Preface

The period 1957 to 1966 was a time in which the author worked with variance component models that were widely used in quantitative genetics, but after 1966 his attention was turned to other subjects, such as evolution, branching processes, and the teaching of probability and statistics. Recently, however, the author became aware that the genomes of large samples of patients with Alzheimer's disease had been sequenced. Furthermore, there was statistical evidence those 11 regions of the human genome were involved in the quantitative expression traits associated with patients with Alzheimer's disease. Subsequently, it was recognized that it would be possible obtain working definitions of 11 loci corresponding to the 11 regions in the human genome, with at least two alleles at each locus defined in terms of markers such as the presence and absence of nucleotide substitutions.

This recognition, in turn, led to awareness that not only variance components but also the effects that were a basis for their definitions could be estimated directly rather than by the indirect methods, based on analysis of variance and covariance procedures, that have been widely used in quantitative genetics. Briefly, this small book, which contains five chapters, is a short and incomplete history of quantitative genetics based on the experience of the author over a period of at least 40 years.

Presented in Chapter 1 is a paper that was developed and written during the period 1956 to 1958, in which attention was focused on analysis of variance and covariance procedures that were used extensively during that period in connection with the estimation of the genetic and variance and covariance components making up models of quantitative genetics. After a

brief discussion of the circumstances that gave rise to the paper, prospective and retrospective views of the paper are given, using properties of matrices. Chapter 2 presents a paper on testing a hypothesis as to whether a major gene was sufficient to explain a quantitative trait that arose in connection with work on human blood. Again, after a brief discussion of the circumstances that led to the paper, a revised version of the paper on fitting models to data, which was published in the 1970s, is republished in a revised form.

The content of Chapter 3 is a reproduction of a recently published theoretical paper containing a detailed account of the direct estimation of effects and variance components for the case of one quantitative trait. In this paper, effects are defined mathematically. The case of one autosomal locus is considered, as well as cases of multiple loci. Similarly, Chapter 4 is a reproduction of a recently published paper, on pleiotropism and the direct estimation of variance and covariance components and effects that arise when several quantitative traits are under consideration. To conclude the book, Chapter 5 contains a republished account, based on artificial data, of the estimation as well as tests of statistical significance as to whether the estimated effects are indeed not equal to zero for the case of one autosomal locus with two alleles. Monte Carlo simulation procedures were employed to conduct these tests as well as to estimate two types of p values, which were used to judge the statistical significance of estimated effects. The last three chapters contain ideas designed for investigating the genetics of some quantitative in big data sets, i.e., large samples and sequenced genomes.