



Protein Structure Prediction Using Parallel Linkage Investigating Genetic Algorithms

Abstract of a presentation at the 1998 IEEE Conference on Systems, Man, and Cybernetics

Karl R. Deerman

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**National Institutes of Health (U.S.).
Division of Computer Research and
Technology**



Protein Structure Prediction Using Parallel Linkage Investigating Genetic Algorithms:

Protein Structure Prediction Using Parallel Linkage Investigating Genetic Algorithms Karl R. Deerman (CAPT, USAF.),1999 **Protein Structure Prediction Using Parallel Linkage Investigating Genetic Algorithms** Karl Deerman,1999-03-01 AFIT has had a long standing interest in solving the protein structure prediction PSP problem The PSP problem is an intractable problem that if solved can lead to revolutionary new techniques for everything from the development of new medicines to optical computer switches The challenge is to find a reliable and consistent method of predicting the 3 dimensional structure of a protein given its defining sequence of amino acids PSP is primarily concerned with predicting the tertiary protein structure without regards to how the protein came to this folded state The tertiary structure determines the protein s functionality **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 Linkage in Evolutionary Computation Ying-ping Chen,2008-09-10 In recent

years the issue of linkage in GEAs has garnered greater attention and recognition from researchers Conventional approaches that rely much on ad hoc tweaking of parameters to control the search by balancing the level of exploitation and exploration are grossly inadequate As shown in the work reported here such parameters tweaking based approaches have their limits they can be easily fooled by cases of triviality or peculiarity of the class of problems that the algorithms are designed to handle Furthermore these approaches are usually blind to the interactions between the decision variables thereby disrupting the partial solutions that are being built up along the way **Evolutionary Computation in Bioinformatics** Gary

Fogel, David W. Corne, 2003 This book offers a definitive resource that bridges biology and evolutionary computation The authors have written an introduction to biology and bioinformatics for computer scientists plus an introduction to evolutionary computation for biologists and for computer scientists unfamiliar with these techniques **Scientific and Technical Aerospace Reports** ,1995 Lists citations with abstracts for aerospace related reports obtained from world wide sources and announces documents that have recently been entered into the NASA Scientific and Technical Information Database *Cumulated Index Medicus* ,1995 **Encyclopedia of Bioinformatics and Computational Biology** ,2018-08-21 Encyclopedia of Bioinformatics and Computational Biology ABC of Bioinformatics Three Volume Set combines elements of computer science information technology mathematics statistics and biotechnology providing the methodology and in silico solutions to mine biological data and processes The book covers Theory Topics and Applications with a special focus on Integrative omics and Systems Biology The theoretical methodological underpinnings of BCB including phylogeny are covered as are more current areas of focus such as translational bioinformatics cheminformatics and environmental informatics Finally Applications provide guidance for commonly asked questions This major reference work spans basic and cutting edge methodologies authored by leaders in the field providing an invaluable resource for students scientists professionals in research institutes and a broad swath of researchers in biotechnology and the biomedical and pharmaceutical industries Brings together information from computer science information technology mathematics statistics and biotechnology Written and reviewed by leading experts in the field providing a unique and authoritative resource Focuses on the main theoretical and methodological concepts before expanding on specific topics and applications Includes interactive images multimedia tools and crosslinking to further resources and databases **Bibliography of Agriculture** ,1999 **Director's Report** National Institutes of Health (U.S.). Division of Computer Research and Technology,1994

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