

Workshop Tutorial: Likelihood-based Network Comparison Using Permutation Models*

Carter T. Butts
Department of Sociology and Institute for Mathematical Behavioral Sciences
University of California, Irvine
Irvine, CA 92697
buttsc@uci.edu

ABSTRACT

A common problem in sociology, psychology, biology, geography, and management science is the comparison of dyadic relational structures (i.e., graphs). Where these structures are formed on a common set of elements, a natural question which arises is whether there is a tendency for elements which are strongly connected in one set of structures to be more – or less – strongly connected within another set. We may ask, for instance, whether there is a correspondence between golf games and business deals, trade and warfare, or spatial proximity and genetic similarity. In each case, the data for such comparisons may be continuous or discrete, and multiple relations may be involved simultaneously (e.g., when comparing multiple measures of international trade volume with multiple types of political interactions).

This session will present an exponential family of permutation models that is suitable for inferring the direction and strength of association among dyadic relational structures. A linear-time algorithm is shown for MCMC simulation of model draws, as is the use of simulated draws for maximum likelihood estimation (MCMC-MLE) and/or estimation of Monte Carlo standard errors. An easily performed maximum pseudo-likelihood estimation procedure is also demonstrated for the permutation model family, which provides a reasonable means of generating seed models for the MCMC-MLE procedure. Use of the modeling framework is illustrated via several applications, including relationships among managers in a high-tech firm, Cholera deaths in London neighborhoods, and intertemporal relations among workers in a Zambian tailor shop.

Keywords

graph comparison, discrete exponential families, permutation models, Markov chain Monte Carlo

*This work was supported in part by NIH award 5 R01 DA012831-05 and NSF ITR award IIS-0331707.