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Mining networks to study rare and common diseases

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Abstract

Networks are scaling-up the analysis of gene and protein functions, hence offering new avenues to study the diseases in which these genes and proteins are involved. I will discuss the exploration of biological networks containing thousands of physical and functional interactions between 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 interaction, molecular complexes or co-expression. We have developed partitioning algorithms to recover communities – or functional modules – from these more complex and data-rich networks, and use them to study the cellular functions of genes and proteins of interest. Recently, we also adapted a random walk strategy to navigate multiplex networks, and extract information about genes and proteins implicated in rare genetic diseases associated to a premature aging phenotype. I will finally show ongoing work dedicated to the disease-contextualization of biological networks thanks to the integration of protein or RNA expression data.

Short bio

Anaïs Baudot is a Systems Biologist with a background in Biology, Genetics and Bioinformatics. She holds a PhD from the Aix-Marseille University (AMU). After a post-doctoral stay at the Spanish National Cancer Research Center (CNIO), she got a Researcher position at French National Center for Scientific Research (CNRS) in 2010. She has been working since then in the Marseille Institute of Mathematics (CNRS-AMU). In September 2017, she joined the Marseille Medical Genetics (MMG) unit to settle network and systems approaches for the study of human disorders. Her research is focused on -omics studies (interactomes), networks (partitioning, boolean modelling), and human diseases, in particular complex diseases, cancers and comorbidities.