

Evolutionary genomics is a relatively new research field with the ultimate goal of understanding the underlying evolutionary and genetic mechanisms for the emergence of genome complexity under changing environments. It stems from an integration of high throughput data from functional genomics, statistical modeling and bioinformatics, and the procedure of phylogeny-based analysis.

Statistical Theory and Methods for Evolutionary Genomics summarizes the statistical framework of evolutionary genomics, and illustrates how statistical modeling and testing can enhance our understanding of functional genomic evolution. The book reviews the recent developments in methodology from an evolutionary perspective of genome function, and incorporates substantial examples from high throughput data in model organisms. In addition to phylogeny-based functional analysis of DNA sequences, the author includes extensive discussion on how new types of functional genomic data (e.g. microarray) can provide exciting new insights into the evolution of genome function, which can lead in turn to an understanding of the emergence of genome complexity during evolution.

This advanced textbook is suitable for graduate students and researchers in (evolutionary) bioinformatics, evolutionary genomics, and molecular evolution. It will also be of relevance and use to scientists in mathematics, statistics, and the computer sciences who are interested in computational biology and bioinformatics.

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