

Evolutionary Algorithm Based on New Crossover for the Biclustering of Gene Expression Data

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R sum  en anglais

Microarray represents a recent multidisciplinary technology. It measures the expression levels of several genes under different biological conditions, which allows to generate multiple data. These data can be analyzed through biclustering method to determinate groups of genes presenting a similar behavior under specific groups of conditions.

This paper proposes a new evolutionary algorithm based on a new crossover method, dedicated to the biclustering of gene expression data. This proposed crossover method ensures the creation of new biclusters with better quality. To evaluate its performance, an experimental study was done on real microarray datasets. These experimentations show that our algorithm extracts high quality biclusters with highly correlated genes that are particularly involved in specific ontology structure.

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