

Brief Review on Bioinformatics

Gedela Vamsi Krishna*

Department of Bio-Technology, GITAM University, AP, India

***Corresponding author:** Gedela Vamsi Krishna, Department of Bio-Technology, GITAM University; AP, India

E-mail: vamsi.oye@gmail.com

Received: March 3, 2017; **Accepted:** March 30, 2017; **Published:** April 06, 2017

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.

REFERENCE

1. Wang D. Unraveling Sugar Chain Signatures of the “Seeds” of Tumor Metastasis. *J Proteomics Bioinform.* 2017; 10:e31
2. Abnizova I, Te Boekhorst R. Computational Errors and Biases in Short Read Next Generation Sequencing. *J Proteomics Bioinform.* 2017;10:1-17.
3. Li H, Lyu Q, Cheng JA. Template-Based Protein Structure Reconstruction Method Using Deep Autoencoder Learning. *J Proteomics Bioinform.* 2016;306-313.

4. Holmes RS. Comparative and Evolutionary Studies of Vertebrate Arylsulfatase B, Arylsulfatase I and Arylsulfatase J Genes and Proteins: Evidence for an ARSB-like Sub-family. *J Proteomics Bioinform.* 2016;9:298-305.
5. Lau D, Dalal K, Hon B. Design and Selection of IFI16-PAAD Mutants with Improved dsDNA Destabilization Properties. *J Proteomics Bioinform.* 2016;9:255-263.
6. Banach M, Kalinowska B, Konieczny L, et.al. Sequence-to-Structure Relation in Proteins-Amyloidogenic Proteins with Chameleon Sequences. *J Proteomics Bioinform.* 2016;9:264-275.
7. Banach M, Kalinowska B. Structural Role of Hydrophobic Core in Proteins-Selected Examples. *J Proteomics Bioinform.* 2016;9:276-286.
8. Appaiah P, Vasu P. In silico Designing of Protein Rich in Large Neutral Amino Acids Using Bovine α 1 Casein for Treatment of Phenylketonuria. *J Proteomics Bioinform.* 2016;9:287-297.
9. Yang R, Liu X, Thakolwiboon S, Protein Markers Associated with an ALDH Sub-Population in Colorectal Cancer. *J Proteomics Bioinform.* 2016;9:238-247.
10. Verma P, Upadhyay A. In-silico Approach Explains Evolution of Beta-lactamases from Penicillin Binding Proteins. *J Proteomics Bioinform.* 2016;9:248-254.
11. Lereim RR, Oveland E. The Brain Proteome of the Ubiquitin Ligase Peli1 Knock-Out Mouse during Experimental Autoimmune Encephalomyelitis. *J Proteomics Bioinform.* 2016;9:209-219.
12. Chiranjeevi P, Swargam S. Inhibitor Design for Vaca Toxin of *Helicobacter pylori*. *J Proteomics Bioinform.* 2016;9:220-225.
13. Reddy HA, Srinivasulu C. A Critical Assessment of *Bombyx mori* Haemolymph Extract on *Staphylococcus aureus* an In vitro and In silico Approach. *J Proteomics Bioinform.* 2016;9:226-231.
14. Castaño SV, Juanes FS. Is MALDI-TOF Mass Spectrometry a Valuable New Tool for Microorganisms Epidemiology? *J Proteomics Bioinform.* 2016;9:232-237.
15. El-Esawi MA. Workshop on Recent Applications of Bioinformatics and Eco informatics (WBE 2015). *J Proteomics Bioinform.* 2016;9:e30.
16. Cole J, Buszka PA, Mobley JA. Characterization of the Venom Proteome for the Wandering Spider, *Ctenus hibernalis* (Aranea: Ctenidae). *J Proteomics Bioinform.* 2016;9:196-199.
17. Kumar R, Mohapatra P, Dubey VK. Exploring Realm of Proteases of *Leishmania donovani* Genome and Gene Expression Analysis of Proteases under Apoptotic Condition. *J Proteomics Bioinform.* 2016;9:200-208.
18. Nair DN, Singh V. Structural Investigation and In-silico Characterization of Plasmeprins from *Plasmodium falciparum*. *J Proteomics Bioinform.* 2016;9:181-194.
19. Siddiqui NY, DuBois LG. Optimizing Urine Processing Protocols for Protein and Metabolite Detection. *J Proteomics Bioinform S.* 2015;14:003.
20. Yang L, Rudser K. Urine Protein Biomarker Candidates for Autism. *J Proteomics Bioinform S.* 2016;14:004.
21. Andreev VP, Gillespie BW. Misclassification Errors in Unsupervised Classification Methods. Comparison Based on the Simulation of Targeted Proteomics Data. *J Proteomics Bioinform S.* 2016;14:005.
22. Mathew AV, Zeng L, Byun J. Metabolomic Profiling of Arginine Metabolome Links Altered Methylation to Chronic Kidney Disease Accelerated Atherosclerosis. *J Proteomics Bioinform S Pennathur S.* 2015;14:001.
23. Sas KM, Nair V. Targeted Lipidomic and Transcriptomic Analysis Identifies Dysregulated Renal Ceramide Metabolism in a Mouse Model of Diabetic Kidney Disease. *J Proteomics Bioinform S.* 2015;14:002.

24. Andreev VP, Gillespie BW. Misclassification Errors in Unsupervised Classification Methods. Comparison Based on the Simulation of Targeted Proteomics Data. *J Proteomics Bioinform S*, 2016;14:005.
25. Naryzhny SN, Maynskova MA. Proteomic Profiling of High-grade Glioblastoma Using Virtual experimental 2DE. *J Proteomics Bioinform*. 2016;9:158-165.
26. Madoz-Gúrpide J, Herrero-Martín D. Proteomic Profiling of Ewing Sarcoma Reveals a Role for TRAF6 in Proliferation and Ribonucleoproteins/RNA Processing. *J Proteomics Bioinform*. 2016;9:166-175.
27. Wright JC, Choudhary JS. DecoyPyrat: Fast Non-redundant Hybrid Decoy Sequence Generation for Large Scale Proteomics. *J Proteomics Bioinform*. 2016;9:176-180.
28. Noronha MA, Linden C. Developments in Cardiovascular Proteomics. *J Proteomics Bioinform*. 2016;9:144-150.
29. Dussaq A, Anderson JC. Mechanistic Parameterization of the Kinomic Signal in Peptide Arrays. *J Proteomics Bioinform*. 2016;9:151-157.
30. Zhao Y, Hou Y. Identification of NaHCO₃ Stress Responsive Proteins in *Dunaliella salina* HTBS using iTRAQ-based Analysis. *J Proteomics Bioinform*. 2016;9:137-143.
31. Sengupta D, Tackett AJ. Proteomic Findings in Melanoma. *J Proteomics Bioinform* 2016;9:e29.
32. Hakim MA, Yang S. Discoveries of Serine Protease Inhibitors from Scorpions. *J Proteomics Bioinform*. 2016; 9:101-106.
33. Wright ML, Pendarvis K. The Effect of Oxygen on Bile Resistance in *Listeria monocytogenes*. *J Proteomics Bioinform*. 2016;9:107-119.
34. Gamberi T, Modesti A. Using Proteomics to Understand Abdominal Aortic Aneurysms: Where Are We? *J Proteomics Bioinform*. 2016;9:120-130.
35. Sood S, Sharma N. Microbial Carboxylesterases: An Insight into Thermal Adaptation Using In Silico Approach. *J Proteomics Bioinform*.
36. Machado I, Coquet L. Proteomic Changes in *Pseudomonas aeruginosa* Biofilm Cells after Adaptive Resistance Development. *J Proteomics Bioinform* 2016.
37. Lippolis R, De Angelis M. Proteomics and Human Diseases. *J Proteomics Bioinform*. 2016.
38. Minafra IP, Cara GD. Proteomic Profiling of In-Vitro Bone-Conditioned Skbr3 Breast Cancer Cells. *J Proteomics Bioinform* 2016.
39. Morris JA. Re-Discovering the Germ Theory of Disease: A Major Role for Proteomics. *J Proteomics Bioinform* 2016.
40. Bo-Yeong C, Lee YS, Ju YR, et al. Proteomics based Development of Biomarkers for Prion Diseases. *J Proteomics Bioinform* 2016.
41. Bachelerie P, Felten A. MLVA_Normalizer: Workflow for Normalization of MLVA Profiles and Data Exchange between Laboratories. *J Proteomics Bioinform* 2016.
42. Silvestrini L, Drosig B. Identification of Four Polyhydroxyalkanoate Structural Genes in *Synechocystis cf. salina* PCC6909: In silico Evidences. *J Proteomics Bioinform* 2016.
43. Barghash A, Arslan T. Robust Detection of Outlier Samples and Genes in Expression Datasets. *J Proteomics Bioinform* 2016.
44. Wu C, Deng J. Metaproteomic Characterization of Daqu, a Fermentation Starter Culture of Chinese Liquor. *J Proteomics Bioinform* 2016.

45. Barkhoudarian G, Whitelegge. Proteomics Analysis of Brain Meningiomas in Pursuit of Novel Biomarkers of the Aggressive Behavior. J Proteomics Bioinform 2016.
46. Barkhoudarian G, Whitelegge. Proteomics Analysis of Brain Meningiomas in Pursuit of Novel Biomarkers of the Aggressive Behavior. J Proteomics Bioinform 2016.
47. Mclean C, He X. Improved Functional Enrichment Analysis of Biological Networks using Scalable Modularity Based Clustering. J Proteomics Bioinform 2016.
48. Ellis ML, Mobley JA. Proteome Dynamics of the Specialist Oxalate Degradator Oxalobacter formigenes 2016.
49. Tiwari V, Solanki V. Significances of OMV and Extracellular Vesicle Proteomics 2016.
50. Li H, Yuan J, Zhai F. Global Analysis of Proteomics for Discovery of Biomarkers in Hepatocellular Carcinoma 2016.
51. Shukla HD. Novel Genomics and Proteomics Based Biomarkers to Predict Radiation Response and Normal Radiotoxicity in Cancer Patients for Personalized Medicine. J Cancer Clin Trials 2016.
52. Harinath BC, Jena N. Genomics and Proteomics of Virulent, Avirulent and Drug Resistant Strains of Tuberculous Mycobacteria 2016.
53. Simonian M Proteomics in Medicine 2016.
54. Mittal P, Jain M. Proteomics: An Indispensable Tool for Novel Biomarker Identification in Melanoma. J Data Mining Genomics Proteomics 2016.
55. Machado I, Coquet L. Proteomic Changes in Pseudomonas aeruginosa Biofilm Cells after Adaptive Resistance Development 2016.
56. Lippolis R, De Angelis M. Proteomics and Human Diseases 2016.
57. Minafra IP, Cara GD. Proteomic Profiling of In-Vitro Bone-Conditioned Skbr3 Breast Cancer Cells 2016.
58. Morris JA. Re-Discovering the Germ Theory of Disease: A Major Role for Proteomics 2016.
59. Bo-Yeong C, Lee YS. Proteomics based Development of Biomarkers for Prion Diseases 2016.
60. Bachelerie P, Felten A. MLVA_Normalizer: Workflow for Normalization of MLVA Profiles and Data Exchange between Laboratories 2016.
61. Silvestrini L, Drog B. Identification of Four Polyhydroxyalkanoate Structural Genes in Synechocystis cf. salina PCC6909: In silico Evidences 2016.
62. Barghash A, Arslan T, Helms V. Robust Detection of Outlier Samples and Genes in Expression Datasets 2016.
63. Wu C, Deng J. Metaproteomic Characterization of Daqu, a Fermentation Starter Culture of Chinese Liquor 2016.
64. Barkhoudarian G, Whitelegge JP. Proteomics Analysis of Brain Meningiomas in Pursuit of Novel Biomarkers of the Aggressive Behavior 2016.
65. Fu G, Song XC. Protein Subcellular localization profiling of Prostate Cells by Dissociable Antibody MicroArray (DAMA) Staining Technology 2016.
66. Mclean C, He X. Improved Functional Enrichment Analysis of Biological Networks using Scalable Modularity Based Clustering 2016.
67. Ellis ML, Mobley JA. Proteome Dynamics of the Specialist Oxalate Degradator Oxalobacter formigenes 2016.
68. Shields B, Shalin SC. Microscopes and Mass Spectrometers 2016.
69. Silvestrini L, Drog B. Identification of Four Polyhydroxyalkanoate Structural Genes in Synechocystis cf. salina PCC6909: In silico Evidences 2016.

70. Samorodnitsky E, Ghosh E. Methylation by DNMT1 is more efficient in Chronic Lymphocytic Leukemia Cells than in Normal Cells 2016.
71. Byrum SD, Burdine MS. A Quantitative Proteomic Analysis of Urine from Gamma-Irradiated Non-Human Primates 2015.
72. Xu X Chemical Cross-linking Mass Spectrometry for Profiling Protein Structures and Protein-Protein Interactions 2015.
73. Tachida Y, Sakurai H. Proteomic Comparison of the Secreted Factors of Mesenchymal Stem Cells from Bone Marrow, Adipose Tissue and Dental Pulp 2015.
74. Meyer MK, Andersen M. Effect of IL-6R Inhibition with Tocilizumab on the Proteome of Peripheral Blood Mononuclear Cells from a Rheumatoid Arthritis Patient 2015.
75. Plummer E, Twin J. A Comparison of Three Bioinformatics Pipelines for the Analysis of Preterm Gut Microbiota using 16S rRNA Gene Sequencing Data 2015.
76. Jung S, Danziger SA. Systematic Analysis of Yeast Proteome Reveals Peptide Detectability Factors for Mass Spectrometry 2015.
77. Mathew AV, Zeng L. Metabolomic Profiling of Arginine Metabolome Links Altered Methylation to Chronic Kidney Disease Accelerated Atherosclerosis 2015.
78. Sas KM, Nair V. Targeted Lipidomic and Transcriptomic Analysis Identifies Dysregulated Renal Ceramide Metabolism in a Mouse Model of Diabetic Kidney Disease 2015.
79. Timpe LC, Li D. Mining the Breast Cancer Proteome for Predictors of Drug Sensitivity 2015.
80. Makhoba XH, Pooe OJ. Molecular Chaperone Assisted Expression Systems: Obtaining Pure Soluble and Active Recombinant Proteins for Structural and Therapeutic Purposes 2015.
81. Katam R, Chibanguza K. Proteome Biomarkers in Xylem Reveal Pierce's Disease Tolerance in Grape 2015.
82. Zheng H, Zhao C. AlbuVoid™ Coupled to On-Bead Digestion - Tackling the Challenges of Serum Proteomics 2015.
83. Sam-Yellowe TY. Immune Complex Proteomes: Tools for Vaccine Discovery. 2015
84. Fu YB, Dong Y. paSNPg: A GBS-Based Pipeline for Protein-Associated SNP Discovery and Genotyping in Non-Model Species 2015.
85. Timta MZ, Yadavalli R. In Silico Characterization of Plasmodium falciparum and P. yoelii Translocon and Exoribonuclease II (RNase II) Identified in the Merozoite Rhoptry Proteome 2015.
86. Jagadeesan G, Vijayakuma V. Pyrazole Based Inhibitors against Enzymes of Staphylococcus aureus: A Computational Study 2015.
87. Kodell RL, Haun RS. Novel Use of Proteomic Profiles in a Convex-Hull Ensemble Classifier to Predict Gynecological Cancer Patients' Susceptibility to Gastrointestinal Mucositis as Side Effect of Radiation Therapy 2015.
88. Voros A, DeLongchamp J. The Secretome of Mycoplasma capricolum subsp. capricolum in Neutral and Acidic Media 2015.
89. Krappmann M, Luthardt M. The Software-Landscape in (Prote) Omic Research 2015.
90. Soloviev M, Milnthorpe AT. Quality Control of Expression Profiling Data 2015.

91. Jia RZ, Zhang RJ. Identification and Classification of Rhizobia by Matrix-Assisted Laser Desorption/Ionization Time-Of-Flight Mass Spectrometry 2015.
92. Smita K, Qadar Pasha MA. Oxidative Stress and Histopathological Evaluation of Rat Lung Tissue during Hypobaric Hypoxia 2015.
93. Paul S, Gangwar A. High Altitude Pulmonary Edema: An Update on Omics Data and Redefining Susceptibility 2015.
94. Ulmer CZ, Yost RA. Liquid Chromatography-Mass Spectrometry Metabolic and Lipidomic Sample Preparation Workflow for Suspension-Cultured Mammalian Cells using Jurkat T lymphocyte Cells 2015.
95. Fang L, Kojima K. Analysis of the Human Proteome in Subcutaneous and Visceral Fat Depots in Diabetic and Non-diabetic Patients with Morbid Obesity 2015.
96. Cho IK, Jeong M. Pulmonary Proteome and Protein Networks in Response to the Herbicide Paraquat in Rats 2015.
97. Minic Z. Proteomic Studies of the Effects of Different Stress Conditions on Central Carbon Metabolism in Microorganisms 2015.
98. Thumfart JO, Abidi N. LC/MS Based Monitoring of Endogenous Decay Markers for Quality Assessment of Serum Specimens 2015.
99. Deng X, Li J, Cheng J. Predicting Protein Model Quality from Sequence Alignments by Support Vector Machines 2013.