Cross disease network analysis

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Disease associated genes (DGs) tend to cluster in cellular networks, defining network modules. Likewise, diseases with shared phenotypes tend to have overlapped network modules and therefore, shared DGs. However, lists of DGs are still incomplete making DG prediction methods central in Network Medicine. We have recently published the S2B method that predicts shared DGs selecting genes frequently and specifically present in shortest paths between DGs of two related diseases (Garcia-Vaquero et al. 2018). Now, we will develop more flexible S2B variants, accounting for short paths that are not necessarily shortest paths. To boost the discovery of relevant molecular mechanisms, we will use multilayer networks combining various cellular networks (protein-protein, co-expression, signaling and transcriptional regulatory interactions). These new method variants will be tested with pairs of diseases with known DGs in common (or with directly interacting DGs) that sample the full spectrum of human diseases. The success of the developed methods will be assessed with performance measures computed through a cross-validation strategy.

Garcia-Vaquero, M.L. et al., 2018. Searching the overlap between network modules with specific betweeness (S2B) and its application to cross-disease analysis. *Scientific Reports*, 8(1), p.11555.