Computational Intelligence in Bioinformatics

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Since the term 'bioinformatics' was coined in 1970 [1], the field of bioinformatics has become relatively mature allowing high-throughput whole genome sequencing and making computer-aided drug design an essential part of drug discovery. With the needs of addressing ever more complex problems in a faster and more accurate manner, the bioinformatics community has exploited many different paradigms. Among them, 'Computational Intelligence' has proved particularly effective since nature-inspired computational approaches are able to extract patterns from large volumes of data, infer rules from sets of examples and adapt according to changing data and/or contexts [2]. Many of those methods have been applied to bioinformatics; they include: Artificial Immune Systems [3], Bayesian Networks [4], Evolutionary Algorithms [5], Fuzzy Logic [6], Hidden Markov Models [7], Neural Networks [8], Rough Sets [9], Support Vector Machines (SVM) [10] and Swarm Intelligence [11]. In this special issue, we present six papers that illustrate the latest applications of Computational Intelligence in Bioinformatics.

Since more and more protein structure prediction tools are now available, it is crucial to be able to assess the quality of the generated models. Using features extracted from sequence alignment between a target and its template(s), Deng et al. [12] developed a SVM-based method to predict the quality score of a model. High correlation between predicted and actual values showed the effectiveness of their method.

Unlike the previous case, the choice of features may not be intuitive. As a consequence, selection methods are required before classification to prevent redundancy and the "curse of dimensionality". To design a system to identify and classify nuclear receptors into sub-classifications to prevent redundancy and the "curse of dimensionality". As demonstrated by these articles, usage of Computational Intelligence has been spreading in bioinformatics. The excellent match between this paradigm and, the nature and complexity of bioinformatics problems makes it suitable for a wide range of applications from sequence annotation, microarray interpretation to protein structure analysis. There is no doubt that in the coming years the impact of Computational Intelligence will grow further, leading to even better understanding of biological data.

References


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