# Appendix: Goodness of fit

The stochastic actor-oriented model (SAOM) is part of the family of inferential network models (Hunter, Handcock, Butts, Goodreau, and Morris 2008; Minhas, Hoff, and Ward 2019), which require unique approaches to assessing goodness of fit (GoF). Standard fit statistics, such as R^2, are not available. Instead, analysts typically assess fit by simulating network (co)evolution an arbitrary number of times, and then comparing high-level features of the simulated networks to the same features of real-world observed networks (Hunter, Goodreau, and Handcock 2008). The specific network statistics used to capture these high-level features should not actually be included as terms in the network model; rather, they should be viewed as emergent properties of the network. GoF is then a matter of determining how well the specified model generates simulated networks that share important emergent features with the observed networks (Lospinoso and Snijders 2019).
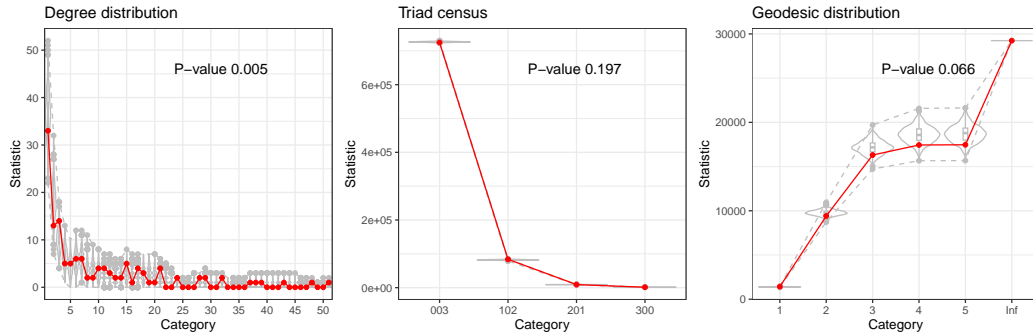
(a) BITs Network
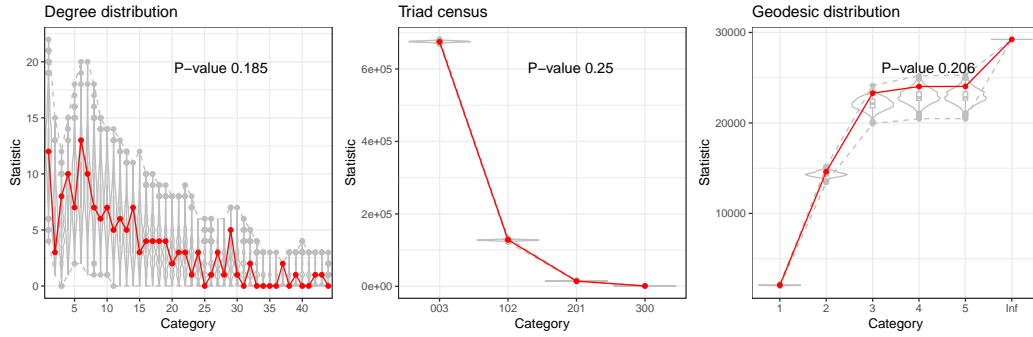
(b) DCAs Network

Figure 1: SAOM Goodness of Fit

Figure 1 illustrates GoF statistics for the BIT and DCA networks. Note that the

listed p-values test the null hypothesis that the observed and simulated networks do not significantly differ. An insignificant p-value (e.g., larger than 0.05) thus indicates a strong fit. P-values in the $0.01 - 0.05$ range are generally acceptable, while p-values less than 0.01, and especially less than 0.001, may require reconsideration of the model.

The figure illustrate fits with regard to three statistics: (1) degree distribution is the overall distribution of nodal degrees in the specified network; (2) the triad census is the overall distribution of four types of undirected triads; and (3) the geodesic distribution is the distribution of minimum path lengths across the network. These are the most commonly used GoF statistics when assessing SAOM fit (Lospinoso and Snijders 2019), and they are also the default statistics in the `RSiena` package (Ripley, Snijders, and Preciado 2012).

Although obtaining good fits with coevolving networks is often very difficult, the fits here are generally quite strong. The only p-value that falls below the 0.05 threshold is the degree distribution for DCAs. Closer inspection reveals that this weaker fit is the result of isolates in the DCA network. If we add a term to the model that controls for the presence of isolates, the fit improves to > 0.2 without significantly affecting any of the other estimates of interest. Given the challenges of fitting coevolution models, the strong fits are reassuring.

References

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