

Contents

About the Authors vii

Acknowledgments ix

Chapter 1 Overview 1

- 1.1 Introduction 1
- 1.2 Book Organization 2
- 1.3 SAS Usage 4
 - 1.3.1 Example of a Basic SAS DATA Step 4
 - 1.3.2 Example of a Basic Macro 5
- 1.4 References 6

PART 1 Classical Quantitative Genetics

Chapter 2 Estimation of Genetic Variances and Covariances by Restricted Maximum Likelihood Using PROC MIXED 11

- 2.1 Introduction 11
- 2.2 The Nested Half-Sib and Related Designs 13
 - 2.2.1 Example of Nested Half-Sib Design, One Trait 13
 - 2.2.2 Example of Nested Half-Sib Design, Two Traits 19
 - 2.2.3 Example of Clonal Design, Two Environments 23
- 2.3 The Diallel and Related Designs 27
 - 2.3.1 Diallel Example 28
 - 2.3.2 Extension to the NC2 Design 33
- 2.4 Pedigreed Populations 34
- 2.5 References 34

Chapter 3 More Estimation of Genetic Parameters 35

- 3.1 Introduction 35
- 3.2 Genetic Parameters Estimated with Regression 35
- 3.3 Genetic Gain and Realized Heritability 41
- 3.4 Inbreeding and Relationship 44
- 3.5 Heterosis, or Hybrid Vigor 49
- 3.6 References 54

Chapter 4 Genetic Selection 55

- 4.1 Introduction 55
- 4.2 Single-Trait Selection 56
 - 4.2.1 Individual Selection 56
 - 4.2.2 Selection on Relatives 57
 - 4.2.3 Indirect Selection 58
- 4.3 Independent Culling 59
- 4.4 Selection Index 62
- 4.5 Selection on BLUP 65
- 4.6 References 66

Chapter 5 Genotype-by-Environment Interaction 69

- 5.1 Introduction 69
- 5.2 Modeling Genotype-by-Environment Interaction 72
 - 5.2.1 ANOVA Model with Fixed GEI 72
 - 5.2.2 Linear-Bilinear Models with Fixed GEI 76
 - 5.2.3 Linear Mixed Model Approach to GEI Analysis 82
 - 5.2.4 Generalized Linear Models to Explore GEI 86
- 5.3 Smoothing Spline Genotype Analysis (SSGA) 90
- 5.4 References 94

Chapter 6 Growth and Lactation Curves 97

- 6.1 Introduction 97
- 6.2 Modeling Lactation and Growth Curves 98
- 6.3 Using PROC REG to Fit Lactation and Growth Data 101
- 6.4 Using PROC NLIN to Fit Non-linear Models 110
- 6.5 Repeated Measures Theory for Lactation and Growth Curves 123
- 6.6 PROC MIXED for Test Day Models 125
- 6.7 Prediction of Individual Test Day Data 138
- 6.8 The SPECTRA and ARIMA Procedures for Time Series Prediction 139
- 6.9 References 146

Chapter 7 Empirical Bayes Approaches to Mixed Model Inference in Quantitative Genetics 149

- 7.1 Introduction 149
 - 7.1.1 Hierarchical Models 151
- 7.2 An Example of Linear Mixed Model Inference 153
- 7.3 Empirical Bayes Inference for Normally Distributed Data 157
 - 7.3.1 Empirical Bayes Analysis in the Linear Mixed Model 158
- 7.4 Generalized Linear Mixed Models 160
 - 7.4.1 Inference on Fixed and Random Effects 162
 - 7.4.2 Using the %GLIMMIX Macro for Quantitative Genetic Inference 163
 - 7.4.3 Empirical Bayes Inference in GLMM 166

- 7.5 Empirical Bayes vs. MCMC 169
- 7.6 Final Comments 174
- 7.7 References 175

PART 2 Molecular Genetics

Chapter 8 Gene Frequencies and Linkage Disequilibrium 179

- 8.1 Introduction 179
- 8.2 Single-Locus Frequencies 180
- 8.3 Hardy-Weinberg Proportions 184
- 8.4 Multiple-Locus Frequencies 188
- 8.5 Marker-Trait Association Tests 191
 - 8.5.1 Analyzing Samples of Unrelated Individuals 192
 - 8.5.2 Analyzing Family Data 195
- 8.6 References 200

Chapter 9 The Extended Sib-Pair Method for Mapping QTL 201

- 9.1 Introduction 202
- 9.2 Statistical Model 203
- 9.3 Inferring the Proportion of Genes IBD Shared by SIBS at QTL 204
 - 9.3.1 Proportion of Alleles IBD at Marker Loci—Parental Genotypes Known 204
 - 9.3.2 Proportion of Alleles IBD at Marker Loci—Parental Genotypes Unknown 206
 - 9.3.3 Multipoint Estimation of Proportion of Genes IBD at QTL 207
- 9.4 Maximum Likelihood Estimation 208
 - 9.4.1 Likelihood Ratio Test 209
 - 9.4.2 Approximate Critical Value for Significance Test 209
- 9.5 Single Marker Analysis and Interval Mapping of QTL 209
- 9.6 Program Implementation 210
 - 9.6.1 Choosing the Scanning Increment 210
 - 9.6.2 Implementing the Multipoint Method 212
 - 9.6.3 Implementing the Mixed Model Methodology through PROC IML 214
 - 9.6.4 Implementing the Mixed Model Methodology through PROC MIXED 216
- 9.7 Executing the Program 216
 - 9.7.1 Data Preparation 217
 - 9.7.2 Running the Main Program 218
 - 9.7.3 Application Notes 219
 - 9.7.4 Example Demo 220
- 9.8 References 222

Chapter 10 Bayesian Mapping Methodology 225

- 10.1 Introduction 225
- 10.2 Two-Point Linkage Analysis 226
 - 10.2.1 Inference Regarding Recombination Rates 227
 - 10.2.2 Example 228
 - 10.2.3 Testing for Linkage 230
- 10.3 Three-Point Analysis 231
- 10.4 Genetic Map Construction 238
- 10.5 QTL Analysis 240
 - 10.5.1 Example 242
 - 10.5.2 Results 246
- 10.6 Final Comments 249
- 10.7 References 249

Chapter 11 Gene Expression Profiling Using Mixed Models 251

- 11.1 Introduction 251
- 11.2 Theory of Mixed Model Analysis of Microarray Data 252
- 11.3 Mixed Model Analysis of Two-Color Microarray Data Using PROC MIXED 254
 - 11.3.1 Data Preparation 254
 - 11.3.2 Computation of Relative Fluorescence Intensities 255
 - 11.3.3 Computation of Gene-Specific Significance Models 257
 - 11.3.4 Explore and Interpret the Results 258
- 11.4 ANOVA-Based Analysis of Affymetrix Data Using SAS Microarray Solution 260
 - 11.4.1 Download Data 260
 - 11.4.2 Examine Data 262
 - 11.4.3 Submit the Analysis 263
 - 11.4.4 Specifications for Mixed Model Analysis 264
 - 11.4.5 Submit the Analysis 266
- 11.5 Discussion 276
- 11.6 References 277

Additional Reading 279

Index 281