The Gerstein lab has created multiple methods for the construction and analysis of biological regulatory networks and has been active in cross-disciplinary network science comparisons. Network science is currently a very popular field, with many new institutes being established to study it and many journals and conferences devoted to it. Network science aims to reveal key unifying principles that govern network behavior across many disciplines, which include molecular networks, neural networks, social networks, electrical networks, and so forth. Biological networks, or networks of biological molecules, emerge as unique because unlike many other networks, such as social networks, they are easily subject to high-throughput experimental observation, and only recently manipulated via precise genome and biomolecular engineering.

The Gerstein lab has developed a network analysis platform to determine small-scale network motifs (*e.g.,* feed-forward and feedback loops) and large-scale structures (*e.g.,* overall network hierarchies, center points of networks, bottlenecks)1-4. Previously we have performed comparisons between biological regulatory networks and also compared regulatory networks with networks in other contexts including governmental hierarchies, assembly line control flows, and the call graph structure of the Linux operating system5. Such a comparative and cross-disciplinary approach enables the transfer of mathematical formalisms from disparate disciplines to help better describe and understand complex biological networks6.

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