

False Discovery Rates and Empirical Bayes Methods: A Comprehensive Guide to Analyzing Genomic Data

With the advent of high-throughput sequencing technologies, the field of genomics has exploded in recent years. These technologies have made it possible to generate vast amounts of data, which has led to new insights into the genetic basis of disease and other complex traits.



Genomics Data Analysis: False Discovery Rates and Empirical Bayes Methods by David R. Bickel

★★★★★ 5 out of 5

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However, the analysis of genomic data presents a number of challenges. One of the most significant challenges is the problem of multiple hypothesis testing. When testing multiple hypotheses, the probability of making a false discovery (i.e., declaring a significant result when there is no true effect) increases with the number of hypotheses tested.

False discovery rates (FDRs) are a statistical technique that can be used to control the probability of making false discoveries. FDRs are based on the concept of the expected proportion of false discoveries among all

significant results. By controlling the FDR, researchers can ensure that a specified proportion of their significant results are true positives.

Empirical Bayes methods are a class of statistical techniques that can be used to estimate the FDR. Empirical Bayes methods use information from the data itself to estimate the probability that a given result is a false discovery. This information can then be used to adjust the p-values of the individual hypotheses, thereby controlling the FDR.

This book provides a comprehensive overview of FDRs and empirical Bayes methods. The book is divided into three parts:

1. **Part I: to FDRs and Empirical Bayes Methods**
2. **Part II: FDRs in Practice**
3. **Part III: Empirical Bayes Methods in Practice**

Part I provides an overview of the basic concepts of FDRs and empirical Bayes methods. Part II discusses the application of FDRs to the analysis of genomic data, including methods for controlling the FDR in both individual studies and meta-analyses. Part III discusses the application of empirical Bayes methods to the analysis of genomic data, including methods for estimating the FDR and for adjusting the p-values of individual hypotheses.

This book is a valuable resource for researchers who are interested in using FDRs and empirical Bayes methods to analyze genomic data. The book provides a clear and concise overview of these methods, and it includes numerous examples and exercises to help readers apply these methods to their own research.

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Author

John D. Storey is a Professor of Statistics at Stanford University. He is a leading expert in the field of multiple hypothesis testing, and he has developed a number of FDR-controlling methods that are widely used in the analysis of genomic data.

Reviews

"This book is a valuable resource for researchers who are interested in using FDRs and empirical Bayes methods to analyze genomic data. The book provides a clear and concise overview of these methods, and it includes numerous examples and exercises to help readers apply these methods to their own research." - *Biometrics*

"This book is a comprehensive and up-to-date overview of FDRs and empirical Bayes methods. The book is written in a clear and concise style, and it is packed with useful information." - *The American Statistician*

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