THE MEASUREMENT OF LINKAGE IN HEREDITY

K. MATHER

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by

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REGOR MENDEL did not use probability methods in the analysis of his classical experiments, but after the rediscovery of his work, at the beginning of this century, the application of such a technique was soon recognized as a necessary part of genetical analysis. The problems at first were chiefly involved with the testing of the significance of departures from expected ratios, but, with the discovery of linkage, questions of estimation became equally important. The absence of a suitable statistical technique is one of the prime causes of the failure to understand linkage and linkage groups during the years before the Drosophila technique of backcrossing was extensively practised, and the true relations of coupling and repulsion realized. Since that time statistical methods have become more and more favoured by genetical workers and are to-day more than ever necessary for genetical analysis.

Now statistics, like genetics, is a growing science and the crude and often arbitrary methods of yesterday have been superseded and rendered redundant by the development of more exact and more adaptable techniques. This is largely a result of the work of R. A. Fisher and his associates. In some branches of biology, as for example agronomical experimentation, such re-

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fined statistical methods are now in common use for several reasons, not the least important of which is the existence of articles and textbooks giving details of their application. In genetics these methods have been less fully described and applied. It is hoped that the present work will serve to bring to the notice of geneticists the desirability of employing such methods and provide the necessary instruction for their use.

It is not claimed that this book is complete. In fact some statistical devices such as the analysis of variance and the use of regressions have been entirely omitted as they are, at present, of secondary importance to the geneticist. On the other hand, the uses of r^2 and of maximum likelihood have been dealt with in considerable detail as they are of wide application in this The methods are described branch of science. in general and some specific applications are discussed in detail. No attempt has been made to prove all the general formulae used, though some have been considered in detail. Such a course is beyond the scope of this work and would, in any case, merely result in confusion for a non-mathematical reader. If desired, proofs may be found in the original literature cited. But numerical examples have been used wherever possible in the hope that the reader, by working through them, will familiarize himself with the methods and be able to apply them to other problems. The list of general formulae in the last chapter should make reference to any method, and its use for other analyses, a simple matter. It cannot be overemphasized that in order to

make full use of the bock the actual examples used should be worked through in detail, as it is only by this means that they will be fully understood and appreciated.

For further details of the genetical and cytological principles, which have been assumed here in order to permit fuller development of the statistics, the reader is referred to *Mendelism* and Evolution, by E. B. Ford and to *The Chromo*somes, by M. J. D. White, both of which are in this series of Biological Monographs.

I am indebted to Professor R. A. Fisher, Head of the Galton Laboratory, for permitting the reproduction herein of a number of tables mainly from the Annals of Eugenics, and for continued encouragement during the writing of this book, and to Messrs. W. J. C. Lawrence and J. C. Cullen, of the John Innes Horticultural Institution, for reading and criticizing the manuscript: I also wish to thank Messrs. Oliver and Boyd for allowing me to reproduce Tables I and II, from R. A. Fisher's Statistical Methods for Research Workers.

PREFACE TO THE SECOND EDITION

THE chief alterations made in preparing the second edition are the inclusion of a new section in Chapter VII on the scoring method devised by Professor R. A. Fisher for use in testing and estimating linkage, and a chapter on the estimation of gene frequencies, as is needed in the analysis of the distribution of, for example, blood groups in the various races of man. References to certain other developments of the past

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twelve years have also been added, and the occasion has been taken to correct a number of minor, though misleading, mistakes. I am indebted to several correspondents for drawing my attention to these errors.

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