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Estimation by DE; 3.5 Simulation and Results; 3.6 Stability Analysis; 3.7 Control Characteristic; 3.8 Conclusions; References; 4 Compute-Intensive Simulations for Cellular Models; 4.1 Introduction; 4.2 Simulation Methods for Stochastic Chemical Kinetics; 4.3 Aspects of Biology - Genetic Regulation

4.4 Parallel Computing for Biological Systems4.5 Parallel Simulations; 4.6 Spatial Modeling of Cellular Systems; 4.7 Modeling Colonies of Cells; References; 5 Parallel Computation in Simulating Diffusion and Deformation in Human Brain; 5.1 Introduction; 5.2 Anisotropic Diffusion Simulation in White Matter Tractography; 5.3 Brain Deformation Simulation in Image-Guided Neurosurgery; 5.4 Summary; References; PART II SEQUENCE ANALYSIS AND MICROARRAYS; 6 Computational Molecular Biology; 6.1 Introduction; 6.2 Basic Concepts in Molecular Biology; 6.3 Global and Local Biological Sequence Alignment

6.4 Heuristic Approaches for Biological Sequence Comparison6.5 Parallel and Distributed Sequence Comparison; 6.6 Conclusions; References; 7 Special-Purpose Computing for Biological Sequence Analysis; 7.1 Introduction; 7.2 Hybrid Parallel Computer; 7.3 Dynamic Programming Communication Pattern; 7.4 Performance Evaluation; 7.5 Future Work and Open Problems; 7.6 Tutorial; References; 8 Multiple Sequence Alignment in Parallel on a Cluster of Workstations; 8.1 Introduction; 8.2 CLUSTAL W; 8.3 Implementation; 8.4 Results; 8.5 Conclusion; References

9 Searching Sequence Databases Using High-Performance BLASTs9.1 Introduction; 9.2 Basic Blast Algorithm; 9.3 Blast Usage and Performance Factors; 9.4 High Performance BLASTs; 9.5 Comparing BLAST Performance; 9.6 UMD-BLAST; 9.7 Future Directions; 9.8 Related Work; 9.9 Summary; References; 10 Parallel Implementations of Local Sequence Alignment: Hardware and Software; 10.1 Introduction; 10.2 Sequence Alignment Primer; 10.3 Smith-Waterman Algorithm; 10.4 FASTA; 10.5 BLAST; 10.6 HMMER - Hidden Markov Models; 10.7 ClustalW; 10.8 Specialized Hardware: FPGA; 10.9 Conclusion; References

11 Parallel Computing in the Analysis of Gene Expression Relationships

Sommario/riassunto

Discover how to streamline complex bioinformatics applications with parallel computingThis 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