

数据库、信号与信息处理

基于蛋白质相互作用网络图的聚类方法

彭利红, 廖波, 刘昊

湖南大学 计算机与通信学院, 长沙 410082

收稿日期 2007-12-13 修回日期 2008-3-7 网络版发布日期 2008-11-9 接受日期

摘要 依据人类AD (Alzheimer's Disease) 相关蛋白质相互作用网络图, 利用基于算术平均最小值——AAMV (Arithmetic Average Minimum Value) 的K-means聚类方法对蛋白质进行聚类并预测4个孤立蛋白质的功能。分析结果表明: 所得结果与用Maryland Bridge 法及Korbel法所得结果非常相似。

关键词 [蛋白质相互作用网络图](#) [算术平均最小值](#) [K-means聚类方法](#) [准则函数](#)

分类号

Clustering method based on protein-protein interaction network graph

PENG Li-hong, LIAO Bo, LIU Hao

School of Computer and Communication, Hunan University, Changsha 410082, China

Abstract

The purpose of this study is to evaluate a novel clustering technique for clustering and detecting the isolated points in protein-protein interaction network, which iteratively refines clusters based on a combination of the K-means clustering algorithm and the Arithmetic Average Minimum Value (AAMV). The result is that the algorithm is found to be effective at detecting clusters and identifying the isolated points in the protein-protein interaction network graph with regard to human Alzheimer's Disease. The algorithm outperforms competing approaches and is capable of effectively predicting the function-unknown protein function.

Key words [protein-protein interaction network graph](#) [Arithmetic Average Minimum Value \(AAMV\)](#) [K-means clustering method](#) [criterion function](#)

DOI: 10.3778/j.issn.1002-8331.2008.32.039

通讯作者 彭利红 simina1221@yahoo.cn

扩展功能

本文信息

- ▶ [Supporting info](#)
- ▶ [PDF\(388KB\)](#)
- ▶ [HTML全文\(0KB\)](#)
- ▶ [参考文献](#)

服务与反馈

- ▶ [把本文推荐给朋友](#)
- ▶ [加入我的书架](#)
- ▶ [加入引用管理器](#)
- ▶ [复制索引](#)
- ▶ [Email Alert](#)
- ▶ [文章反馈](#)
- ▶ [浏览反馈信息](#)

相关信息

- ▶ [本刊中 包含 “蛋白质相互作用网络图” 的相关文章](#)
- ▶ [本文作者相关文章](#)

- [彭利红](#)
- [廖波](#)
- [刘昊](#)