



Algebraic Statistics for Computational Biology

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The quantitative analysis of biological sequence data is based on methods from statistics coupled with efficient algorithms from computer science. Algebra provides a framework for unifying many of the seemingly disparate techniques used by computational biologists. This book, first published in 2005, offers an introduction to this mathematical framework and describes tools from computational algebra for designing new algorithms for exact, accurate results. These algorithms can be applied to biological problems such as aligning genomes, finding genes and constructing phylogenies. The first part of this book consists of four chapters on the themes of Statistics, Computation, Algebra and Biology, offering speedy, self-contained introductions to the emerging field of algebraic statistics and its applications to genomics. In the second part, the four themes are combined and developed to tackle real problems in computational genomics. As the first book in the exciting and dynamic area, it will be welcomed as a text for self-study or for advanced undergraduate and beginning graduate courses.

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