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**Guest Editorial: Computational Biology****Puspendra K Gupta, FNA, FNASc, FNAAS, FASc**

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Computational Biology  
Knowledge Mining**ABSTRACT**

With the availability of massive datasets, it has become possible to study different systems in an organism in its entirety. The availability of recent hardware and software has enabled the researcher to analyse and model this vast amount of biological data, aiding to the sciences of systems biology and integrative biology.

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In recent years, massive datasets using living organisms generated through different emerging technologies have been increasingly used in biology. These emerging technologies mainly include different areas of omics research, including genomics, proteomics, transcriptomics, metabolomics, phenomics, etc. While this availability of data has provided new opportunities for biologists, there are also challenges in dealing with the data, which are relevant for the study of the principles underlying all disciplines of biology, including taxonomy, morphology, anatomy, physiology, pathology, genetics, molecular biology, systems biology, etc. Despite these challenges, computational biology has generated considerable interest in utilizing computations in different areas of study in biology, and that has allowed well-funded centers to boom at a number of prestigious universities globally.

Computational biology is the science of using the aforementioned biological data for deriving meaningful information. Although the term has often been used interchangeably with that of “bioinformatics”, attempts have been made to distinguish them. For instance, according to National Institute of Health (NIH) (<http://www.nih.gov/>) in the US, computational/mathematical biology is the use of such approaches to address theoretical and experimental questions in biology, while bioinformatics is the application of information science to understand complex life-science data.

Bioinformatics as a science for analyzing data began to develop as early as 1970s, when Ben Hesper and Paulien Hogeweg, the latter being a theoretical biologist from the Netherlands who works on complex biological systems (treating them as dynamic information processing systems), defined the term bioinformatics as “the study of information processes in biotic systems”. This was later followed and extended in by Hwa Lim 1987 and by Temple Smith in 1991. The quantity of data being shared began to grow exponentially by the end of the 1980s. This required the development of new computational methods in order to quickly analyze and interpret relevant information, which then gave birth to pervasive science of computational biology during 1990s. Computational biology has been used to help sequence the human genome, create accurate models of the human brain, and assist in modeling biological systems. With the availability of massive datasets, it has also become possible to study different systems in an organism in its entirety, thus aiding the sciences of systems biology and integrative biology. Additionally, physiologists have been looking at the functioning of an organism

as a whole for decades, if not centuries, applying network analysis to cell signaling, metabolism and genetics using some form of bioinformatics. And there are several flourishing sub-areas of computation biology that have been created for convenience. These include computational genomics, computational modeling, computational pharmacology, computational neuroscience, computational evolutionary biology, computational ecology, taxonomy, etc. Thus, computation has pervaded all areas of biology, and no student of biology today can conduct research without having access to massive data and a plethora of software.

In view of the importance and universality of the use of computational biology and to boost the growth of this subject, a number of societies, networks and organizations were established. At the international level, the International Society for Computation Biology (ISCB) (<http://www.iscb.org/>) and the Bioinformatics Organization, Inc. (Bioinformatics.Org) (<http://www.bioinformatics.org/>) were established. Societies were also born at the regional and national levels, which include the Hellenic Society for Computational Biology and Bioinformatics (<http://www.hscbb.gr/>), the Bioinformatics Society of India (InBios) (<http://www.newindigo.eu/biotech/>), Bioclues.org, Bioinformatics Italian Society (BITS) (<http://www.bioinformatics.it/>), MidSouth Computational Biology and Bioinformatics Society (MCBIOS) (<http://www.mcbios.org/>), the Japanese Society for Bioinformatics (<https://www.jsbi.org/en/>), the Society for bioinformatics in Nordic countries (Socbin) ([www.socbin.org/](http://www.socbin.org/)), the European Bioinformatics Institute (Cambridge, UK) ([www.ebi.ac.uk/](http://www.ebi.ac.uk/)), the Australian Bioinformatics Network, the Asia Pacific Bioinformatics Network (APBioNet.org) ([www.apbionet.org/](http://www.apbionet.org/)), the African Bioinformatics Network ([www.h3abionet.org/](http://www.h3abionet.org/)), the Helmholtz Network for Bioinformatics (HNB) ([www.bioinf.med.uni-goettingen.de/projects/hnb/](http://www.bioinf.med.uni-goettingen.de/projects/hnb/)), etc. In 1998, the Bioinformatics Organization, Inc., based in Boston, was initiated to serve the scientific and educational needs of bioinformatics practitioners and the general public. Some of these societies/organizations also have their own journals. For instance, Bioinformatics (published from Oxford) ([bioinformatics.oxfordjournals.org](http://bioinformatics.oxfordjournals.org)) and PLOS Computational Biology ([www.ploscompbiol.org](http://www.ploscompbiol.org)) (published as open-access, peer-reviewed journal by the Public Library of Science or PLOS) are the two official journals of the ISCB. ISMB Proceedings are also published as part of a regular, online, open-access issue of Bioinformatics. In addition to the journals sponsored by societies, some of the other journals dedicated to computational biology include the following : BMC Bioinformatics ([www.biomedcentral.com/bmcbioinformatics](http://www.biomedcentral.com/bmcbioinformatics)), Briefings in Bioinformatics (<http://bib.oxfordjournals.org>), Computational Molecular Biology ([cmb.sophiapublisher.com](http://cmb.sophiapublisher.com)), Database (journal) ([database.oxfordjournals.org](http://database.oxfordjournals.org)), EMBnet.journal ([journal.embnet.org](http://journal.embnet.org)), IEEE/ACM Transactions on Computational Biology and Bioinformatics ([www.computer.org/portal/web/tcbb](http://www.computer.org/portal/web/tcbb)), Journal of Bioinformatics and Computational Biology ([www.worldscientific.com/worldscinet/jbcb](http://www.worldscientific.com/worldscinet/jbcb)), Journal of Computational Biology (<http://www.liebertpub.com/overview/journal-of-computational-biology/31/>), and Journal of Integrative Bioinformatics (<http://www.liebertpub.com/overview/omics-a-journal-of-integrative-biology/43/>). These journals have many notable research projects in the field of computational biology, provide reviews on software, tutorials on open source software, and also display information on upcoming computational biology conferences.

Large conferences are also periodically organized to assess and facilitate further the growth of computational biology. Some notable examples are Conferences of ISCB ([www.iscb.org/about-ismb](http://www.iscb.org/about-ismb)), Intelligent Systems for Molecular Biology (ISMB) (<http://www-lbit.iro.umontreal.ca/ISMB98/>), European Conferences on Computational Biology (ECCB) ([www.ebi.ac.uk/eccb/](http://www.ebi.ac.uk/eccb/)) and Research in Computational Molecular Biology (RECOMB) ([www.recomb.org](http://www.recomb.org)). Several articles come out as effective publications from the proceedings of these conferences. Despite the plethora of information published in different journals and the proceedings of national and international conferences, further need for rapid, peer review and most importantly ethical publishing cannot be overestimated. Most recently, the Nobelist Randy Schekman, a US Biologist, who is also the Editor-in-Chief of the journal eLife ([www.elifesciences.org](http://www.elifesciences.org)) criticized the journals like Nature, Cell and Science for artificially restricting the number of papers they accept, and also discussed the need for bringing magnanimity to the journals. It is time that young scientists think about what impact their work has on the community, rather than delving on the impact factors or citation factors of journals. Although many argue that to be cited is the key, the impact that bioinformatics can have in lessening the scale of experimentation on society at large should be more important. I hope International Journal for Computational Biology (IJCB) will truly meet this demand and serve biology in a true sense.

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