

工程与应用

## 一种新算法在基因表达谱聚类中的应用

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收稿日期 2008-7-10 修回日期 2008-11-17 网络版发布日期 2009-12-30 接受日期

**摘要** 聚类分析是从基因表达数据中提取生物学信息的主要方法。针对基本粒子群优化算法易陷入局部极值和对可调参数敏感的问题, 提出了一种新型粒子对算法来解决基因聚类问题。算法初始化四个粒子, 随机分成两对, 将K-均值快速聚类的结果作为每个粒子对中一个粒子的初始位置。在每次迭代中, 粒子仅依靠自身速度和粒子对的最佳位置来完成自身更新。每个粒子对产生的精英粒子, 组成一个新的粒子对, 继续搜索, 新粒子对的最佳位置即为聚类算法的最优解。实验结果表明算法具有良好的同质性和差异性, 且在计算时间和收敛速度方面具有相当的优势。

**关键词** [基因表达谱](#) [粒子群优化](#) [粒子对](#) [聚类分析](#)

**分类号** [TP391](#)

## Application of new algorithm in gene expression profile clustering

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### Abstract

Clustering techniques can extract biomedical information from gene expression data. The basic particle swarm optimization is liable to be trapped in local convergence and sensitive to adjustable parameters. A new algorithm is proposed to solve gene clustering problem. Four particles are initialized and two of them are chosen randomly as a pair. The result of K-means is assigned to one particle in the pair. At each iteration, every particle updates itself only according to its velocity and the best position of the pair it belongs to. One elitist particle is generated from each pair respectively and they are combined into a new pair. The new particle pair continues to search and its best position is just the global optima of the algorithm. Experiment results show that the algorithm has perfect homogeneity and separation in yeast gene expression data and has an advantage in computation time and convergence rate.

**Key words** [gene expression profile](#) [particle swarm optimization](#) [particle pair](#) [clustering analysis](#)

DOI: 10.3778/j.issn.1002-8331.2009.36.061

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