

Abstract Submitted
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Network Approach to Disease Diagnosis¹ AMITABH SHARMA, AMIR BASHAN, ALBERT-LASZLO BARABASI, Channing Division Of Network Medicine, 181 Longwood, Harvard Medical School, Boston -02115 — Human diseases could be viewed as perturbations of the underlying biological system. A thorough understanding of the topological and dynamical properties of the biological system is crucial to explain the mechanisms of many complex diseases. Recently network-based approaches have provided a framework for integrating multi-dimensional biological data that results in a better understanding of the pathophysiological state of complex diseases. Here we provide a network-based framework to improve the diagnosis of complex diseases. This framework is based on the integration of transcriptomics and the interactome. We analyze the overlap between the differentially expressed (DE) genes and disease genes (DGs) based on their locations in the molecular interaction network ("interactome"). Disease genes and their protein products tend to be much more highly connected than random, hence defining a disease subgraph (called disease module) in the interactome. DE genes, even though different from the known set of DGs, may be significantly associated with the disease when considering their closeness to the disease module in the interactome. This new network approach holds the promise to improve the diagnosis of patients who cannot be diagnosed using conventional tools.

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