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In biology, networks play an important role in gene prioritization, an essential process for disease-gene discovery because of limited validation and characterization resources [82]. For example, network properties (e.g. hubbiness) have been used to distinguish functionally essential and loss-of-function tolerant genes [65]. One could also prioritize uncharacterized genes based on how they are connected to characterized ones. If a gene, say, is one step away from a group of genes associated with a particular disease, it is very likely that it too is associated with this disease. The influence of a node may not be restricted to its nearest neighbors; network flow algorithms are widely used to examine long-range influence [83][84]. For instance, in a social science context, researchers use cascade-structured models to capture the information propagation on blog networks, predicting a blog's popularity [85].

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Box 2. Network topology

· **Modularity** value to measure strength of network division. Apart from measuring degrees and paths, one can easily observe that social networks tend to have communities within them due to the relatively larger number of interactions between people in the same neighborhood, school, or work place. People within the same social group naturally form strong ties and, in the extreme, constitute a single cohesive group (or a fully connected graph, or clique). Analogous to these closely-knit social groups, a large number of biological components can form a single functional macromolecular complex such as the ribosome. More generally, a common feature of a large number of social, technological and biological networks is that they are composed of modules such that nodes within the same module have a larger number of connections to each other compared to nodes belonging to different modules. A quantity dubbed modularity attempts to measure this, comparing the number of intra and inter module links in a network [19].

· **Missing links** connections unobservable or missing. Another type of formalism making use of properties of nodes is link prediction. High-throughput experiments can be noisy, and the resultant networks may contain spurious links; missing data is also very common. Methods for link prediction and denoising are therefore useful. This can be done solely using network structure. For instance, in a protein-protein interaction network, defective cliques can be used to find missing interactions and determine the parts required to form a functional macromolecular complex [86]. Moving beyond network structure, whether two nodes are connected often depends on their intrinsic properties (e.g. their gene-expression level, conservation, and subcellular localization, etc.). A number of machine learning methods (e.g. collaborative filtering [87], maximum likelihood [88], and probabilistic relational models [89]) have been proposed to combine various node and edge features for link prediction [90]. One method that has not been used much in biological sciences is stochastic block models [91]. These have been popular in computational social science for link prediction [92]. They require comprehensive gold-standards for validation and may catch-on more in the biological sciences as these develop.

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