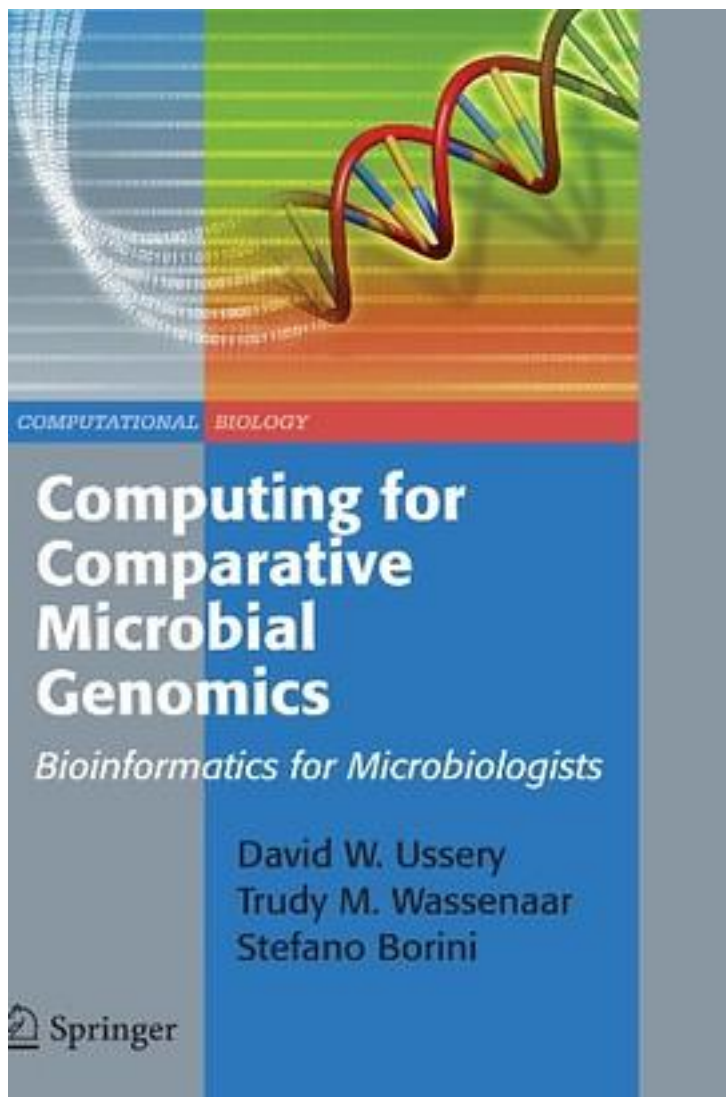


Computing for Comparative Microbial Genomics



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The problem many microbiologists face is simply that of too much information. This book details many published methods for comparison of genomes, and provides examples of how custom comparisons can be made. The choice of methods obviously depends on the questions to be asked, and of course on the quantity of genomes to be compared. Two similar bacterial chromosomes can simply be aligned with each other, and regions of inversions and deletions can be readily visualised. However, this method won't work to compare hundreds of genomes, where 2-Dimensional clustering heat maps would be useful. This text is built around teaching COMPUTATIONAL / BIOINFORMATIC methods for comparison of microbial genomes, and includes detailed examples of how to compare them at the level of DNA, RNA, and protein, in terms of structural / functional analysis. Aimed at advanced undergraduate and graduate students in Bioinformatics and Microbiology, this book will prove an invaluable reference to computational and bioinformatics tools.

作者介绍:

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