After the great expansion of genome-wide association studies, their scientific methodology and, notably, their data analysis have matured in recent years, and they are a keystone in large epidemiological studies. Newcomers to the field are confronted with a wealth of data, resources, and methods. This book presents current methods to perform informative analyses using real and illustrative data with established bioinformatics tools and guides the reader through the use of publicly available data.

- Includes clear, readable programming codes for readers to reproduce and adapt to their own data
- Emphasizes extracting biologically meaningful associations between traits of interest and genomic, transcriptomic, and epigenomic data
- Uses up-to-date methods to exploit omic data
- Presents methods through specific examples and computing sessions
- Supplemented by a website, including code, datasets, and solutions

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