Advances in metaheuristics for gene selection and classification of microarray data

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Résumé en anglais	Gene selection aims at identifying a (small) subset of informative genes from the initial data in order to obtain high predictive accuracy for classification. Gene selection can be considered as a combinatorial search problem and thus be conveniently handled with optimization methods. In this article, we summarize some recent developments of using metaheuristic-based methods within an embedded approach for gene selection. In particular, we put forward the importance and usefulness of integrating problem-specific knowledge into the search operators of such a method. To illustrate the point, we explain how ranking coefficients of a linear classifier such as support vector machine (SVM) can be profitably used to reinforce the search efficiency of Local Search and Evolutionary Search metaheuristic algorithms for gene selection and classification.
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