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Disease spread on networks: integrating structure and dynamics through a generalized inverse.

A fundamental issue for understanding disease dynamics on networks is how network structure and node characteristics combine to influence disease spread. I will discuss a generalized inverse, called the absorption inverse, that arises naturally in this context. The absorption inverse is connected to transient random walks on the graph, and can be used to derive a distance metric, centrality measures, and community detection algorithms that integrate both structure and dynamics. I will describe some of these measures, together with implications for disease dynamics. This is joint work with Karly Jacobsen. (Received February 04, 2017)