Dynamical overlap of protein interaction networks: a method to predict protein functions

Irene Sendiña-Nadal[1], Yanay Ofran[2], Juan Antonio Almendral[1], Daqing Li[3], Inmaculada Leyva[1], Javier M. Buldú[1], Shlomo Havlin[3], & Stefano Boccaletti[4,5]

[1] Complex Systems Group, Dept of Signal Theory and Communications, Rey Juan Carlos University, Camino del Molino s/n, 28943 Fuenlabrada, Madrid, Spain
[2] The Mina and Everard Goodman Faculty of Life Sciences, Bar Ilan University, 52900 Ramat Gan, Israel
[3] Department of Physics, Minerva Center, Bar Ilan univeristy, 52900 Ramat Gan, Israel
[4] Embassy of Italy in Tel Aviv, 25 Hamered St., 68125 Tel Aviv, Israel
[5] CNR-Istituto dei Sistemi Complessi, Via Madonna del Piano 10, 50019 Sesto Fiorentino, Firenze, Italy
irene.sendina@urjc.es

The latest advances in the field of genome sequencing technologies have tremendously increase the number of known proteins. The challenge is now how to characterize those proteins and elucidate their function within the different biological processes. One recent approach to assign a function to one protein is by means of the network of its interactions with other proteins [Sharan07]. Novel high-throughput techniques for protein-protein interaction measurements have let to obtain those networks of protein interaction from different organisms [Aebersold03, Field05]. Using this network representation, proteins as nodes and detected physical interactions among them as links, it is possible to apply the tools from complex networks theory to predict and annotate a function to a given protein.

While most of the works on functional annotation of proteins via their network of interactions are exclusively based in topological measurements from the properties of the PIN, we propose the application of an algorithm based on the synchronization behavior emerging from a modular network organization. The method relies on how phase oscillators organize in a network structure of dynamical interactions, and on a recently proposed technique for the identification of synchronization interfaces and overlapping communities [Li08] in ensembles of networking dynamical systems. The combination of the synchronization behavior of the PIN structure and an initial modular classification of proteins drawn from a manual assignment available from a ten years old database from the Munich information Center for Protein Sequences (MIPS) allows for protein function predictions that is in genuine agreement with more recent and better refined manual assignments obtained from Gene Ontology database.

[Aebersold03] R. Aebersold, and M. Mann, Mass spectrometry-based proteomics, Nature 422, 198 (2003).

[Fields07] S. Fields, High-throughput two-hybrid analysis. The promise and the peril, FEBS J 272, 5391 (2005).

[Li08] D. Li et al., Synchronization Interfaces and Overlapping Communities in Complex Networks, Phys Rev Lett 101, 168701 (2008).

[Sharan07] R. Sharan, I. Ulitsky, and R. Shamir, Network-based prediction of protein function, Molecular Systems Biology 3, 88 (2007).