BioISI - Biosystems & Integrative Sciences Institute

Development of computational methods to characterize human diseases through the analysis of biomolecular networks

Place of work/: BioISI/FCUL

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Abstract / MSc thesis project proposal

The main goal of this proposal is to develop computational methods to discover genes associated with complex diseases. Network medicine approaches aim to identify disease associated genes using the concept of disease modules, that is, genes associated with a given disease tend to interact closely in biological networks, defining specific network neighborhoods associated with that disease [1]. Biological networks identify physical and functional interactions between biomolecules, and provide us with a map of cell components and processes [2].
It is still a major challenge to identify genes that, when their activity is perturbed, have the capacity to either cause or modify the disease phenotype. Knowing these genes is fundamental to devise new therapeutic approaches or to apply a personalized medicine approach.

Our lab has developed a couple of approaches to analyze biomolecular networks and potentiate our understanding of human diseases [1,3]. This master thesis proposal will build upon our previous approaches along one of the following axis:

1. Optimization and performance evaluation of network cross-disease analysis methods
2. Prediction of gene-disease associations (or gene-process associations) through machine learning models trained with network embeddings based in node connectivity to other diseases or biological processes
3. Discovery of network features correlated with tissue-specific cancer driver genes
4. Understanding metastasis tropism patterns through within-cell and between-cells molecular interaction networks

Students selected for this project, after thesis registration, are eligible to apply to the BioISI Junior Programme (supporting 8 students with a 6-month Scholarship(BII), being the selection criterium the academic merit of the candidates).

Bibliography

1. Garcia-Vaquero, M. L., Gama-Carvalho, M., Rivas, J. D. L. & Pinto, F. R. Searching the overlap between network modules with specific betweenness (S2B) and its application to cross-disease analysis. *Scientific Reports* **8**, 11555 (2018).
2. Liu, C. *et al.* Computational network biology: Data, model, and applications. *Physics Reports* 1–66 (2020) doi:10.1016/j.physrep.2019.12.004.
3. Loureiro, C. A. et al. Network Biology Identifies Novel Regulators of CFTR Trafficking and Membrane Stability. *Frontiers in Pharmacology* **10**, 249–13 (2019).