# Introduction to the Special Section

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Network Science arises naturally in social sciences, biology, neuroscience, and many other disciplines. In the past decade, network analysis has been an active research area in statistics, applied mathematics, computer science, physics and information theory. The main purpose of this special issue is to introduce some recent advances of network research in our field to help students and researchers who are new to this area.

Advances in statistical network analysis could be broadly divided into the following four categories: modeling, inference, computation and applications. Each of the six papers of this special issue covers at least one aspects of those categories.

Crane and Dempsey introduce a general framework for network modeling. It encompasses classical network models, such as stochastic blockmodels, exponential random graph models and graphon models, and some more recently proposed classes of models including vertex exchangeable models, relatively exchangeable models, edge exchangeable models and relationally exchangeable models. Hoff extends the stochastic blockmodel and the latent space model to a general regression framework that combines both additive and multiplicative effects, and accommodates continuous, binary and ordinal network model relations.

Gao and Ma review recent results on information-theoretic limits in statistical inference including graphon estimation, community detection and hypothesis testing for stochastic blockmodels. Algorithms to obtain the optimal rates are discussed.

The likelihood function for community detection for (degree corrected) stochastic blockmodels is nonconvex. Li, Chen and Xu review convex relaxation methods for community detection, and discuss techniques based on the primal and dual analysis to obtain weak and strong consistencies. Spectral method is one of the most popular convex relation methods. Athreya, Tang, Park and Priebe define the latent structure model which includes stochastic block models and random dot product graphs, and consider spectral estimates of latent positions.

Complementing the applications in social networks, Wang, Li, Li and Huang introduce two challenging and fruitful applications of network analysis in biology: gene network and brain networks. Novel modeling, inference and computation are needed to construct (dynamic) networks and to extract biological knowledge.

We want to thank the authors for their expertise and contributions to make this special issue possible. We hope this special issue would have an impact on introducing network research to a broader audience of statisticians.