

Dictionary-driven protein annotation

Isidore Rigoutsos*, Tien Huynh, Aris Floratos¹, Laxmi Parida and Daniel Platt

Bioinformatics and Pattern Discovery Group, IBM T.J. Watson Research Center, Yorktown Heights, NY 10598, USA and ¹First Genetic Trust Inc., 9 Polito Avenue, Lyndhurst, NJ 07071, USA

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ABSTRACT

Computational methods seeking to automatically determine the properties (functional, structural, physicochemical, etc.) of a protein directly from the sequence have long been the focus of numerous research groups. With the advent of advanced sequencing methods and systems, the number of amino acid sequences that are being deposited in the public databases has been increasing steadily. This has in turn generated a renewed demand for automated approaches that can annotate individual sequences and complete genomes quickly, exhaustively and objectively. In this paper, we present one such approach that is centered around and exploits the Bio-Dictionary, a collection of amino acid patterns that completely covers the natural sequence space and can capture functional and structural signals that have been reused during evolution, within and across protein families. Our annotation approach also makes use of a weighted, position-specific scoring scheme that is unaffected by the over-representation of well-conserved proteins and protein fragments in the databases used. For a given query sequence, the method permits one to determine, in a single pass, the following: local and global similarities between the query and any protein already present in a public database; the likeness of the query to all available archaeal/bacterial/eukaryotic/viral sequences in the database as a function of amino acid position within the query; the character of secondary structure of the query as a function of amino acid position within the query; the cytoplasmic, transmembrane or extracellular behavior of the query; the nature and position of binding domains, active sites, post-translationally modified sites, signal peptides, etc. In terms of performance, the proposed method is exhaustive, objective and allows for the rapid annotation of individual sequences and full genomes. Annotation examples are presented and discussed in Results, including individual queries and complete genomes that were released publicly after we built the Bio-Dictionary that is used in our

experiments. Finally, we have computed the annotations of more than 70 complete genomes and made them available on the World Wide Web at <http://cbscrv.watson.ibm.com/Annotations/>.

INTRODUCTION

The automatic elucidation of protein function directly from sequence has been the focus of research activity for many years. Such an elucidation has an obvious appeal for it tries to minimize the amount of associated manual labor by reducing a large number of possibilities to one or a handful of choices. This is typically achieved by tapping into repositories of previously accumulated knowledge and by trading computation (i.e. *in silico* approaches) for typically tedious manual analysis. The discovery of protein function directly from sequence, in an automated or semi-automated manner, has become a fundamental question as thousands of unknown proteins and increasing numbers of complete genomes are made available daily in the public domain. Of course, one should not lose sight of the fact that protein annotation is the first step in the attempt to fully describe a particular organism through characterization of its metabolic pathways and transcription regulation networks.

During the last three decades, numerous methods have been proposed for determining protein function from sequence, all of which are essentially instances of a 'guilty by association' approach to solving this problem. Depending on the nature of the information exploited and the manner in which the information is used, these methods can essentially be divided into a handful of well-differentiated categories.

The chronologically earliest examples of protein annotation methods rely on the determination of a local or global similarity between a query protein and proteins with known annotation that are contained in a database (1–4). If two sequences of comparable length share a large portion of their extent, the previously uncharacterized sequence will inherit the function of the annotated one. The validity of this scheme relies on the implicit assumption that two sequences that 'look the same' at the sequence level also have the same function and structure. This is a reasonable assumption, but counter-examples such as the dehydrogenase/z-crystallin case have also been documented in the literature (for a discussion of this particular case see for example 5). The methods in this category are known as 'similarity-based' or 'homology-based' and are numerous. The approach we present in this paper belongs to this category as well.

*To whom correspondence should be addressed. Tel: +1 914 945 1384; Fax: +1 914 945 4104; Email: rigoutsos@us.ibm.com

Dictionary Of Protein

AW Chickering



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Dictionary of Protein Barbara Kraus,1976-04-01 **THE BARBARA KRAUS DICTIONARY OF PROTEIN** ,1975

Hands on Data Science for Biologists Using Python Yasha Hasija,Rajkumar Chakraborty,2021-04-08 Hands on Data Science for Biologists using Python has been conceptualized to address the massive data handling needs of modern day biologists With the advent of high throughput technologies and consequent availability of omics data biological science has become a data intensive field This hands on textbook has been written with the inception of easing data analysis by providing an interactive problem based instructional approach in Python programming language The book starts with an introduction to Python and steadily delves into scrupulous techniques of data handling preprocessing and visualization The book concludes with machine learning algorithms and their applications in biological data science Each topic has an intuitive explanation of concepts and is accompanied with biological examples Features of this book The book contains standard templates for data analysis using Python suitable for beginners as well as advanced learners This book shows working implementations of data handling and machine learning algorithms using real life biological datasets and problems such as gene expression analysis disease prediction image recognition SNP association with phenotypes and diseases Considering the importance of visualization for data interpretation especially in biological systems there is a dedicated chapter for the ease of data visualization and plotting Every chapter is designed to be interactive and is accompanied with Jupyter notebook to prompt readers to practice in their local systems Other avant garde component of the book is the inclusion of a machine learning project wherein various machine learning algorithms are applied for the identification of genes associated with age related disorders A systematic understanding of data analysis steps has always been an important element for biological research This book is a readily accessible resource that can be used as a handbook for data analysis as well as a platter of standard code templates for building models **Image Analysis and Processing -- ICIAP 2009** Carlo Sansone,2009-09-03

This book constitutes the refereed proceedings of the 15th International Conference on Image Analysis and Processing ICIAP 2009 held in Vietri sul Mare Italy in September 2009 The 107 revised full papers presented together with 3 invited papers were carefully reviewed and selected from 168 submissions The papers are organized in topical sections on computer graphics and image processing low and middle level processing 2D and 3D segmentation feature extraction and image analysis object detection and recognition video analysis and processing pattern analysis and classification learning graphs and trees applications shape analysis face analysis medical imaging and image analysis and pattern recognition **Peptide and Protein Design for Biopharmaceutical Applications** Knud Jensen,2009-09-01 Peptides serve as effective drugs in the clinic today However the inherent drawbacks of peptide structures can limit their efficacy as drugs To overcome this researchers are developing new methods to create tailor made peptides and proteins with improved pharmacological properties Design of Peptides and Proteins provides an overview of the experimental and computational methods for peptide

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Structural Bioinformatics Jenny Gu, Philip E. Bourne, 2011-09-20 Structural Bioinformatics was the first major effort to show the application of the principles and basic knowledge of the larger field of bioinformatics to questions focusing on macromolecular structure such as the prediction of protein structure and how proteins carry out cellular functions and how the application of bioinformatics to these life science issues can improve healthcare by accelerating drug discovery and development Designed primarily as a reference the first edition nevertheless saw widespread use as a textbook in graduate and undergraduate university courses dealing with the theories and associated algorithms resources and tools used in the analysis prediction and theoretical underpinnings of DNA RNA and proteins This new edition contains not only thorough updates of the advances in structural bioinformatics since publication of the first edition but also features eleven new chapters dealing with frontier areas of high scientific impact including sampling and search techniques use of mass spectrometry genome functional annotation and much more Offering detailed coverage for practitioners while remaining accessible to the novice Structural Bioinformatics Second Edition is a valuable resource and an excellent textbook for a range of readers in the bioinformatics and advanced biology fields Praise for the previous edition This book is a gold mine of fundamental and practical information in an area not previously well represented in book form Biochemistry and Molecular Education destined to become a classic reference work for workers at all levels in structural bioinformatics recommended with great enthusiasm for educators researchers and graduate students BAMBED a useful and timely summary of a rapidly expanding field Nature Structural Biology a terrific job in this timely creation of a compilation of articles that appropriately addresses this issue Briefings in Bioinformatics *Medical Record* George Frederick Shrady, Thomas Lathrop Stedman, 1913

Bioinformatics Peter V. Yan, 2005 The genomic revolution that has spawned microarrays and high throughput technologies has produced vast amounts of complex biological data that require integration and multidimensional analysis Bioinformatics incorporates sub disciplines ranging from databases and ontologies to the modelling of complex biological systems by way of molecular evolution and protein structure prediction This new book provides state of the art research from around the world

Pediatrics, 1912 *Management of Data*, 2010

Bioinformatics Andreas D. Baxevanis, B. F. Francis Ouellette, 2005 Reviews of the Second Edition In this book Andy Baxevanis and Francis Ouellette have undertaken the difficult task of organizing the knowledge in this field in a logical

progression and presenting it in a digestible form And they have done an excellent job This fine text will make a major impact on biological research and in turn on progress in biomedicine We are all in their debt Eric Lander from the Foreword to the Second Edition The editors and the chapter authors of this book are to be applauded for providing biologists with lucid and comprehensive descriptions of essential topics in bioinformatics This book is easy to read highly informative and certainly timely It is most highly recommended for students and for established investigators alike for anyone who needs to know how to access and use the information derived in and from genomic sequencing projects Trends in Genetics It is an excellent general bioinformatics text and reference perhaps even the best currently available Congratulations to the authors editors and publisher for producing a weighty authoritative readable and attractive book Briefings in Bioinformatics This book written by the top scientists in the field of bioinformatics is the perfect choice for every molecular biology laboratory The Quarterly Review of Biology This fully revised version of a world renowned bestseller provides readers with a practical guide covering the full scope of key concepts in bioinformatics from databases to predictive and comparative algorithms Using relevant biological examples the book provides background on and strategies for using many of the most powerful and commonly used computational approaches for biological discovery This Third Edition reinforces key concepts that have stood the test of time while making the reader aware of new and important developments in this fast moving field With a new full color and enlarged page design Bioinformatics Third Edition offers the most readable up to date and thorough introduction to the field for biologists This new edition features New chapters on genomic databases predictive methods using RNA sequences sequence polymorphisms protein structure prediction intermolecular interactions and proteomic approaches for protein identification Detailed worked examples illustrating the strategic use of the concepts presented in each chapter along with a collection of expanded more rigorous problem sets suitable for classroom use Special topic boxes and appendices highlighting experimental strategies and advanced concepts Annotated reference lists comprehensive lists of relevant Web resources and an extensive glossary of commonly used terms in bioinformatics genomics and proteomics Bioinformatics Third Edition is essential reading for researchers instructors and students of all levels in molecular biology and bioinformatics as well as for investigators involved in genomics clinical research proteomics and computational biology www.wiley.com/bioinformatics [Essays in Bioinformatics](#) David S. Moss, Sibila Jelaska, Sándor Pongor, 2005 **Protein Bioinformatics** Ingvar Eidhammer, Inge Jonassen, Willie R. Taylor, William R. Taylor, 2004-02-13 Pairwise global alignment of sequences Pairwise local alignment and database search Statical analysis Multiple global alignment and phylogenetic trees Scoring matrices Profiles Sequence patterns Structures and structure descriptions Superposition and Dynamic programming Geometric techniques Clustering Combining local similarities Significance and assessment of structure comparisons Multiple structure comparison Protein structure classification Structure prediction Threading Basics in mathematics probability and algorithms Introduction to molecular biology **In Silico Technologies in Drug Target Identification and Validation**

Darryl Leon, Scott Markel, 2006-06-13 The pharmaceutical industry relies on numerous well designed experiments involving high throughput techniques and in silico approaches to analyze potential drug targets These in silico methods are often predictive yielding faster and less expensive analyses than traditional in vivo or in vitro procedures In Silico Technologies in Drug Target Ide *Atlas of Protein Sequence and Structure*, 1976 Issued as supplements to vol 5 of Atlas of protein structure which was published in 1972 The American Physician, 1920 **SUCCESSFUL FARMING**, 1915 **National Union Catalog**, 1973 Includes entries for maps and atlases *Rift-lines within European regulatory framework for Biosimilars when taking heterogeneity and variation during lifecycle of the reference biologic and the biosimilar into account*

Malik Osmane, 2013-10-15 Master s Thesis from the year 2013 in the subject Medicine Pharmacology Pharmacy grade 1 st CLASS HONS Dublin Institute of Technology Chemistry course Pharmaceutical Quality Assurance Regulatory Affairs language English abstract During the course of this thesis evidence was presented and discussed related to the research questions The fundamental question related to the heterogeneity and variation through the life cycle of the biosimilar and the reference biologic remains neglected based on the results collected during this thesis by the stakeholders mainly because those issues were not addressed in any official regulatory guidance document As clear guidance from the EMA is lacking with the only available guidance being that once a marketing authorization is issued it is accepted that the quality profiles of the reference biologic and the biosimilar will have different quality profiles Abstract Within the biosimilar development context there are unaddressed questions by the European Medicines Agency EMA with regard to the impacts of shifts of the quality profile purity and impurity levels of the reference biologic for the biosimilar development program This dynamic is an open issues has potentially implications on the comparability exercise of the before mentioned Opinions from experts involved in the guidance drafting process of EMA and other were evaluated with regard to the issue **The Literary Digest**

Edward Jewitt Wheeler, Isaac Kaufman Funk, William Seaver Woods, Arthur Stimson Draper, Wilfred John Funk, 1911

Decoding **Dictionary Of Protein**: Revealing the Captivating Potential of Verbal Expression

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