

Introduction to the Special Issue on Bioinformatics and Computational Biology

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Communication: received 31 December 2019, revised 31 December 2019, accepted 31 December 2019

Digital Object Identifier: 10.32913/mic-ict-research.v2019.n2.917

The Editor coordinating the review of this article and deciding to accept it was Prof. Nguyen Linh Trung

Abstract: The Special Issue on Bioinformatics and Computational Biology in the Journal of Research and Development on Information and Communication Technology (ICT Research) aims at bringing together researchers in Vietnam for exchange of new developments in all areas of bioinformatics and computational biology.

Keywords: *Bioinformatics, computational biology.*

In the last ten years, since the Human Genome Project [1] and the development of the next-generation sequencing technologies, the cost for whole-genome sequencing has reduced substantially. A number of large-scale human genome projects have been launched to characterize genetic variation at both global and specific population levels, finally created large-scale genetic databases. The produced databases from these massive sequencing projects have been used to implement association mapping studies of complex disorders and other phenotypic traits. The availability of genetic databases has facilitated the integration of genetic factors into risk prediction models. A polygenic risk score (PRS) combines the effect of many single nucleotide polymorphisms (SNP) into a single score, and has lately been shown to have a clinically predictive value in various common diseases.

In this special issue, the first study of Nguyen Tran The Hung and Le Duc Hau [2] aims to articulate the evidence supporting the clinical usage of PRS, the concepts behind the validity of PRS, approaches to implement PRS in Vietnamese population and cautions in selecting methods and thresholds in developing an appropriate PRS. In addition, the genetic databases have paved the way for the study of evolutionary relationships among populations by phylogenetic trees. Computational methods for building phylogenetic trees from gene/protein sequences have been developed for decades and come of age.

The next study of Le Sy Vinh [3] analyses widely-used methods to construct large phylogenetic trees, and available methods to build phylogenomic trees from whole-genome datasets. It also makes a recommendation for best practices when performing phylogenetic and phylogenomic analyses.

Finally, the next-generation sequencing technologies have also facilitated the study of liquid biopsies for tracking the genomic evolution of tumors over time with application in cancer early detection by analyzing cell-free DNA. The liquid biopsy technology helps avoid the need to conduct repeated biopsies, thus reduce the risk for patients. The last study of Nguyen Ngoc Tran [4] summarizes major advances in liquid biopsy assay technologies and discusses the types of cancers that most likely benefit from early detection.

Through these researches, a picture of advanced applications of next-generation sequencing technologies especially in Vietnam has been depicted and summarized.

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Le Duc Hau obtained his PhD degree in Bioinformatics from the University of Ulsan, Republic of Korea in 2012. He is now leading the Department of Computational Biomedicine at Vingroup Big Data Institute, Vietnam. He has been focusing on proposing computational methods for disease- and drug-related problems in personalized medicine, especially on identification of disease-associated biomarkers, prediction of drug targets and response. In parallel, he has been developing bioinformatics tools. So far, he has published more than fifty papers in well-recognized journals and conferences, nearly a half of those are in ISI-indexed journals. In addition, he has been a member of program committees and reviewer of several international conferences/journals. Moreover, he is a principal investigator and a key member of some national/ministry-level projects. Specially, he is the principal investigator of the biggest genome project in Vietnam (i.e., building databases of genomic variants for Vietnamese population). Finally, he has been collaborating with some well-recognized international research institutes.



Le Hoang Son obtained the Ph.D. degree in mathematics and informatics from the University of Science of Vietnam National University, Hanoi (VNU), in conjunction with the Politecnico di Milano University, Italy, in 2013. From 2007 to 2018, he was a Senior Researcher and Vice-Director of the Center for High Performance Computing at VNU University of Science. Since, he has been an Associate Professor of information technology in Vietnam. Since August 2018, he has been a Senior Researcher of the Department of Multimedia and Virtual Reality at the Information Technology Institute of VNU. His research interests include artificial intelligence, data mining, soft computing, fuzzy computing, fuzzy recommender systems, and geographic information systems. He is a member of Vietnam Journalists Association, the International Association of Computer Science and Information Technology, Vietnam Society for Applications of Mathematics, the Key Laboratory of Geotechnical Engineering, and Artificial Intelligence at the University of Transport Technology. He is an Associate Editor of the Journal of Intelligent and Fuzzy Systems (SCIE), IEEE ACCESS (SCIE), Data Technologies and Applications (SCIE), International Journal of Data Warehousing and Mining (SCIE), Neutrosophic Sets and Systems (ESCI), Vietnam Research and Development on Information and Communication Technology, VNU Journal of Science: Computer Science and Communication Engineering, and Frontiers in Artificial Intelligence. He serves as an Editorial Board for Applied Soft Computing (SCIE), Plos One (SCIE), International Journal of Web and Grid Services (SCIE), International Journal of Ambient Computing and Intelligence (ESCI), and Vietnam Journal of Computer Science and Cybernetics. He is a Guest Editor of several Special Issues at International Journal of Uncertainty, Fuzziness and Knowledge Based Systems (SCIE) and Journal of Ambient Intelligence and Humanized Computing.