

Brief Review on Bioinformatics

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Abstract

During the last years, the enthusiasm for applying feature selection methods in bioinformatics has get rid of from being a clarifying example to becoming a real precondition for perfect structure. In separate, the high dimensional nature of many modeling tasks in bioinformatics, going from sequence analysis over microarray analysis to spectral analyses and literature mining has given rise to a wealth of feature selection techniques being presented in the field. The most common problems are forming in biological developments at the molecular level and creating inferences from collected data. A bioinformatics solution collect statistics from biological data form various fields. Build a computational model. Solve a computational modeling problem. Test and evaluate a computational algorithm. Bioinformatics is a fusion of computing, biotechnology and biological.

Keywords: Bioinformatics; Biostatistics; Comparative genomics; Database Management; Protein Prediction; Sequence Analysis; Biocomputing

Introduction

Bio-Informatics: Bioinformatics is concept of biology in terms of molecules and applying “informatics techniques” to understand and organize the information associated with these molecules, on a large scale. Bioinformatics is a managing information system for molecular biology and has many practical applications of its own.

Applications of Bioinformatics

1. Associating among protein, DNA, and RNA sequences.
2. Examining for related sequences in other organisms.
3. Searching for functional patterns in proteins and nucleic acids.
4. Determine if there are known interactions among proteins.
5. Managing data.

Bioinformatics Databases:

A few popular databases are GenBank from NCBI. Swiss Prot from the Swiss Institute of Bioinformatics and PIR from the Protein Information Resource.[1-9]

GenBank:

GenBank (Genetic Sequence Databank) is one of the fastest rising repositories of known genetic sequences.[10-17] A biological database is a large, organized body, usually related with computerized software calculated to apprise, inquiry, and save components of the data stored within the system. The size of data type may be small but database might be a single file holding many records, all of them consist of similar set of data.[18-23]

EMBL:

The EMBL (European Molecular Biology Laboratory) Nucleotide Sequence Database is a complete database of DNA and RNA sequences collected from the scientific works and flagrant applications and directly succumbed by researchers and sequencing sets[24-30]

Swiss Port:

Swiss Port is a protein sequence database that provides a great number of integration with other databases and also has a very less number of termination (means less identical sequences are present in the database)[31-42]

Open access journals provide more brightness and convenience to the readers to achieve the required information. The ongoing researches all over the world, which are being exhibited through open access journals, serve as the main source of information in various fields[43-54] Open Access literature plays a key role in proving the information and present researches across the earth Journal of Applied Bioinformatics & Computational Biology provides information[55-62] In order to create responsiveness among the people, group of researchers unite to form a society or an organization. The main aim of these societies is to advice and creates awareness in the public [63-69].

Open access Journal of Applied Bioinformatics & Computational Biology are the peer-reviewed journals that maintain the quality and standard of the journal content, reviewer's agreement and respective editor's acceptance in order to publish an article[70-76] These journals ensures the barrier-free distribution of its content through online open access and thus helps in improving the citations for authors and attaining good journal impact factors [96-100].

The 9th International Conference on Bioinformatics is going to be held during October 23-24, 2017 in France's most populous city Paris. The conference focuses on foremost topics such as Proteomics, Systems Biology, Evolutionary Bioinformatics, Genomics, Immunology, Algorithms & Databases, Clinical Informatics, Biostatistics, Structural Bioinformatics Drug Discovery, and Clinical Case Reports.[77-78] OMICS Group world class International conferences organizers and Open Access Publications organizes 100 International conferences across the globe every year scientific discoveries on recent and current developments in various departments in the scientific world for acceleration, OMICS Group Conference is International recognized by ICCA (International Congress and Convention Association).[79-82] Journal of Proteomics & Bioinformatics on 7th International Conference on Proteomics & Bioinformatics October 24-26, 2016 Rome, Italy speakers like Boris Zaslavsky Cleveland Diagnostics, USA presented his views on a disease process is commonly

related with changes in protein structure or protein-protein interaction.[83-89] Such type of changes are under-utilized in clinical practice. In diseases such as cancer, structural changes in proteins within the tumor cells are vast, ranging from alternative splicing to post-translational modifications and can be used as highly efficacious markers for clinical diagnostics. Finally, we discuss the future of structure-based tactics to protein biomarkers as a basis for high performance clinical-grade protein biomarkers[90-93]

Unraveling Sugar Chain Signatures of the “Seeds” of Tumor Metastasis is the article which is being published by author Denong Wang, Tumor Glycomics Laboratory, SRI International Biosciences Division, CA, USA in which he states Circulating Tumor Cells (CTCs) are rare cancer cells in blood circulation that are shed from the primary tumor and play key roles in disseminating metastatic tumor cells to remote sites.[94-96] Detection of CTCs has been explored as a non-invasive “liquid biopsy” for tumor diagnosis and prognosis. CSCs belong to a subpopulation of undifferentiated tumor cells with embryonic characteristics. Finally, these studies suggest epithelial tumor expression of blood group substance-related auto antigens. The potential of this class of carbohydrate-based immunological targets for tumor vaccine development and targeted immunotherapy has yet to be explored.

Editors like Dr. Ning Li obtained his bachelor’s degree from Beijing Forestry University in China in late 80s began to pursue his graduate study in the United States from 1983, have been working as the Editorial Chief. [97-99] Research Interest: Post-translational modification (PTM) networks in plant cell biology, Quantitative PTM proteomics, interatomic and molecular systems biology and Plant Biotechnology. Serological Biomarkers of Dermatomyositis – Associated Interstitial Lung Disease is one of his recent publications.

Conclusion

Bioinformatics predominantly focus on these types of datasets available in molecular biology: genome sequences, macromolecular structures, and the results of functional genomics experiments (e.g. expression data). Additional info includes the text of scientific papers and relationship data from metabolic pathways, taxonomy trees, and protein-protein interaction networks. The person who deals with bioinformatics has a wide range of computational techniques including sequence and structural alignment, database design and data mining, macromolecular geometry expression data clustering, phylogenetic tree construction, prediction of protein structure and function and gene finding,. We survey some representative applications, such as finding homologues, designing drugs, and performing large-scale censuses. All area’s regarding bioinformatics are all set to play a key role taking a step for which bioinformatics field can come into existence to world.

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