

Computational Methods for Understanding Social Interactions in Animal Populations

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Population biology is at the threshold of a new era. Recent breakthroughs in data collection technology enable deployment of sensing devices to automatically track the locations of individual animals via GPS. These technologies will supply data about animal populations that are orders of magnitude richer than any previously collected. Such data offer the promise of answering some of the big ecological questions about animal populations: Which individuals are leaders and to what degree do these leaders control the behavior of others? How do social groups change when individuals join or leave the population or with external events such as the presence of a predator? To what degree can we predict future social interactions based on past information?

Unfortunately, in this domain, our ability to analyze data lags substantially behind our ability to collect it. In particular, most previous approaches to analyzing social data are essentially static in that the interactions are aggregated over time and all information about the time and ordering of social interactions is discarded. These static approaches have two serious weaknesses. First, they can give inaccurate or inexact information about patterns in the data. Second, they can prevent us from even being able to ask fundamental questions about the causes or consequences of social interactions.

The goal of the proposed research is to create analytical and computational tools that explicitly address the time and order of social interactions between individuals. The proposed approach will be to combine ideas from social network analysis, Internet computing, distributed computing, and machine learning to solve problems in population biology. The diverse computational tasks of this project include design of algorithmic techniques to identify social entities such as a communities, leaders, and followers, and to use these structures to predict social response patterns to danger or disturbances. Nowhere is the impact of social structure likely to be greater than when species come in contact with predators. Thus, the accuracy and predictive power of the proposed computational tools will be tested by characterizing the social structure of horses and zebras (equids) both before and after human-or predator-induced perturbations to the social network.

The proposed interdisciplinary research will have broader impacts on diverse research communities. New methods for analysis of social interactions in animal populations will be useful for behavioral biologists in such diverse fields as behavioral ecology, animal husbandry, conservation biology, and disease ecology. The machine learning algorithms we will develop are relevant to many studies in which researchers need to classify temporal interaction data. The proposed network methods have broader relevance to human societies: disease transmission, dissemination of ideas, and social response to crises are all dynamic processes occurring via social networks. Further, through teaching and participation in outreach, students and school teachers will gain access to opportunities for hands-on, interdisciplinary experiences in a new area of computational biology. The research and software resulting from the proposed project will be disseminated both in computational and biological communities and enhanced by cross-disciplinary training activities and will serve to train a new generation of interdisciplinary scientists.