

Editorial

# Computational Biology and Bioinformatics. What? Why? How?

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## Editorial

Do we know details on biology in general and biological processes in particular? Do we know yet what life is all about or where does life originate at? Do we even know all of the cellular processes? Answers to these queries would bring confusing, contradictory or incomplete statements. Human curiosity on knowing biological structures and functions is ever alive. A biological body, in its interior world, is a collection of various systems, building blocks, processes, mechanisms, etc. From surface, they look different or classified but in their inner kingdom they are not so different, functionally. Yet, little differences make them different with abilities to perform differently. Computational biology is apparently a new field that helps us characterizing various biological processes through certain types of information extracted from the system 'biology'. Storage of information and processing fall in the field of Bioinformatics, Going beyond observation based techniques, we, now-a-days. Do computation by mimicking biological systems *in silico* with the utilization of the power of mathematical formalism and computer programming. This is what we now call as computational biology and the information we extract there from are processed using techniques that make Bioinformatics.

Understanding biological structures relies mainly on the use of advanced available techniques. Once curious minds would invest efforts to dissect a biological body and look into the interior structural components using naked eyes. Then came optophysics and related instruments in the 17th century when the enhanced microscopic look helped to show tiny objects and as a result biological structural unit 'cell' got discovered. Since then continued progresses have been made in microscopy technology and scientists now can easily observe biological systems as tiny as filaments, microtubule, cell's small constituents, etc. The development of technology continues and the observation of even smaller units will be possible. But understanding! Only observation is not enough. Dynamics, interactions, responses, etc. together make obvious nature of biological processes and most of those characteristics are either poorly addressed or yet un-understood. Modelling, analytical analysis, numerical simulation, computation of dynamics, etc. have been, in recent days, invading in the biological exploration with novel techniques and approaches. Computational biology draws biological processes in virtual world and explores the

statistical nature quite clearly that is often impossible using traditional observation based biological research techniques. A protein moves or stay static: directionality of the movement, probability of moving towards any specific targets, reverse dynamics, correlated dynamics, thermodynamic fluctuations, chemical/reaction kinetics, etc. follow physical (popularly known as 'biophysical') laws. They often require physical ways of understanding. Computational biology adopts parameters in programming to tune the *in silico* designed biological system and calculates values of parameters evolving from excited systems that address most of the biophysical criteria.

Creating biological system in computer always relies on the attitude of approach 'simple'. Going out of complicacies as are found in real system we need to develop models or cartoons that hold most of the general properties of the system but not the details. Often we need to focus at one or two parameters only and keep the others unchanged. For example, when we try to understand the interaction energetics between two biomolecules we can perform a pinpointed address of the distance dependent change of binding energies [1-3]. The binding energies at short and long distances follow certain physical formalisms namely charge based Coulomb and van der Waals interactions, hydrophobic, hydrophilic coupling energetics, hydrogen bonding energetics, various mechanical property based coupling energetics, etc. But in these specific example studies in computational biology many such energy sources and parameters related to long time equilibration, exploration of thermodynamic fluctuations, and other important related aspects were ignored due to limited programming capability. As the power of computation increases more parameters that can address better dynamics, vibrations, and fluctuations of the system can be adopted in computation.

Bioinformatics stores the information, helps them to be processed and thus newer systems find stronger background to be explored on. A combined approach using areas of computer science, condensed matter physics, mathematics, statistics and engineering are utilized in bioinformatics to process biological data. Data related to structure and function of the nucleic acid, protein, membrane, microtubule, nervous system, etc. at their both normal and disease states are stored and processed in bioinformatics. Besides knowing the systems' history a time dependent track of the order/disorder transitions, dynamic trends, related energetics are computationally addressed. Thus the pathways of various diseases are discovered. Bioinformatics and computational biology are therefore complimentary to each other and at the end both appear with tools that help biology to be not only explored but also get manipulated for adjustment with environment and time.

Quality research in computational biology, developments in bioinformatics are happening at a fast pace. Publication of the findings has to be ensured in quality journals that are dedicated specifically to the related themes. This journal has created such a platform for all

from around the globe.

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