2018 Research Interest/Project Ideas

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Dynamic Processes, Evolutionary Trajectories, and Control of Complex Systems

An important class of complex systems can be modeled as a set of one or more dynamic (time-evolving) interacting entities. Examples of such systems include infection and disease networks, IoTs, supply chains and manufacturing processes, and social networks. Owing to their scale, scope, and complexity, it is often infeasible to sample the complete dynamic state of these systems in real time. Sampled system state is typically available in the form of snapshots in time, either of all entities in the system, or a subset thereof. Additional modeling complexities arise when the same set of entities manifest distinct interactions, corresponding to different modalities. For instance, in an IoT network, a set of entities may be linked through communication channels (the communication network), control-actuation links, the proximity network (entities that sense identical phenomena), and other context-specific networks. Each of these networks may themselves be sampled at widely varying spatio-temporal rates. In such a modeling framework, there are important questions relating to structure, function, evolution, and control of underlying processes: (i) from sparsely sampled interactions, can we infer underlying *dynamic processes* governing network evolution. More specifically, can we infer unsampled *spatio-temporal* regions of the network, arrival and departure sequences, and network features such as modularity and clustering coefficient; (ii) with an understanding of the *dynamic processes*, can we derive *control strategies* that optimize given objectives. For instance, in a social network, can we maximize both quality and quantity of information flow (for some defined measure of information quality); (iii) can we predict long term evolution (forward evolution) of the network state; i.e., tracking the inferred dynamic process in time to understand network trajectories. Some of these problems have been studied in literature, using largely ad-hoc models and methods, with limited empirical evidence of success. We propose the first comprehensive formal modeling and study of these problems, with a view to characterizing the inherent complexity of the problems, bounds on inference, methods that achieve these bounds, software implementations of methods at scale, and validation on applications of broad interest.

Our approach is rooted in the principles underlying the Science of Information, developed as part of our NSF funded Science and Technology Center on Science of Information. We exemplify our approach using our recent result on the inference of the arrival order of nodes in a dynamic network from a single observed snapshot. This problem arises in applications ranging from reverse engineering complex systems to understanding time evolution (e.g., social networks (where arrival orders may be anonymized), biomolecular networks (were arrival orders are unknown), or infection networks (where order of infection is only weakly known from timetags on phenotype). Even this simple instance of our proposed problem is profoundly important -- in social networks, using arrival orders, one can map the spread of information, and use it to design personalized channels by prioritizing information of shared interest. In networks of biochemical interactions (e.g., protein interaction networks), one can identify early biomolecules (e.g., proteins in prokaryotic species), which are known to be preferentially implicated in cancers and other diseases. In infection networks the arrival order allows one to identify early patients, yielding clues

to genetic origin, evolution, and mechanisms of transmission. In battlefield systems, arrival orders often reveal chains of command and control -- the earliest strategic decisions are typically made at highest levels of command and control.