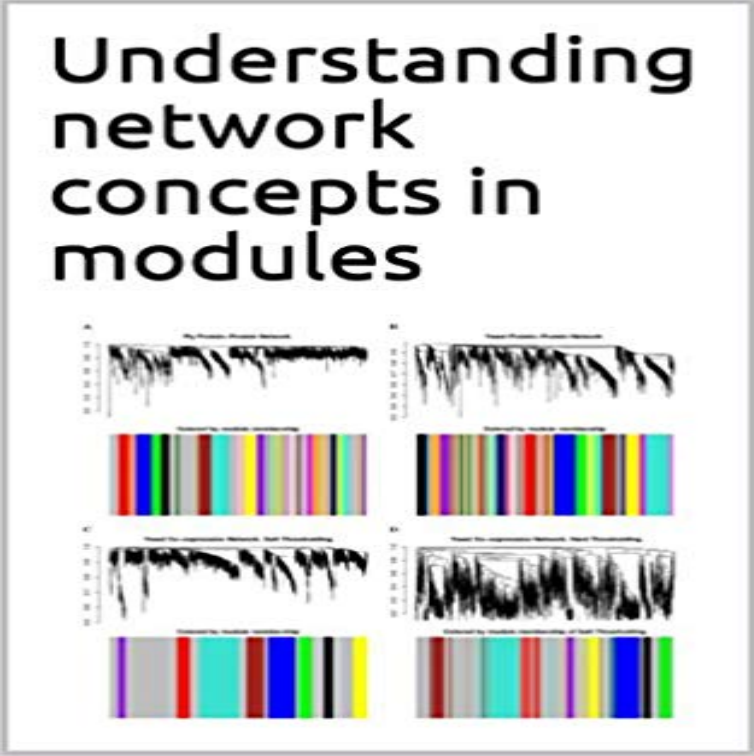


Understanding network concepts in modules



Background Network concepts are increasingly used in biology and genetics. For example, the clustering coefficient has been used to understand network architecture; the connectivity (also known as degree) has been used to screen for cancer targets; and the topological overlap matrix has been used to define modules and to annotate genes. Dozens of potentially useful network concepts are known from graph theory. Results Here we study network concepts in special types of networks, which we refer to as approximately factorizable networks. In these networks, the pairwise connection strength (adjacency) between 2 network nodes can be factored into node specific contributions, named node conformity. The node conformity turns out to be highly related to the connectivity. To provide a formalism for relating network concepts to each other, we define three types of network concepts: fundamental-, conformity-based-, and approximate conformity-based concepts. Fundamental concepts include the standard definitions of connectivity, density, centralization, heterogeneity, clustering coefficient, and topological overlap. The approximate conformity-based analogs of fundamental network concepts have several theoretical advantages. First, they allow one to derive simple relationships between seemingly disparate networks concepts. For example, we derive simple relationships between the clustering coefficient, the heterogeneity, the density, the centralization, and the topological overlap. The second advantage of approximate conformity-based network concepts is that they allow one to show that fundamental network concepts can be approximated by simple functions of the connectivity in module networks.

Conclusion Using protein-protein interaction, gene co-expression, and simulated data, we show that a) many networks comprised of module nodes are

approximately factorizable and b) in these types of networks, simple relationships exist between seemingly disparate network concepts. Our results are implemented in freely available R software code, which can be downloaded from the following webpage:

<http://www.genetics.ucla.edu/labs/horvath/ModuleConformity/ModuleNetworks>

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correlation network analysis (6.56) If NCF is a continuous function, then the fundamental network concept NCF(C)
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