Master Thesis proposal
Investigating the structure and organization of a drug-target network

Claudio Altafini
Division of Automatic Control, Dept. of Electrical Engineering,
Linköping University, SE-58183, Sweden.
email: claudio.altafini@liu.se

November 19, 2014

This proposal is for a Master thesis in in the field of **Systems Biology.**

In databases such as DrugBank (www.drugbank.ca/), all currently known annotation of the effects of a drug on its molecular targets is publicly available and can be queried. In particular, the DrugBank database is a unique bioinformatics and cheminformatics resource containing 7680 drug entries (small molecules, peptides, nutraceuticals and over 6000 experimental drugs) and 4270 non-redundant drug targets (e.g. enzymes, ion channels, receptors). Each DrugCard entry contains more than 200 data fields, among which there is often a field describing whether the drug acts as an agonist (activator) or as an antagonist (inhibitor) on a target. The objective of the proposed thesis is to construct a *drug-target network*, i.e., a bipartite graph in which one type of nodes are the drugs and the other the targets, see [4, 1] for examples. The edges we are interested in are those carrying information on the agonistic/antagonistic nature of the drug-target interactions. The bipartite graph that we intend to construct is therefore a *signed bipartite graph*. This type of graph is related to a so-called "spin glass" in Statistical Physics, a prototype "disordered system". The plan for the thesis is to study a series of properties related to the ordered or disordered organization of the resulting network (in the style of [3, 2], where analogous concepts are used in different contexts), and to apply them to the understanding of drug synergies and drug repurposing.

The ideal candidate for the thesis will have a curriculum in Engineering or Computer Science or Bioinformatics. Given that the nature of the work is essentially computational, a background in Biology is not strictly necessary, although willingness to acquire some basic notions is a prerequisite.

References

[1] F. Cheng, C. Liu, J. Jiang, W. Lu, W. Li, G. Liu, W. Zhou, J. Huang, and Y. Tang. Prediction of drug-target interactions and drug repositioning via network-based inference. *PLoS Comput Biol*, 8(5):e1002503, 05 2012.

[2] G. Facchetti, G. Iacono, and C. Altafini. Computing global structural balance in large-scale signed social networks. *Proc. Nat. Ac. Sci.*, 108:20953–8, 2011.

[3] G. Iacono and C. Altafini. Monotonicity, frustration, and ordered response: an analysis of the energy landscape of perturbed large-scale biological networks. *BMC Syst. Biol.*, 4:83, 2010.

[4] M. A. Yildirim, K. I. Goh, M. E. Cusick, A. L. Barabási, and M. Vidal. Drug-target network. *Nat Biotechnol*, 25(10):1119–1126, Oct 2007.