
Preface

We wrote this book to fill the gap between textbooks of quantitative genetic theory and software manuals that provide details on analytical methods but little context or perspective on which methods may be most appropriate for particular applications. We do not cover the basics of quantitative genetics theory; we recommend readers be familiar with two of the classic introductory texts on the subject, *Introduction to Quantitative Genetics*, 4th Ed. by D.S. Falconer and Trudy Mackay, and *Genetics and Analysis of Quantitative Traits* by Michael Lynch and Bruce Walsh. We hope to apply the concepts of quantitative genetics to particular analytical solutions that will be useful to plant and animal breeders, focusing mainly on methods to predict breeding values. We attempt to demonstrate analyses in freely available software (such as R packages) where possible, but we also include considerable attention to the commercial software ASReml because it provides so much flexibility and utility to analysis of breeding program data. Free (but time-limited) trials of ASReml are available, and “Discovery” versions of the software are freely available to public institutions in many developing countries (<http://www.vsnl.co.uk/free-to-use/asreml-discovery>). In addition, we include some information on SAS analyses for comparison, because SAS is widely used in the breeding community.

This book is composed of two major sections. The first section (Chaps. 1, 2, 3, 4, 5, 6, 7, and 8) covers the topic of classical phenotypic data analysis for prediction of breeding values in animal and plant breeding programs. In Chap. 1, we introduce ASReml software because it is one the more popular, and we believe one of the most powerful, softwares available for analyzing data in breeding programs using mixed models analyses. Chapter 2 includes a brief review of linear mixed models and compares them to ordinary least squares analyses of variance, with which some readers may be more familiar. This is followed by a general introduction to variance-covariance structures used in mixed models (Chap. 3). Chapters 4 and 5 cover prediction of breeding values using sire (or general combining ability) models and animal models. Chapter 6 is about multivariate models used when breeders want to analyze multiple traits simultaneously and estimate genetic correlations among traits. Chapter 7 introduces spatial analyses for field experimental designs used in tree and crop breeding to account for environmental heterogeneity *within* environments. Chapter 8 introduces genotype-by-environment (GE) interactions in multi-environmental trials and various variance-covariance structures to model GE and the heterogeneity of error variation *among* environments.

In the second section (Chaps. 9, 10, 11, and 12), we provide the concepts and an overview of available tools for using DNA markers for predictions of genetic merit in breeding populations. With recent advancements in DNA sequencing technologies, genomic data, especially single nucleotide polymorphism (SNP) markers, have become widely available for animal and plant breeding programs in recent years. Analyses of DNA markers for prediction of genetic merit are a relatively new and very active research area, with new methods and improvements of older methods being proposed and tested constantly. The algorithms and software to implement these algorithms are changing as we speak. Therefore, Sect. 2 intends to be an introduction to the topic, touching on some of the more widely used

methods and softwares currently available. Readers should be aware that the methods discussed here are likely to be modified and improved in the near future, and that new statistical packages will be introduced. We present this material, however, in the hopes of providing a solid grounding in the basics of handling large marker data sets and using them to predict breeding values. In Chap. 9, we describe characteristics of typical DNA marker data sets and introduce some software tools useful for exploratory analyses (visualization, summary, and data manipulation) of marker data. Chapter 10 focuses on imputation of missing genotypes. Chapter 11 covers the use of DNA markers to predict genomic relationships between individuals in breeding populations and the use of genomic best linear unbiased prediction (GBLUP) to predict breeding values even of individuals that have not been phenotyped. Chapter 12 reviews the statistical background of more advanced genomic selection methods with several examples.

This book is intended for students in plant or animal breeding courses and for professional breeders interested in using these tools and approaches in their breeding programs. We love to hear from users about suggestions for improvements and corrections to the text.

We tried our best to give credit to resources we used to write this book. Apologies if we missed something; please let us know so that we can include the source in a future edition. Many friends, colleagues, and graduate students helped with the writing, revising, and editing the original lecture notes and exercises, which turned out to be a huge task. We acknowledge the contributions of Greg Dutkowski, Salvador Gezan, Steve McKeand, Jérôme Bartholome, Trevor Walker, Jaime Zapata-Valenzuela, Funda Ogut, Kent Gray, YiJian Huang, Patrick Cumbie, Alfredo Farjat, Terrance Ye, Jeremy Howard, Francesco Tiezzi, Brian Cullis, Tori Batista Brooks, Austin Heine, April Meeks, Paula Barnes Cardinale, Onur Troy Isik, Amanda Lee, Mohammad Nasir Shalizi, Edwin Lauer, and Miroslav Zoric for reviewing drafts of chapters and providing feedback. Thiago Marino, Jason Brewer, Heather Manching, and Randy Wissner generously provided unpublished maize data to use as an example in Chap. 11. Christophe Plomion (INRA, France) provided maritime pine data to use in Chaps. 9, 10, 11, and 12. Tree Improvement Program at NC State University provided unpublished pine progeny test data to use in several chapters.

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