Pilot study: Network structure and TB transmission

We will generate scale-free networks according to the parameters listed in Table 1 using the Sah et al. (2014) algorithm:

Table 1: Design of pilot study I for generating networks.

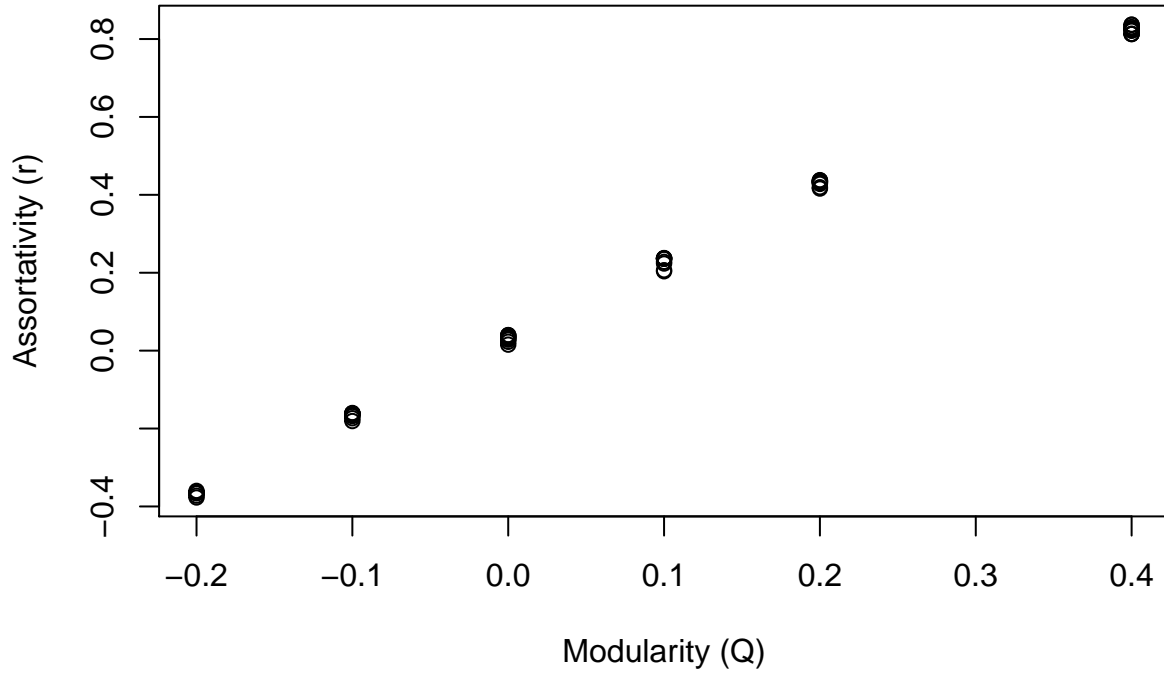| Variable	Value
Modularity, Q	- 0.2, -0.1, 0, 0.1, 0.2, 0.4
Degree distribution, $p(k)$	$\frac{k^{-\alpha}}{\zeta(\alpha)}$
Mean degree, $< k >$	10
Network size, N	$2 \cdot 10^3$

Network structure

Figure 1: Comparison between measures of community structure from Newman 2003 and Sah 2014.
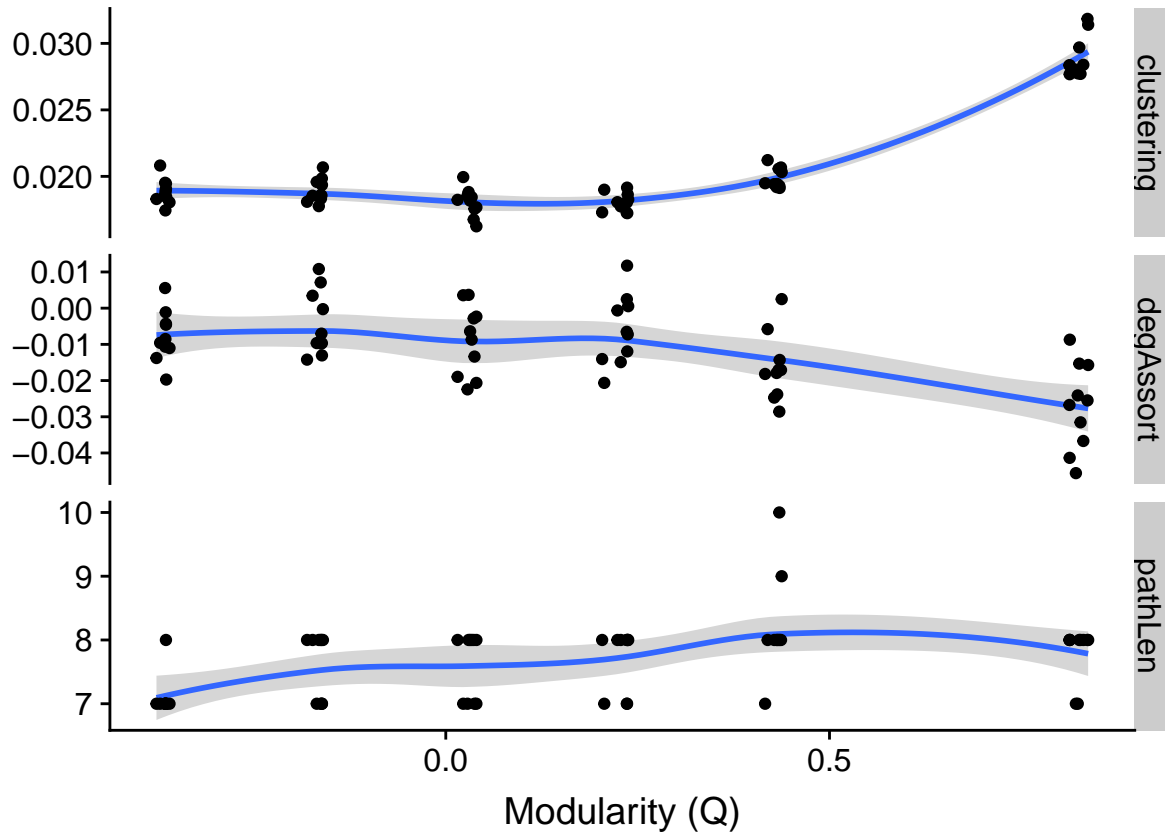

Figure 2: Values of clustering, degree assortativity, and path length with varying modularity for networks generated using rewiring algorithm.
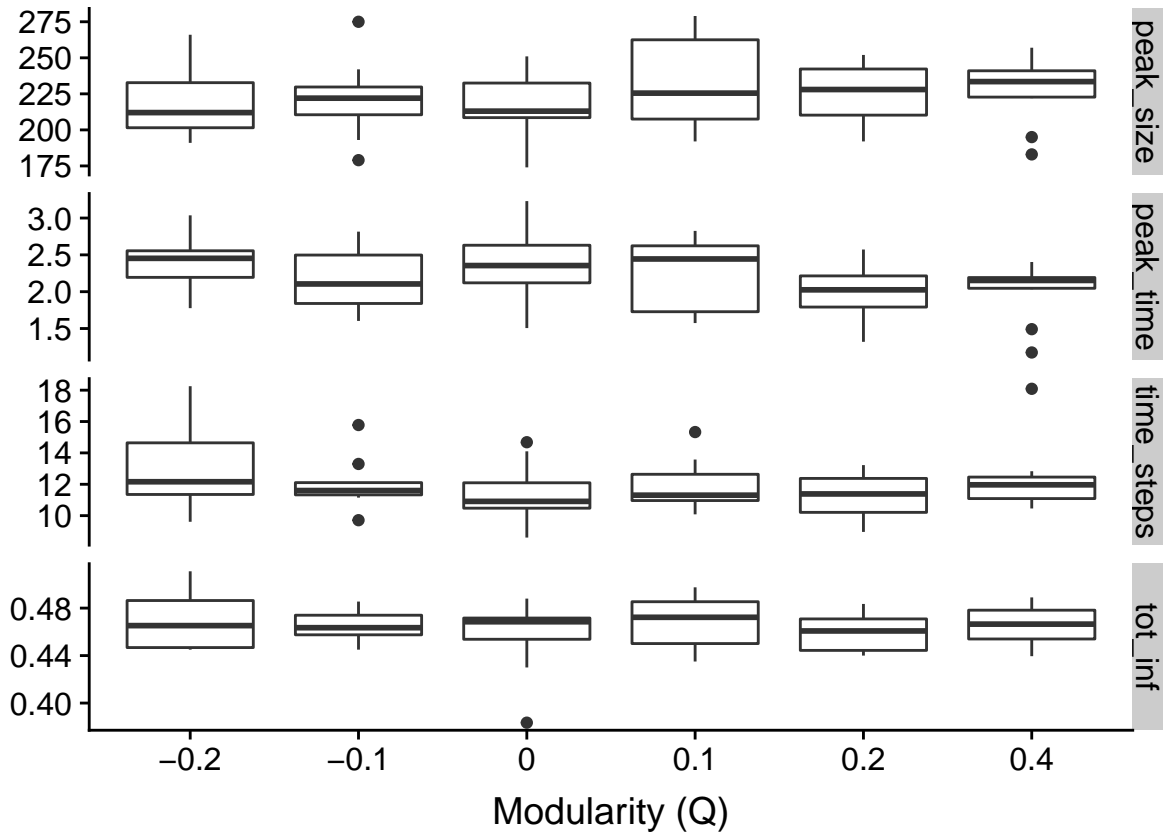
Disease spread

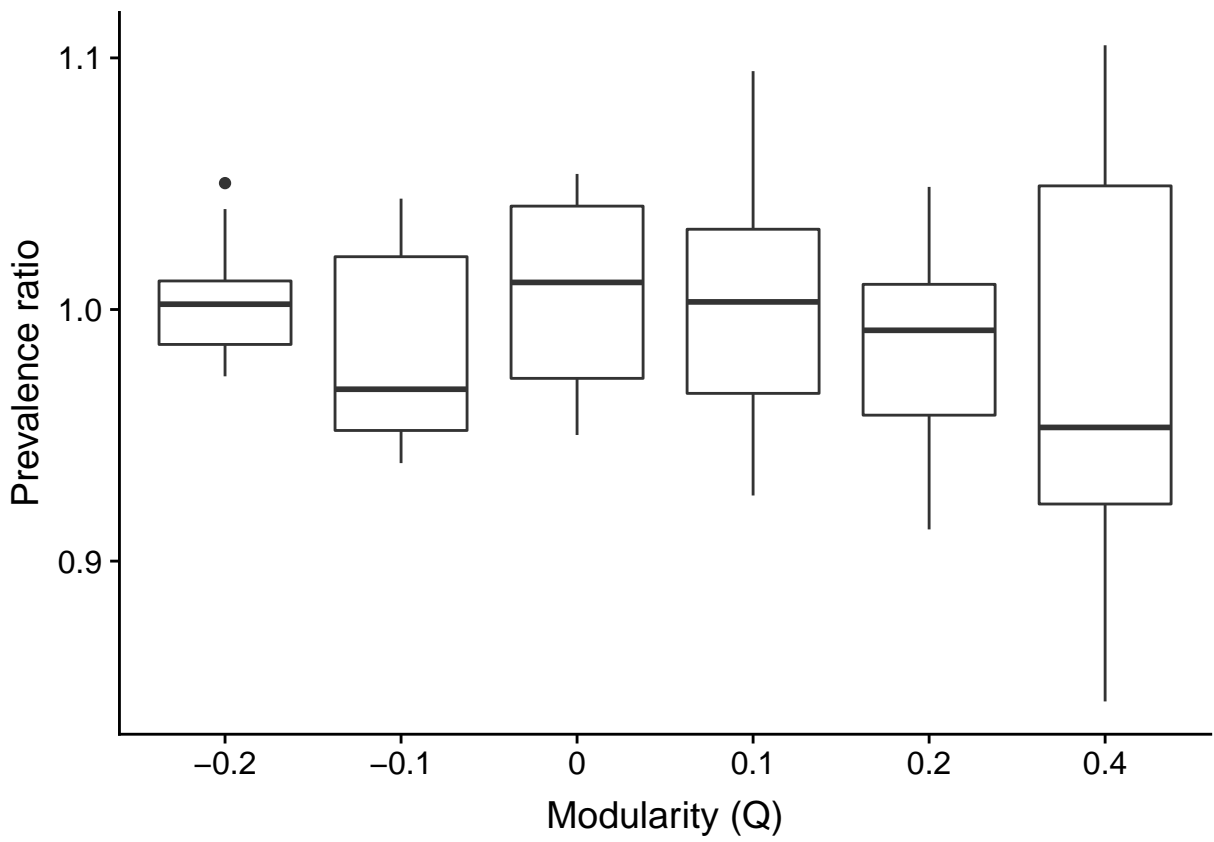Figure 3: Epidemic parameters across modularity values.

Figure 4: Ratio of cases in module 1 to module 2 across modularity values.

Notes

- Generated using Sah algorithm
- Pilot study shows results for 10 network replicates
- One epidemic simulated per network