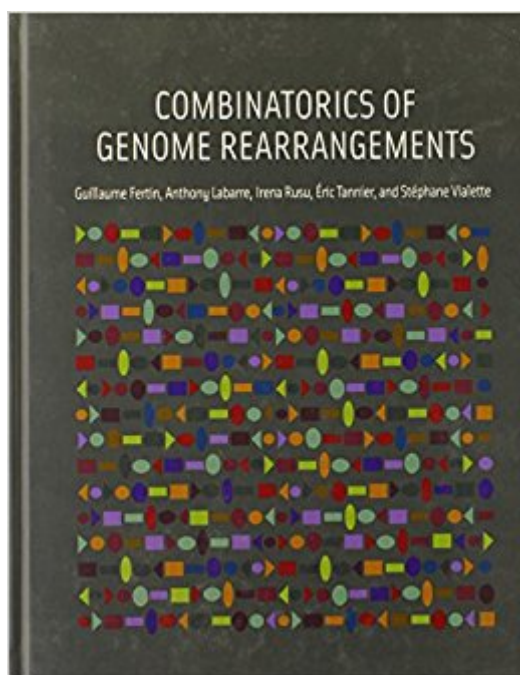


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Combinatorics Of Genome Rearrangements (Computational Molecular Biology)



Synopsis

From one cell to another, from one individual to another, and from one species to another, the content of DNA molecules is often similar. The organization of these molecules, however, differs dramatically, and the mutations that affect this organization are known as genome rearrangements. Combinatorial methods are used to reconstruct putative rearrangement scenarios in order to explain the evolutionary history of a set of species, often formalizing the evolutionary events that can explain the multiple combinations of observed genomes as combinatorial optimization problems. This book offers the first comprehensive survey of this rapidly expanding application of combinatorial optimization. It can be used as a reference for experienced researchers or as an introductory text for a broader audience. Genome rearrangement problems have proved so interesting from a combinatorial point of view that the field now belongs as much to mathematics as to biology. This book takes a mathematically oriented approach, but provides biological background when necessary. It presents a series of models, beginning with the simplest (which is progressively extended by dropping restrictions), each constructing a genome rearrangement problem. The book also discusses an important generalization of the basic problem known as the median problem, surveys attempts to reconstruct the relationships between genomes with phylogenetic trees, and offers a collection of summaries and appendixes with useful additional information.

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Customer Reviews

This book will be a defining book for the field of genome rearrangement and is destined to become a classic as soon as it hits the bookshelves. The authors have done an excellent job in presenting one of the most technically challenging areas of computational biology in an easily understood manner. Dobzhansky and Sturtevant would not be disappointed. (Pavel Pevzner, Ronald R. Taylor Chair of Computer Science, Director, Interdisciplinary Bioinformatics Program, University of California, San Diego) *Combinatorics of Genome Rearrangement* is the first computer science monograph on this rapidly expanding field. The authors have managed the seemingly impossible feat of combining scope and coherence; they have pulled together all the disparate research lines and integrated them through a common treatment and notation. This volume is simultaneously an accessible computational biology textbook for computer science and bioinformatics students, an easy and thorough entry to the field for professionals attracted by the novelty and diversity of the problems in the field, and an up-to-date reference book for specialists. (David Sankoff, Department of Mathematics and Statistics, University of Ottawa)

Guillaume Fertin is Professor of Computer Science at the University of Nantes. Anthony Labarre received a PhD in Mathematics and Computer Science from the Université libre de Bruxelles. Irena Rusu is Professor of Computer Science at the University of Nantes. Eric Tannier is a Researcher at the INRIA, in the Laboratory of Biometrics and Evolutionary Biology of the University of Lyon. Stéphane Vialette is a Researcher in the Gaspard-Monge Institute of Electronics and Computer Science at the University of Paris-Est Marne-la-Vallée. Guillaume Fertin is Professor of Computer Science at the University of Nantes. Anthony Labarre received a PhD in Mathematics and Computer Science from the Université libre de Bruxelles. Irena Rusu is Professor of Computer Science at the University of Nantes. Eric Tannier is a Researcher at the INRIA, in the Laboratory of Biometrics and Evolutionary Biology of the University of Lyon. Stéphane Vialette is a Researcher in the Gaspard-Monge Institute of Electronics and Computer Science at the University of Paris-Est Marne-la-Vallée.

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