

Interdisciplinary Researches in Iran II

Genome-wide sequencing has empowered us to relate more and more events in healthy as well as disease-affected cells and tissues to the genomic sequence. Bioinformatics is a highly interdisciplinary field that aims to analyze genomic sequences and biological data. For this reason, methods and technologies from various disciplines from biology and medicine to mathematics, statistics, computer sciences, and physics are employed.^[1] In fact extracting knowledge from biological data is a very complex task because usually all the knowledge and skills needed to understand biological mechanisms are not available in a research group. As an example, after several decades of biological researches and a quarter century from establishment of biomedical engineering as an interdisciplinary field in Iran, only a few research groups are being founded that possess different expertise to solve bioinformatics problems. Although single disciplinary research teams have been worked in the field of bioinformatics from years ago, nowadays high-throughput experimental methods in molecular biology result in an enormous amount of data, including interactions, networks, and pathways^[2] that could not be evaluated only by a single discipline. Therefore, it is essential to have a research team with intensive interaction among a multitude of actors such as mathematicians and computer scientists in order to provide new tools to reveal the essential biological mechanisms from a system perspective for the next-generation sequencing (NGS).^[3]

Now, NGS encompasses almost complete genomes of the many species, illuminating more and more facts about how individual genomes as well as individual aspects of their regulation differ from each other. However, it is currently well known that the difference is not directly correlated with the number of genes but somewhat to the complexity of regulation of the expression of these genes. The different derivative variants (alternative transcripts and proteins including post-translational modifications) from the genes of an organism show a relationship with the functional complexity. In other words, the most important part is not the blueprint of the genome, but the way its modules interact.

A living organism or even a single cell is a greatly organized system of interacting macromolecules and metabolites, which can be regarded as a molecular machine formed by

local interactions of molecular network. To elucidate the essential behaviors of a cellular system, it is necessary to study the bimolecular networks,^[4] rather than analyzing individual components or partial aspects of the organism. So, from this point of view, an organism can be viewed as a dynamical interaction network of genes, proteins, and biochemical reactions that organizes the complex functions of the cells and thus gives rise to life. Living organisms differ from each other not only because of the differences of their genes and proteins but also because of the architectures of their molecular networks. Furthermore a complicated living organism cannot be fully understood by merely analyzing individual components, and the global network of those components is eventually responsible for an organism's behavior. Selecting the network model and fitting the available data into the network are the most important steps in this area. These models range from Boolean networks that involve less biological detail and display only qualitative dynamic behavior to very concrete models that use continuous variables in the modeling procedure and are able to model biochemical interactions with stochastic kinetics.^[4]

In conclusion, the biologists need to mine and organize knowledge generated from high-throughput techniques to achieve new biological insight by further interpreting them in a systematic manner. They should make new satisfactory stories to enhance our understanding of complicated biological functions by integrating comprehensive data of molecular components and make new solutions for many serious human health problems in coming century. This can only be done by constructing groups possessing different expertise by themselves in order to understand biological mechanisms. It seems after several years of researches in single/multidisciplinary research teams in Iran; our researchers found that we really need to establish interdisciplinary groups in order to be able to analyze biological data such as NGS that enables us to elucidate dynamic context-dependent connections of biological networks.

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