Mining and modeling networks to study diseases

Networks are scaling-up the analysis of gene and protein functions, thereby offering new avenues to study the diseases in which these macromolecules are involved. I will discuss the exploration of *omics* networks containing thousands of physical and functional interactions between genes and proteins. In particular, we now focus on multiplex networks, i.e., networks composed of layers containing the same nodes but different interaction categories, such as protein-protein interactions, molecular complexes or correlations of expression. We develop algorithms (e.g., community detections, random walks) to explore these large and complex biological networks, integrate information (e.g., expression), and mine the functional knowledge they contain. I will show how we use these tools to study human diseases, and in particular diseases-disease comorbidity relationships.

I will finally briefly mention strategies to decipher drug synergies in cancer thanks to logical modeling of signaling pathways and networks.

Selected Associated publications

The DREAM Module Identification Challenge Consortium, Choobdar S, Ahsen ME, Crawford J, Tomasoni M, Fang T, et al. Assessment of network module identification across complex diseases. Nature Methods. 2019 Sep;16(9):843–52.

Valdeolivas A, Tichit L, Navarro C, Perrin S, Odelin G, Levy N, et al. Random Walk with Restart on Multiplex and Heterogeneous Biological Networks. Bioinformatics. 2018 Jul 18;

Flobak Å, Baudot A, Remy E, Thommesen L, Thieffry D, Kuiper M, et al. Discovery of Drug Synergies in Gastric Cancer Cells Predicted by Logical Modeling. Xenarios I, editor. PLOS Computational Biology. 2015 Aug 28;11(8):e1004426;

Ibáñez K, Boullosa C, Tabarés-Seisdedos R, Baudot A, Valencia A. Molecular Evidence for the Inverse Comorbidity between Central Nervous System Disorders and Cancers Detected by Transcriptomic Meta-analyses. Horwitz MS, editor. PLoS Genetics. 2014 Feb 20;10(2):e1004173.