The Gerstein Lab has extensive experience in biological network science and has developed a network analysis platform. This platform encompasses tools to determine small-scale network motifs such as feed-forward loops and feedback loops as well as large-scale structures such as overall network hierarchies, center points of networks, bottlenecks of networks, and so forth. These have been published in numerous analyses including identifying enriched network motifs with Loregic1, cross-species network clustering with OrthoClust2, and calculating the impact of conserved or species specific regulatory networks on gene expression with DREISS3. Additional network analysis methods have formulated in a web-accessible network toolkit called TYNA4.

This platform has been used to analyze the human regulatory network, the network associated with cancer, the phosphorylation network in yeast, the yeast regulatory network, and other model organism networks5. We have performed extensive comparisons between these regulatory networks and also compared regulatory networks with networks in other contexts such as governmental hierarchies, assembly line control flows, and the call graph structure of the Linux operating system6. We have published many comparative network papers including a review exploring comparing networks across disciplines7. Such an approach enables the transfer of mathematical formalisms from disparate disciplines to help better describe and understand complex biological networks. We also have an extensive toolkit for mining literature networks in the biological sciences, looking at the patterns and the dynamics of the development of these networks, and how they are mediated by certain key individuals. We have published a number of papers on the analysis of literature in social networks and sciences8,9.

The Gerstein lab has previous experience in mining the yeast regulatory network10,11, finding the occurrence of various motifs used by the phosphorylation network and the transcriptional regulatory network.

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