

# CONTRIBUTIONS TO QUANTITATIVE AND POPULATION GENETICS

A collection of publications with Introduction submitted by

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# CONTRIBUTIONS TO QUANTITATIVE AND POPULATION GENETICS

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## 1. INTRODUCTION

Over my research career, more than half of my effort has been devoted to the increase of understanding of the genetical basis of quantitative variation. For this reason, the major part of this document is devoted to this topic. I have tried to set my work in its context and to show how it relates to current areas of advance.

Much of my work has related either to evolutionary theory or plant breeding theory, so that I make frequent reference to my books [52, 62]. The plant breeding book's acceptability may be gauged from the fact that it is now in a second edition [73] and has been translated into Russian [65]. It is novel in its attempt to provide a synthesis of population and quantitative genetics in the plant breeding context.

The short book on natural selection [62] also contains work unpublished elsewhere, but its originality lies principally in its attempt to explain, very briefly, what can and what cannot be accounted for by natural selection, as currently understood.

As a theoretical geneticist, rather than an experimenter, I have frequently used the technique of Monte Carlo simulation of populations of Mendelian individuals. Though this was not entirely novel when I began using it, I believe that my first paper [1] was the first use of such simulation to test a current hypothesis of interest: that a high rate of mutation was not needed to maintain large numbers of self-incompatibility alleles in a small population (Ewens, 1964), contrary to the conclusion of Fisher and

Wright. Fisher and Wright proved, in fact, to have been correct [1]. The problem of the origin of such alleles remains, though it is closer to solution than for a long time by the methods of molecular genetics (Anderson *et al.* 1986). The properties of multi-locus systems of self-incompatibility are unlikely to be readily explicable in these terms, however (e.g. 76,80).

Simulation has been useful in many other investigations [4, 8, 9, 15, 24, 31, 43, 44, 54, 58, 66, 68, 80], one of the most recent being a demonstration of the inutility of a class of functions called the major gene index, discussed in Section 2.4.2 below.

Papers of some significance other than those discussed below in Section 2 include the following.

[9] was a relatively early use of Monte Carlo simulation by computer for the testing of statistical methodology. It highlighted the limitations of the lod score method of linkage analysis.

[15] showed how the frequency of a lethal recessive trait with advantageous heterozygote trait in a small population is expected to be very different from its large population equilibrium frequency. This is an important result for the attempt to explain the high frequency of certain deleterious human traits such as cystic fibrosis.

[18] showed (what was to be expected from the work of Fisher (1930)) that if fixation of neutral alleles was expected to be very frequent in evolution (Kimura 1968), slightly deleterious alleles were expected to be fixed even more frequently. This result has been developed and shown to be important by Ohta (1973).

[20 and 23] were among a substantial number of papers published at about the same time, which showed that genetical counselling posed no threat to the human gene pool.

[29, 46] has been an influential reference work for what might be called the 'protein era' of human biochemical genetics, now overtaken by the 'DNA era'. It presented a synthesis of knowledge of normal and pathological biochemical variation, as clarified by genetics.

[3] was one of the first studies of gene frequency change in defined populations of large domestic animals of known ancestry, illustrating the well known importance of genetical drift in the determination of gene frequency at loci apparently unrelated to the traits for which selection was being practised [17].

[57,58,60] introduce a novel statistical methodology for the control of variability in field trials. However, my contribution to this development was relatively minor, as in [64] and [79], which develop and demonstrate a new approach to the analysis of structure in correlation matrices.

# The Biochemical Genetics of Man

## Second Edition

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# The Theory of Plant Breeding

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# natural selection and its constraints

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