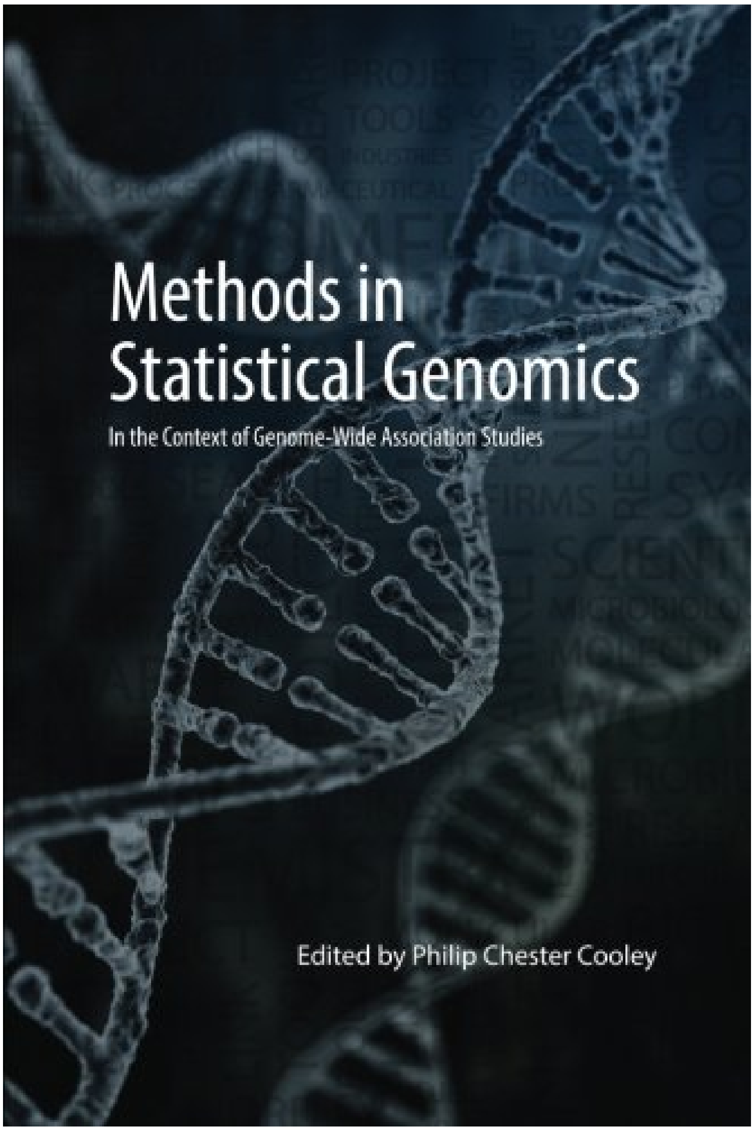
Methods in Statistical Genomics: In the Context of Genome-Wide Association Studies

Philip Chester Cooley



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Philip Chester Cooley : Methods in Statistical Genomics: In the Context of Genome-Wide Association Studies before purchasing it in order to gage whether or not it would be worth my time, and all praised Methods in Statistical Genomics: In the Context of Genome-Wide Association Studies:

This groundbreaking work uses a simulated data set to evaluate new analytic methods in genome-wide association studies (GWAS). The human genome is very complex, and the effect of a genetic variant depends on many factors including where the gene is expressed, when it is expressed, how it interacts with other genes that themselves may harbor variants, and the effect of the environment. GWAS have identified many new genetic risk factors for a number of common human diseases, but much work remains to be done and can only be accomplished by using new approaches. The role of this book is to help jump-start the investigation of such new approaches. Identifying which computational strategy is best suited for investigating a specific aspect of genomics is a daunting task. Using simulated data to evaluate new analytic methods provides a truth set against which to assess methods predictive properties. In this book, Cooley and colleagues use simulated data to test a variety of analytic methods, starting with single-gene models and progressing to more complex polygene and gene-by-environment scenarios. The methods that Cooley and colleagues use are straightforward, easily applied, and thoroughly documented.