Table of Contents

List of Figures

List of Tables

Chapter 1

**Introduction**

* 1. QTL mapping/Marker Regression
  2. Stepwise forward selection
  3. Chapter Over
  4. …

Chapter 2

**Inferring the Global Genetic Architecture of Gene Transcripts From Ultra-High Dimensional Molecular Data (ENAR Presentation Title/Title of first paper)**

2.1 Introduction

2.2 Model

2.3 Results

2.4 Discussion

Chapter 3

**An ultrahigh-dimensional high-order epistatic mapping model of complex traits. (Second Paper)**

3.1 Introduction

3.2 Methods  
 3.2.1 Extension of iForm procedure  
 3.2.2 Considerations made with data model  
 3.2.3 Testing Additive and Dominant effects after iForm procedure? (like in marker regression section of Statistical Genetics of Quantitative Traits)

3.3 Application  
 3.3.1 Caenorhabditis elegans data (Rockman et al. 2010)  
 3.3.2 Simulation

3.3.3 Mei Trees Growth parameters

3.4 Results  
 3.4.1 Results of running model on data  
 3.4.2 Comparison to original paper (cis and trans-QTL comparisons / marker hotspots)

3.5 Discussion

Chapter 4

4.1 Introduction

4.1.1 Functional Mapping component to response variable

4.2 Methods

4.2.1 Legendre Polynomials

4.3 Application

4.3.1 Mei Trees full dataset not just growth parameters

4.4 Results

4.5 Discussion

4.5.1 Useful for screening in GWAS studies involving functional components

4.5.2 Data reduction techniques for both response and predictor space

4.5.3 Limitations: A lot of moving parts, need for clinical validation, useful for hypothesis generation and research ideas, Useful for EDA at beginning of projects

Chapter 5  
 **Summary and future work**

5.1 Summary

Use Cover letter and Research statement for guidance and inspiration

5.2 Future Aims  
 5.2.1 Aim 1  
 5.2.2 Aim 2  
 5.2.3 Aim 3