BRIGHAM AND WOMEN'S HOSPITAL

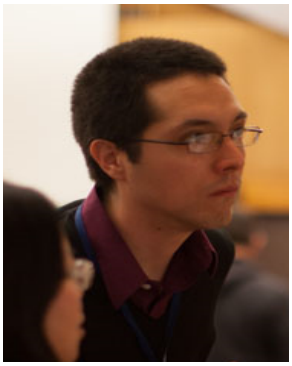
HARVARD MEDICAL SCHOOL

181 Longwood Avenue
Boston, Massachusetts 02115-5804

Department of Medicine
Channing Division of Network Medicine

Channing Network Science Seminar

Oct 21 (Friday), 2016, 11am @ 5th floor conference room



Jorge G. T. Zañudo, Ph.D.
Postdoctoral researcher at Department of Physics, Pennsylvania State University
Visiting Scientist at Dana-Farber Cancer Institute and Broad Institute

Network-based Dynamic Modeling and Control Strategies in Complex Diseases

In order to understand how the interactions of molecular components inside cells give rise to cellular function, creating models that incorporate the current biological knowledge while also making testable predictions that guide experimental work is of utmost importance. To model the dynamics of the networks underlying complex diseases we use network-based models with discrete dynamics, which have been shown to reproduce the qualitative dynamics of a multitude of cellular systems while requiring only the combinatorial nature of the interactions and qualitative information on the desired/undesired states. Here I present some recently developed analytical and computational methods for analyzing network-based models with discrete dynamics. The methods presented are based on a type of function-dependent subnetwork that stabilizes in a steady state regardless of the state of the rest of the network, and which we termed stable motif. Based on the concept of stable motif, we proposed a control method that identifies targets whose manipulation ensures the convergence of the model towards a dynamical attractor of interest (which are identifiable with the cell fates and cell behaviors of modeled organisms). We illustrate the potential of these methods by collaborating with wet-lab cancer biologists to construct and analyze a model for a process involved in the spread of cancer cells (epithelial-mesenchymal transition). These methods allowed us to identify the subnetworks responsible for the disease and the healthy cell states, and show that stabilizing the activity of a few select components can drive the cell towards a desired fate or away from an undesired fate, the validity of which is supported by experimental work.

Bio: Jorge G. T. Zañudo is a postdoctoral researcher (Stand Up To Cancer - The V Foundation Convergence Scholar) at the Department of Physics of The Pennsylvania State University where he works under the supervision of Réka Albert. He is currently a visiting scientist at the Dana-Farber Cancer Institute and at the Broad Institute in Levi Garraway's lab. He received his B.S. in Physics from Universidad de Guadalajara and his Ph.D. in Physics from The Pennsylvania State University, where his Ph.D. advisor was Réka Albert. His Ph.D. work consisted on developing theoretical and computational methods for analyzing logic-based models of the dynamics of signal trandsuction and regulatory networks. His current work is in developing control methods for network models, and in building and analyzing logic-based network models of drug resistance in breast cancer and melanoma.

Hosted by Yang-Yu Liu