

Optimization, classification and dimensionality reduction in biomedicine and bioinformatics

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Abstract

Summary. Research in biomedicine is faced with various problems connected to high-throughput processing –the need to handle the high frequency of incoming data and its high-dimensionality by means of a large number of measured features. Biomedicine needs efficient methods to deal with the enormous amount of collected data as well as effective tools to extract meta-data and information. It needs methods to explore data by means of classification and to evaluate data and models with respect to accuracy and reliability. Optimization methods have been successfully applied to these problems, but the complexity of the data, i.e. varying data density, high dimensionality and model reliability, is still very challenging. This paper addresses some important issues concerning the classification of a large amount of data: k-nearest-neighbor (kNN)-based and support vector machine (SVM)-based classification, dimensionality reduction for kNN and SVM classification, and optimal parameter settings for a SVM-based classifier. Dimensionality reduction and parameter selection are accomplished by using an electromagnetism-like metaheuristic (EM). The same EM is used for solving another optimization problem studied in this paper –the maximum betweenness problem (MBP). During radiation hybrid experiments, X-rays are used to fragment the chromosome. The probability that the given dose of an X-ray will break the chromosome rises with the distance between chromosomes. In this way, markers are placed on two separate chromosomal fragments. By estimating the frequency of the breaking points, and thus the distances between markers, it is possible to determine their order in a manner analogous to meiotic mapping. In this context, improvement of the radiation experiment is achieved by solving the MBP, i.e. by determining the total ordering of the markers that maximizes the number of satisfied constraints.

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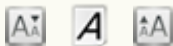
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