

Special Issue

Bioinformatics: From Gene to Networks

Message from the Guest Editors

The applied areas of bioinformatics are based on the analysis of accumulated data on DNA, RNA and protein sequences, protein structures, gene expression profiles, and biochemical pathways that have been experimentally confirmed to be involved into metabolic processes (and, consequently, phenotypic traits of organisms). Functional, structural and comparative genomics, oligonucleotide-based and recombinant DNA technologies, and medical informatics are most advanced of biological approaches, covered by bioinformatics. The identification of single genes and their functions allows us to predict the structures and functions of proteins, and their involvement into metabolic pathway networks. By the means of bioinformatics, it is possible to measure the levels of gene expression in different cells or tissues, construct expression vectors, provide addressed gene editing, develop models for pathogenesis, and design drugs for medical treatment. We invite submissions in the fields of all interdisciplinary sciences using bioinformatics. Both theoretical and experimental studies are welcome, as well as comprehensive review and survey papers.

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Message from the Editor-in-Chief

As the world of science becomes ever more specialized, researchers may lose themselves in the deep forest of the ever increasing number of subfields being created. This open access journal Applied Sciences has been started to link these subfields, so researchers can cut through the forest and see the surrounding, or quite distant fields and subfields to help develop his/her own research even further with the aid of this multi-dimensional network.

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