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Book Review

Advances in Genetics, Vol. 42, Genetic Dissection of Complex Traits

Edited by D.C. Rao and Michael A. Province

Academic Press, San Diego, San Francisco, New York, Boston, London, Sydney, Tokyo, 2001,
583 pp., ISBN 0-12-017642-4

This book is based on a symposium held in honor of the 70th birthday of Newton E. Morton, one of the famous genetic epidemiologists. Forty-six authors, leading experts in genetic epidemiology and in biostatistics, contributed to 32 chapters, divided into nine sections. Section 1, which summarizes Newton's contribution to genetic epidemiology, is supplemented by a complete list of Dr. Morton's research activities in the appendix.

The genetic dissection of complex traits is important not only for genetic epidemiology and human genetics; it also has a great impact on the animal and plant genetics and practical applications in breeding methodology.

This volume documents state-of-the-art methods and strategies for genetic dissection of complex traits and is also useful for the recognition of the limitations of current approaches. The book has three objectives: to provide scientists and students with a comprehensive review, to place contemporary methodologies in their proper perspective, and finally, to project promising new directions for the future.

Section 2 contains an overview and preliminaries of the methods and a summary of the concepts of heritability, linkage, and association. Definition of the phenotype as a key issue in designing any genetic study and genotyping for human whole-genome scans is included in Section 3. The model-based and model-free methods for linkage and association analysis are presented in Sections 4 and 5. The latest methods, meta-analysis classification methods, application of neural networks for gene finding, genome partitioning and whole-genome analysis, deciphering the genetic architecture of a multivariate phenotype, are comprehensively discussed in Section 6. Other important topics, the resolution and feasibility of genome scanning approaches, the role of interacting determinants in the localization of genes, linkage disequilibrium mapping and optimum study designs are overviewed in Section 7. Multiple comparisons and significance levels are discussed in Section 8. Section 9 presents views on the 21st century and the future of new strategies and directions in this field.

This volume should be recommended to the scientists and experts in biostatistics, genetics and also to breeders – to obtain a quick but thorough overview of current methodological trends in the genetic dissection of complex traits.

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