Computer Science and Systems Biology: Integration towards Improvement

Dhilleswara Rao V*

Department of Biotechnology, Bharathidasan University, Tamil Nadu, India

Computer Science and Systems Biology have heralded remarkable technological advances in understanding the complex biological systems including human biochemical, molecular and neural pathways and networks. Systems biology integrates the computer applications and experimental biology in modeling's, predictions and characterizations of complex and dynamic properties of biological systems. Particularly, multi-omics studies, high-throughput sequencing techniques and microarray techniques made possible the generation of large datasets from biological systems that could help in understanding the comprehensive molecular pathways, systems functions and behaviors. In the last decade, the computer science and systems biology approaches increased the interest in pathway based biomarker identification, identifying disease genes and drug targets, generation of global genetic interaction maps, and development of new diagnosis and therapeutics methods for deadly diseases and contemporary outbreaks. In this letter, I summarize the breakthroughs of the decade and future challenges in uncover the complex components of biological systems.

The integration of basic sciences with computer science and technological approaches is a revolutionary event in human life. The basic and applied biological techniques provided morphological and anatomical understanding, which is not quite enough to study the basis of biochemistry and molecular biology at cellular levels. Human biological systems are composed of complex biochemical and molecular pathways. Hence, uncover the 3-dimentional (3-D) architecture of the cell was the biggest challenge before the integration of biology and computational approaches. Before the collaboration, however, basic analytical techniques helped in identifying various biomolecules, many questions unanswered due to the lack of availability of large scale data analysis. Computer aided concepts led to the new direction in biological sciences, which provided insights into understanding biomolecules, genes and networks. The inception of bioinformatics paved a new path towards the development of DNA, RNA and protein databases, where the large sets of data can be stored. Further research advancements in biological systems opened doors for a new branch of integrated science, named 'Systems Biology' that provided updated knowledge about networks of biological systems, genetics, gene products, genomics and the 3-D architecture of cell.

The integrated studies established a framework in intelligent systems, data mining, and visualization. Moreover, the development of large data sets of disease causing genes, pathogenic process allowed identifying disease markers, drug targets, which further provided insights into drug design models, novel diagnosis and therapeutic strategies. In addition, improved mathematical and mechanism based modeling, simulation studies, and quantitative system studies, combined with data-driven analytics increased the interest in drug discovery, validation and optimization of clinical development. A fast-growing area developed from integration of bioinformatics and systems biology is system medicine, which provide integrated treatment options at individual level. As of now the clinical applications are limited; however, it is believed that the continuous efforts in analyzing physiological networks, data from multiple sources and highly monitored biological changes would change the pace of development in system medicine. In future, in precision medicine, accumulation of data points from individual makes each person as a longitudinal study.

Indeed, there are remarkable breakthroughs witnessed, significant challenges limiting the progression of computational and systems biology in changing directions towards the development in personalized medicine. Of course, the large data sets are available for modeling and comparative studies, the curation of large data sets and creating a global infrastructure to access the data is a major challenge. Creation of high level information models is on great demand to map the biological systems. As systems biology is multi-dimensional area, matter of community (an engineer, a biochemist, a computer scientist, and a physician) is another biggest challenge; in fact, it is much bigger than technical aspects related to clinical studies. Establishing worldwide collaborations to transfer the knowledge and technology and creating space to analyze global data, is another challenge. In recent time, data science (big data) artificial intelligence (neural networks) becoming more powerful tools in the study of biological systems by using informatics approaches; hence, availability of expertise in these emerging dimensions are also significant.

In summary, the future in biological science, integrated with computational biology will create more opportunities to the researchers to understand all biological systems at deeper levels. It is expected that there will be a large shift towards mathematical, computational aided biology that eventually improve the healthcare and quality of life of human beings.

Journal of Computer Science and Systems Biology: A Decade Move-on

Owing to the benefits of open access publishing in disseminating knowledge across various fields including science, medicine and technology, I would appreciate efforts made by the editors, reviewers and contributors of Journal of Computer Science and Systems Biology on its successful completion of 10 years in open access publishing. In the highly competitive open access market, it is difficult to attract the contributors and readers by publishing high quality original works and reviews in timely fashion. Journal of Computer Science and Systems Biology showed the commitment in selecting papers and maintaining history of quality publication over a decade. The survival of such

*Corresponding author: Dhilleswara Rao V, Department of Biotechnology, Bharathidasan University, Tamil Nadu, India, Tel: +918106544565; E-mail: drvana.biotech@gmail.com

committed publications is becoming questionable now-a-days, because of the commercial perspectives of many emerging publishers. The communities from computer sciences, systems biology are looking for the decades ahead and expected endless efforts from the editor of the journal to continue the legacy.