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Mathematical and Computational Biology Series

Molecular biologists are performing increasingly large and complicated experiments, but often have little background in data analysis. The book is devoted to teaching the statistical and computational techniques molecular biologists need to analyze their data. It explains the big-picture concepts in data analysis using a wide variety of real-world molecular biological examples such as eQTLs, ortholog identification, motif finding, inference of population structure, protein fold prediction and many more. The book takes a pragmatic approach, focusing on techniques that are based on elegant mathematics yet are the simplest to explain to scientists with little background in computers and statistics.

Key Features

- Assumes no background in statistics or computers
- Covers most major types of molecular biological data
- Covers the statistical and machine learning concepts of most practical utility (P-values, clustering, regression, regularization and classification)
- Intended for graduate students beginning careers in molecular biology, systems biology, bioengineering and genetics

About the Author

Alan M Moses is currently Associate Professor and Canada Research Chair in Computational Biology in the Departments of Cell & Systems Biology and Computer Science at the University of Toronto. His research touches on many of the major areas in computational biology, including DNA and protein sequence analysis, phylogenetic models, population genetics, expression profiles, regulatory network simulations and image analysis.

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