

## Application of hierarchical local modularity maximum method to biological networks

DeWu Ding

Department of Mathematics and Computer Science, Chizhou College, Chizhou 247000, China

E-mail: [dwding@yahoo.com.cn](mailto:dwding@yahoo.com.cn)

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### Abstract

This study showed that the network communities with biological significance could be identified by using hierarchical local modularity maximum method.

**Keywords** biological network; community; metabolic network.

### 1 Introduction

Many computational studies focus on the building, validating and analyzing biological networks, e.g., gene regulatory networks, protein interaction networks, metabolic networks, etc (Barabasi and Oltvai, 2004). Among lots of analytical methods, the concept of network communities from complex networks has been widely used for decades. In a general way, the study of biological network communities could helpful for understanding the structure and function of these networks (Newman, 2006, 2010; Fortunato, 2010).

Generally speaking, limited network community studies have been achieved for biological networks. Almost all of current studies consider biological networks as general complex networks (Ibrahim et al., 2011; Kuang and Zhang, 2011; Huang and Zhang, 2012; Zhang, 2012). As a result, the communities obtained are often biological insignificance (Ding and He, 2011). However, in present study I herein showed that the network communities with biological significance could be identified by using hierarchical local modularity maximum (Blondel et al., 2008).

### 2 Method and Application

The hierarchical local modularity maximum method is mainly represented by two steps

- (1) Find a local maximum of modularity according to

$$\Delta Q = \left[ \frac{\sum_{in} + k_{i,in}}{m} - \left( \frac{\sum_{tot} + k_i}{2m} \right)^2 \right] - \left[ \frac{\sum_{in}}{2m} - \left( \frac{\sum_{tot}}{2m} \right)^2 - \left( \frac{k_i}{2m} \right)^2 \right]$$

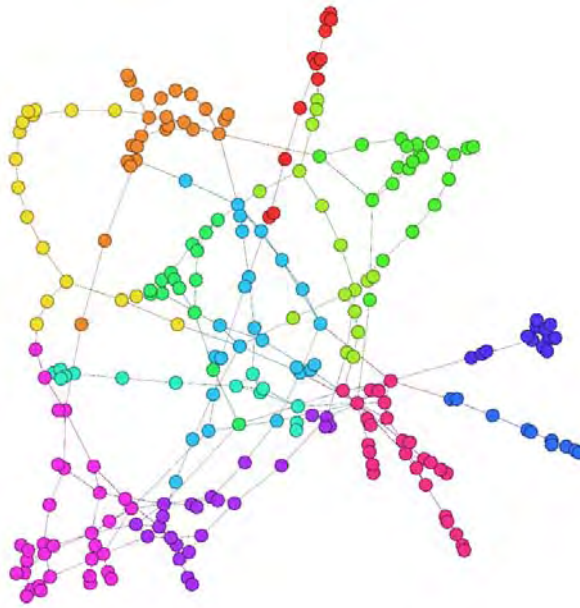
- (2) Build a new network whose nodes are the communities.

Repeating above two steps will generate a hierarchical decomposition of network (Blondel et al., 2008).

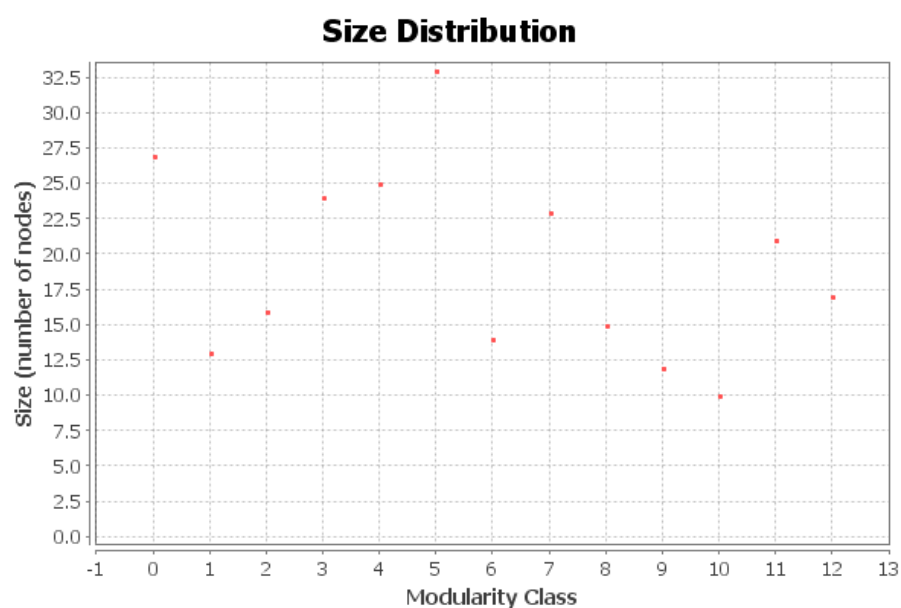
To apply the method, I constructed a metabolite graph model for a recent reconstructed high-quality *S. aureus* metabolic network. I revised the model and extracted the giant strong component (Ding and Li, 2009)

for network communities study. It contained 250 nodes and 560 connections. At last, using hierarchical local modularity maximum method, I identified 13 communities in the giant strong component of *S. aureus* metabolic network (Fig. 1).

The modularity in the partition of the giant strong component of *S. aureus* metabolic network is 0.792. The 13 communities are all biologically significant. For example: community 0 mainly corresponded to pyruvate metabolism; valine, leucine and isoleucine degradation; community 1 mainly corresponded to bile acid biosynthesis, and valine, leucine and isoleucine degradation; community 2 mainly corresponded to glycine, serine and threonine metabolism, glyoxylate and dicarboxylate, and folate biosynthesis, etc. See Fig. 2 for the size distribution of these 13 communities.



**Fig. 1** The 13 communities in the giant strong component of *S. aureus* metabolic network (each community is marked by a distinct color).



**Fig. 2** The size distribution of 13 communities in the giant strong component of *S. aureus* metabolic network.

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