Network sensitivity analysis for TB-assortativity

How does the way we generate assorted networks affect results?
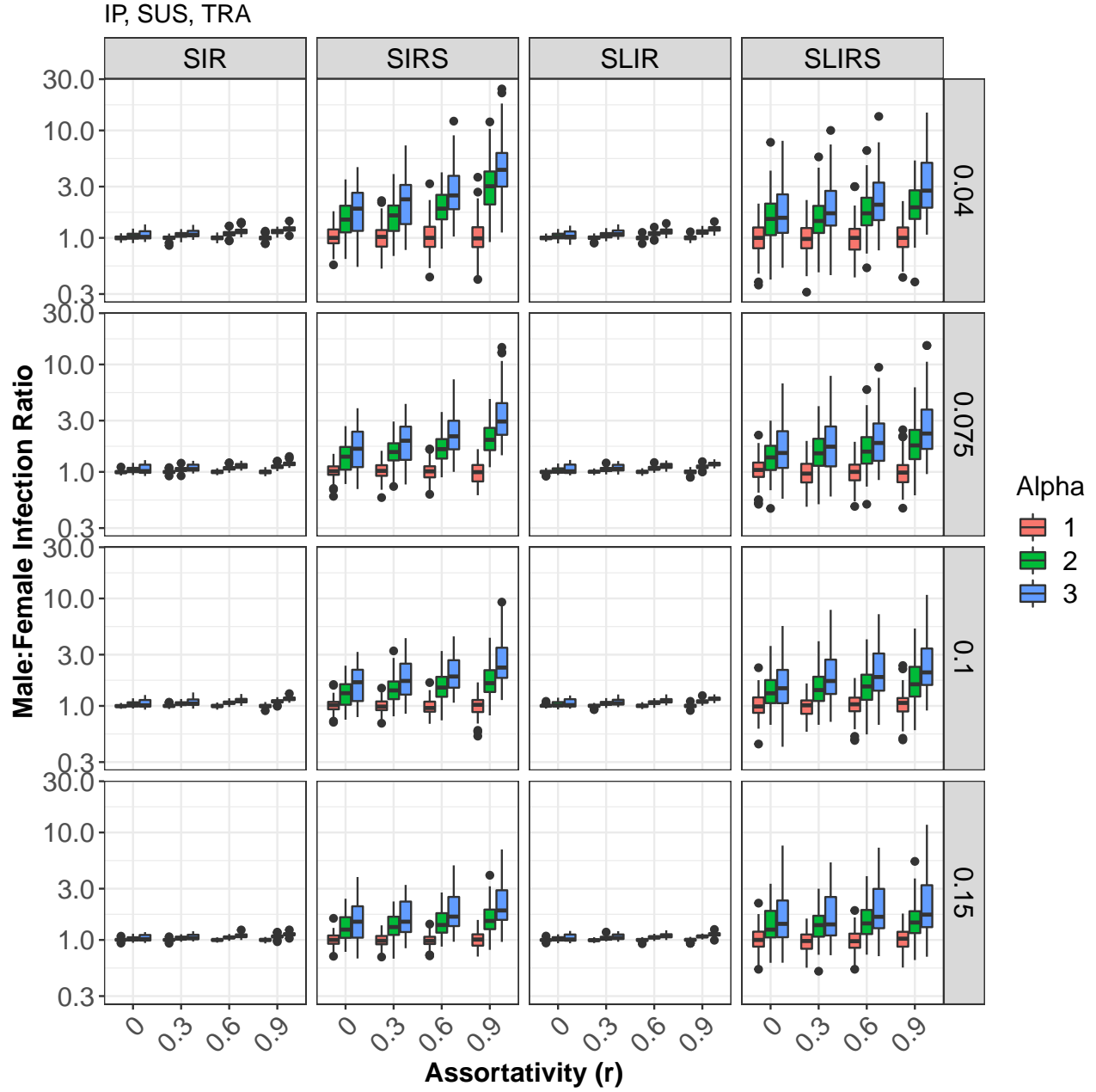
Figure 1: The effects of sex-traits and assortativity on male-bias in simulations on Sah-networks. Faceted by transmission rate. Results shown for combined sex-traits (IP, SUS, TRA)
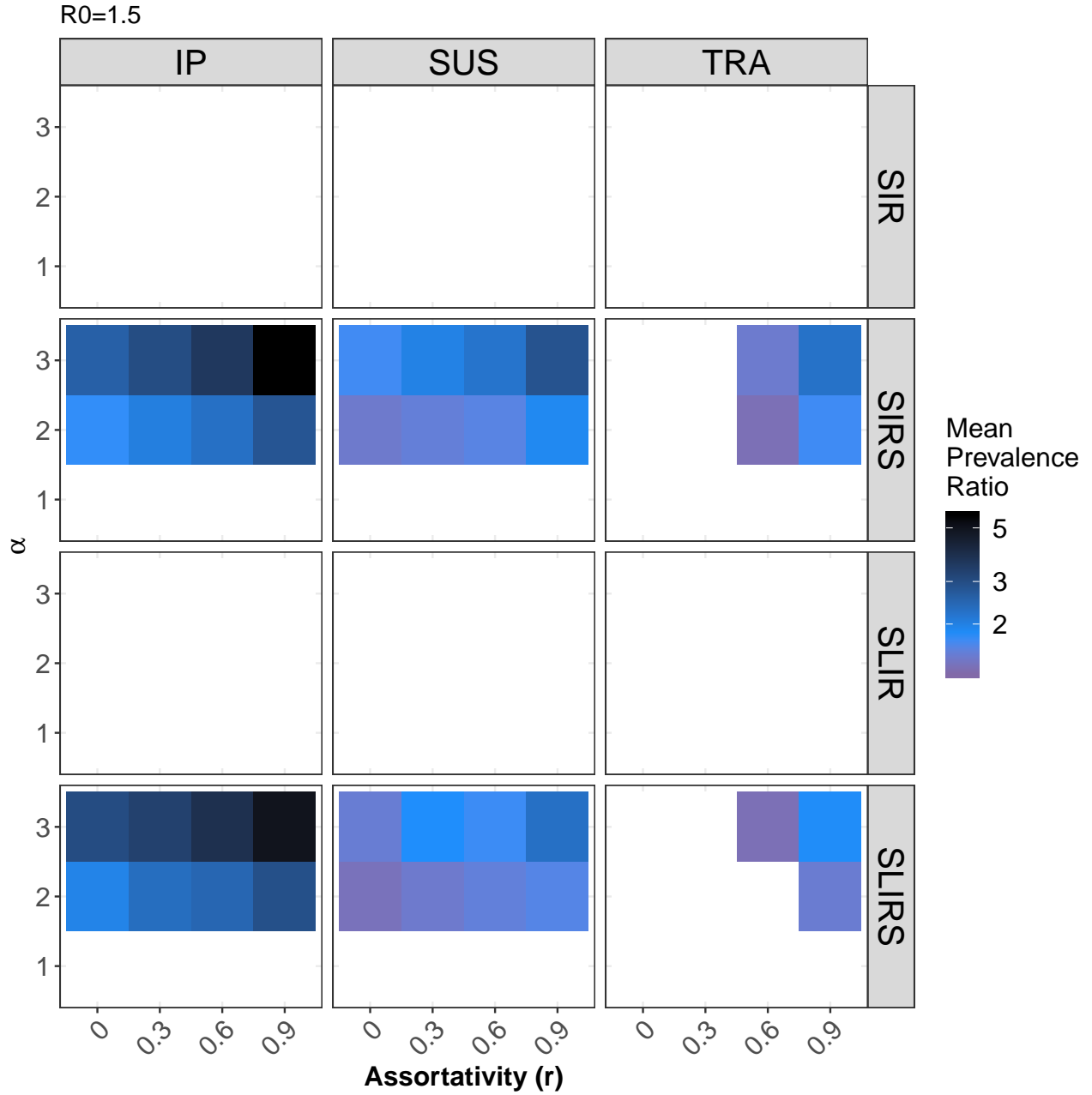
Figure 2: The effects of sex-traits and assortativity on male-bias in simulations on Sah-networks. Results shown for low transmissability pathogen. Only ratios above 1.25 are shown to visualize which parameter combinations can lead to male-bias.
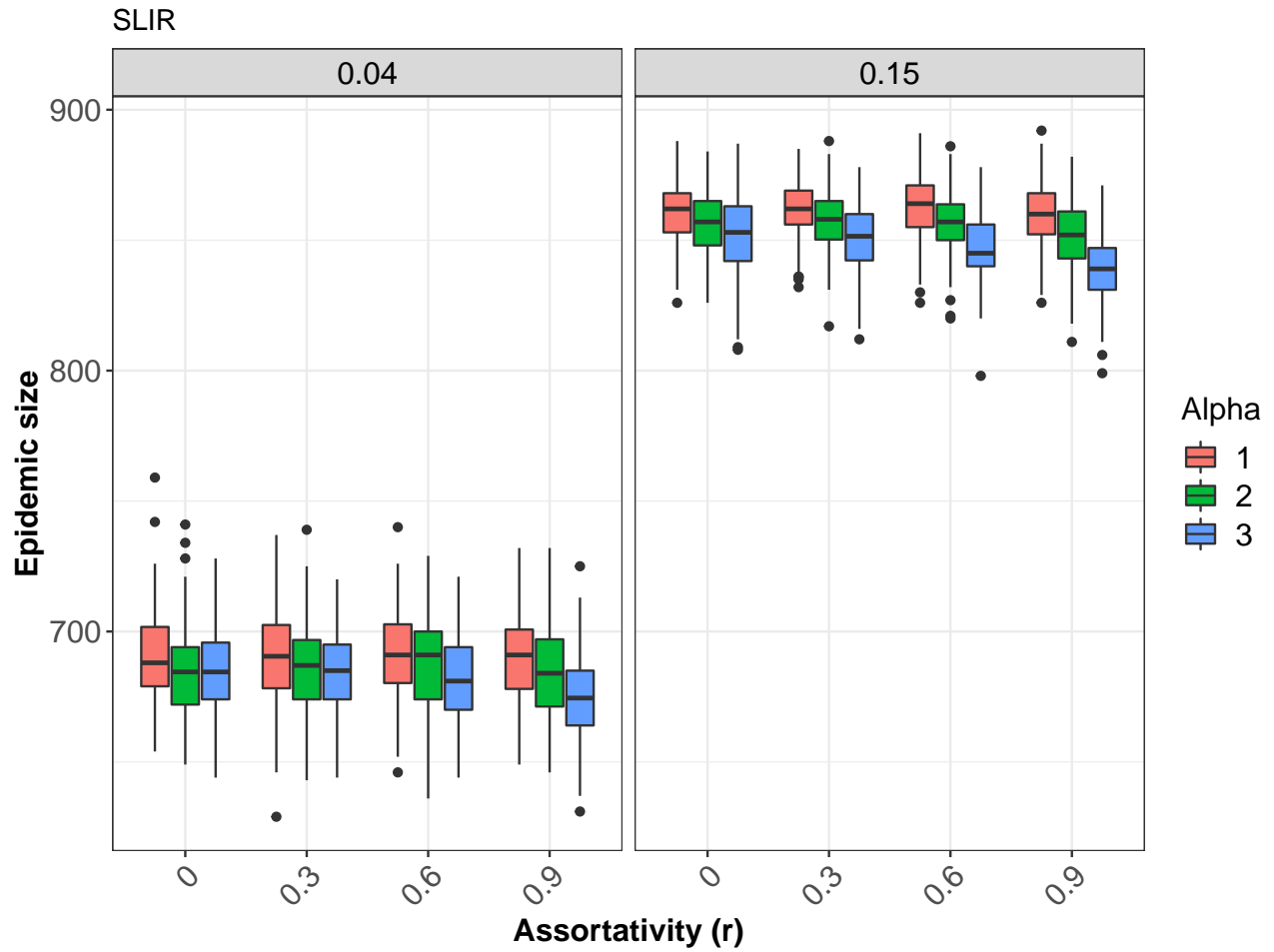
Figure 3: Epidemic size in SLIR model simulations on Sah networks across assortativity values. Faceted by transmission rate. Colors show sex-trait ratios.
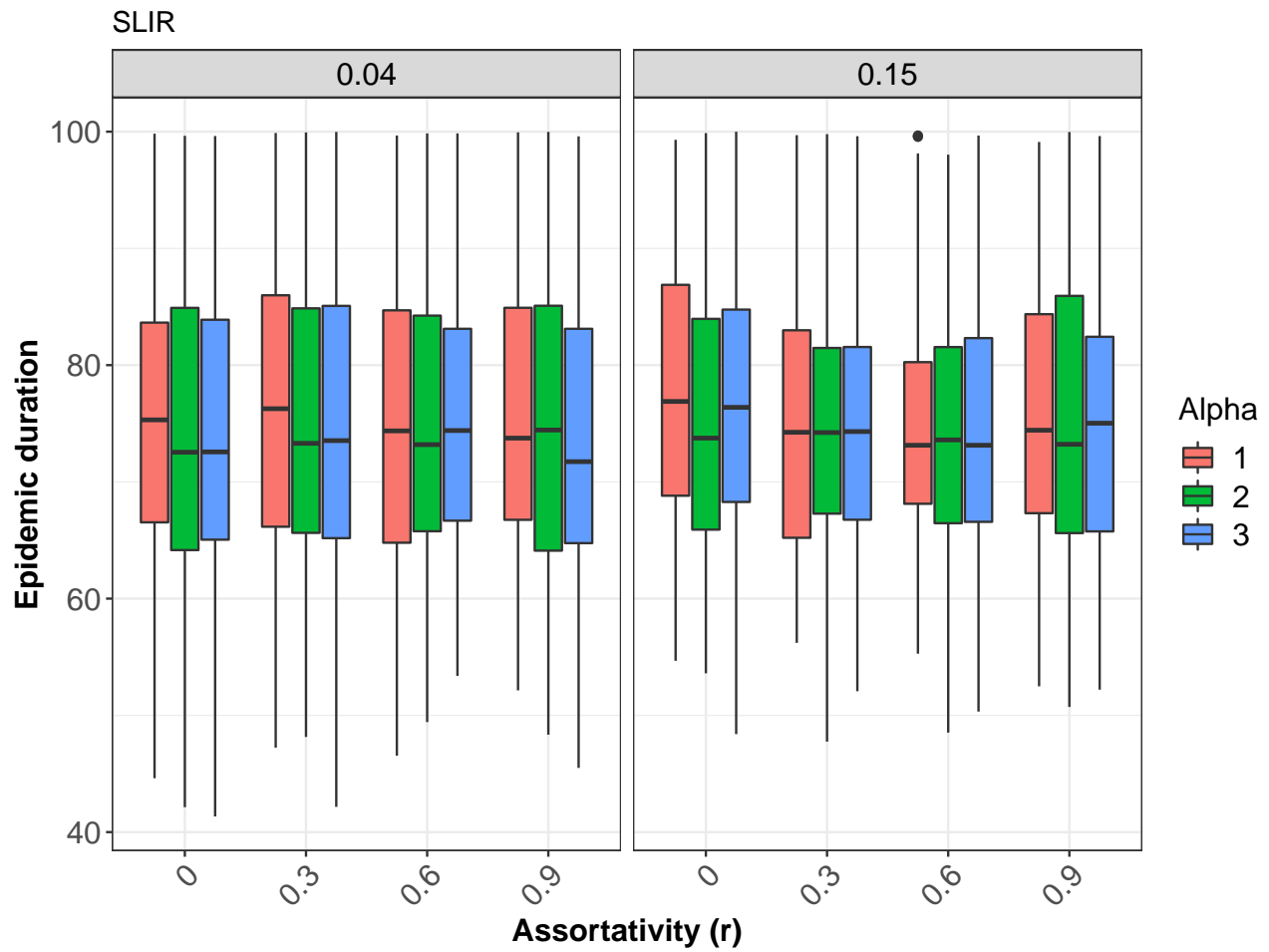
Figure 4: Epidemic duration in SLIR model simulations on Sah networks across assortativity values. Faceted by transmission rate. Colors show sex-trait ratios.
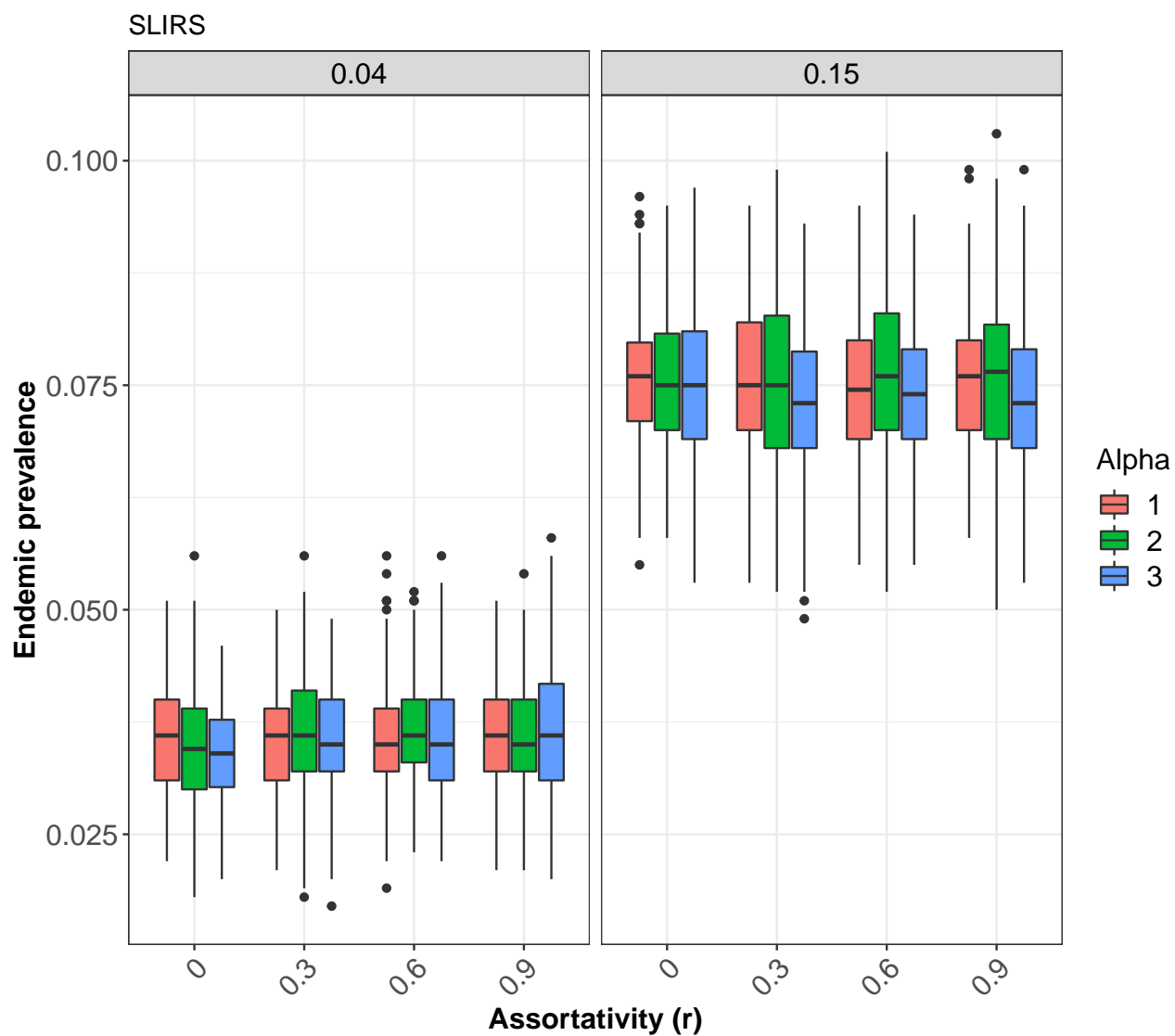
Figure 5: Endemic prevalence in SLIRS model simulations on Sah networks across assortativity values. Faceted by transmission rate. Colors show sex-trait ratios.
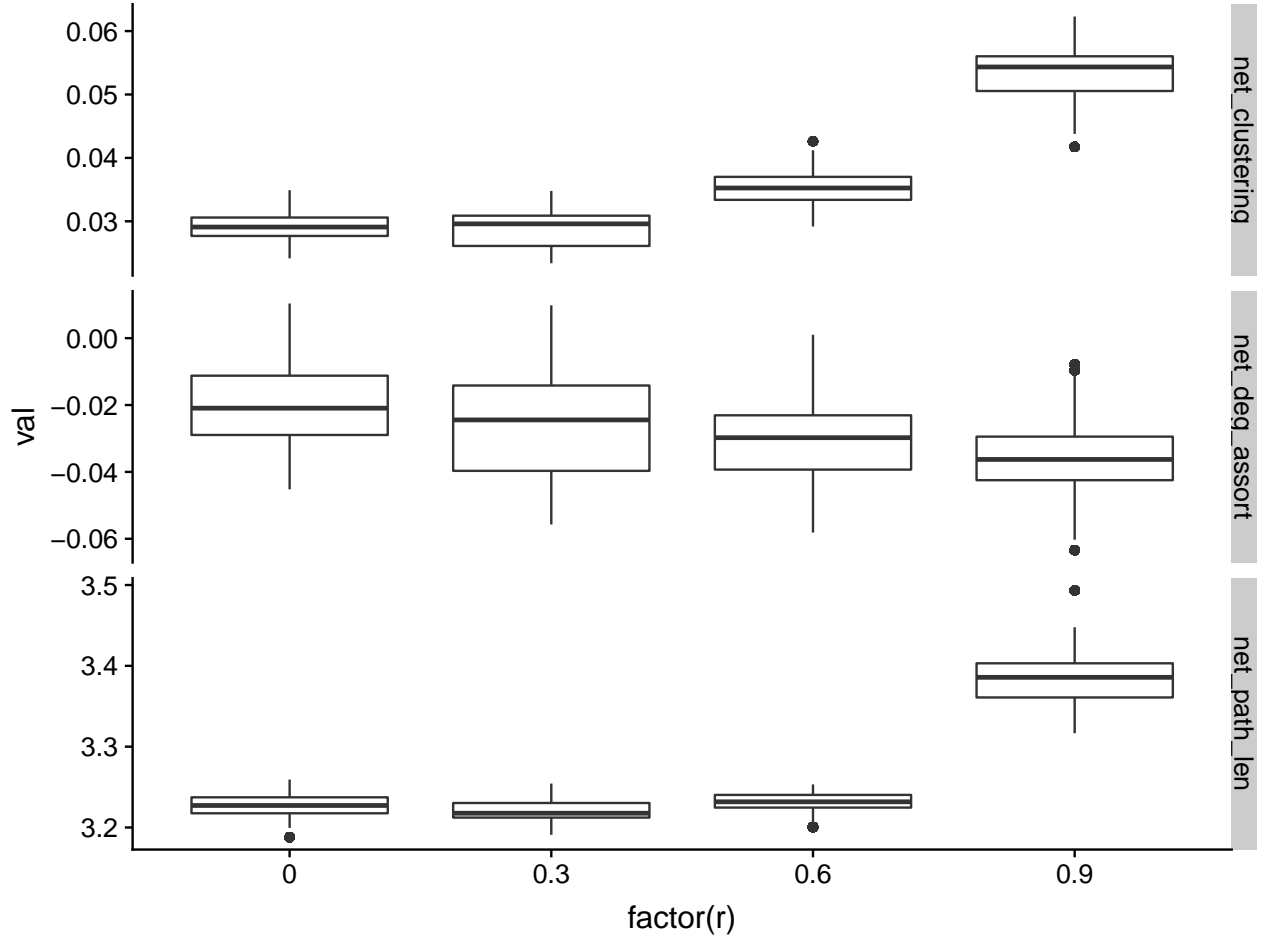
Figure 6: The effects of assortativity on network structural characteristics in Sah networks.

Sensitivity analyses

- Preliminary results for 50 replicates on networks generated with Sah algorithm (r=0, .3, .6, .9)

- One epidemic simulated per network

- Simulations stopped after 150 time steps, need to increase reps & length of simulation

- Results largely similar to re-wiring. Assortativity doesn't inrease male-bias alone. Sex-traits, especially longer male infecitous period, are likely the culprit. Any differences found in outbreak size are likely due to changes in network statistics, including changing clustering, degree assortativity, and network path length rather than assortativity.
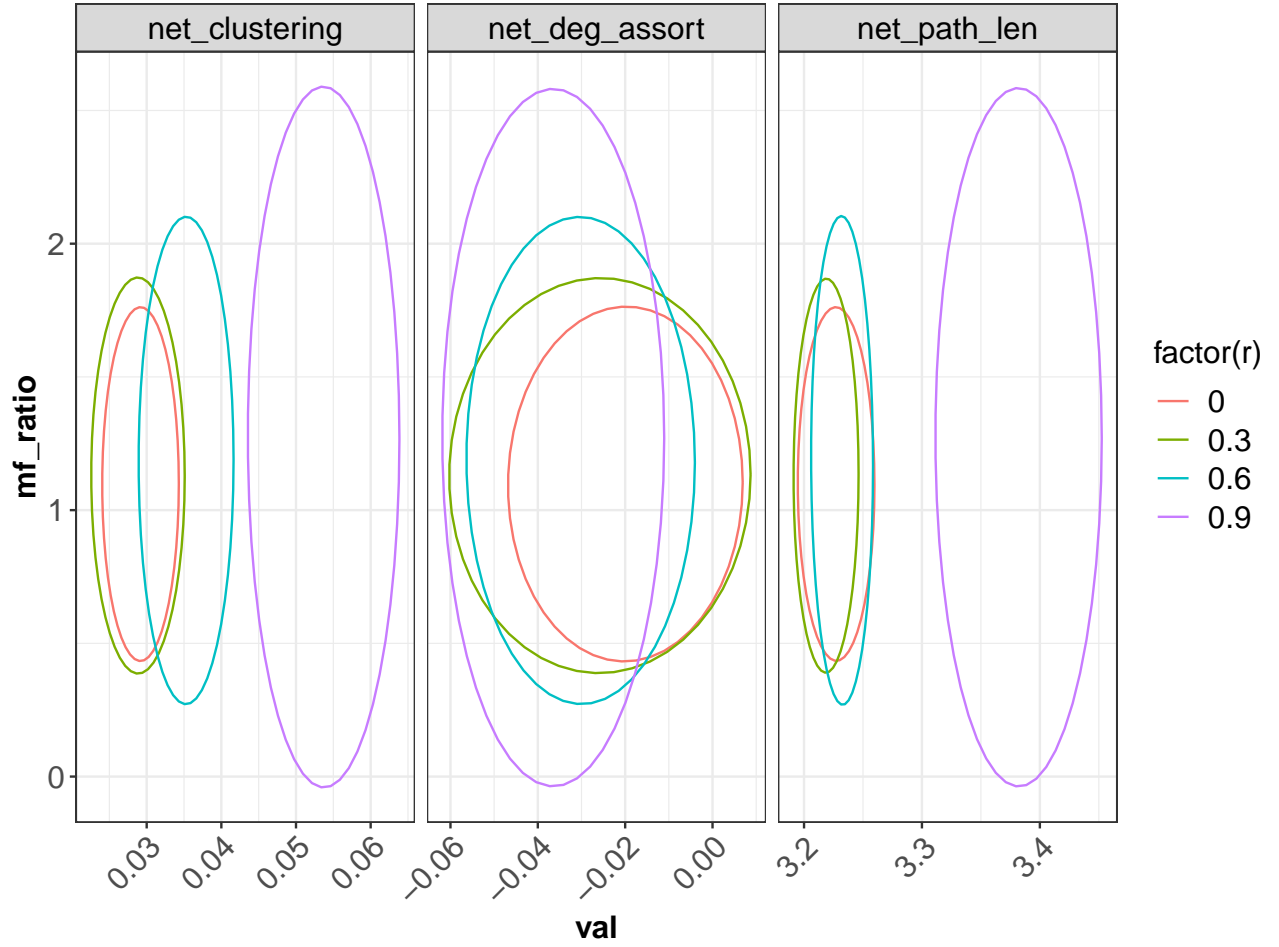
Figure 7: The relationship between network structural characteristics and male-bias. Results shown for all model types (SIR, SLIR, SIRS, SLIRS) and sex-traits.