MINT, SIGNOR 2.0 and their ancillary databases, contextualization of molecular networks for human diseases.

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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.
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 (protein A up-regulates/down-regulates protein B etc.) between biological entities (proteins, chemicals, protein families, complexes, small molecules, phenotypes and stimuli).

SIGNOR 2.0 contains over 24,000 interactions between more than 6,300 biological entities and features tools such as the extraction of networks from a custom lists of entities, as well as access to a collection of pre-assembled signaling pathways. These relationships can be represented as a generic network by capturing observations made in different experimental contexts as such as disease onset. SIGNOR 2.0 also collects information on causal interactions between Human Coronavirus proteins (HCoV) and the human host involved in cellular pathways that are modulated by infection during HCoV infection. This information can be used to retrieve and organize logical models that allow users to infer the perturbations caused by viral infection on cellular networks and to predict the effect of molecules that are candidates for therapeutic treatments.

Through the analysis of the signaling events whose disruption causes pathological phenotypes, MINT, SIGNOR 2.0 and their ancillary databases (DISNOR, http://signor.uniroma2.it/disease_browser.php and CancerGeneNet, https://signor.uniroma2.it/CancerGeneNet/) can be utilised as a platform for precision medicine and their data can be exploited to build an a priori "disease logic model" useful for diseases analysis.

References and useful links

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