

## **BIOLOGICALLY INSPIRED COMMUNITY DETECTION:**

We discuss a biologically inspired “community detection” method that enables the determination of network structure on all scales. Using information theory correlations, this approach ascertains the stability of network structure and function to external perturbations. We discuss applications ranging from communication networks to computer vision.

“Community detection” is a graph theory inspired problem that seeks to identify groups or “communities” of basic elements (or “nodes”) that are strongly linked within their own group and weakly connected to other groups. As its name suggests, “community detection” is rooted and intimately related to social and biological systems. This problem is of considerable importance not only in systems biology but also to other disciplines such as smart grid applications and homeland security.

We investigate general aspects of this problem and a biologically inspired approach to address it. In this approach, inspired by social and biological networks, different “replicas” (or copies of the systems) are considered. The correlations between different candidate partitions (“replica solutions”) of the graph into communities are evaluated with the aid of information theory measures. High correlations signify a stability of the partitions to small perturbations. By examining these correlations, it is possible to ascertain the natural structures in biological (and other) systems on *all scales*.

The resulting method may be applied to both static and dynamic networks. It is very fast and extremely accurate. With the aid of the inter-replica information theory correlations it is also possible to examine the computational complexity of the system and to numerically evaluate the quality of the partitions and to see how meaningful they are in general cases. The complexity of this problem shares some features with hard combinatorial problems (and their phase diagram).

We have applied the method to numerous networks including those of dolphins, C-elegans, anthropological systems, hierarchical and random networks with billions of links, and the analysis of chemical and physical systems with 10000 atoms.

More recently, this approach was applied to computer vision. An unsupervised image segmentation (with no prior training sets) based on this method can detect features that are not recognized by most humans.

The field of community detection is in its infancy and its use in the analysis of biological systems and biologically inspired applications is certain to provide many new insights and aid other approaches.

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