

INTRODUCTION

Open Access



Current trend and development in bioinformatics research

Yuanyuan Fu¹, Zhougui Ling^{1,2}, Hamid Arabnia³ and Youping Deng^{1*}

From The 20th International Conference on Bioinformatics & Computational Biology (BIOCOMP 2019) Las Vegas, NV, USA. 29 July-01 August 2019

*Correspondence: dengy@hawaii.edu
¹ Department of Quantitative Health Sciences, John A. Burns School of Medicine, University of Hawaii at Manoa, Honolulu, HI 96813, USA
Full list of author information is available at the end of the article

Abstract

This is an editorial report of the supplements to BMC Bioinformatics that includes 6 papers selected from the BIOCOMP'19—The 2019 International Conference on Bioinformatics and Computational Biology. These articles reflect current trend and development in bioinformatics research.

Keywords: Bioinformatics, Biomarkers, Human disease, Microbiome

The supplement to BMC Bioinformatics was proposed to launch during the BIOCOMP'19—The 2019 International Conference on Bioinformatics and Computational Biology held from July 29 to August 01, 2019 in Las Vegas, Nevada. In this congress, a variety of research areas was discussed, including bioinformatics which was one of the major focuses due to the rapid development and requirement of using bioinformatics approaches in biological data analysis, especially for omics large datasets. Here, six manuscripts were selected after strict peer review, providing an overview of the bioinformatics research trend and its application for interdisciplinary collaboration.

Cancer is one of the leading causes of morbidity and mortality worldwide. There exists an urgent need to identify new biomarkers or signatures for early detection and prognosis. Mona et al. identified biomarker genes from functional network based on the 407 differential expressed genes between lung cancer and healthy populations from a public Gene Expression Omnibus dataset. The lower expression of sixteen gene signature is associated with favorable lung cancer survival, DNA repair, and cell regulation [1]. A new class of biomarkers such as alternative splicing variants (ASV) have been studied in recent years. Various platforms and methods, for example, Affymetrix Exon-Exon Junction Array, RNA-seq, and liquid chromatography tandem mass spectrometry (LC-MS/MS), have been developed to explore the role of ASV in human disease. Zhang et al. have developed a bioinformatics workflow to combine LC-MS/MS with RNA-seq which provide new opportunities in biomarker discovery. In their study, they identified twenty-six



© The Author(s) 2020. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

alternative splicing biomarker peptides with one single intron event and one exon skipping event; further pathways indicated the 26 peptides may be involved in cancer, signaling, metabolism, regulation, immune system and hemostasis pathways which validated by the RNA-seq analysis [2].

Proteins serve crucial functions in essentially all biological processes and the function directly depends on their three-dimensional structures. Traditional approaches to elucidation of protein structures by NMR spectroscopy are time consuming and expensive, however, the faster and more cost-effective methods are critical in the development of personalized medicine. Cole et al. improved the REDRAFT software package in the important areas of usability, accessibility, and the core methodology which resulted in the ability to fold proteins [3].

The human microbiome is the aggregation of microorganisms that reside on or within human bodies. Rebecca et al. discussed the tissue-associated microbial detection in cancer using next generation sequencing (NGS). Various computational frameworks could shed light on the role of microbiota in cancer pathogenesis [4]. How to analyze the human microbiome data efficiently is a huge challenge. Zhang et al. developed a non-parametric test based on inter-point distance to evaluate statistical significance from a Bayesian point of view. The proposed test is more efficient and sensitive to the compositional difference compared with the traditional mean-based method [5].

Human disease is also considered as the cause of the interaction between genetic and environmental factors. In the last decades, there was a growing interest in the effect of metal toxicity on human health. Evaluating the toxicity of chemical mixture and their possible mechanism of action is still a challenge for humans and other organisms, as traditional methods are very time consuming, inefficient, and expensive, so a limited number of chemicals can be tested. In order to develop efficient and accurate predictive models, Yu et al. compared the results among a classification algorithm and identified 15 gene biomarkers with 100% accuracy for metal toxicant using a microarray classifier analysis [6].

Currently, there is a growing need to convert biological data into knowledge through a bioinformatics approach. We hope these articles can provide up-to-date information of research development and trend in bioinformatics field.

Abbreviations

BIOCOMP'19: The 2019 International Conference on Bioinformatics and Computational Biology; LC-MS/MS: Liquid chromatography tandem mass spectrometry; ASV: Alternative splicing variants; NMR: Nuclear Magnetic Resonance; REDCRAFT: Residual Dipolar Coupling based Residue Assembly and Filter Tool; NGS: Next generation sequencing.

Acknowledgements

This supplement will not be possible without the support of the International Society of Intelligent Biological Medicine (ISIBM).

About this supplement

This article has been published as part of BMC Bioinformatics Volume 21 Supplement 9, 2020: Selected Articles from the 20th International Conference on Bioinformatics & Computational Biology (BIOCOMP 2019). The full contents of the supplement are available online at <https://bmcbioinformatics.biomedcentral.com/articles/supplements/volume-21-supplement-9>.

Authors' contributions

YF drafted the manuscript, ZL, HA, and YD revised the manuscript. All authors read and approved the final manuscript.

Funding

Publication of this supplement has been supported by NIH grants R01CA223490 and R01 CA230514 to Youping Deng and 5P30GM114737, P20GM103466, 5U54MD007601 and 5P30CA071789.

Availability of data and materials

Not applicable.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author details

¹ Department of Quantitative Health Sciences, John A. Burns School of Medicine, University of Hawaii at Manoa, Honolulu, HI 96813, USA. ² Department of Pulmonary and Critical Care Medicine, The Fourth Affiliated Hospital of Guangxi Medical University, Liuzhou 545005, China. ³ Department of Computer Science, University of Georgia, Athens, GA 30602, USA.

Published: 3 December 2020

References

1. Mona Maharjan RBT, Chowdhury K, Duan W, Mondal AM. Computational identification of biomarker genes for lung cancer considering treatment and non-treatment studies. 2020. <https://doi.org/10.1186/s12859-020-3524-8>.
2. Zhang F, Deng CK, Wang M, Deng B, Barber R, Huang G. Identification of novel alternative splicing biomarkers for breast cancer with LC/MS/MS and RNA-Seq. *Mol Cell Proteomics*. 2020;16:1850–63. <https://doi.org/10.1186/s12859-020-03824-8>.
3. Casey Cole CP, Rachele J, Valafar H. Increased usability, algorithmic improvements and incorporation of data mining for structure calculation of proteins with REDCRAFT software package. 2020. <https://doi.org/10.1186/s12859-020-3522-x>.
4. Rebecca M, Rodriguez VSK, Menor M, Hernandez BY, Deng Y. Tissue-associated microbial detection in cancer using human sequencing data. 2020. <https://doi.org/10.1186/s12859-020-03831-9>.
5. Qingyang Zhang TD. A distance based multisample test for high-dimensional compositional data with applications to the human microbiome. 2020. <https://doi.org/10.1186/s12859-020-3530-x>.
6. Yu Z, Fu Y, Ai J, Zhang J, Huang G, Deng Y. Development of predictive models to distinguish metals from non-metal toxicants, and individual metal from one another. 2020. <https://doi.org/10.1186/s12859-020-3525-7>.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more biomedcentral.com/submissions

