

Use R!

Foulkes

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Andrea S. Foulkes

Applied Statistical Genetics with R

For Population-based Association Studies

The vast array of molecular level information now available presents exciting opportunities to characterize the genetic underpinnings of complex diseases while discovering novel biological pathways to disease progression. In this introductory graduate level text, Dr. Foulkes elucidates core concepts that undergird the wide range of analytic techniques and software tools for the analysis of data derived from population-based genetic investigations. *Applied Statistical Genetics with R* offers a clear and cogent presentation of several fundamental statistical approaches that researchers from multiple disciplines, including medicine, public health, epidemiology, statistics and computer science, will find useful in exploring this emerging field. Couched in the language of biostatistics, this text can be easily adopted for public health and medical school curricula.

The text covers key genetic data concepts and statistical principles to provide the reader with a strong foundation in methods for candidate gene and genome-wide association studies. These include methods for unobservable haplotypic phase, multiple testing adjustments, and high-dimensional data analysis. Emphasis is on analysis of data arising from studies of unrelated individuals and the potential interplay among genetic factors and more traditional, epidemiological risk factors for disease. While theoretically rigorous, the analytic techniques are presented at a level that will appeal to researchers and students with limited knowledge of statistical genetics. The text assumes the reader has completed a first course in biostatistics, uses publicly available data sets for illustration, and provides extensive examples using the open source, publicly available statistical software environment R.

Dr. Foulkes is an Associate Professor of Biostatistics at the University of Massachusetts, Amherst, where she has been recognized for teaching excellence. Her active research program includes the development of methods for characterizing the relationships among high-dimensional molecular and cellular level data and measures of disease progression. She has authored numerous technical manuscripts in this field and currently serves as the principal investigator of an individual research award from the National Institute of Allergy and Infectious Diseases, a division of the National Institutes of Health.

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