 1's. This could propose a problem because three out of the four scenarios of epistasis between markers would result in a coding of 0 for the level in the interaction effect. This has the potential to falsely skew the data of no additive effect for interactions terms because of the sparseness of coding. By centering the coding to $(-\frac{1}{2}, \frac{1}{2})$, it would result in an interaction effect being coded as $(-\frac{1}{4}, \frac{1}{4})$. This coding would happen for different scenarios for each of the levels. The $-\frac{1}{4}$ could arise when the interaction is made up of a homozygote interacting with a heterozygote

genotype. A coding of $\frac{1}{4}$ would arise by either a homozygote interacting with another homozygote genotype, or when a heterozygote interacts with another heterozygote genotype.

2.3 Application

2.3.1 Simulation Results

Simulations studies were conducted to test the theoretical properties of the selection procedures and the results 2.1, 2.2 and 2.3. The results were compared to several other commonly used methods for eQTL mapping. In each of the examples the response was generated from model (2) with $\gamma = 1, 2, \text{ and } 3$ for the random error with a sample size of $n = 200$. The X_i 's were all independently and identically distributed realizations generated from $Binomial(0.5)$ and then orthogonal contrasts were made making each $x_{ij} \in (-\frac{1}{2}, \frac{1}{2})$. The true $\beta = (3, 0, 0, 3, 0, 3, 3, 0_{493})$, therefore making $T_1 = 1, 4, 6, 7$ and $p_0 = 4$. The relevant interactions were set to the pairs $\mathcal{T}_2 = (1, 6), (1, 7), (4, 7), (4, 7)$ and $q_0 = 4$ all with $j, k = 3$ where $(j, k) \in \mathcal{T}_2$. There were several methods compared during each of the simulations 2.1, 2.2 and 2.3. The methods that were used to model the data were single marker analysis, forward selection involving only main effects (FS), forward selection involving all main effects and interaction (FS2) and the iFORM procedure. Several outcomes were evaluated to compare across each of the models. The outcomes are separated into three parts. The first part focuses on the selection of main effects, the second part focuses on the selection of interaction effects and the third part is the overall model performance. Simulations of $M=100$ replicates were run and the outcomes considered include

Convergence Probability (Cov) $\sum_{m=1}^M I(\mathcal{T} \subset \hat{\mathcal{T}})/M$ *Percentage of correct zeros (Cor0)*
 $\sum_{m=1}^M \sum_{j=1}^p I((\hat{\beta}_j = 0, \beta_j = 0)/[M(p - p_0)])$ *Percentage of incorrect zeros (Inc0)* $\sum_{m=1}^M \sum_{j=1}^p I(\hat{\beta}_j \neq$

$0, \beta_j \neq 0)/[M(p_0)]$ Exact Selection probability (Exact) $\Sigma_{m=1}^M I(\mathcal{T} = \hat{\mathcal{T}})/M$ The average model size
 Mean Square Error (MSE) *Adjusted R-square* Computation Time in seconds

In each instance of the simulation, the iFORM procedure was closest to the simulated data, indicated as Oracle. Single marker analysis was conducted on each of the main effects individually and the significant markers were then designated as eQTLs. When comparing the single marker analysis, we can see it rarely designated the full set of main effects as significant from the simulated data. Also, no consideration for interactions could be assessed in single marker analysis. The iFORM procedure contains the identified main effects over 90% of the time across all simulations. The procedure also includes interaction selection. The interaction screening shares a similar success rate where the interaction effects are correctly selected over 90% of the time as well. Focusing on the computation time, we observed only a few seconds, on average, increase than running single marker analysis. The final models selected by the iFORM procedure had similar adjusted R-square values as the Oracle results, on average. Looking at the exact selection percentage, we can see that the vast majority of the time the correct predictors were selected and indicated as significant each time. To compare the interaction screening effectiveness, forward selection was implemented on both the main effects and interactions effects. The time it took to create the design matrix in order to implement forward selection was not included in the computation time. As can be seen from the results, using forward selection on the full set of main effects and pair-wise interactions took substantially longer to run on average than any of the other methods, including the iFORM procedure. Another drawback to implementing forward selection on such a large set seemed to come with over fitting the model. The selection included the maximum number of predictors allowed by the designated stopping value and did not use the BIC criteria for final model selection. This resulted in 19 additional predictors selected (**Tables 1 -3**)**2.1**. This increased the adjusted R-square value of the final model, however this is suspected because of over fitting the data and not to be a true prediction of the response.

Table 2.1: Simulation 1 Table (sigma=1)

Method	Cov	Cor0	Inc0	Exact	Cov.1	Cor0.1	Inc0.1	Exact.1	Size	MSE	X	Time
Single Marker	0.00	1.000	0.2500	0.00	NA	NA	NA	NA	3.00	23.630	0.216	0.8
FS	0.85	0.953	0.0625	0.85	NA	NA	NA	NA	27.00	10.230	0.660	3.4
FS2	1.00	0.996	0.0000	1.00	0.95	0.981	0	0.0	27.00	0.302	0.989	72.3
iFORM	0.90	0.999	0.0500	0.90	0.90	1.000	0	0.9	7.55	2.930	0.894	4.0
Oracle	1.00	1.000	0.0000	1.00	1.00	1.000	0	1.0	8.00	1.023	0.965	N

Table 2.2: Simulation 2 Table (sigma=2)

Method	Cov	Cor0	Inc0	Exact	Cov.1	Cor0.1	Inc0.1	Exact.1	Size	MSE	X	Time
Single Marker	0.02	0.999	0.529	0.029	NA	NA	NA	NA	1.97	27.02	0.178	0.69
FS	0.80	0.953	0.050	0.800	NA	NA	NA	NA	27.00	11.49	0.651	3.22
FS2	1.00	0.996	0.000	1.000	0.98	0.98	0	0.00	27.00	1.17	0.964	68.20
iFORM	0.97	0.998	0.007	0.970	0.95	1.00	0	0.93	8.70	4.41	0.865	3.84
Oracle	1.00	1.000	0.000	1.000	1.00	1.00	0	1.00	8.00	3.92	0.880	NA

```
knitr::kable(
  read.csv("Chapter02_Table1Sim1.csv"), caption = 'Simulation 1 Table (sigma=1)',
  booktabs = TRUE
)
```

```
knitr::kable(
  read.csv("Chapter02_Table1Sim2.csv"), caption = 'Simulation 2 Table (sigma=2)',
  booktabs = TRUE
)
```

```
knitr::kable(
  read.csv("Chapter02_Table1Sim3.csv"), caption = 'Simulation 3 Table (sigma=3)',
  booktabs = TRUE
)
```


Table 2.3: Simulation 3 Table (sigma=3)

Method	Cov	Cor0	Inc0	Exact	Cov.1	Cor0.1	Inc0.1	Exact.1	Size	MSE	X	Time
Single Marker	0.00	0.999	0.612	0.000	NA	NA	NA	NA	1.65	33.90	0.138	0.69
FS	0.82	0.953	0.043	0.827	NA	NA	NA	NA	27.00	14.44	0.633	3.22
FS2	1.00	0.997	0.000	1.000	0.98	0.97	0	0.00	27.00	2.69	0.931	68.20
iFORM	0.89	0.995	0.060	0.896	0.96	1.00	0	0.94	7.93	11.10	0.713	3.83
Oracle	1.00	1.000	0.000	1.000	1.00	1.00	0	1.00	8.00	8.98	0.771	NA

2.3.2 Real Data Analysis

? reported an eQTL mapping study of *C. elegans* using 208 recombinant inbred advanced intercross lines (RIAIL) from a cross between the laboratory strain, N2, and a wild isolate from Hawaii, CB4856. Abundances of 20,000 gene transcripts were measured by microarray in developmentally synchronized young adult hermaphrodites of these lines, providing a genome-wide coverage of *C. elegans* from WormBase, a public *C. elegans* genome database. The microarray data was preprocessed through a normal-exponential convolution background correction and normalized using quantile standardization. Although they are closely related, the two strains used for the cross are considered relatively divergent for *C. elegans*. The two strains differ roughly at approximately 1 base pair per 900. Their RIAILs were genotyped at 1454 ordered single-nucleotide polymorphism (SNP) markers that cover the whole genome of *C. elegans* including five autosomes (denoted as I – V) and one sex chromosome (denoted as X).

? used a classic interval mapping approach to detect 2309 eQTLs by testing and scanning associations of each SNP with each gene transcript over the entire genome. Rockman et al’s analysis allowed a rectangular map of eQTL positions gene positions to be constructed 2.1 , from which one can identify cis-eQTLs on the diagonal and trans-eQTLs off the diagonal. However, because their association analysis was conducted individually for each SNP, the detection of eQTLs was based on

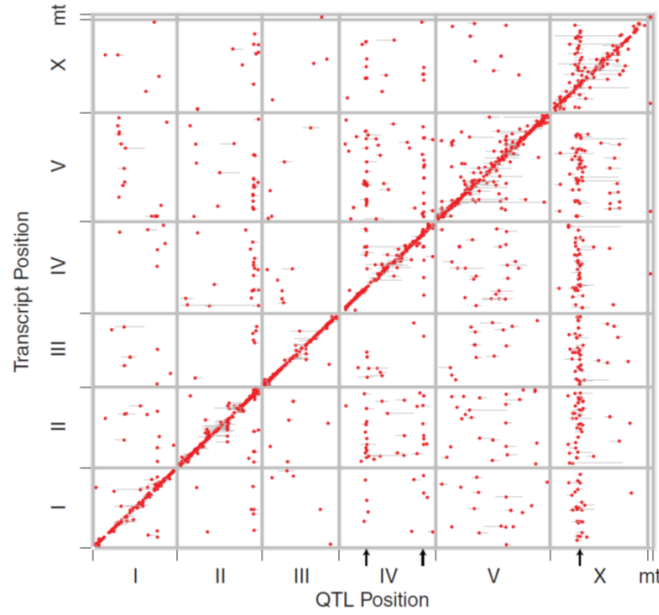


Figure 2.1: SNP Picture

the marginal effects of individual eQTLs, which may lead to two issues being unsolved. First, of those eQTLs detected for the same gene transcript, some may include confounded effects by others. Second, the effects of genetic epistasis may take place but were not detected. By analyzing all SNPs simultaneously under a single framework, the high-dimensional model, iFORM, implemented in this study can more precisely characterize the genetic machinery underlying variation in each gene transcript. More specifically, we treat each transcript as a response with all SNP markers and their interactions as predictors by building a big regression model. Significant predictors were then selected based on the iFORM procedure. A final model including both main and interaction effects can be evaluated by calculating adjusted R-square values

2.2 illustrates the map of how a particular gene transcript is controlled by its eQTLs through main effects and interaction effects. For clarity of our presentation, we only chose one representative gene transcript from each chromosome. For example, gene transcript A_12_P103290 located at position 2069088 – 2069147 of chromosome I was detected to be controlled by main effects due

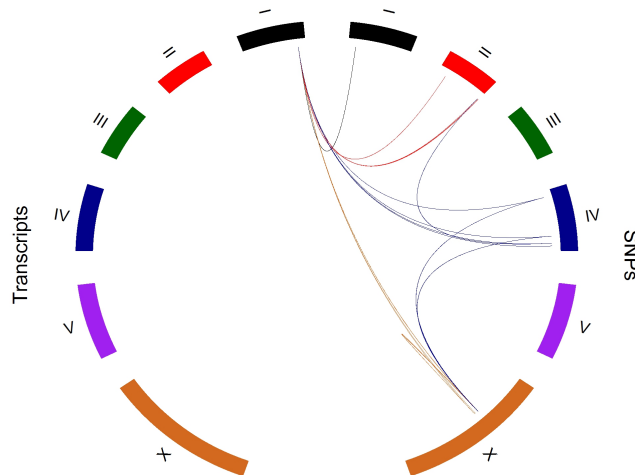


Figure 2.2: SNP Picture

to X2_13516256 eQTLs on chromosomes II and X4_15632637 eQTLs on chromosome IV and X2_13516256:X4_15632637 interactions between some of these eQTLs on these two chromosomes.

iFORM provides the estimates of each effect (either main effect or interaction effect), standard errors of each estimate and the significance tests of each effect. As an example, 2.4 gives the result of how gene transcript A_12_P103290 can be predicted by its eQTLs and their interactions. It can be seen that the final predictive model (adjusted $R^2 = 0.896$) contains 14 markers which exert their main effects and/or interaction effects on the transcript. Of the 14 final markers, a half shows significant main effects ($p < 0.05$), with several (i.e., X_14636404, X4_15568674, X4_15632637 and X_14542103) explaining about 5% heritability (defined as a proportion of genetic variance due to a predictor over the total phenotypic variance). Of these final markers, we identified eight significant epistatic interactions. Each epistasis accounts for 4.6 – 5.5% heritability 2.4.

Table 2.4: iFORM Single Marker Analysis

eQTL	Effect	SE	p.value	Heritability...	Effect	SE	pvalue
X1_2068168 (cis-eQTL)	-0.197	0.035	0.000	0.060	-0.210	0.074	0.005
X2_13516256	-0.069	0.039	0.080	0.007	-0.138	0.075	0.068
X2_13813025	-0.023	0.052	0.665	0.001	-0.095	0.074	0.201
X2_13694563	0.074	0.062	0.238	0.008	-0.089	0.075	0.242
X2_2482896	0.064	0.027	0.017	0.006	-0.057	0.076	0.453
X_15500580	0.073	0.064	0.253	0.008	0.010	0.076	0.899
X_14636404	-1.768	0.092	0.000	4.794	0.024	0.076	0.751
X4_16403215	0.028	0.040	0.489	0.001	0.087	0.075	0.252
X4_15568674	-1.972	0.134	0.000	5.964	0.094	0.075	0.213
X4_1873297	0.044	0.026	0.086	0.003	0.095	0.071	0.185
X4_15632637	1.960	0.143	0.000	5.892	0.104	0.075	0.169
X4_13532205	0.064	0.028	0.024	0.006	0.111	0.075	0.143
X_15820520	-0.014	0.055	0.796	0.000	0.146	0.075	0.054
X_14542103	1.786	0.087	0.000	4.892	0.162	0.075	0.031
X2_13516256.X4_15632637	-3.799	0.268	0.000	5.534	NA	NA	NA
X2_13516256.X4_15568674	3.753	0.276	0.000	5.401	NA	NA	NA
X_15820520.X_14636404	-3.771	0.172	0.000	5.453	NA	NA	NA
X_15820520.X_14542103	3.691	0.172	0.000	5.224	NA	NA	NA
X_14636404.X4_1873297	-3.534	0.163	0.000	4.789	NA	NA	NA
X_14636404.X4_13532205	-3.567	0.166	0.000	4.879	NA	NA	NA
X_14542103.X4_1873297	3.629	0.164	0.000	5.050	NA	NA	NA
X_14542103.X4_13532205	3.469	0.167	0.000	4.614	NA	NA	NA

```
knitr::kable(
  list(
    read.csv("OutputTable1.csv"),
    read.csv("OutputTable2.csv")
  ),
  caption = "iFORM Single Marker Analysis",
  booktabs = TRUE
)
```

It is interesting to note that all predictors jointly contribute to 62.6% heritability for transcript

A_12_P103290, of which main effects account for 26.7% and epistatic effects account for 35.9%. It is very surprising that epistasis contributes to more than a half of heritability. Of the eight epistatic interactions, only one occurs due to the interaction between two significant eQTLs, X_14542103 and X4_13532205 2.4. All the remaining is due to interactions between one significant eQTL and one non-significant marker. Some eQTLs, such as X_14542103 and X_14636404, produce epistasis with a greater frequency than others. Despite their involvement in the final predictive model, some markers were tested to be insignificant in terms of both main and interaction effects, suggesting that they regulate a gene transcript in a subtle but important fashion. In summary, iFORM can not only provide an estimate of the overall heritability of gene transcript A_12_P103290 (i.e., the sum of individual heritabilities explained by each predictor), but also chart a detailed picture of how each genetic variant contributes to transcript variation. In particular, iFORM can characterize epistasis and its role in trait control, thus equipped with a capacity to retrieve so-called missing heritabilities (?), a significant issue arising from current genome-wide association studies.

Through analyzing associations between all markers and each transcript by iFORM, we can identify the difference of cis- and trans-eQTLs for a particular transcript. For example, of the eQTLs affecting A_12_P103290, we detected that X1_2068168 is a cis-eQTL, whereas all others are trans-eQTLs 2.4. We list the number and distribution of these two types of eQTLs and the pattern of how they interact with each other to determine gene transcripts 2.5. By detecting cis-eQTLs and trans-eQTLs, iFORM detected that genetic interactions take place mostly between trans-eQTLs.

```
knitr::kable(
  read.csv("Chapter02_OutputTable_cisQTL.csv"),
  caption = "Distribution of cisQTLs",
  booktabs = TRUE
```

Table 2.5: Distribution of cisQTLs

eQTL.Type	Count	Proportion
Cis-eQTL	14	0.0024
Trans-eQTL	5509	0.9628
Cis-eQTL x cis-eQTL	0	0.0000
Trans-eQTL x cis-eQTL or cis-eQTL x trans-eQTL	2	0.0003
Cis-eQTL x trans-eQTL	196	0.0340

)

2.4 Discussion

With the recent development of genotyping and sequencing techniques, the collection of genome-wide genetic and genomic data from any tissue of an organism has been made much easier and more efficient. Because of this, genetic studies of complex diseases or traits have developed during the past decade to a point at which we can draw a complete picture of genetic architecture for disease or trait formation and progression by genome-wide association studies (GWAS) (?). Traditional marginal analysis based on simple regression has been instrumental for the detection of important genetic variants or quantitative trait loci in a variety of organisms, but its bottleneck has emerged quickly due to its limitation in precisely and comprehensively charting genetic control landscapes. Many GWAS studies published are bothered by missing heritabilities because of their incapacity to detect genome-wide epistasis and genotype environment interactions (?).

Epistasis is a phenomenon by which the influence of a gene on the phenotype depends critically upon the context provided by other genes (?). It has been increasingly recognized that epistasis is an important source for trait variation (?; ?; ?), thus inclusion of epistasis would enhance the prediction accuracy of phenotypic performance and shed more light on the global genetic architecture

of trait control (?). However, epistasis is extremely hard to detect as an interaction term, whose inclusion may complicate the inference of the predictive model (?; ?). Thanks to recent progresses in high-dimensional data modeling, we have been able to implement several cutting-edge statistical models for systematical detection and characterization of genome-wide epistasis.

? proposed a new high-dimensional model, iFORM, that can tackle an issue of interaction selection simultaneously from a large pool of continuous predictors. This model is based on forward-selection-based procedures, characteristic of computational feasibility and efficiency. The authors further proved that the detection of interactions by iFORM is consistent, even if the dimension increases exponentially for a sample size. As one of the first attempts to introduce high-dimensional models into genetic studies, we modified iFORM to accommodate to the discrete nature of molecular markers. Our simulation studies indicate that iFORM can provide reasonably accurate and precise estimates of genetic main effect and interaction effects. Also, it shows greater power to detect significant genes and their interactions which may not be detected by traditional single marker analysis.

We

results confirmed those by the traditional approach, the new model provides some new findings including new eQTLs and epistasis, thus allowing a complete set of genetic variants to be characterized. As an important tool to understand the genetic mechanisms underlying both complex traits and diseases, eQTL mapping has been widely used to identify key regulatory pathways toward endophenotype and end-point phenotypes (?; ?; ?; ?; ?). A typical eQTL study may not only include a large number of molecular markers as like in a GWAS, but also record tens of thousands of gene transcripts throughout the entire genome. Our current version of iFORM can only take into account one gene transcript as a response at a time, thus having a limitation to model the

correlation and dependence among different genes. It is our next step to formulate a multivariate multiple regression model by which to test how an individual predictor, main effect or epistatic effect, pleiotropically affects correlated expression profiles of different genes.

Given the complexity of biological phenomena, pair-wise epistasis may be insufficient to explain phenotypic variation. ? argued that high-order interactions among more than two genes may provide a key pathway toward complex traits. Three-way interactions have been detected in trait control (?; ?). A model for modeling three-way interactions has been developed in a case-control GWAS design (?) and a genetic mapping setting (?). It is crucial to extend iFORM to map main effect, two-way epistasis and three-way epistasis in an eQTL mapping study although no substantial change is needed in the computational algorithm, except for an enlarged test set and extra computing time. Our work is based on a backcross population in which there are only two genotypes at a locus. The backcross population can facilitate our estimation and test of genetic effects owing to a smaller number of parameters at each locus or locus pair, but its utility is very limited in the F2 design of model systems and natural populations of outcrossing species such as humans. A more general model of iFORM should consider three genotypes at each locus, which provides estimates of additive and dominant effects at each locus and four types of epistasis, i.e., additive-additive, additive-dominant, dominant-additive and dominant-dominant, between each pair of loci (?). Each of these epistatic types may affect a phenotype through a different pathway.

With continuous falling of sequencing price, we will have desirable opportunities to study the dynamic behavior and pattern of gene expression profiles across time and space scales (?; ?). Many previous studies suggest that gene expression during cell and organ development may follow a particular form, which can be quantified by mathematical equations (?). For example, abundance of gene expression may change periodically in human's brain during circadian clock. Many researchers

used Fourier's series approximation to model the periodic changes of gene expression by estimating the period and amplitude of the cycles (?). By integrating Fourier series into iFORM, we will be able to map dynamic eQTLs for gene expression and make a quantitative prediction of temporal and spatial patterns of genetic control by eQTLs.

Chapter 3

High-order Epistatic Networks

3.1 Motivation

Quantitative traits are very difficult to study because these traits are controlled by many genes that interact in a complicated way (??). Genome-wide mapping and association studies increasingly available due to next-generation high-throughput genotyping techniques have proven to be useful for characterizing gene-gene interactions, coined epistasis, that contribute to phenotypic variation (??; ??). Powerful statistical methods have been developed to analyze all possible markers simultaneously, from which to search for a complete set of epistasis for quantitative traits (??). The joint analysis of all markers is particularly needed to chart an overall picture of genetic interactions, in comparison with computationally less expensive marginal analysis.

Epistasis reported in the current literature is mostly due to interactions between two genes. However, a growing body of evidence shows that genetic interactions involving more than two loci play a pivotal role in regulating the genetic variation of traits (??; ??; ??). For example, in a mapping

population deriving from crossing two chicken lines, three-locus interactions were detected to determine body weight (?). A mapping study established by two yeast strains identified genetic interactions involving five or more loci for colony morphology (?). Other studies have demonstrated that high-order epistasis is of critical importance in regulating metabolic networks in yeast (?) and *Escherichia coli* and *Saccharomyces cerevisiae* (?; ?), whereas lower-order (pairwise) epistasis may be insufficient to explain metabolic variation for these organisms.

The theoretical models of high-order epistasis have well been established by mathematical biologists (?; ?). These models provided a foundation to interpret high-order epistasis from a biological standpoint. A few statistical models have been derived to estimate and test high-order epistasis in case-control designs (?) and population-based mapping settings (?). ? developed a Bayesian version of detecting high-order interactions for both continuous and discrete phenotypes. However, these models were based on a marginal analysis, thus less powerful to illustrate a global view of genetic control mechanisms due to high-order epistasis.

In this article, we deploy a variable selection procedure within a genetic mapping or association setting to characterize the genetic architecture of complex traits composed of main effects of individual genes, pairwise epistasis between two genes, and three-way epistasis among three genes. The model was built on greedy interaction screening forward selection developed under the marginality principle (named iFORM) by ?. These approaches, proved to possess sure screening property for ultrahigh-dimensional modeling, have been implemented to model the genetic architecture of main effects and pairwise epistasis due to eQTLs for gene transcripts (?). Here, we extend the implementation of iFORM to systematically capture three-way interactions that are expressed among all possible markers studied. To show the statistical power of the extended model, we performed computer simulation studies. The model was further validated through analyzing a real

data of genetic mapping for shoot growth in a woody plant, mei (*Prunus mume*). The model should be used in any other mapping or association studies of quantitative traits.

3.2 Methods

3.2.1 Mapping and association studies

Genetic mapping and association studies are two types of designs used to dissect quantitative traits. The former is based on a controlled cross derived from distinct parents, whereas the latter samples different genotypes from a pool of accessions or a natural population. In both types of design, a set of individuals are sampled to be phenotyped for quantitative traits of interest and genotyped by molecular markers distributed throughout the entire genome. For a particular genetic experiment, the number of markers is much larger than that of samples, thus, it is impossible to estimate the genetic effects of all markers simultaneously using traditional regression models. This issue becomes much intractable when we aim to estimate genetic interactions of different orders. To tackle the issue of the number of predictors \gg the number of samples, several variable selection approaches have been implemented in association studies. One approach is forward selection which was shown to be robust for estimating pairwise interactions of predictors (?). With sure screening properties and controlling for false positives, this approach, named iFORM, performs very well in capturing important information in explaining the response variable. On top of these nice theoretical properties it is computationally efficient by using ordinary least squares calculations and only requiring a predetermined set up steps. Here, we extended the iForm procedure to include HGI's to capture more relevant information. In the following sections, the notation and model set-up will be introduced. After this theoretical properties will be explored. Finally simulated and real data

analysis will be conducted to help confirm the theoretical properties and show the feasibility of using the model for screening across whole genomes to more precisely explain phenotypes of interest.

3.2.2 Epistatic model

Consider a linear model that underlies the true genotype-phenotype relationship. Assume that the phenotype, as the response of the model, is controlled by a set of p SNPs that act singly and/or interact with each other. These main and interaction effects of markers, i.e., the predictors of the model, need to be estimated. Let $\mathbf{Y} = (y_1, \dots, y_n)^T$ denote the phenotypic value of n samples from a mapping or association population. When considering pairwise and three-way interactions, the linear model is expressed as

$$\mathbf{Y} = \alpha + X^T \beta + Z^T \gamma + W^T \eta + \epsilon \quad (3.1)$$

where $X = (X_1, \dots, X_p)^T$ is the design matrix that specifies the genetic effects of each marker $\beta = (\beta_1, \dots, \beta_p)$, $Z = (X_j X_k)^T (1 \leq j \leq k \leq p)$ is the design matrix that specifies the epistatic effects between two markers, expressed in γ , $W = (X_j X_k X_l)^T (1 \leq j \leq k \leq l \leq p)$ is the design matrix that specifies the epistatic effects among three markers, expressed in η , and $\epsilon \sim N(0, \sigma^2)$ is the residual error normally distributed with mean zero and variance σ^2 . We denote the index sets for the linear, order-2 and order-3 effects in equation (3.1), respectively, as $P_1 = 1, 2, \dots, p$, $P_2 = \{(j, k) : 1 \leq j \leq k \leq p\}$, $P_3 = \{(j, k, l) : 1 \leq j \leq k \leq l \leq p\}$. With the significant main, order-2 interaction and order-3 interaction effect sets being, $T_1 = \{j : \beta_j \neq 0, j \in P_1\}$, $T_2 = \{(j, k) : \gamma_{jk} \neq 0, (j, k) \in P_2\}$, $T_3 = \{(j, k, l) : \eta_{jkl} \neq 0, (j, k, l) \in P_3\}$.

The true size of \mathcal{T}_1 , will be p_1 and similarly for \mathcal{T}_2 and \mathcal{T}_3 will have sizes p_2 and p_3 respectively. There will be a total of 3 sets referred to throughout the procedure, the candidate set \mathcal{C} , the selection set \mathcal{S} and the model set, \mathcal{M} . The candidate set is the set of all possible predictors at a given step in the selection process. The selection set contains the predictors that have previously been selected from the candidate set from each iteration of the procedure. Finally, the model set is the final model that is fit from the selection set at the end of the procedure. The BIC is used to determine the optimal cutoff for the final model size.

3.2.3 iForm with high-order epistasis

The iForm procedure is a forward selecting procedure. In traditional forward selection the procedure starts with the empty set and then iterates through the entire set of possible predictors in \mathcal{C} and selects the best predictor and includes it in \mathcal{S} at the end of each step. The best predictor can be determined in many ways but usually is defined by the predictor that results in the least amount of error. For our purposes we use the residual sum of squares. This continues with selecting the best predictor from \mathcal{C} at each step until a designated stopping criterion is met or until some information criterion is met. Common information criteria used for selecting predictors to be in \mathcal{M} are AIC, BIC, R^2 and Mallows's C_p statistic.

The iForm procedure for high-order epistatic detection parallels the forward selection procedure, but \mathcal{C} will grow dynamically with the creation of order-2 and order-3 interaction effects between main effects that were included from previous iterations of the procedure. There are three steps to the model selection. The first step is to initialize the 3 sets mentioned above. The sets, \mathcal{S} and \mathcal{M} are set to the empty set while the candidate set, \mathcal{C} , is first set to P_1 , all the main effects. The next step starts the forward selection procedure selecting predictors from \mathcal{C} . The selected predictor will

be a main effect at the first step. At subsequent steps, after interaction effects are included, selected predictors could be either be a main effect, order-two or order-three interaction effect. The final step involves repeating the second step until a designated stopping criterion is met. This can be a certain amount of predictors to be considered in the final model, or it can be based off of other factors such as the sample size. The designated stopping criterion will be denoted as d . For our purposes we use d as a function of the sample size, $d = n/\log_2 a(n)$. The procedure will run up until d iterations, and the optimal model will then be constructed from the selection set. This is done by an information criterion. Here we used the Bayesian Information Criterion proposed by ? denoted as the BIC_2 . This was derived by them to control the false discovery rate in high dimensional model selections.

$$BIC_2(\hat{M}) = \log(\sigma_{\hat{M}}^2) + n^{-1}|\hat{M}| * (\log(n) + 2 * \log(d^*)) \quad (3.2)$$

Once the selection procedure is done and there are d predictors in the selection set the BIC is used to determine the cutoff value for the optimum number of predictors in the model set. Then linear regression is performed on the model set.

Two guiding principles are used to help dynamically select the main effects and epistasis effects throughout the procedure. The first is the marginality principle, which states that an effect will not be removed from the model once it has been selected. A previous selected effect may become marginal by the inclusion of subsequent effects. This especially can be the case when an interaction effect is included. One of the parent effects may become less significant or even not significant at all by considering both in the model. The next principle we state as the heredity principle but has also been referred to in other work as the hierarchy principle (? and ?). There are two cases of the heredity principle considered. The strong case would not allow for an order-2 epistasis

effect to be included into the candidate set without both the parent main effects that make up the interaction are first included in the model. More formally this can be written as, $\gamma_{jk} \neq 0$ only if $\beta_j, \beta_k \neq 0 \forall 1 \leq j, k \leq p$. Similarly with order-3 epistasis, you would need to have all order-2 epistatic parent effects included in the model before including as a candidate predictor. This would translate to, $\eta_{jkl} \neq 0$ only if $\gamma_{jk}, \gamma_{jl}, \gamma_{kl} \neq 0 \forall 1 \leq j, k, l \leq p$. The weak case relaxes the need for all parent effects to be included in the model before considering the epistatic effects as candidates. Only one parent effect would be required to be in the model for candidates to be included. In the scenario with order-2 epistatic effects we would need, $\gamma_{jk} \neq 0$ only if $\beta_j^2 + \beta_k^2 \neq 0 \forall 1 \leq j, k \leq p$ and with order-3 epistatic effects to be considered as a candidate we would need, $\eta_{jkl} \neq 0$ only if $\gamma_{jk}^2 + \beta_l^2 \neq 0 \forall 1 \leq j, k, l \leq p$.

The heredity (hierarchy) principle help reduce the search space by making the assumption that previously selected main effects would be involved in the interaction effects. By considering this principle it substantially reduces the search space making this feasible for ultra-high dimensional situations. Even larger than ram datasets can be used with efficient memory mapping of the dataset while running the procedure. The weak version of the heredity principle for three-way interactions states that at least one of the main effects needs to be selected into the model to consider an interaction effect that contains that predictor. Considering a moderately high set of predictors say $p = 5000$, if trying to include all order-2 interactions upfront, will make the candidate set be as high as 12,498,000. This alone could exceed most ram requirements of standard computers. This is before even stepping up to order-3 interactions. The weak heredity principle would decrease the candidate set substantially. Assuming a sample size of $n = 200$, would give a cut off of $n/\log_2(n) = 200/\log_2(200) = 26$ steps in the procedure. The 5000 original predictors plus up to 5000 epistatic predictors included in the candidate set at each step in the procedure would give a maximum of approximately 135,000 candidate predictors. This would give a maximum of

approximately 135,000 candidate predictors. This gives a 100 fold decrease in the candidate set. This could substantially make ultra-high dimensional analysis more feasible and also speed it up in the process. This is the weak case. If considering the strong case the decrease in candidate space is even more apparent. Aside from the efficiency by lowering the search space of the candidate set, the heredity principle is usually taken into account by researchers when selecting models involving the consideration for interaction effects.

3.2.4 Theoretical Properties

The theoretical properties of the iForm procedure with high-order epistasis follow closely with the forward selection procedure. ? summarize forward selection nicely as follows. At each step, the response is regressed on the most correlated covariate, and the residual is calculated and used as the new response in next step. After the most correlated covariate (say, X_1) is selected, all other covariates are regressed on X_1 , and then the covariates are substituted by the corresponding normalized residuals, which are used as the new covariates in next step. By viewing forward selection in this sense the computational complexity of the procedure depends upon the size of the candidate set. The candidate set in the iForm's case does grow dynamically at each step, by at most the number of predictors currently selected in C for each step. If we denote the current size of the candidate set as m then each iteration of the procedure grows with complexity of $O(nm)$, where n is the sample size. Leaving the selection unrestricted we would not be able to fit more than n predictors for a linear model and therefore n would be the most main effects that would be able to be selected. Considering the weakest form of the heredity principle at the current iteration there would be at most $p + (n(n-1)(n-2))/6$ predictors in the candidate set. This would make the total complexity of the selection procedure to be $nO(n(p + n(n-1)(n-2))) = O(n^3p + n^5)$. This

makes the total complexity grow linearly as p grows.

The theoretical properties of the iForm procedure show sure screening properties (?). By this we mean that all the import predictors, whether that is a main effect or epistatic effect will be selected with probability tending to 1. This is important to capture as much of the signal as possible through all the noise that comes with $p \gg n$ or ultra-high dimensional situations. It is also important not to ‘over-fit’ the model with unnecessary predictors that actually explain more noise in the data than the model is being fitted on than the actual signal you would like to pick up on.

To show the property from above the following conditions would need to be met for regulatory purposes. ? showed how under these conditions sure screening properties for interaction models like FS2 and iForm are satisfied. This also applies to order-3 interaction models like FS3 and iForm with higher order epistasis, like we do with the high-order epistasis model. The following assumptions need to be met for these conditions. The first is that the $X = (X_1, \dots, X_p)^T$ are jointly and marginally normal with independent normally distributed error. Next we would need the eigenvalues of the covariance matrix to be positive and bounded by two constants $0 < \tau_{min} < 1 < \tau_{max} < \infty$, such that $\sqrt{\tau_{min}} < \lambda_{min}(\Sigma) < \lambda_{max}(\Sigma) < \sqrt{\tau_{max}}/4$. Also, the genetic effects, β need a certain level of signal strength. This we would assume to be $|\beta| > C_\beta$ for some positive constant C_β and $\beta_{min} \nu \beta^{-\xi_{min}}$, with $\beta_{min} = \min(\beta)$. Lastly, there needs to be a certain level of sparsity to the number of important effects. Denoting the total number of important effects as d_0 , and positive constants ξ, ξ_0 and ν we would need $\log(p) \nu n^\xi, d_0 \nu n^{\xi_0}$ and $\xi + 6\xi_0 + 12\xi_{min} \frac{1}{2}$. The conditions stated are accepted standards in the literature when studying ultra-high dimensional situations. (?, ?, ?).

3.3 Application

3.3.1 Simulation Studies

To study the numeric properties of the selection procedure, simulation studies were conducted. Data was generated using R 3.1. The X_i 's were all independently and identically distributed realizations generated from Binomial(0.5) and the true effects for both the main and epistatic effects were included following different heredity scenarios. The phenotype was generated from the linear model setup described previously. To capture relevant data structures, there were several different scenarios considered. For each scenario 50 predictors were generated with a sample size of 300 observations. The data was split into training and a testing set to study both the fitted properties of the model as well as the generalizability of the model. There were a variety of metrics obtained to assess the suitability of each model utilized in the simulations. The first metrics that were taken into account were the rates for the true positives, false positives, true negatives and false negatives. Since we have a variety of levels to each of the models each of the rates were evaluated for the different hierarchical levels. Some of the models only have main effects and/or two-way interactions, therefore the rates were only given for the area applicable to model and the rest were reported as NA. The generalizability of the models was also assessed by withholding 100 random observations as a test set. All the data was generated from the same scenario and then 100 of the observations were randomly selected and stored for out of sample measures. The data was generated from the given scenario and randomly split before assessing the models. The exact same training and testing sets were used to fit and assess each of the models in order to make as fair of a comparison as possible. Each scenario was replicated 100 times and measures were averaged over all replicates. The two measures assessed were mean square error and the coefficient of determination. The analogous in-sample

measures were also calculated for comparison. The models being compared in the simulation studies are Forward Selection, Forward Selection with all order-2 interactions (FS2), Forward Selection with all order-2 interactions (FS3), iForm strong heredity order-2, iForm weak heredity order-2, iForm strong heredity order-3, iForm weak heredity order-3, Glinternet (?), and finally hierNet (?)

Covering a variety of settings the following scenarios were evaluated and compared.

Scenario 1: $\mathbf{Y} = \beta_1x_1 + \beta_4x_4 + \beta_6x_6 + \beta_7x_7 + \gamma_{1,4}x_1x_4 + \gamma_{1,6}x_1x_6 + \gamma_{1,7}x_1x_7 + \gamma_{6,7}x_6x_7 + \eta_{1,6,7}x_1x_6x_7$

The first is where the data were generated from the interactions of the model follow a strong heredity (hierarchy) with $\sigma = 1$. Notice we have all parent effects of the order-2 epistatic effects and also all parent effects of the order-3 epistatic effect are also in the model.

Scenario 2: $\mathbf{Y} = \beta_1x_1 + \beta_4x_4 + \beta_6x_6 + \beta_7x_7 + \gamma_{1,4}x_1x_4 + \gamma_{1,6}x_1x_6 + \gamma_{1,9}x_1x_9 + \gamma_{6,7}x_6x_7 + \eta_{1,6,9}x_1x_6x_9$

The second, the data is generated to have the interactions in follow a weak heredity (hierarchy) with $\sigma = 1$. In this scenario the main effect of x_9 is not included in the model but you can see it is part of both an order-2 and the order-3 effect.

Scenario 3: $\mathbf{Y} = \beta_1x_1 + \beta_4x_4 + \beta_6x_6 + \beta_7x_7 + \gamma_{2,3}x_2x_3 + \gamma_{3,8}x_3x_8 + \gamma_{5,8}x_5x_8 + \gamma_{5,9}x_5x_9 + \eta_{3,9,11}x_3x_9x_{11}$

The third scenario is anti-heredity (hierarchical) where the interaction effects are only among predictors not present as main effects in the model. We still have main effects and epistatic effects in the model. However, the parent effects of the interactions are not the main effects included in the model.

Scenario 4: $\mathbf{Y} = \gamma_{1,4}x_1x_4 + \gamma_{1,6}x_1x_6 + \gamma_{1,9}x_1x_9 + \gamma_{6,7}x_6x_7 + \eta_{1,6,9}x_1x_6x_9$ Finally the last scenario only generates data that come from pure interactions between predictors with no main effects present in the model used to generate the data.

For the first scenarios where the truth obeys strong heredity where all of the parent main effects

need to be selected before interactions are selected. The models that appeared to do the best in this simulation were forward selection on all order-3 interactions included from the beginning (FS3), iForm order-3 weak heredity and iForm order-3 strong heredity @ref(tab:Chap3sim1. The FS3 took over a 40 fold increase in time to run. The other comparison models, glinternet and hierNet seemed to perform well on the training set but not as well on the testing set. This would indicate that some overfitting was occurring with those types of regularization models. The next scenario was when the truth obeys weak heredity. With the underlying model obeying the weak heredity, the iForm order-3 strong heredity version dropped off in performance slightly. However, the FS3 and iForm order-3 remained as top performers @ref(tab:Chap3sim2. The third scenario assessed was from an underlying model with an anti-heredity structure. Both main effects and interaction effects were used in the model to generate the data. However the interactions included in the model were of combinations of main effects in the candidate set, that were not in the model. The iForm seems to drop in performance with this scenario @ref(tab:Chap3sim3. This is to be expected because it is in direct violation of the underlying assumptions of the model hierarchy. Even with these violations of the heredity it still performed reasonably well. Lastly, making the scenario a little more extreme, the underlying model generating the data was only of interactions. There were no main effects included in the model. The results of this scenario are shown in @ref(tab:Chap3sim4. Performance appeared to drop off for all models explored in the simulation.

```
knitr::kable(
  read.csv("Chapter03_TableSim1.csv"), caption = 'Table 1 Simulation results when the truth obeys weak heredity'
  booktabs = TRUE
)
```

Table 3.1: Table 1 Simulation results when the truth obeys strong heredity

Model	T1.tpr	T1.fpr	T2.tpr	T2.fpr	T3.tpr	T3.fpr	Train.MSE	Train.Rsq	Test.MSE
Forward select	1	0.001	0	0.000	0	0	3.330	0.727	3.490
Iform weak(2)	1	0.000	0	0.000	0	0	1.128	0.907	1.252
Iform strong(2)	1	0.000	0	0.000	0	0	1.102	0.909	1.198
Forward select(2)	1	0.000	0	0.000	0	0	1.086	0.910	1.198
Forward select(3)	1	0.000	0	0.000	0	0	0.992	0.918	1.121
Iform weak(3)	1	0.000	0	0.000	0	0	1.020	0.916	1.135
Iform strong(3)	1	0.000	0	0.000	0	0	0.968	0.920	1.060
glinternet	1	0.441	1	0.018	0	0	1.246	0.898	1.446
hierNet	1	0.303	1	0.024	0	0	0.906	0.925	1.421
Oracle	NA	NA	NA	NA	NA	NA	0.953	0.921	1.050

Table 3.2: Table 2 Simulation results when the truth obeys weak heredity

Model	T1.tpr	T1.fpr	T2.tpr	T2.fpr	T3.tpr	T3.fpr	Train.MSE	Train.Rsq	Test.MSE
Forward select	1	0.001	0	0.000	0	0	3.326	0.731	3.480
Iform weak(2)	1	0.000	0	0.000	0	0	1.119	0.910	1.200
Iform strong(2)	1	0.008	0	0.000	0	0	1.580	0.872	1.707
Forward select (2)	1	0.000	0	0.000	0	0	1.083	0.912	1.167
Forward select (3)	1	0.000	0	0.000	0	0	0.979	0.921	1.089
Iform weak(3)	1	0.000	0	0.000	0	0	1.003	0.919	1.079
Iform strong (3)	1	0.008	0	0.000	0	0	1.578	0.872	1.705
Glinetnet	1	0.531	1	0.020	0	0	0.906	0.927	1.425
hierNet	1	0.343	1	0.027	0	0	0.856	0.931	1.412
Oracle	NA	NA	NA	NA	NA	NA	0.940	0.924	1.034

```
knitr::kable(
  read.csv("Chapter03_TableSim2.csv"), caption = 'Table 2 Simulation results when the truth obeys strong heredity',
  booktabs = TRUE
)
```

```
knitr::kable(
  read.csv("Chapter03_TableSim3.csv"), caption = 'Table 3 Simulation results when the truth is weakly hereditary',
  booktabs = TRUE
)
```

Table 3.3: Table 3 Simulation results when the truth is anti-heredity

Model	T1.tpr	T1.fpr	T2.tpr	T2.fpr	T3.tpr	T3.fpr	Train.MSE	Train.Rsq	Test.MSE
Forward select	1	0.000	0	0.000	0	0	3.284	0.729	3.510
Iform weak (2)	1	0.004	0	0.000	0	0	3.140	0.741	3.435
Iform strong(2)	1	0.000	0	0.000	0	0	3.284	0.729	3.510
Forward select (2)	1	0.000	0	0.000	0	0	1.081	0.911	1.171
Forward select (3)	1	0.000	0	0.000	0	0	0.989	0.918	1.095
Iform weak(3)	1	0.003	0	0.000	0	0	3.155	0.739	3.448
Iform strong(3)	1	0.000	0	0.000	0	0	3.284	0.729	3.510
glinternet	1	0.710	1	0.029	0	0	0.844	0.931	1.578
hierNet	1	0.858	1	0.085	0	0	0.307	0.975	2.216
Oracle	NA	NA	NA	NA	NA	NA	0.952	0.921	1.031

Table 3.4: Table 4 Simulation results when the truth is constructed of pure interactions

Model	T1.tpr	T1.fpr	T2.tpr	T2.fpr	T3.tpr	T3.fpr	Train.MSE	Train.Rsq	Test.MSE
Forward select	NaN	0.020	0	0.000	0	0	3.316	0.025	3.445
Iform weak(2)	NaN	0.028	0	0.000	0	0	3.007	0.115	3.181
Iform strong(2)	NaN	0.021	0	0.000	0	0	3.294	0.031	3.429
Forward select (2)	NaN	0.000	0	0.000	0	0	1.117	0.669	1.170
Forward	NA	NA	NA	NA	NA	NA	NA	NA	NA
Select(3)	NaN	0.000	0	0.000	0	0	1.005	0.703	1.081
Iform weak(3)	NaN	0.025	0	0.000	0	0	3.043	0.106	3.209
Iform strong(3)	NaN	0.021	0	0.000	0	0	3.294	0.031	3.429
glinternet	NaN	0.571	1	0.017	0	0	1.002	0.699	1.445
hierNet	NaN	0.853	1	0.045	0	0	0.672	0.802	1.758
Oracle	NA	NA	NA	NA	NA	NA	0.968	0.713	1.022

```
knitr::kable(
  read.csv("Chapter03_TableSim4.csv"), caption = 'Table 4 Simulation results when the truth is
  booktabs = TRUE
)
```

In the scenarios where the data was assumed to follow some form of a hierarchical structure for the epistasis effects the iForm procedure for higher-order epistasis effects appeared to perform the best. Not only did it result in selecting the correct model, the false positive rate was also among the

lowest. The out of sample error was also among the lowest between each of the models compared. With the procedure using OLS calculations, it also performed the fastest out of the models including epistasis effects. All of the combined show the promise of the iForm procedure for GWAS type studies. With the other scenarios, the underlying structure of the data does not follow a typical intuition about the structure of data in biology.

3.3.2 Worked Example

We validated the biological usefulness of the model by analyzing a mapping data for a woody plant, mei (*Prunus mume*). Originated in China, mei has been cultivated for its ornamental flowers for thousands of years (?). Its many desirable properties, such as cold-hardiness, colors and flavors, are appraised as a symbol of persistence and beauty in Chinese culture. Recent sequencing of its genome has made it an ideal model system to study the genetics and evolution of woody plants (?). To improve the growth rigor and form of mei important to its ornamental value, a cross was made between two distinct cultivars, Fenban (female parent) and Kouzi Yudie (male parent), aimed to select superior genotypes from hybrids. To the end, an F1 mapping population of 190 hybrids was established and further genotyped for 4,934 SNP markers over eight linkage groups which correspond to eight chromosomes across the entire genome.

To test genotypic differences in growth performance, each of these hybrids was grafted on an established root stock using multiple budding scions. Next spring, buds on the scions sprouted into shoots. The lengths and diameters of 10 randomly selected shoots were measured once every two weeks during an entire growth season from March to October. It was found that both shoot length and diameter growth was well fitted to the three-parameter growth equation expressed as

$$g(t) = a/[1 + b * \exp(-rt)] \quad (3.3)$$

where $g(t)$ is the amount of shoot growth at time t , a is the asymptotic value of growth when time tends to be infinite, b is a parameter that reflects the amount of growth at time 0, and r is the relative growth rate. These three parameters determine the overall form of growth curve jointly, although they function differently. Thus, by estimating these parameters for individual hybrids using a nonlinear least squares approach, we can draw the growth curve of each hybrid. Differences in growth curve among hybrids may be controlled by specific genes or quantitative trait loci (QTLs). Although tremendous efforts have been made to map growth QTLs and their epistasis (??; ?), none has characterized the contribution of high-order epistasis although it has been thought to regulate growth processes.

By treating the estimates of growth parameters for individual hybrids as “phenotypic traits,” we used iFORM to map growth QTLs and QTL-QTL interactions. Of 4,934 markers, 2,100 are the testcross markers at which markers are segregating due to only one heterozygous parent and 2,834 are the intercross markers whose segregation results from the heterozygosity of both parents. For a testcross marker, there is only one main genetic effect, whereas an intercross marker contains additive and dominant main effects. Thus, a pair of testcross markers produces only type of epistasis, but a pair of intercross markers forms four types of epistasis, additive \times additive, additive \times dominant, dominant \times additive and dominant \times dominant. For two markers with one from the testcross and the other from the intercross, there are two types of epistasis, i.e., additive \times additive and additive \times dominant (?). The number and type of epistasis can be characterized for any three markers accordingly. Here, the iFORM was implemented in a way that allows both marker markers to be modeled and analyzed simultaneously.

Table 3.5: Table 5 The detection of epistasis for the relative growth rate (r) of shoot length in the full-sib family of mei tree by a low-order epistatic model

Coefficient	Estimate	SE	T.value	P.value
(Intercept)	0.18285	0.07613	2.402	0.0174 *
AATTC_nn_np_2517_a	0.40013	0.06509	6.147	5.13e-09 ***
AATTC_nn_np_2815_a	0.15792	0.06837	2.310	0.0221 *
CATG_nn_np_3479_a	0.23433	0.05285	4.434	1.63e-05 ***
CATG_nn_np_1284_a	0.22200	0.05313	4.179	4.61e-05 ***
AATTC_nn_np_2815_a×AATTC_lm_ll_3034_a	0.45783	0.09244	4.953	1.71e-06 ***

To demonstrate the possible importance of high-order epistasis, we analyze the data by assuming that growth parameters are controlled by low-order epistasis only and by both low- and high-order epistasis, respectively. The weak heredity (hierarchical) was used to screen every SNP and possible interaction of the main effects selected and the rest of the SNPs left in the candidate set. It was not restricted to the strong case where both main effects had to be in the model for the interaction to be considered. For the pairwise epistatic model, this grew the candidate set to almost 20,000 predictors to choose from. It turned out that 5 predictors were chosen, i.e., four main additive effects of markers, AATTC_nn_np_2517, AATTC_nn_np_2815, CATG_nn_np_3479 and CATG_nn_np_1284 and one epistatic effect due to markers AATTC_nn_np_2815 and AATTC_lm_ll_3034, for growth parameter r of shoot length 3.5. The main effect of marker AATTC_lm_ll_3034 was detected to be insignificant. These main and epistatic effects together explained 32.41% of the total variance of parameter r.

```
knitr::kable(
  read.csv("Chapter03_Table5.csv"), caption = 'Table 5 The detection of epistasis for the rela
  booktabs = TRUE
)
```

When opening up the iForm procedure to the possibility to creating higher order interactions

to be placed into the candidate set, a more complete picture of the phenotypal variation was revealed. The amount of predictors included in the final model grew to 12, with one of them being three-way interactions among markers AATTC_nn_np_2815, AATTC_lm_ll_3034 and AATTC_nn_np_1615. The adjusted R^2 jumped up to over 70% 3.5. This astonishing jump in predictive power is an exemplar case as to the importance of higher-order interactions in genetic models. Not only did higher-order interactions become one of the most significant predictors in the model selected, it also allowed for other order-two interactions and main effects to be kept in the model that were previously left out. At the next step of every iteration, the new candidate effect was conditioned on everything previously selected. With the conditional effect of the higher-order interaction it enabled for other lost effects to be modeled as well.

```
knitr::kable(
  read.csv("Chapter03_Table6.csv"), caption = 'Table 6 The detection of epistasis for the rela
  booktabs = TRUE
)
```

The purpose of the mei genetic project is to study the genetic control of shoot growth form. Here, we further analyze how three-way interactions detected by our model affect growth form. Assume that there are three testcross markers, A (with two alleles A, a), B (with two alleles B, b), and C (with two alleles C, c), which interact jointly to affect shoot growth. The three markers form eight genotypes AABBCC, AABBCc, AABbCC, AABbCc, AaBBCC, AaBBCc, AaBbCC and AaBbCc whose genotypic means at time t are partitioned into different components, respectively, expressed as

Table 3.6: Table 6 The detection of epistasis for the relative growth rate (r) of shoot length in the full-sib family of mei tree by a high-order epistatic model

Coefficient	Estimate	SE	T.value
(Intercept)	0.16859	0.05801	2.906
AATTC_nn_np_2517_a	0.27773	0.04396	6.318
AATTC_nn_np_2815_a	0.26382	0.05295	4.983
CATG_nn_np_3479_a	0.20767	0.03467	5.990
CATG_nn_np_1284_a	0.04522	0.04265	1.060
AATTC_nn_np_2815_a×AATTC_lm_ll_3034_a	1.82572	0.17925	10.185
AATTC_nn_np_2815_a×AATTC_hk_hk_278_a	0.25935	0.03888	6.671
CATG_lm_ll_3153_a	0.14877	0.03491	4.262
CATG_nn_np_1284_a×AATTC_nn_np_554_a	0.22994	0.05104	4.505
AATTC_nn_np_2815_a.AATTC_lm_ll_3034_a×AATTC_nn_np_1615_a	-1.51714	0.19060	-7.960
AATTC_nn_np_2815_a×AATTC_nn_np_929_a	-0.30805	0.05477	-5.624
AATTC_hk_hk_479_d	0.16044	0.03443	4.660
AATTC_nn_np_2517_a×CATG_hk_hk_648_a	0.14537	0.02840	5.118

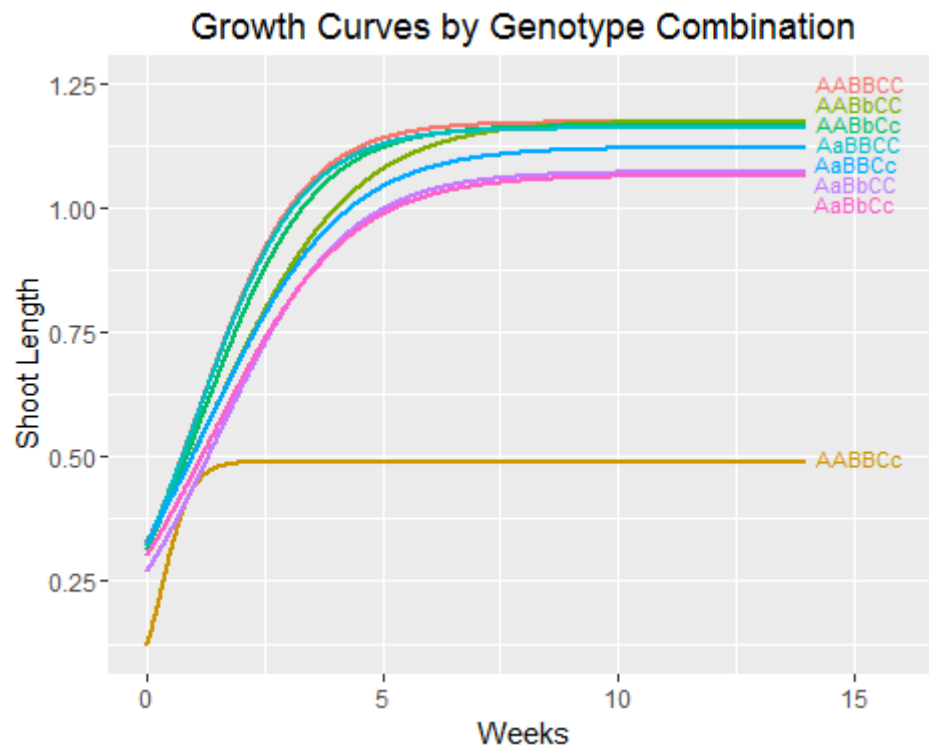


Figure 3.1: Growth Curve Comparison

$$\begin{aligned}
\mu_{111}(t) &= \mu(t) + \alpha_1(t) + \alpha_2(t) + \alpha_3(t) + i_{12}(t) + i_{13}(t) + i_{23}(t) + i_{123}(t) \\
\mu_{112}(t) &= \mu(t) + \alpha_1(t) + \alpha_2(t) \smile \alpha_3(t) + i_{12}(t) \smile i_{13}(t) \smile i_{23}(t) \smile i_{123}(t) \\
\mu_{121}(t) &= \mu(t) + \alpha_1(t) \smile \alpha_2(t) + \alpha_3(t) \smile i_{12}(t) + i_{13}(t) \smile i_{23}(t) \smile i_{123}(t) \\
\mu_{122}(t) &= \mu(t) + \alpha_1(t) \smile \alpha_2(t) \smile \alpha_3(t) \smile i_{12}(t) \smile i_{13}(t) + i_{23}(t) + i_{123}(t) \\
\mu_{211}(t) &= \mu(t) \smile \alpha_1(t) + \alpha_2(t) + \alpha_3(t) \smile i_{12}(t) \smile i_{13}(t) + i_{23}(t) \smile i_{123}(t) \\
\mu_{212}(t) &= \mu(t) \smile \alpha_1(t) + \alpha_2(t) \smile \alpha_3(t) \smile i_{12}(t) + i_{13}(t) \smile i_{23}(t) + i_{123}(t) \\
\mu_{221}(t) &= \mu(t) \smile \alpha_1(t) \smile \alpha_2(t) + \alpha_3(t) + i_{12}(t) \smile i_{13}(t) \smile i_{23}(t) + i_{123}(t) \\
\mu_{222}(t) &= \mu(t) \smile \alpha_1(t) \smile \alpha_2(t) \smile \alpha_3(t) + i_{12}(t) + i_{13}(t) + i_{23}(t) \smile i_{123}(t)
\end{aligned} \tag{3.4}$$

where $\mu(t)$ is the population mean at time t ; $\alpha_1(t)$, $\alpha_2(t)$, and $\alpha_3(t)$ are the genetic effects of markers A, B and C at time t , respectively; $i_{12}(t)$, $i_{13}(t)$, and $i_{23}(t)$ are the pairwise epistatic effects between markers A and B, A and C and B and C at time t , respectively; and $i_{123}(t)$ is the three-way epistatic effect among three the markers at time t . From the above equations, we solve the pairwise and three-way epistatic effects as

$$\begin{aligned}
i_{12}(t) &= [(\mu_{111}(t) + \mu_{112}(t) + \mu_{221}(t) + \mu_{222}(t)) \smile (\mu_{121}(t) + \mu_{122}(t) + \mu_{211}(t) + \mu_{212}(t))] \\
i_{13}(t) &= [(\mu_{111}(t) + \mu_{121}(t) + \mu_{212}(t) + \mu_{222}(t)) \smile (\mu_{112}(t) + \mu_{122}(t) + \mu_{211}(t) + \mu_{221}(t))] \\
i_{23}(t) &= [(\mu_{111}(t) + \mu_{122}(t) + \mu_{211}(t) + \mu_{222}(t)) \smile (\mu_{112}(t) + \mu_{121}(t) + \mu_{212}(t) + \mu_{221}(t))] \\
i_{123}(t) &= [(\mu_{111}(t) + \mu_{122}(t) + \mu_{212}(t) + \mu_{222}(t)) \smile (\mu_{112}(t) + \mu_{121}(t) + \mu_{211}(t) + \mu_{222}(t))]
\end{aligned} \tag{3.5}$$

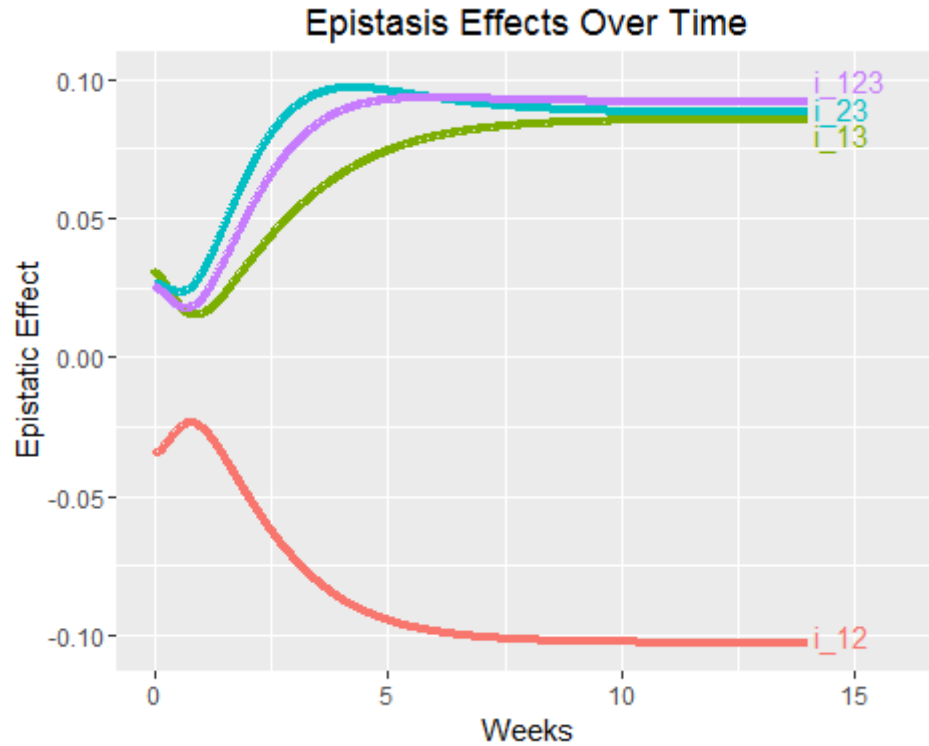


Figure 3.2: Epistasis Comparison

Each genotype can draw a growth curve using its growth parameters (a , b , r) estimated from raw data, from which we can chart the curves of pairwise and three-way epistatic effects using equation (3.4). Three markers AATTC_nn_np_2815(AA/Aa), AATTC_lm_ll_3034(BB/Bb) and AATTC_nn_np_1615(CC/Cc) that produce a significant three-way interaction for parameter x of shoot length display pronounced differences in growth curve 3.1. The epistasis of low- and high-order performs differently to affect growth form, with three-way interactions playing a more remarkable role than pairwise epistasis 3.2.

The figures display the variation between each of the growth curves for the eight combinations of the three marker genotypes focused on 3.1. Differences of each of the growth parameters can be observed when studying the figures. There is clear separation in the shoot length that is observed at the end of the 16 weeks. This difference can be visually grouped into four clusters that show the

effect a genotype combination can have on the asymptotic growth parameter, a . Another noticeable difference between the curves displayed is the rate at which the growth developed. At the earlier weeks of development you can see some of the genotype combinations grew faster, manifesting in a steeper slope and other genotypes had shallower slopes. All of these visually show what was picked up on when modeling the shoot length growth and the impact of the higher-order interactions between the genotypes have on such growth. By solving the system of linear equations in (3.5) we can dissect the epistatic effects of the genotype combinations. The effects over time are displayed 3.2 and in this you can see the non-linear influence of the interactions between the markers included.

3.4 Discussion

Genetic interactions have been thought to contribute to a significant portion of genetic variance for quantitative traits of critical importance to evolutionary biology, agriculture and medicine (?; ?). While pairwise interactions have been a major focus of quantitative genetic studies, there has been growing evidence that genetic interactions involving three or more loci play an important role in affecting the phenotypic differentiation of traits (?; ?; ?; ?; ?; ?; ?). Because of its complexity due to a network of interactions, the detection of high-order epistasis is extremely difficult (?). More importantly, interpretation of high-order epistasis and its contribution to overall genetic architecture can be better made by jointly analyzing all possible low- and high-order interactions among genes. This has added an extra challenge to statistical modeling and detection of this important phenomenon. Thanks to the recent development of statistical models for high-dimensional variable selection, we have reformed a statistical modeling framework for detecting high-order epistasis by focusing on three-way interactions.

Our model extends ? forward selection-based algorithm iFORM that has proven to be robust and efficient for computing and detecting two-way interactions between predictors (including continuous predictors). A favorable property of iFORM is its capacity to detect interactions even if the dimension of predictors is extremely high relative to a sample size used. The fundamental assumption used by iFORM is the heredity principle, i.e., the existence of interactions between a pair of variables that each has at least weak main effects. After extending it to characterize three-way interactions, this assumption can be relaxed for the third variable; i.e., even if there is no detectable main effect for the third marker, then extended iFORM can still detect the three-way interaction. This property may explain the reason why high-order epistatic model outperforms low-order epistatic model, as demonstrated from the detection of significant genetic interactions in a real data of a woody plant, mei (*Prunus mume*). It was found from a recent study that loci participating in high-order genetic interactions may not individually have measurable effects (?). As a result, our model can be used as a general tool to detect genetic interactions of various orders and, therefore, elucidate the overall picture of genetic architecture by capturing the so-called missing heritability.

The model was investigated by simulation studies whose result help users to determine an optimal design of mapping or association studies in terms of sample size, phenotyping precision and the number of markers. Its application to *P. mume* genetic mapping leads to the detection of key loci and their interactions expressed at the low- and high-order levels for the growth form of shoots. The curve of three-way epistasis on mei shoot length growth was observed to increase exponentially during the first five weeks of shoot sprouting and become stable after five weeks. Such integration of the model into growth equation shed light on the developmental mechanisms of growth processes through epistasis, a question that has evoked a tremendous interest of researchers globally in the area of evolutionary developmental biology (?, ?, ?). We have created an R package that has implemented the model which adds a function to allow epistasis of any orders to be searched. The

package can be uploaded at <http://statgen.psu.edu/software/> and will be made available through CRAN (Comprehensive R Archive Network).

Chapter 4

iForm Functional Mapping (A computational method)

4.1 Motivation

As we have seen and also has been noted by several researchers while conducting biometric analysis (???) or molecular dissection (?, ?) is that quantitative traits are very complex and much is still needed to be learned. The researchers cited note that the traits are most likely polygenic, including gene-gene interactions and other sources of interaction effects. (??; ??; ?) Higher order interactions of complex traits are not well studied because of their difficulty to detect in mapping studies as well. The lack of data should not be construed as proof that this order of interaction does not exist. (?). The difficulty in detection leads a way for new computational methods to be developed and approaches to describe how to distinguish such effects. As noted in chapter 3, new theoretical models of high-order epistasis have well been established by mathematical biologists (??). These

models provided a foundation to interpret high-order epistasis from a biological standpoint. A few statistical models have been derived to estimate and test high-order epistasis in case-control designs (?) and population-based mapping settings (?)

Growth and developmental traits are mostly better described by a functional process (?, ?), it is more biologically meaningful to map these traits as growth curves (?). There have been a few different approaches that have integrated growth equations into genetic mapping via the likelihood function, leading to the birth of a so-called functional mapping models (?, ?, ?, ?). These style of approaches can allow for the developmental change of genetic control to be characterized across both time and as well as space (?, ?). Treating the phenotype as a complex trait it would be likely it would follow a more functional or dynamic process. This information could be lost or greatly limited by treating the response as a single static predictor. Modeling the longitudinal structures in this fashion, functional mapping has proven to be of great statistical power in gene identification and the utilization of sparse phenotypic data (?). In an attempt to capture all relevant information and be as parsimonious as possible principles from biophysical and biochemical processes were considered. The logistic growth equations are both biologically relevant (?, ?) and have few parameters that can be mapped to growth QTLs by estimating these parameters for each genotype and interactions between genotypes.

There are many approaches for gene mapping with genome-wide association studies (GWAS) being one of the most popular one, achieving a considerable success since their first publication in 2005 (?). Analytical approaches are constantly being developed to perform GWAS studies. There are a few areas of challenges in statistical modeling and analysis of genetic data that account for the complexity of phenotypic information. Generally GWAS studies associate genetic markers with static, single valued phenotypes. As we have discussed, most analysis revolve around point wise

estimates and do not always take the entirety of the system during the analysis. Incorporating selections are starting to become more common but further work in this area still needs to be explored. Extending the forward selecting procedure previously state in 2 and 3 in order to handle a functional phenotype would be very beneficial with GWAS level studies. A few challenges do arise while considering to conduct a genome-wide association study (GWAS) on interacting traits measured at a sequence of time points. The model needs to be flexible enough to fit different situations, independence of the error structure needs to be maintained or accounted for with the time dependencies and finally computational efficiency needs to be good enough to fit such complex models. All of these issues combined make it a difficult exertion to take on but with computational power increasing, it is becoming more feasible to handle.

In applications like the scenario described where we have a functional value phenotype and a high dimensional predictor space with dynamically considering interaction effects it may be too restrictive to suppose that the effect of all of the predictors is captured by a simple linear fit. Reframing the regression problem to help code in the longitudinal data into the structure of the data in a biologically meaningful manner and making some sparsity assumptions about the number of significant genetic and epistatic effects that affect the phenotype will help in the development of such a model to tackle such a task.

Also included in iFormFunctional Mapping Part

Monitoring the change in expression patterns over time provides the distinct possibility of unraveling the mechanistic drivers characterizing cellular responses. Gene arrays measuring the level of mRNA expression of thousands of genes simultaneously provide a method of high-throughput data collection necessary for obtaining the scope of data required for understanding the complexities of living organisms. Unraveling the coherent complex structures of transcriptional dynamics is the goal of

a large family of computational methods aiming at upgrading the information content of time-course gene expression data. In this review, we summarize the qualitative characteristics of these approaches, discuss the main challenges that this type of complex data present, and, finally, explore the opportunities in the context of developing mechanistic models of cellular response. ?

4.2 Methods

4.2.1 Regression by linear combination of basis functions

One common approach to regression problems is to frame the model as a linear combination of basis functions. In typical multiple regression the design matrix would be the values of the observed predictors and these would be used to fit the model, usually with a least squares approach. The goal then being to fit the expected value of the phenotype of interest in terms of the values of the predictors. This would result in a linear model of the form,

$$Y = \beta_0 + \beta_1 X_1 + \cdots + \beta_p X_p + \epsilon(\#eq : lin - mod) \quad (4.1)$$

This model is nice for a single response but can be too restrictive at times. With a functional response over time, having a model with more flexibility could more accurately estimate the phenotype especially when considering a functional phenotype like a growth model. A fit like the one mentioned would only restrict growth to be a straight line and that may not be applicable in real world applications. By treating the problem as linear combination of basis functions, the general form would look like,

$$f(x) = \sum_{i=0}^P \theta_i \phi_i(x) \quad (4.2)$$

where the ϕ are the basis functions of the researchers choosing. Under this format you can choose any function that would fit the need of the given problem and has relevance to the application area. A common choice is to use polynomial regression, where ϕ_i would be the predictors raised to different degrees in order to invoke a non-linear relationship into the model. This works well but it comes with some drawbacks. The first being that for each degree considered, it could grow the predictor set even larger. Instead of just one effect for each predictor you could have up to the order of the polynomial effects for each predictor. With the predictor set being at a high dimensional level already, this may not be something feasible to do. The other area of concern is that it would give a way for higher correlation between effects in the model. This would violate the initial assumptions of the model.

Standard polynomial regression is just one case of using basis functions in linear regression. There are many transformations that are able to be performed to invoke nicer properties to the data. The basis functions that are going to be focused on in this work are orthogonal polynomials. This would be a special case of polynomial regression that would alleviate some of the drawbacks mentioned above. Orthogonal polynomials by definition are orthogonal to each other and therefore would not have any correlation between predictors when used as basis functions. Also as an advantage, polynomial regression can be used to make similar types of interest as other types of multiple regression analysis. It does this while modeling a non-linear relationship between the phenotype and genetic markers without having to use complex optimization methods. Ordinary least squares would still apply in this framework, making it more computationally efficient as well. One specific class of orthogonal polynomials that will be used are the Legendre polynomials because of the nice

properties they possess.

4.2.2 Legendre Polynomials

Remove R Code

```
library(ggplot2)

library(data.table)

library(RColorBrewer)

Legendre<-function( t, np.order=1,tmin=NULL, tmax=NULL )
{
  u <- -1

  v <- 1

  if (is.null(tmin)) tmin<-min(t)

  if (is.null(tmax)) tmax<-max(t)

  nt <- length(t)

  ti    <- u + ((v-u)*(t-tmin))/(tmax - tmin)

  np.order.mat <- matrix(rep(0,nt*np.order),nrow=nt)

  if(np.order >=1)

    np.order.mat[,1] <- rep(1,nt)

  if (np.order>=2)

    np.order.mat[,2] <- ti

  if (np.order>=3)

    np.order.mat[,3] <- 0.5*(3*ti*ti-1)
```



```

if (np.order>=4)

  np.order.mat[,4] <- 0.5*(5*ti^3-3*ti)

if (np.order>=5)

  np.order.mat[,5] <- 0.125*(35*ti^4-30*ti^2+3)

if (np.order>=6)

  np.order.mat[,6] <- 0.125*(63*ti^5-70*ti^3+15*ti)

if (np.order>=7)

  np.order.mat[,7] <- (1/16)*(231*ti^6-315*ti^4+105*ti^2-5)

if (np.order>=8)

  np.order.mat[,8] <- (1/16)*(429*ti^7-693*ti^5+315*ti^3-35*ti)

if (np.order>=9)

  np.order.mat[,9] <- (1/128)*(6435*ti^8-12012*ti^6+6930*ti^4-1260*ti^2+35)

if (np.order>=10)

  np.order.mat[,10] <- (1/128)*(12155*ti^9-25740*ti^7+18018*ti^5-4620*ti^3+315*ti)

if (np.order>=11)

  np.order.mat[,11] <- (1/256)*(46189*ti^10-109395*ti^8+90090*ti^6-30030*ti^4+3465*ti^2-63)

return(np.order.mat)
}

L <- data.frame(t = seq(0, 1, by = 0.01), Legendre(seq(0, 1, by = 0.01), 10))

L_melt <- melt(L, id = "t")

ggplot(L_melt, aes(x = t, y = value, group = variable, color = brewer.pal(10, "Set3")[variable]))
  geom_line() + theme(legend.position="none")

```

Figure 4.1: First 10 Legendre Polynomials

The definition of the Legendre polynomials are the solutions for $n = 0, 1, 2, \dots$ (with the normalization $P_n(1) = 1$) form a polynomial sequence of orthogonal polynomials called the Legendre polynomials. Each Legendre polynomial $P_n(x)$ is an n th-degree polynomial. It may be expressed using Rodrigues' formula:

$$P_n(x) = \frac{1}{2^n n!} \frac{d^n}{dx^n} [(x^2 - 1)^n] \quad (4.3)$$

An important property of the Legendre polynomials is that they are orthogonal with respect to the L2-norm on the interval $-1 \leq x \leq 1$:

$$\int_{-1}^1 P_m(x) P_n(x) dx = \frac{2}{2n+1} \delta_{mn} \quad (4.4)$$

δ_{mn} denotes the Kronecker delta equal to 1 if $m = n$ and 0 otherwise. These polynomials can be generated by using the following recursively. Each Legendre polynomial would be the next order n in the expression below.

$$\begin{aligned} P_n(x) &= \frac{1}{2^n} \sum_{k=0}^n \binom{n}{k}^2 (x-1)^{n-k} (x+1)^k \\ &= \sum_{k=0}^n \binom{n}{k} \binom{-n-1}{k} \left(\frac{1-x}{2}\right)^k \\ &= 2^{-n} \sum_{k=0}^n x^k \binom{n}{k} \binom{\frac{n+k+1}{2}}{k} \end{aligned} \quad (4.5)$$

With nature of the Legendre orthogonal polynomials, it was advantages for both dimension reduction and also handling unevenly spaced, missing or non-uniform time measurements from different subjects in the dataset. By seeing which polynomial curve fits the given phenotype, it removes some of the challenges when fitting the model. Different orders of the polynomial are tried throughout the procedure to allow for flexibility in the fitting the genetic variation from the mean curve for each of the genotypes or epistasis between genotypes considered in the model.

4.2.3 Model

The layout of the underlying model is first fit to an asymptotic growth model described by a logistic curve of the form,

$$\mu(t) = a / (1 + b * \exp(-r * t))$$

It is biologically meaningful to implement a growth equation, like a logistic curve, to describe growth trajectory ?. Here the population is described by a mean growth curve by this growth equation where a, b and r are growth parameters each provide a biological interpretation, with a being the asymptotic growth, b being the initial amount of growth and r being the relative growth rate. Time varying additive and dominant effects of significant SNPs are modeled by the Legendre orthogonal polynomial used in quantitative genetic studies, mentioned above. (?, ?, ?). This representation can be expressed as

$$\alpha_j(t) = (L_0(t), L_1(t), \dots, L_s(t)) * (u_{j0}, u_{j1}, \dots, u_{js})^T$$

$$\beta_j(t) = (L_0(t), L_1(t), \dots, L_{s'}(t)) * (v_{j0}, v_{j1}, \dots, v_{js'})^T$$

where $L_0(t), L_1(t), \dots, L_s(t)$ and $L_0(t), L_1(t), \dots, L_{s'}(t)$ are the LOP of orders s and s' , respectively; and $u_{j0}, u_{j1}, \dots, u_{js}$ and $v_{j0}, v_{j1}, \dots, v_{js'}$ are the vectors of time-invariant additive and dominant effects, respectively. Orders s and s' , selected from information criteria, for the purposes of this procedure the Bayesian information criterion (BIC_2), originally developed by ? was implemented. A nice feature that comes from modeling the fit in this manner is that the dimension of response phenotypic data is reduced through LOP modeling. (?, ?, ?, ?, ?). Writing the model out more explicitly we would have,

$$\begin{aligned}
 y(t) = \mu(t) + \sum_{j=1}^J \alpha_j(t) \xi_j + \sum_{k=1}^K \beta_k(t) \zeta_k \\
 + \sum_{I_1 < I_2 = 1}^I \gamma_I^{aa}(t) \xi_{I_1} \xi_{I_2} \\
 + \sum_{I_1 < I_2 = 1}^I \gamma_I^{ad}(t) \xi_{I_1} \zeta_{I_2} \\
 + \sum_{I_1 < I_2 = 1}^I \gamma_I^{da}(t) \zeta_{I_1} \xi_{I_2} \\
 + \sum_{I_1 < I_2 = 1}^I \gamma_I^{dd}(t) \zeta_{I_1} \zeta_{I_2} \\
 + \epsilon(t)
 \end{aligned} \tag{4.6}$$

4.2.4 Integrating with the iForm Procedure

An outline of the selection procedure used following the model described is as follows. At first the mean growth curve is estimated for the presented data following the logistic growth curve.

This could be adjusted depending on the functional process the researcher is studying. Once the mean curve is fit the selection procedure is initialized in a similar fashion as mentioned in previous chapters @ref{highdeqtl}. Both the solution set and the model set are assigned to the empty set, $S_0 = \emptyset$ and $M_0 = \emptyset$. The candidate set starts off containing all main effects for the additive and dominant effects of each SNP. The selection procedure then begins and each SNP is assessed and the best fitting candidate is then placed in the selection set. While assessing each candidate SNP, an additional search is performed for the best fitting polynomial fit up to a pre-specified order that is determined at the beginning of the procedure. The orthogonal polynomials are used to assist in fitting the genetic effects for each marker or epistatic interaction between the markers. This would allow the genetic effect some flexibility over time and give a more representative fit. This could also be used with other functional models or other types of non-linear functions that characterizes the biological systems being evaluated. We are treating the polynomials as a basis function for the regression problem and therefore the Residual Sum of Squares is calculated similar to multiple regression but replacing the design matrix with the necessary basis functions. This continues until a designated stopping value is reached. The BIC_2 is then used to find the optimal fit given the selection procedure performed. The following graphics show how the process works at each step

4.3 Application

4.3.1 Simulation Studies

As statistical issues become more complex they are going to be more analytically intractable and computational methods will need to close that gap to show the effectiveness of new models and procedures. Simulation studies were performed to ascertain the validity of the model. Rates at which

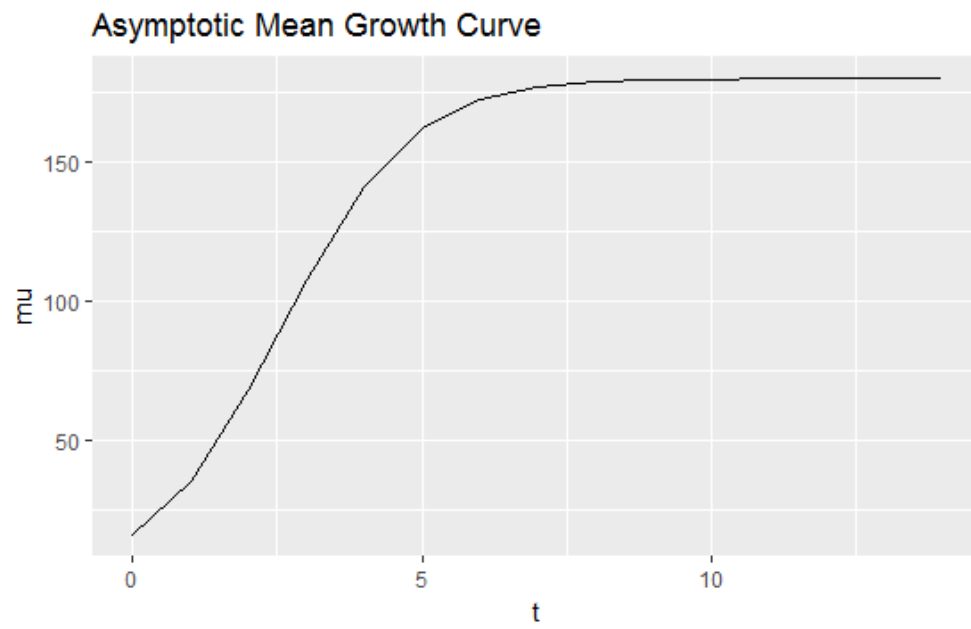


Figure 4.2: Example Growth Curve

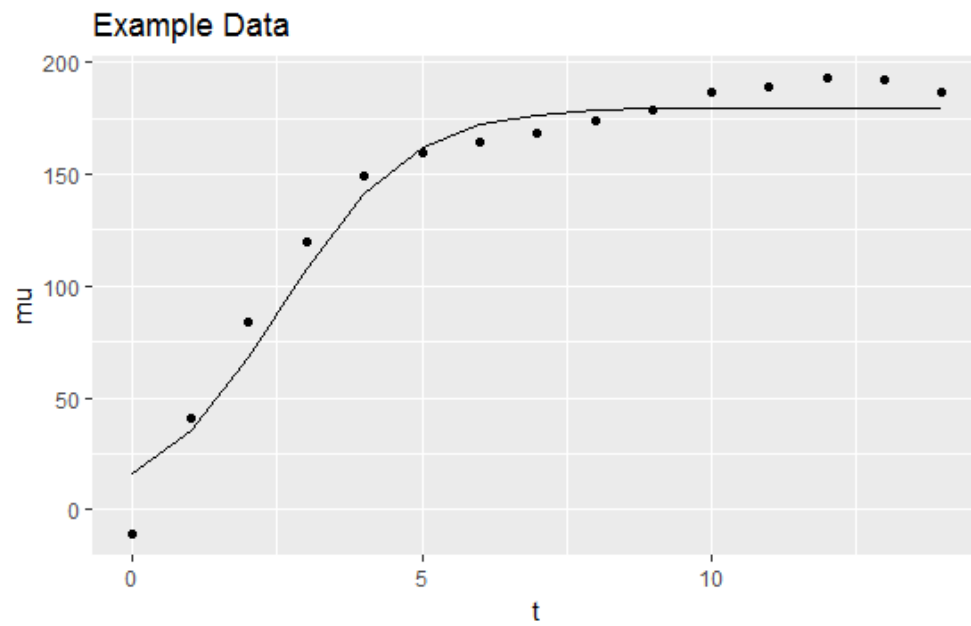


Figure 4.3: Example Data with Growth Curve

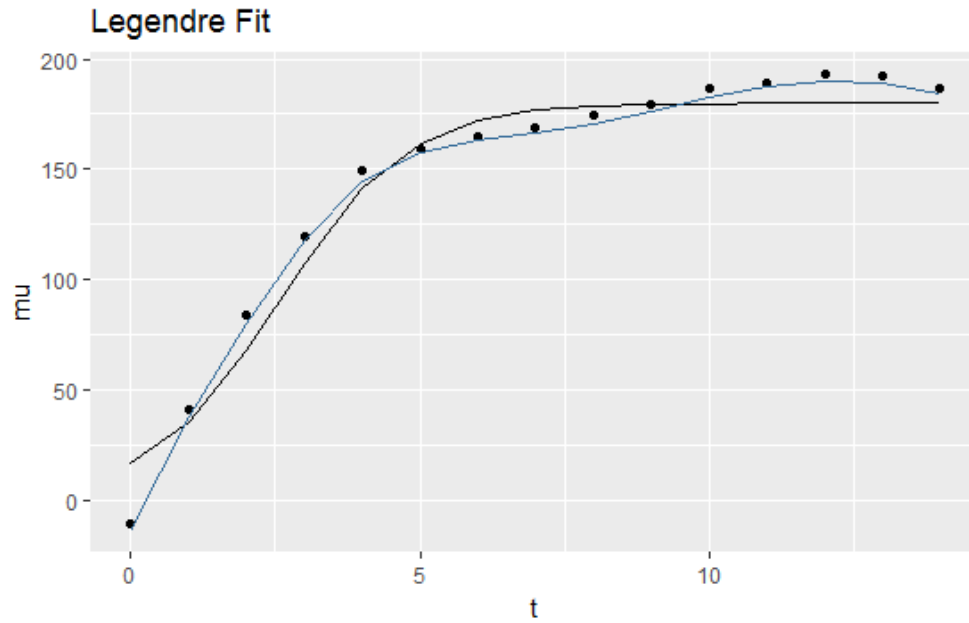


Figure 4.4: Additional Legendre Fit to Data

correct markers/epistasis were selected and overall model true model size was assessed. Data was original generated from a mean curve following the growth equation described above. It was then sampled from a multivariate normal distribution with the mean vector following the generated and with correlated errors over time. Significant effects were also included in the model to simulate different marker levels. These effects could be main effects of SNPs, or epistatic effects of interaction between SNPs. There were a total of 4 main effects and three interaction effects simulated. This simulation was replicated 100 times and then the selection procedure was ran. It performed well with 93% of the replicates selecting all main and interaction effects and the other 7% of the models select a majority of the effects. The model size simulated was of size 7. The average model size of the replicates fit was around 13.5. This would indicate some slight over-fitting but all important effects were included in the model. Some considerations for this need to be looked into further for future work.

4.3.2 Worked Example

As a comparison to what was done before in 3 the same mei tree dataset used in this chapter was studied again. This serves as a comparison to previous performance and also to see if any new discoveries can be made by incorporating the time component and fitting the growth parameters simultaneously throughout the procedure. The previous model only fit one parameter of the growth equation as a time and assessed the genetic markers that had a significant impact of this parameter. The parameter focused on was the rate parameter, r for the shoot height of the progeny. The initial results running the analysis with a single predictor and using the selection procedure are,

As a comparison here are the results for simultaneously fitting the growth curve and allowing for a more flexible genetic effect to be fit to the data. As you can see there are overlapping markers identified in the models. This shows the robustness of the new selection technique to be consistent with previous models. You can also see that the fit of the overall model has also increased. By including all effects at once, you gain more statistical power and it boost the adjusted R square value from 0.71 to above 0.9. This boost in model performance could be partially due to some over-fitting like we observed in the simulation studies and therefore a very strict bonferroni correction was implemented to assess whether individual markers were truly significant. Even with a strict cut-off we still observed 3 epistatic predictors to be highly significant. This shows the importance of including such terms while performing such a GWAS. The other area to note is the highly significant intercept term, which in our case is the result of the growth curve fit before implementing the selection procedure. This indicates also the importance of including biologically relevant information in the model to help better understand the genetic architecture being studied of the phenotype.

4.4 Discussion

The new model proposed has some very nice features and seems to perform well in the given application. Considering the complexity of working high dimensional data coupled with including epistatic effects as well as a functional component to the phenotype, it performs relatively efficiently. **Using generalize least squares, GLS type calculations aided in this efficiency**, while taking into account the correlation that would naturally arise between the repeated measurements are the same trees over time. This was enabled by the framing of the regression problem as a linear combination of basis functions. The agreeable properties of orthogonal polynomials helped ensure model assumptions are being met as closely as possible in order to use the calculations. Also by including the biologically meaningful logistic growth equations it helps fit a baseline fit to the data and would better allow for individual genetic effects to be found throughout the selection. These would of course have to be lab verified in order to assess the true biological mechanisms at play for the genetic control of the phenotype.

Some possible areas of concern for fitting the genetic effects to the polynomials could be that the effect does not conform to the polynomial curve under consideration. This can be alleviated by using other types of basis functions such as splines, but this would also cost a huge amount in computational efficiency with such a high dimensional data set. You need to be as efficient as possible when implementing a GWAS style study with the inclusion of possible epistasis. False positives could be of concern as well throughout the selection. The flexibility of the model and the wide range of polynomial fits that are considered could result in artifacts in the data to be picked up on. This is partially alleviated by using improved selection criteria like the BIC_2 and also having stricter than conventional cut-off values for significance testing. However these would still need to be assessed further through computational techniques such as cross-validation and

bootstrapping. The selection procedure is effective as a screening tool for exploratory data analysis and hypothesis generation. Lab verification would be another area that would help validate the findings even further. The comparison to previously run models is promising step in assessing the validity of the model at hand.

Chapter 5

Conclusions

5.1 Summary

5.1.1 HighDeQTL

- advantages
- disadvantages steps to improve

5.1.2 Higher Order Epistasis

- advantages
- disadvantages steps to improve

5.1.3 iForm Functional Mapping

- advantages
- disadvantages steps to improve

what else will be done before submitting for publication.

What areas need developed more and what areas will be looked into and discussed in further detail?

5.1.4 Previously written summary paragraph

In my disseration I have applied, adapted and extended the forward selection procedure under the marginality assumption first proposed by ? that is able to reduce search space substantially by making some reasonable assumptions about the data. These assumptions can be relaxed a little to broaden the scope of the space. The procedure ahs been applied in both simulated and real datasets in all areas of study. There are many advantages to using such a procedure with some being it is a computationally efficient way for high dimensional data situations that arise from high throughput data, especially when considering epistasis between gene markers or other type of interaction effects in the model. Guided search space based off of commonly used principles in model selection that are relevant in real world situations. It is able to perform a GWAS with included epistatic interactions a fairly quick manner. Able to relax assumptions to widen the search space. This may decrease the speed of the algorithm but makes the search more comprehensive. Also it is able to screen for complex scenarios that would be hard to find in a lab setting otherwise. Having said that with the flexibilty of the initial model, false posiive rates could be a concern and need to be taken into consideration. Adjustment to the significance level and the model selection criteria have been made

to account for this. This would still need to be followed up on independently by checking with other datasets and/or lab verification.

Functional components were also considered to such a selection procedure. This also increases the computational complexity of the model and therefore decreases some efficiency gains previously seen. Use biologically relevant information to guide the fitting of the model. Initially considers well established growth equations as a baseline for the underlying structure. It then performs a GWAS level analysis with considering epistatic interactions throughout the process.

5.2 Discussion

Needs Expanded

The selection procedures proposed attempt to address problems that are complex and have many moving parts to the procedure. Using a flexible model is very helpful to fulfill such requirements but this could have it be prone to over fitting at times if not well controlled. Need to heavily consider this as part of interpreting the model. Using stricter selection criteria and corrections to multiple testing for significance is extremely important. The main purpose is to use a screening to guide future research, use for exploratory data analysis and hypothesis generation.

With the complexity and expense that comes with genetic mapping, especially with a functional traits that needs repeatedly measured over time. Correlation structures are inherent in this data that need be addressed and usually done so at a heavy computational cost. Framing the problem as a regression problem and being able to use OLS calculations help to reduce the cost. Verification steps are important steps 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.

Also included in iFormFunctional Mapping Part

Monitoring the change in expression patterns over time provides the distinct possibility of unraveling the mechanistic drivers characterizing cellular responses. Gene arrays measuring the level of mRNA expression of thousands of genes simultaneously provide a method of high-throughput data collection necessary for obtaining the scope of data required for understanding the complexities of living organisms. Unraveling the coherent complex structures of transcriptional dynamics is the goal of a large family of computational methods aiming at upgrading the information content of time-course gene expression data. In this review, we summarize the qualitative characteristics of these approaches, discuss the main challenges that this type of complex data present, and, finally, explore the opportunities in the context of developing mechanistic models of cellular response. ?

5.3 Future Steps

- Aim 1
- Continue testing properties of the iForm procedure used with the Legendre Polynomials
- Submit by Summer
- Aim 2

- Consider other multivariate responses and correlated error structures.
- Expression levels of different cell lines or tissue types as multivariate response
- Aim 3
- Combine functional component and multivariate response into complete functional network
 - Time-Series of gene expression from cell lines or tissue types

More extensive explanation of future aims will be necessary for the final write up.

5.3.1 Aim 1

Incorporating other mean curves for the intercept term could help extend and relate to other areas of biology that follow a functional trait. There are also other types of orthogonal polynomials that could be explored as well. Using others polynomials would allow for other fits to the data that may be more applicable in other scenarios. Also using other basis functions in general could open up opportunities for other areas of application.

5.4 Aim 2

Other interesting areas would be to consider different levels of interactions with other omics data. Gene-gene interactions considered are only a portion of the picture and this type of modeling could also handle more levels of interactions that occur in a biological system. One area that

I am particularly interested in applying would be in methylation studies of the gene expression. This level of interaction is very important and a selection procedure like the one proposed could help screen and generate of possible effects and hypothesis to continue to look into. It would also apply in gene-environment interactions. This does not have to be restricted to just within the biological system under study. Environmental factors are important areas that could vastly impact the development of a phenotype.

5.4.1 Aim 3

Statistical areas that could as be considered to extend the model would be to include multivariate reponses to the system. For example having gene and protein expression being a bivariate reponse and to see how genetic markers and epistasis between the markers would better predict this by taking the correlation between those two response variables into account. Other statistical considerations would be to extend selection criteria to help further reduce the possibility of false positives being selected given a growing dataset like the one that occurs while dynamically including interaction effects throughout the selection. Making the model even more computational efficient would always be beneficial as well. The faster a model can accurately run the more likely a researcher will use it. It will also help process all the high throughput data that is being constantly developed.

5.4.2 Closing Remarks

Continuing on, my aim would be to work with datasets of this scale and incorporate the types of statistical methods mentioned and machine learning techniques to aid in analysis. The results could help gain larger insights into the genomic/epigenetic architecture of biological systems. On top of

the importance of a functional component to the phenotype, considering other types of multivariate responses would be interesting to study in context of such a system. Integrating different level of omics data and the challenges that arise with such complicated and large datasets has interested me throughout my PhD work. Translating such a complex system into usable information that can be shared in order to prevent and fight disease would be ideal research for me. This type of research would need both methodological development as well as application of existing statistical and machine/deep learning techniques to handle the magnitude of the problem.

Chapter 6

Appendix

This needs more work. Only includes first part of the appendix pdf

