

Abstract Submitted
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Viral Disease Networks? NATALI GULBAHCE, Northeastern University and Dana Farber Cancer Institute, Harvard Medical School, HAN YAN, MARC VIDAL, Dana Farber Cancer Institute, Harvard Medical School, ALBERT-LASZLO BARABASI, Northeastern University and Dana Farber Cancer Institute, Harvard Medical School — Viral infections induce multiple perturbations that spread along the links of the biological networks of the host cells. Understanding the impact of these cascading perturbations requires an exhaustive knowledge of the cellular machinery as well as a systems biology approach that reveals how individual components of the cellular system function together. Here we describe an integrative method that provides a new approach to studying virus-human interactions and its correlations with diseases. Our method involves the combined utilization of protein - protein interactions, protein – DNA interactions, metabolomics and gene - disease associations to build a “viraldiseasome”. By solely using high-throughput data, we map well-known viral associated diseases and predict new candidate viral diseases. We use microarray data of virus-infected tissues and patient medical history data to further test the implications of the viral diseasome. We apply this method to Epstein-Barr virus and Human Papillomavirus and shed light into molecular development of viral diseases and disease pathways.

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