

Computational Biology

K. Erciyes

Distributed and Sequential Algorithms for Bioinformatics



Springer

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Albert Y. Zomaya



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organisms Although molecular genetics and microbiology were among the scientific fields that have mostly benefited from the discoveries made in bacteria our current state of knowledge has gone beyond what anyone could have ever imagined The present Research Topic aims to cover new and exciting broad aspects of the importance of bacteria to human life both positive and negative influences Regulation of bacterial gene expression replication and segregation control mechanisms cell to cell communication via quorum sensors and the relatively recent finding of bacterial immunity via CRISPR have led to the development of many and very important new tools in biotechnology and the emerging field of molecular medicine The battle against infectious diseases has also benefited from the genetic approaches that have been developed in the quest for finding new targets and novel drugs against pathogenic bacteria At the next level the human microbiome project has opened up new avenues in understanding the role of bacteria in human health and wellbeing Finally the relationship between bacterial infections and human cancers will also be covered a subject that is still under verification through rigorous experimental approaches Special emphasis will be given to the bacterial accessory genome i e the mobilome as the primary cause of health threatening antimicrobial resistance and the production of toxins and virulence factors Taking into account the evolutionary importance of horizontal gene transfer and the additional beneficial roles of certain bacterial mobile genetic elements they help project best the Good the Bad and the Ugly outline of this topic At the time this eBook is about to be published our Research Topic has registered nearly 55 000 views

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Computational Intelligence Kurosh Madani, António Dourado, Agostinho Rosa, Joaquim Filipe, Janusz Kacprzyk, 2015-11-19 The present book includes a set of selected extended papers from the fifth International Joint Conference on Computational Intelligence IJCCI 2013 held in Vilamoura Algarve Portugal from 20 to 22 September 2013 The conference was composed by three co located conferences The International Conference on Evolutionary Computation Theory and Applications ECTA the International Conference on Fuzzy Computation Theory and Applications FCTA and the International Conference on Neural Computation Theory and Applications NCTA Recent progresses in scientific developments and applications in these three areas are reported in this book IJCCI received

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Philosophical Transactions ,2008 Each issue of Transactions B is devoted to a specific area of the biological sciences including clinical science All papers are peer reviewed and edited to the highest standards Published on the 29th of each month Transactions B is essential reading for all biologists Science John Michels (Journalist), 2005 A weekly record of scientific progress *ACM SIGPLAN Notices* ,2006 *Parallel Computing for Bioinformatics and Computational Biology* Albert Y. Zomaya, 2006-05-24 Discover how to streamline complex bioinformatics applications with parallel computing This publication enables readers to handle more complex bioinformatics applications and larger and richer data sets As the editor clearly shows using powerful parallel computing tools can lead to significant breakthroughs in deciphering genomes understanding genetic disease designing customized drug therapies and understanding evolution A broad range of bioinformatics applications is covered with demonstrations on how each one can be parallelized to improve performance and gain faster rates of computation Current parallel computing techniques and technologies are examined including distributed computing and grid computing Readers are provided with a mixture of algorithms experiments and simulations that provide not only qualitative but also quantitative insights into the dynamic field of bioinformatics Parallel Computing for Bioinformatics and Computational Biology is a contributed work that serves as a repository of case studies collectively demonstrating how parallel computing streamlines difficult problems in bioinformatics and produces better results Each of the chapters is authored by an established expert in the field and carefully edited to ensure a consistent approach and high standard throughout the publication The work is organized into five parts Algorithms and models Sequence analysis and microarrays Phylogenetics Protein folding Platforms and enabling technologies Researchers educators and students in the field of bioinformatics will discover how high performance computing can enable them to handle more complex data sets gain deeper insights and make new discoveries

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