



**Computational Methods for Understanding
Bacterial and Archaeal Genomes (Advances in
Bioinformatics and Computational Biology) (Series
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Over 500 prokaryotic genomes have been sequenced to date, and thousands more have been planned for the next few years. While these genomic sequence data provide unprecedented opportunities for biologists to study the world of prokaryotes, they also raise extremely challenging issues such as how to decode the rich information encoded in these genomes. This comprehensive volume includes a collection of cohesively written chapters on prokaryotic genomes, their organization and evolution, the information they encode, and the computational approaches needed to derive such information. A comparative view of bacterial and archaeal genomes, and how information is encoded differently in them, is also presented. Combining theoretical discussions and computational techniques, the book serves as a valuable introductory textbook for graduate-level microbial genomics and informatics courses.

Contents: General Characteristics of Prokaryotic Genomes (J Mrázek & A O Summers); Genes in Prokaryotic Genomes and Their Computational Prediction (R K Azad); Evolution of the Genetic Code: Computational Methods and Inferences (G Fournier); Dynamics of Prokaryotic Genome Evolution (P Lapierre); Mobile Genetic Elements and Their Prediction (M G I Langille et al.); Horizontal Gene Transfer: Its Detection and Role in Microbial Evolution (J P Gogarten & O Zhaxybayeva); Genome Reduction During Prokaryotic Evolution (F J Silva & A Latorre); Comparative Mechanisms for Transcription and Regulatory Signals in Archaea and Bacteria (A Martínez-Antonio & J Collado-Vides); Computational Techniques for Orthologous Gene Prediction in Prokaryotes (M Poptsova); Computational Elucidation of Operons and Uber-Operons (P Dam et al.); Prediction of Regulons Through Comparative Genome Analyses (Z-C Su et al.); Prediction of Biological Pathways Through Data Mining and Information Fusion (F-L Mao et al.); Microbial Pathway Models (S R Veflingstad et al.); Metagenomics (K Arima & J Wooley).

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