



## Channing Network Science Seminar

March 13, 2015, 11am @ 5th floor conference room



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#### Systematic drug efficacy screening using network-based drug-disease proximity

Abstract: Recent analyses of drug targets and disease genes, typically using shortest path lengths between the two groups of nodes in the human interaction network, provided limited insights on the effect of targeted interventions on diseases. Accordingly, the community still lacks a network-based formalization of the impact of drugs on the interrelated web of genes perturbed in the cellular network. In this talk, I will introduce a novel network-based relative proximity measure to quantify the closeness between any two sets of nodes (e.g., drug targets, the proteins that the drug binds, and disease genes, the genes associated with the disease). The relative proximity takes into account the scale-free nature of the human interaction network and corrects for known bias towards drug targets that are often high-degree nodes by incorporating various distance definitions between the two sets of nodes and comparison of these distances to those of randomly selected nodes in the network (i.e. the distance relative to random expectation). We have tested the developed measure on 112 drugs used in 29 diseases and found that the therapeutic effect of drugs is localized within the two-step neighborhood of the disease genes. We observe that the majority of the drugs are closer to the diseases they are recommended for compared to random proteins in the network. Furthermore, we find that relative proximity distinguishes symptomatic and effective treatments based on a systematic analysis of the adverse event reports collected by Federal Drug Administration. In brief, relative proximity offers a formal framework to characterize the distance between two sets of nodes in the network with key applications in various domains from network pharmacology (e.g., discovering novel uses for existing drugs) to social sciences (e.g., defining similarity between groups of individuals).

*Bio: Emre Guney is a postdoctoral research associate in the Center for Complex Network Research at Northeastern University and the Center for Cancer Systems Biology at Dana Farber Cancer Institute. He holds a BS in Computer Engineering from Middle East Technical University in Turkey and a PhD in Biomedicine from Universitat Pompeu Fabra in Spain. His research interests include disease bioinformatics and systems medicine with a particular focus on network-based approaches to understand biological processes perturbed in complex diseases.*

Hosted by Yang-Yu Liu