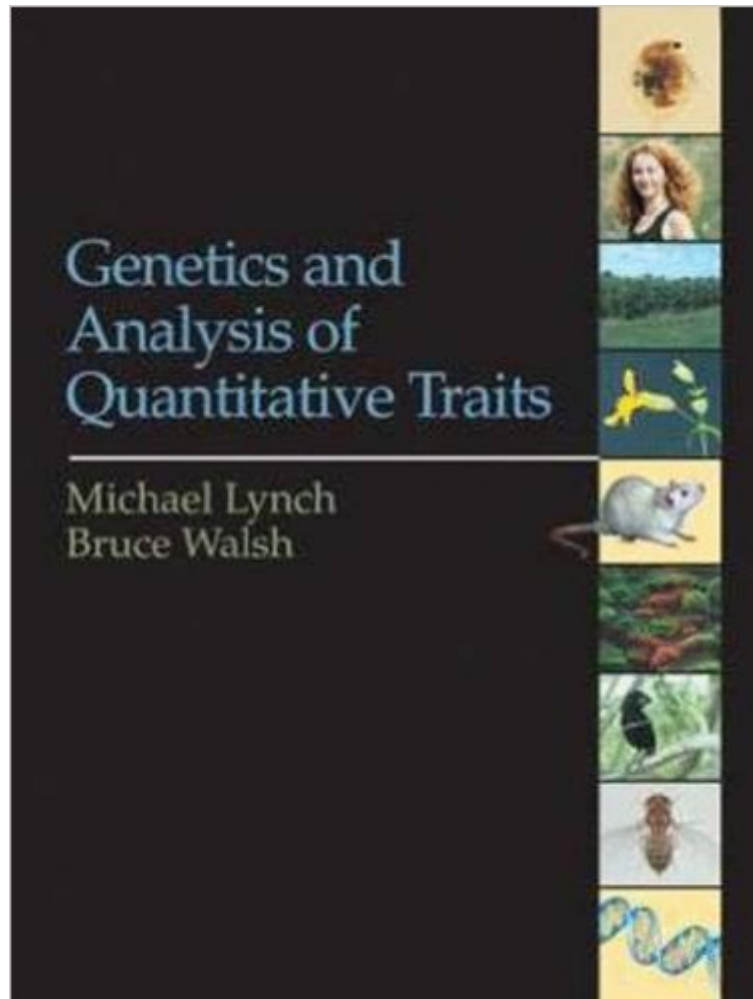# Genetics And Analysis Of Quantitative Traits

Synopsis

Genetics and Analysis of Quantitative Traits brings together the diverse array of theoretical and empirical applications of quantitative genetics under one cover, in a way that is both comprehensive and accessible to anyone with a rudimentary understanding of statistics and genetics. What was originally envisioned as a single text has now become two, with the focus of this first book being on the basic biology and methods of analysis of quantitative characters. (The second book, Evolution and Selection of Quantitative Traits, will address the basic principles that govern the evolutionary dynamics of quantitative characters under the forces of mutation, random genetic drift, and natural and/or artificial selection, integrating the theory of evolution of such characters with existing empirical data from natural and domesticated plant and animal populations.) Written as a general text in quantitative genetics, the book will also be useful as a basic reference for the seasoned professional. Throughout, central theoretical concepts are developed from first principles. To aid the less statistically sophisticated reader, several chapters and appendices focus on the basic statistical tools needed to digest the book. Wherever possible, theoretical and analytical concepts are illustrated with empirical examples from diverse settings. Three major features of Genetics and Analysis of Quantitative Traits distinguish it from earlier work. First, it reflects the explosive influx over the past few years of quantitative-genetic thinking into evolutionary biology. Second, in animal breeding, enormous strides have been made in the development of new techniques for estimating breeding values (for the purposes of identifying elite individuals in selection programs) and for estimating variance components from samples of complex pedigrees. In this text's last two chapters, the authors outline the basic principles of complex pedigree analysis, without getting bogged down in technical details. Third, Genetics and Analysis of Quantitative Traits provides a broad overview of the newly emerging array of techniques for quantitative-trait loci (QTL) analysis, currently one of the most active fields of quantitative-genetic research. Genetics and Analysis of Quantitative Traits contains numerous fully-worked examples and illustrations of theoretical concepts, as well as over 2,000 references with indices by subject, author, and organism. In addition, the authors maintain a World Wide Web site featuring up-to-date lists of computer programs and on-line resources, and added information on various topics presented in the text.

Book Information

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Customer Reviews

This is overall a decent treatment of what its title claims it to be. The main flaw, as I see it, is the lack of exercises. The material is fairly heavy on mathematics and statistics and I find it hard to internalize a lot of the mathematical machinery without going through the calculations myself.Apart from this lack of exercises I like the book. It is a bit too long (and far too heavy!), and it contains more historical background than what I need, but it gives a very thorough overview of the theory of the field, which is what is most important in the end. The great amount of text makes it more useful as a book to learn from than as a reference, but since there isn't anything else out there I suppose we are stuck with this for reference as well.

Along with Falconer and MacKay, this is one of my favourite intro textbooks to quantitative genetics. I use it as a reference frequently. I find it an easier read than "Introduction to Quantitative Genetics" (this was especially true when I was starting out), and a little more comprehensive.

Great book! Clear explanations and good examples. What makes it a really interesting book is that it explains both animal breeding, plant breeding and natural selection in ecological context. So this book has a very broad angle of subjects, but greatly focussed on the common factor: genetical quantitative traits and how to analyse them. The mathematical level might be slightly difficult for not so mathematic orientated people, but most is very well explained and some (parts of) chapters might actually not be misplaced in a mathematics teaching book as well. I have been waiting for such a book and expect it to become a classic. I highly recommend this book!

The book is great in breadth and depth, and well-written for a genetics text. I'm sure it will be a resource of mine for a long time... unfortunately it seems to be cheaply printed and bound. I had an

entire chapter fall out the first time I read it!

I read this book with the expectation that it would give me an idea of the extent to which organism traits or phenotypes are determined optimally. Discussions on evolution frequently regard the functioning and attributes of an organism as being optimal at the particular time in its evolutionary history. A successful theory of evolution as a theory of mathematical optimization would entail a thorough understanding of the evidence for this hypothesis of optimality of phenotypes. Another interesting question as to what effect a certain mixing of genetic factors, each one of these factors determining a phenotype separately (and optimally), would determine an optimal phenotype. An answer to this question would be important from the standpoint of transgenic strategies. But this book is not about optimization theory in genetics, but one that introduces the reader to an analysis, in the authors view, of how evolution happens, and not a predictive tool of what ought to evolve. And, as the authors correctly point out, the time scales needed to evolve an optimal phenotype are not usually dealt with in discussion on optimization strategies. The authors also argue that optimization theories do not consider the expected phenotypic variance or the influence of random drift or mutation. Quantitative genetics does this, they state, and they define it as a mechanistic theory of the evolutionary process. What is also interesting about quantitative genetics is that it was responsible directly or indirectly for a large body of statistical theory, many of these results being standard material in modern classes in statistics. It is also beginning to find an intersection with the theory of molecular genetics. The authors remark that eventually both quantitative and molecular genetics will have to answer to each other, and they give a taste of this in the chapter on marked-based analysis and QTLs. There is no question that the reading of this book will give the reader a comprehensive overview of quantitative genetics. But, it takes an very long time to get through, and there are no exercises to test the understanding. Readers will need a fair knowledge of statistics to read the book, but there are three chapters and appendices in the back of the book outlining some of the necessary statistical concepts. The level of mathematics is the most sophisticated in the last chapter, which uses techniques such as maximum likelihood, expectation maximization, and restricted maximum likelihood. Readers with a background in bioinformatics will be very familiar with these techniques. Newton-Rhapson methods and Fisher's scoring method are discusses as derivative-based methods for solving the ML/REML equations and compared with the EM methods for doing the same. The authors are very convincing in informing the reader of the difficulty in estimating genetic variance components in real populations. Also, and most importantly, there are myriads or real-world examples given to illustrate the theory. For molecular geneticists,

and for those very curious about the connection between molecular biology and quantitative genetics, chapter 14, covering the principles of marker-based analysis, would probably be the most interesting in the book. The treatment is both historical, discussing the effects of entire chromosomes, and modern, discussing topics such as using markers or the construction of nearly isogenic lines and cloning individual QTLs. In the 'classical' approach to marker-based methods the authors discuss chromosomal assays, wherein a chromosome from one line is substituted into a standard genetic background chosen to have minimum variance. Since a chromosomal segment may contain a large position of the total genome, the authors take what could be called a 'coarse-grained' approach that utilizes genetic factors rather than a 'microscopic' one emphasizing individual genes. Such a strategy requires large sample sizes if one is to detect factors that result in extremely small effects. Examples of this approach are given, and the authors discuss its weaknesses, one being that a large chromosomal section can have QTLs that have effects in opposite directions, resulting in a net effect close to zero. Thoday's method is also discussed in order to point out the limitations of using flanking-marker mapping methods. The genetics of Drosophila bristle number is also briefly treated, but many references are given. Recoginizing that direct sequencing of DNA gives a measure of genetic variation, the authors point out though that restriction fragment length polymorphisms are suitable for most purposes, assuming that these are detectable. The advantages and disadvantages of other techniques, such as randomly amplified polymorphic DNAs, are also discussed. The arithmetic involved in genetic mapping is treated in fair detail, the authors overviewing what is involved mathematically in map distances, recombination frequencies, and in the estimation of how many randomly distributed markers are needed to gaurantee that a portion of the genome is within a given number of map units of a marker. The strategies for mapping and cloning of QTLs are the main emphasis in the rest of the chapter. Some of the more interesting discussions here include: 1. The phenomena of 'linkage drag', wherein linked undesirable geness can be dragged along with the marker; 2. Candidate loci and their use in the study of genetic disorders. The authors outline in great detail the problems with this approach, such as linkage disequilibrium; 3. Gene cloning and its use in the study of QTLs. The authors discuss two different cloning strategies, namely that of transposon tagging and positional cloning. The authors emphasize the need for inbred lines for the detection of QTLs by transposon tagging to reduce variance from segregation at other loci. Because of this need, they seem skeptical of the general use of this technique, but give a brief argument as to its possible success using homologies in sequence data between species. The authors also emphasize the complexity involved in the use of positional cloning and comparative mapping and then outline an algorithm as to how to use NILs to

do positional cloning of a QTL.

This book is an excellent resource in the field of genetics, a classic in the area of quantitative trait analysis. Beware, however, that it is a bit dated. The field has moved a lot in the last 10 years.

This is, I think, the most comprehensive book on the subject of Quantitative trait design and analysis I have seen. In particular, it has an excellent section on modeling multi-locus models, something incredibly important nowadays.

This book is great when you want to understand quantitative genetics. I used it for my major thesis in dairy cattle breeding en fount it very useful. It will help you get the point in the confusing world called genetics.

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