Evaluation and Assessment of Bioinformatics Methods and Their Applications

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Abstract : Bioinformatics, in its broad sense, involves application of computer processes to solve biological problems. A wide range of computational tools are needed to effectively and efficiently process large amounts of data being generated as a result of recent technological innovations in biology and medicine. A number of computational tools have been developed or adapted to deal with the experimental riches of complex and multivariate data and transition from data collection to information or knowledge. These bioinformatics tools are being evaluated and applied in various medical areas including early detection, risk assessment, classification, and prognosis of cancer. The goal of these efforts is to develop and identify bioinformatics methods with optimal sensitivity, specificity, and predictive capabilities. The recent flood of data from genome sequences and functional genomics has given rise to new field, bioinformatics, which combines elements of biology and computer science. Bioinformatics is conceptualizing biology in terms of macromolecules (in the sense of physical-chemistry) and then applying "informatics" techniques (derived from disciplines such as applied maths, computer science, and statistics) to understand and organize the information associated with these molecules, on a large-scale. Here we propose a definition for this new field and review some of the research that is being pursued, particularly in relation to transcriptional regulatory systems.
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