Contextualization of molecular networks for human diseases

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Molecular and signalling interactions described in the scientific literature are systematically captured into several publicly available databases. The interaction data is organized in structured formats that can be easily processed and exploited to perform functional and network analyses to, for instance, infer the function of uncharacterized proteins or to investigate their potential role in cellular pathways.
I will give an overview of the main bioinformatics resources that store molecular and signalling interactions, how they represent biological interactions, the community standards, curation rules and ontologies adopted, and which information are available. I will discuss more in detail about the resources developed in our group, MINT and SIGNOR 2.0.

MINT, the Molecular INTeractions Database (https://mint.bio.uniroma2.it/) is a public database that stores information about experimentally verified protein-protein interactions mined from the scientific literature. MINT is an active member of the IMEx consortium, whose purpose is to coordinate curation efforts between its members to make available a unified, non-redundant and standardised molecular interaction dataset.
SIGNOR 2.0, the SIGnaling Network Open Resource (https://signor.uniroma2.it/) is a manually curated database that captures, organizes and displays signaling information into binary causal relationships between biological entities.

Through the analysis of the molecular interactions whose disruption causes pathological phenotypes, bioinformatic resources such as MINT and SIGNOR 2.0 can be exploited to build interaction networks useful for gaining insights on disease molecular mechanisms and to predict novel and effective pharmacological strategies.