Title	Exploring the world of metabolite association networks
Group	Systems and Synthetic Biology
Project type	Thesis
Credits	36
Supervisor(s)	Dr. Edoardo Saccenti (SSB)
Examiner(s)	Dr. Edoardo Saccenti, Dr. Robert Smith
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Begin date	

Used skills: Network inference, data analysis and multivariate statistics; programming; relating results to existing or novel biological knowledge.

Requirements: Ability to program in R, basic statistics and biological knowledge are highly desired skills.

Description: Different types of information can be represented in the shape of networks in order to model a biological system. A network is a graphical representation of different biological entities (nodes) and their relationships (edges): the meaning of the nodes and edges used in a network representation depends on the type of data used to build the network. Some of the most common types of biological networks are: protein-protein interaction networks, Metabolic networks, Genetic interaction networks, Gene / transcriptional regulatory networks and Cell signalling networks.

In this project we will focus on metabolite-metabolite association networks that can be built from metabolomics data: the ultimate goal is to characterize the properties of these networks and to answer to questions like: *Which topological measures best reflect a set of metabolites participating in the same pathway? Are metabolite-metabolite association networks scale free? Do they exhibits small world properties? Which measures better described metabolites associated with a disease?*

At the end of the project you will have gained ample experience in network analysis, network topology, statistics and in handling and modelling complex information.

References

Alm, E. and A. P. Arkin (2003). "Biological networks." Current opinion in structural biology **13**(2): 193-202.
Embar, V., A. Handen and M. K. Ganapathiraju (2016). "Is the average shortest path length of gene set a reflection of their biological relatedness?" Journal of bioinformatics and computational biology **14**(06): 1660002.

Glass, L. (1975). "Classification of biological networks by their qualitative dynamics." Journal of Theoretical Biology **54**(1): 85-107.

van Tilborg, D. and E. Saccenti (2021). "Cancers in Agreement? Exploring the Cross-Talk of Cancer Metabolomic and Transcriptomic Landscapes Using Publicly Available Data." Cancers **13**(3): 393.