

Accepted Manuscript

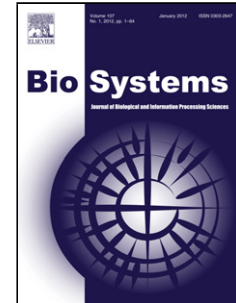
Title: Multiobjective optimization to reconstruct biological networks

Author: Ahmed Naef Rosni Abdullah Nuraini Abdul Rashid

PII: S0303-2647(18)30131-X
DOI: <https://doi.org/doi:10.1016/j.biosystems.2018.09.003>
Reference: BIO 3877

To appear in: *BioSystems*

Received date: 8-4-2018
Revised date: 16-7-2018
Accepted date: 11-9-2018



Please cite this article as: Ahmed Naef, Rosni Abdullah, Nuraini Abdul Rashid, Multiobjective optimization to reconstruct biological networks, *BioSystems* (2018), <https://doi.org/10.1016/j.biosystems.2018.09.003>

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

Multiobjective Optimization to Reconstruct Biological Networks

Ahmed Naef^{a,*}, Rosni Abdullah^{a,b}, Nuraini Abdul Rashid^c

^a*School of Computer Sciences, Universiti Sains Malaysia, 11800 USM, Penang*

^b*National Advanced IPv6 Centre (Nav6) 6th Floor, School of Computer Sciences, Universiti Sains Malaysia, 11800 USM, Penang*

^c*College of Computer and information sciences, Princess nourah bint Abdulrahman university, KSA*

Abstract

Automated methods for reconstructing biological networks are becoming increasingly important in computational systems biology. Public databases containing information on biological processes for hundreds of organisms are assisting in the inference of such networks. This paper proposes a multiobjective genetic algorithm method to reconstruct networks related to metabolism and protein interaction. Such a method utilizes structural properties of scale-free networks and known biological information about individual genes and proteins to reconstruct metabolic networks represented as enzyme graph and protein interaction networks. We test our method on four commonly-used protein networks in yeast. Two are networks related to the metabolism of the yeast: KEGG and BioCyc. The other two datasets are networks from protein-protein interaction: Krogan and BioGrid. Experimental results show that the proposed method is capable of reconstructing biological networks by combining different omics data and structural characteristics of scale-free networks. However, the proposed method to reconstruct the network is time-consuming because several evaluations must be performed. We parallelized this method on GPU to overcome this limitation by parallelizing the objective functions of the presented method. The parallel method shows a significant reduction in the execution

*Corresponding author

Email address: ahmdnaef@gmail.com (Ahmed Naef)

Download English Version:

<https://daneshyari.com/en/article/11015370>

Download Persian Version:

<https://daneshyari.com/article/11015370>

[Daneshyari.com](https://daneshyari.com)