Spontaneous emergence of modularity in cellular networks

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Modularity is known to be one of the most relevant characteristics of biological systems and appears to be present at multiple scales. Given its adaptive potential, it is often assumed to be the target of selective pressures. Under such interpretation, selection would be actively favouring the formation of modular structures, which would specialize in different functions. Here we show that, within the context of cellular networks, no such selection pressure is needed to obtain modularity. Instead, the intrinsic dynamics of network growth by duplication and diversification is able to generate it for free and explain the statistical features exhibited by small subgraphs. The implications for the evolution and evolvability of both biological and technological systems are discussed.

Keywords: complex networks; modularity; evolvability; tinkering; network biology

1. INTRODUCTION

Biological and technological systems both exhibit a common pattern of modular organization. A modular system is formed by quasi-independent parts that not only are tightly integrated within themselves but also exhibit a certain degree of interdependency among themselves (Schlosser & Wagner 2004). Modularity is considered to be a prerequisite for the adaptation of complex organisms and their evolvability (Raff 1996; Gerhart & Kirschner 1997; Calabretta et al. 2000).

Modularity is particularly obvious in cellular networks (Ravasz et al. 2002), where it can be detected at the topological level. These networks include the webs of interactions among proteins, genes, enzymes and metabolites or signalling molecules. It has been argued that modularity is likely to have been selectively favoured by evolution. In that case, explaining its origins would require a functional view of biological networks (Hartwell et al. 1999).

Within the context of network theory (Bornholdt & Schuster 2003; Dorogovtsev & Mendes 2003; Boccaletti et al. 2006; Koonin et al. 2006), the given system is represented as a graph \( G = (V, E) \) composed of a set of \( N \) nodes (say proteins), \( V = \{v_i\} \), and a set of links, \( e_{ij} \in E \), indicating if a connection exists between nodes \( v_i \) and \( v_j \). An example is shown in figure 1: the human protein interaction network. Here we can see a few proteins having a large number of links (the hubs) surrounded by many proteins having just a few connections. This type of heterogeneous networks is very common and is characterized by a probability distribution \( P(k) \) of having a node with \( k \) links, which falls off as a power law with a cut-off, i.e.

\[
P(k) \sim (k + k_0)^{-\gamma} e^{-k/k_0},
\]

where \( k_0 \) is a constant and \( 2 < \gamma < 3 \) denotes the scaling exponent (typically close to \( \gamma \approx 2.5 \)). The cut-off \( k_0 \) is a characteristic degree indicating the presence of a maximum number of links. The hubs tend to have important roles (Albert et al. 2000), particularly when looking at regulatory elements such as transcription factors (Rodriguez-Caso et al. 2005), where the most connected nodes are often proto-oncogenes or tumour suppressor genes and their failure typically involves some proliferative disorder.

At its smallest scale, modules are defined by means of subgraphs involving three or four elements (Wolf & Arkin 2003). These subgraphs have received considerable attention in relation to the so-called network motifs (Milo et al. 2002, 2004). Roughly speaking, motifs are patterns of interconnections occurring in complex networks at numbers that are significantly higher than those in randomized networks. The analysis of their statistical distribution reveals that each class of natural and artificial networks seems to display a common pattern of motif abundances. The statistical pattern is thus interpreted as functionally meaningful. Under this view, motif abundances—as well as modularity—would be a consequence of selective forces. Is that the case? Recently, a model for the evolution of modularity and network motifs has been suggested, based on a genetic programming approach (Lipson et al. 2002; Kashtan & Alon 2005). The model evolves electronic circuits under an environment that changes itself in a modular manner. However, the view of network substructures as resulting from pure selection or optimization has been questioned in a number of studies (Guimerà et al. 2004; Solé et al. 2002a; Banzhaf & Kuo 2004; Mazurie et al. 2005; Rice et al. 2005; Valverde & Solé 2005; Kuo et al. 2006; Solé & Valverde 2006), suggesting that the abundance of motifs does not necessarily reflect functional advantages.

In this paper we show that an alternative explanation for modularity exists, associated with the inevitable constraints imposed by the rules driving the growth of cellular networks. Specifically, since biological entities typically evolve by tinkering (Jacob 1976; Solé et al. 2002a), widely reusing, combining and reconnecting available parts, some patterns of network organization will be essentially inevitable. As a consequence, both subgraph patterns and modular

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After gene duplication has taken place, rapid divergence occurs and many redundant genes become silenced (i.e. become pseudogenes). Changes in wiring are associated with the emergence of novelty and new functionalities (Patthy 1999). In our work presented here we consider only such simple approximation based on single-gene events. We will use one of the simplest DD models of protein network evolution (Vazquez et al. 2003), which involves the following set of rules, to be applied a given number of times, until \( N \) nodes are present. Assuming that we have a graph of size \( n \), we iterate the following rules.

(i) **Duplication.** Choose a node \( v_i \in V \) at random and duplicate it, thus generating a new node \( v_{n+1} \).

(ii) **Link deletion.** The new node shares a set of neighbouring nodes \( \{ v_j \} \) with its predecessor. For each common pair of common links, i.e. \( e_{ij} \) and \( e_{n+1,p} \) we choose one of them and delete it with probability \( \delta \). This rule thus removes (probabilistically) redundant relations among proteins.

(iii) **Link addition.** A link is added among nodes \( v_i \) and \( v_{n+1} \) with probability \( \alpha \). This is a small number and allows new functionalities to emerge by linking the twin proteins.

This model has been solved analytically and it has been shown that it exhibits a phase transition at a given deletion rate. This can be shown by constructing a dynamical equation for the average degree \( K_n \) of the simulated protein network after \( n \) nodes have been introduced. It can be shown that \( K_n \) evolves following the discrete system (Vazquez et al. 2003)

\[
K_{n+1} = \frac{nK_n + 2\alpha + (1 - 2\delta)K_n}{n+1},
\]

(2.1)

where we can see that the number of proteins \( n \) is also a time scale. Using the continuous approximation \( K_{n+1} - K_n \sim dK_n/dn \) and assuming that \( n \) is large, we have a differential equation

\[
dK_n/dn = 2\alpha K_n/n + 1 - 2\delta K_n.
\]

(2.2)

By solving it, we obtain the time evolution of the average degree

\[
K_n = \frac{2\alpha}{2\delta - 1} + \left( K_1 - \frac{2\alpha}{2\delta - 1} \right) n^{1 - 2\delta}.
\]

(2.3)

It is easy to check that a steady degree \( K^* \) is achieved for \( \delta > \delta_c = 1/2 \), namely

\[
K^* = \lim_{n\to\infty} K_n = \frac{2\alpha}{2\delta - 1}.
\]

(2.4)

whereas for \( \delta < \delta_c \), link removal is too slow and the average connectivity is high. There is thus a critical deletion rate \( \delta_c = 1/2 \) separating a strongly connected proteome from a sparse one (which would also include many small subgraphs). Since real protein maps are known to be rather sparse (with average connectivities around \( \langle k \rangle \sim 3-5 \)), we should expect to find appropriate removal rates at \( \delta > \delta_c \). Actually, it has been shown (Vazquez et al. 2003) that for \( \alpha = 0.1 \) and \( \delta = 0.7 \), the model is consistent with several properties observed in the yeast proteome (such as scale-free topology, small-world behaviour, graph correlations and robustness against node deletion). By using appropriate measures, we will show that both modules and non-random distributions of subgraphs are an expected by-product of network growth by duplication.
Figure 2. Modularity in tinkered model networks. Here we show (a–d) the average number of modules ($\mu$) of networks generated using the DD model. Here $\mu$ is computed on the largest connected component for each $\delta$ and averaged over 50 replicas. We used four different $\alpha$ values ((a) $\alpha = 0.005$, (b) $\alpha = 0.01$, (c) $\alpha = 0.10$ and (d) $\alpha = 0.50$) and a maximal network size $N=1000$. A well-defined maximum is observed at $\delta^* \approx 0.7$ in all cases. The network shown in (e) is an example of the modular graphs obtained at $\delta^*$.

3. MODULARITY FROM TINKERING

3.1. Modules

We will first analyse the emergence of modular patterns in the previously described model. In order to provide a quantitative measure, we will use a specific algorithm\(^1\) of community detection (Clauset et al. 2004; see also Newman 2006; Reichardt & Bornholdt 2006). The method considers a decomposition of the graph $\mathcal{Q}$ (figure 2) into a set $\Gamma_{\mu}$ of subgraphs $C'_i \in \Gamma_{\mu}$ defining a partition $\mathcal{C}$. Obviously, many possible $\mathcal{C}$-partitions are possible. Using the adjacency matrix of the graph, $A = (a_{ij})$, and assuming a given partition, the fraction of edges that fall within subsets of $\mathcal{C}$ will be given by

$$f(C) = \frac{\sum_{i,j} a_{ij} \delta(C_i, C_j)}{\sum_{i,j} a_{ij}},$$

(3.1)

where $\delta(a, b) = 1$ if $a = b$ and zero otherwise. Using $m = \sum_{i,j} a_{ij}/2$, we can also write

$$f(C) = \frac{1}{2m} \sum_{i,j} a_{ij} \delta(C_i, C_j).$$

(3.2)

In order to define an appropriate modularity index, the previous measure needs to be compared with the expectation from a randomly wired graph with identical number of nodes and links. Let us indicate as $k_i$ the degree of $v_i$, which is obtained from the adjacency matrix as $k_i = \sum_j a_{ij}$.

The expected probability of having a link connecting two arbitrary nodes $v_i$ and $v_j$ will be simply $k_i k_j/2m$, and thus we can define modularity $Q$ in terms of the average difference between the observed and the expected value of $f$, namely

$$Q = \frac{1}{2m} \sum_{i,j} \left[ a_{ij} - \frac{k_i k_j}{2m} \right] \delta(C_i, C_j),$$

(3.3)

\(^{1}\) All these approaches are heuristics. It has been shown that modularity maximization is an NP-complete problem (Brandes et al. 2006) and thus there is in general no optimal partition.

which is properly normalized between 0 (random network) and 1 (a single module is present).

The modularity of a network will be defined as the maximum $Q = \max \{ Q \}$ as evaluated by the search algorithm (Clauset et al. 2004). The size of the best partition $\mu$ defines the (potential) number of modules. Here we apply this measure to the largest connected component of the network generated by the algorithm described in §2. For each $\delta$, and a fixed $\alpha$ value, we generate 50 simulated networks, each one starting from a small graph of four fully connected elements and ending once a graph with $N = 10^4$ nodes is obtained. Four different values of $\alpha$ have been used. The results are shown in figure 2, where a one-hump curve $\mu(\delta)$ is obtained in all four cases. A maximum is reached for $\delta^* \approx 0.7$, which is actually the deletion rate that gave best-fit statistics compared with yeast proteome data (Vazquez et al. 2003).

The origins of the maximum can be understood in terms of two basic conflicting components associated with the growth rules. At low $\delta$ values, the system is highly connected, being all node members of the giant component and having a large degree. As a consequence, we should not expect to observe a large number of modules. On the other hand, as $\delta$ increases, the network becomes more and more sparse and for $\delta > \delta_c$, it starts to get fragmented. The largest component in this domain will be formed by highly heterogeneous groups of loosely linked subgraphs. Close to the transition $\delta_c$, many elements belong to the largest connected component, but the number of modules is not large since they share many links. With increasing $\delta$, it is more likely to find groups of connected nodes that still share few links. But further increasing $\delta$ implies breaking of $\mathcal{Q}$ into many small subgraphs, which will display a low modularity.

3.2. Subgraph census

A second level of analysis can be performed by considering the frequency of subgraphs of a given size, also known as subgraph census (see Wasserman & Faust 1994).
and references therein). Here we have studied the census
of $n=4$ subgraphs, since it provides a reasonable number
of different structures. More importantly, most examples
whose functional relevance has been described in detail
fall within this class (Milo et al. 2002, 2004; Klemm &

The results are shown in figure 3a,b, where we can
compare the observed patterns of subgraph abundances
in real and simulated networks, respectively. For the real
datasets, we have used the human interactome, the
subset of transcription factors and the yeast proteome.
The plots display the per cent of subgraphs found in each
network against the subgraph rank $r$. After a plateau,
the frequency of subgraphs rapidly decays as an
exponential function, i.e.

$$N(r) \sim e^{-\eta r},$$

with $\eta \approx 1.8$. Such pattern is also found in the
distribution of subgraphs obtained from the DD model.
Using the $\delta$ value that gives the maximum number
of modules, we also obtain an exponential decay, with
$\eta_{DD} = 1.71 \pm 0.20$, consistently with the real datasets.

The common pattern shared by both real and
simulated graphs is consistent with a rule-driven
mechanism of network evolution. In this context, it is
interesting to see that the different subgraphs are easily
connected through DD events (figure 3c).

4. DISCUSSION

What drives the emergence of modularity in evolution? Is
it a function-driven mechanism or instead the by-product
of more fundamental, dynamical rules, as it has been
suggested in other contexts (Kauffman 1993)? Although
it is true that modularity is an essential feature of
biological structures, our analysis suggests that it might
be a by-product of the multiplicative nature of duplica-
tion–rewiring mechanisms. Such a tinkering process
(Jacob 1976; Solé et al. 2002a,b) inevitably leads to
fluctuations in network structure due to its multiplicative
nature: the rich gets richer and the graph will be
organized around hubs. Moreover, the local amplification
of subgraph abundances obtained from the DD process is
also responsible for the decay observed in $N(r)$.

The presence of an optimal level of modularity at a
given $\delta$ value is an important result of our study with
potential implications for evolution by selection, at least
at some levels. Selection might have been present at the
level of link deletion. By removing the right amount of
links, a large connected graph can be obtained, which
will be both heterogeneous (and thus robust against
random node deletion) and modular. In this context,
although our results do not rule out the role of selection
and functional adaptation in explaining modularity,
they suggest that strong constraints are imposed by the
rules of network growth. Thus, topological patterns
(including heterogeneity and modular organization)
would be an emergent property of evolutionary tinker-
ing. Evolvability might have strongly benefited from
such features, since heterogeneity and modularity
immediately favour robustness and specialization,
respectively. Further work should explore how these
results can be extended to a more detailed level of
description of network evolution.

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REFERENCES

Albert, R. & Barabási, A.-L. 2002 Statistical mechanics of
1103/RevModPhys.74.47)
Albert, R., Jeong, H. & Barabási, A.-L. 2000 Error and attack
(doi:10.1038/35019019)