

M³ : Merging Module Model for a Network with Scale-Free Properties and Modularity

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1 Introduction

Many graphical and statistical properties have been found in a large size of complex networks such as WWW, social and biomolecular networks [1, 3]. One of the common properties is scale-free, shows that the degree distribution $P(k)$ of the networks follows power law $P(k) \sim k^{-\gamma}$. Recent study demonstrates that metabolic networks in different organisms also have both modularity and hierarchy [5]. To get an insight into their origin and growing mechanisms of the networks, here we present a simple model that consists of deterministic and stochastic process.

2 Model and Method

Our model can produce networks with scale-free and modularity as follows. **1)** Prepare a module that the fixed number of nodes is E and clustering coefficient of the module is 1 (Fig.1, $t = 0$). **2)** Merge one of nodes of the module by joining new module (Fig.1, $t = 1$). **3)** When joining modules, preferential attach [2] is used (Fig.1, $t = 2$). **4)** Stop developing process when the total number of nodes reaches $N \gg 0$.

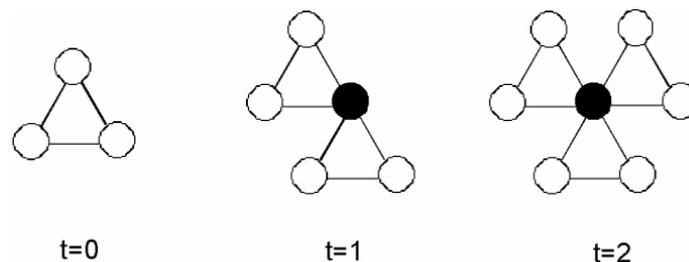


Figure 1: Growing process with $E = 3$. Node and edge correspond to metabolite and reaction path respectively. Filled node is shared node by joining new module. Time step t denotes the number of iterative process of the model.

3 Results and Discussion

Distributions of degree and clustering coefficient are shown in Fig.2 and Fig.3 respectively that demonstrate that our model can reproduce topological features of metabolic network. $C(k)$ decreases as K

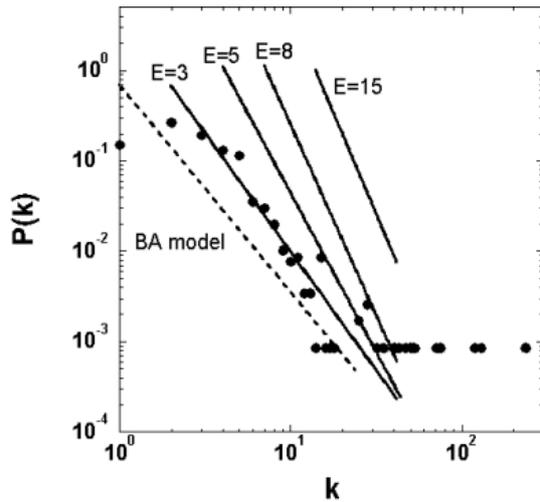


Figure 2: Degree distributions. Solid lines are produced by our model. Filled circles are base on metabolic network of *Escherichia coli* [6]. Dashed line comes from circles BA model [2].

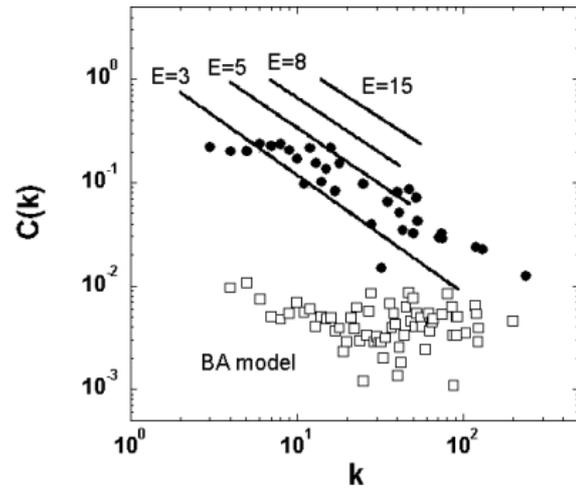


Figure 3: Dependence of clustering coefficient on the node's degree of Figure 2. Filled circles are base on metabolic network of *Escherichia coli* [6]. Open squares are based on BA model.

increases in Fig.3, which indicates the networks have module structure. BA model [2] can generate degree of distribution, and fails to produce modularity in the network (Fig. 3).

We present a model for generating networks have the same properties of metabolic networks. It is little known that how real metabolic networks developed under different environmental conditions. Our method may provide some information developing and/or evolutionary mechanism of biomolecular networks, including metabolic and other complex networks. Because of ability to produce biological network features one can apply the model for construction other network model such as Boolean networks [4].

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