

The effects of mixing patterns and sex-traits on transmission and male-bias of TB

Can assortativity drive male bias or are sex-trait differences required to explain male-bias?

Preliminary results for simulations of pathogen spreading on contact networks with varying levels of assortativity ($r = 0, 0.3, 0.6, 0.9$) and sex-trait ratios (α). Sex-traits were susceptibility (SUS), infectious period (IP), and transmissibility (TRA).

Rates of susceptibility for nodes (SUS) was modeled as

Source -> Target	Overall transmission rate, β
F->F	$\frac{2\tau}{(\alpha+1)}$
M->M	$\frac{2\tau\alpha}{(\alpha+1)}$
M->F	$\frac{2\tau}{(\alpha+1)}$
F->M	$\frac{2\tau\alpha}{(\alpha+1)}$

Rates of transmissibility (TRA) for nodes was modeled as

Source -> Target	Overall transmission rate, β
F->F	$\frac{2\tau}{(\alpha+1)}$
M->M	$\frac{2\tau\alpha}{(\alpha+1)}$
M->F	$\frac{2\tau\alpha}{(\alpha+1)}$
F->M	$\frac{2\tau}{(\alpha+1)}$

Infectious period (INF) for nodes modeled as

Source	Overall transmission rate, β
F	$\frac{\gamma(\alpha+1)}{2}$
M	$\frac{\gamma(\alpha+1)}{2\alpha}$

Each sex-trait was modeled separately.

Sensitivity parameters tested:

1. transmission rate ($\tau = 0.04, 0.075, 0.1, R_0 = 1.5, 2.5, 3.5$)
2. model type (SIR, SLIR, SIRS, SLIRS). SIRS and SLIRS models ran for 200 time units.

Response variables:

1. Male-bias: calculated differently for SIR/SLIR and SIRS/SLIRS. For models without recovery: number of male recovered nodes at end of simulation divided by number of female recovered nodes at end of simulation. For models with recovery: average ratio of male cases to female cases in last 100 time units for each simulation.
2. Epidemic duration: calculated for SIR/SLIR models as the number of time units before infectious population reached 0.
3. Total number infected: calculated for SIR/SLIR models as the total number of individuals that became infected before infectious population reached 0.

4. Endemic equilibrium: calculated for SIRS/SLIRS models as the average size of the infected population in the last 100 time units.
5. Prevalence of latent infection: calculated for SLIRS model as the average size of the latent population in the last 100 time units.

Notes

- Began with scale-free (300) and small-world networks (300) then re-wired
- Results for 100 network replicates shown
- One epidemic simulated per network

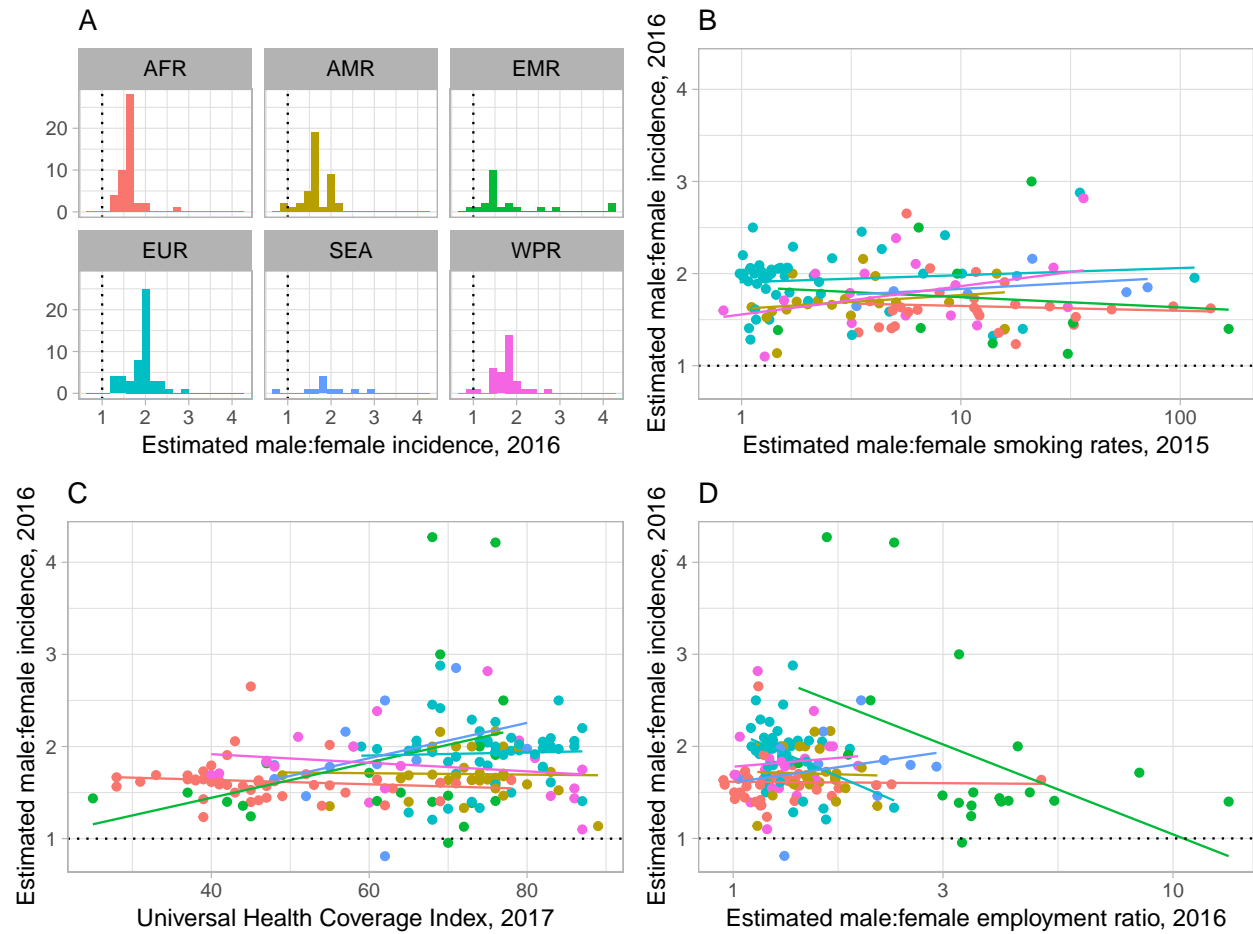


Figure 1: Across the world, more cases of TB occur among men than women (A). These patterns are remarkably similar across regions and are not explained by rates of smoking (B), health coverage (C), or employment (D). Colors indicate regions shown in A. Not all variables were available for the same set of countries for each plot. B & D are log-scale. Data from WHO and ILO.

Take-aways for data exploration:

- Male-bias similar across regions
- Commonly cited drivers of male-bias not strongly predicting male-bias at the country or regional level
- There has to be something physiological

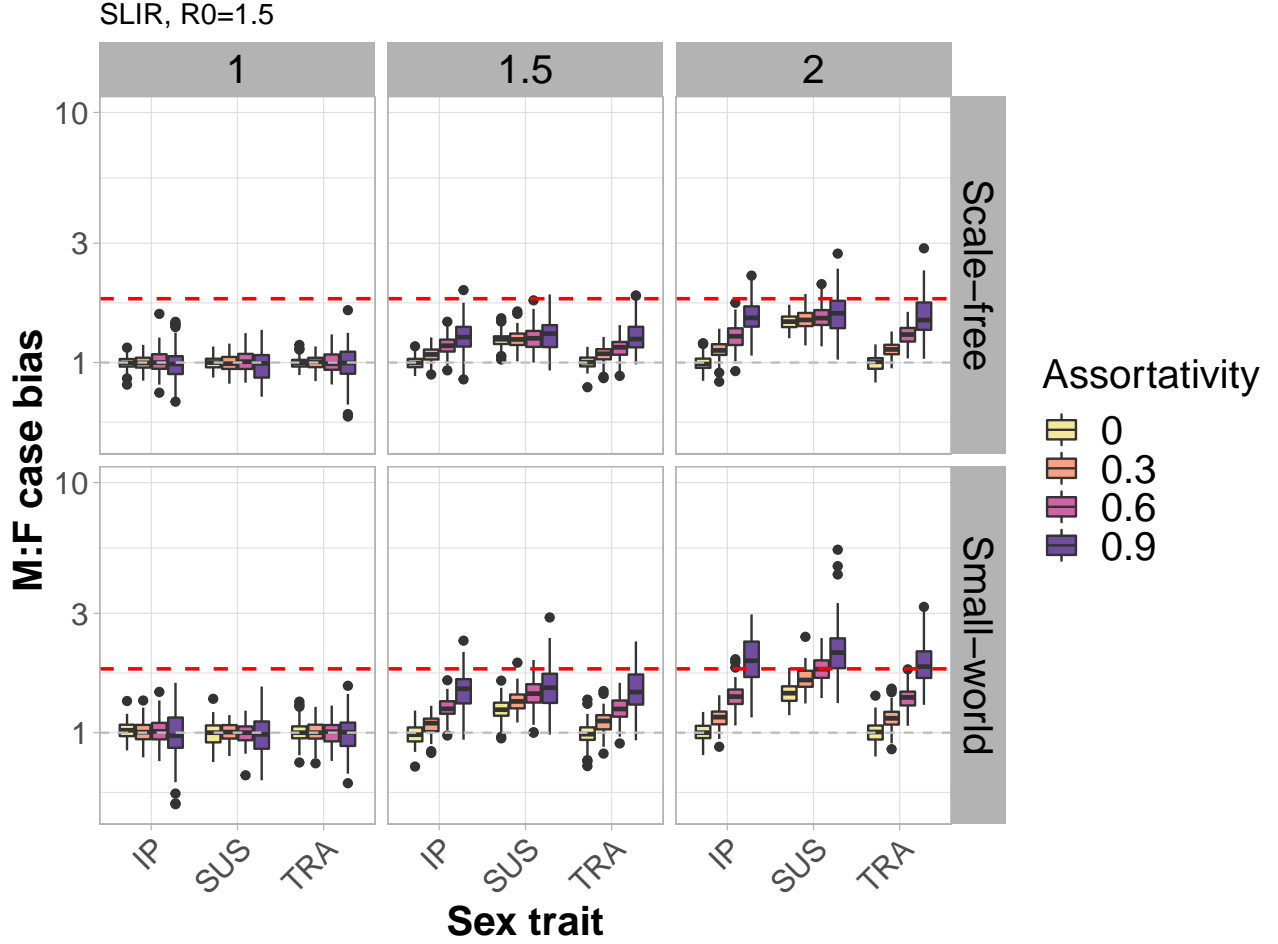


Figure 2: The effects of assortativity on male-bias in SLIR model. Vertical panels show sex-trait ratios (α) for sex-traits shown at the bottom including male:female infectious period (IP), susceptibility (SUS), and transmissibility (TRA). Horizontal panels show different network types (scale-free and small-world). The red dashed line shows the observed ratio of male:female cases globally and the grey dashed line represents even distribution of cases between men and women. Results for $\tau = 0.075$ shown.

Take-aways for male-bias:

- Low transmissibility
- With endemic (SLIRS) dynamics
- Infectious period especially, and also susceptibility can lead to male bias
- Interaction between sex-traits and assortativity on male-bias

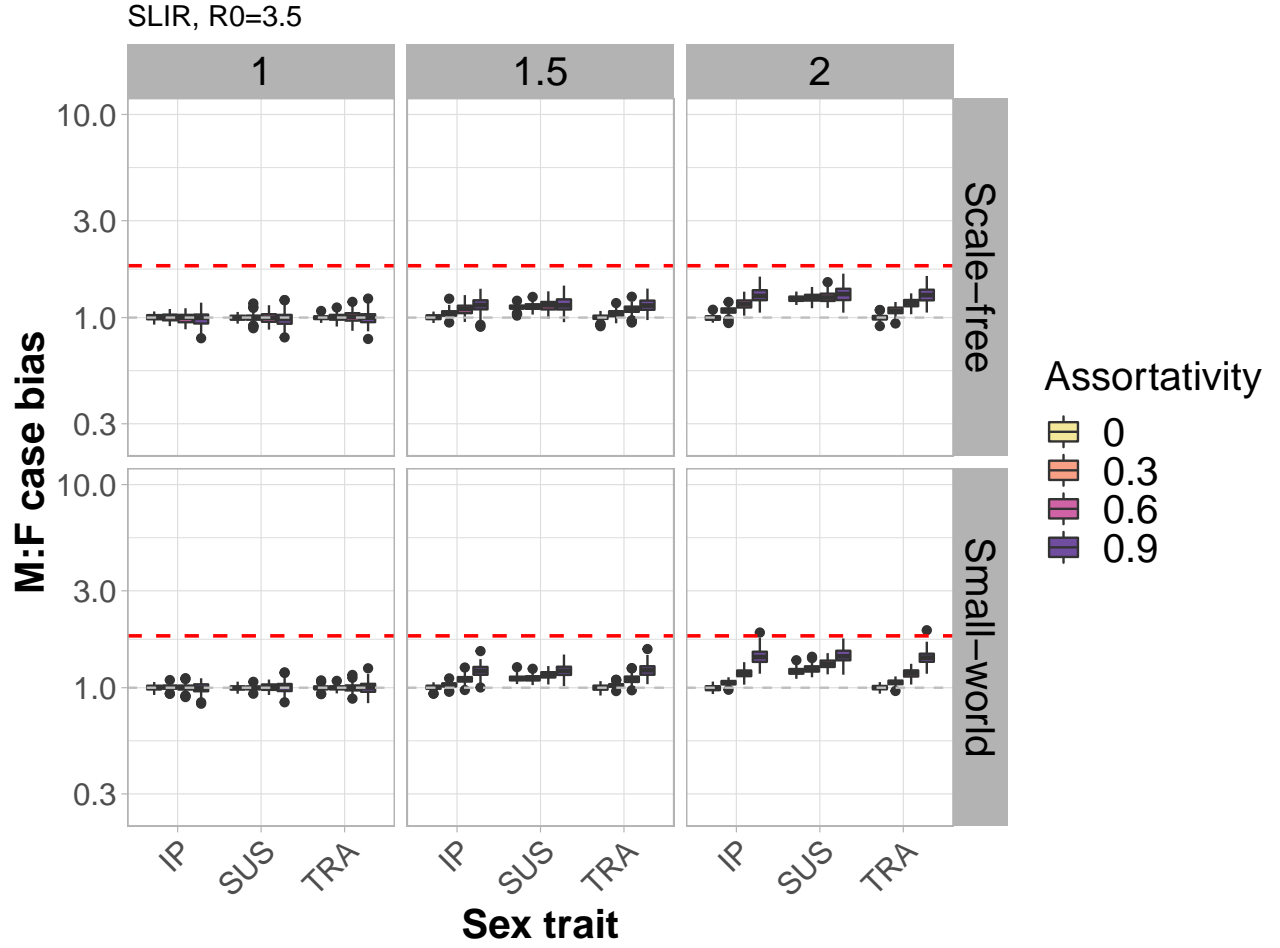


Figure 3: The effects of assortativity on male-bias in SLIR model. Vertical panels show sex-trait ratios (α) for sex-traits shown at the bottom including male:female infectious period (IP), susceptibility (SUS), and transmissibility (TRA). Horizontal panels show different network types (scale-free and small-world). The red dashed line shows the observed ratio of male:female cases globally and the grey dashed line represents even distribution of cases between men and women. Results for $\tau = 0.15$ shown.

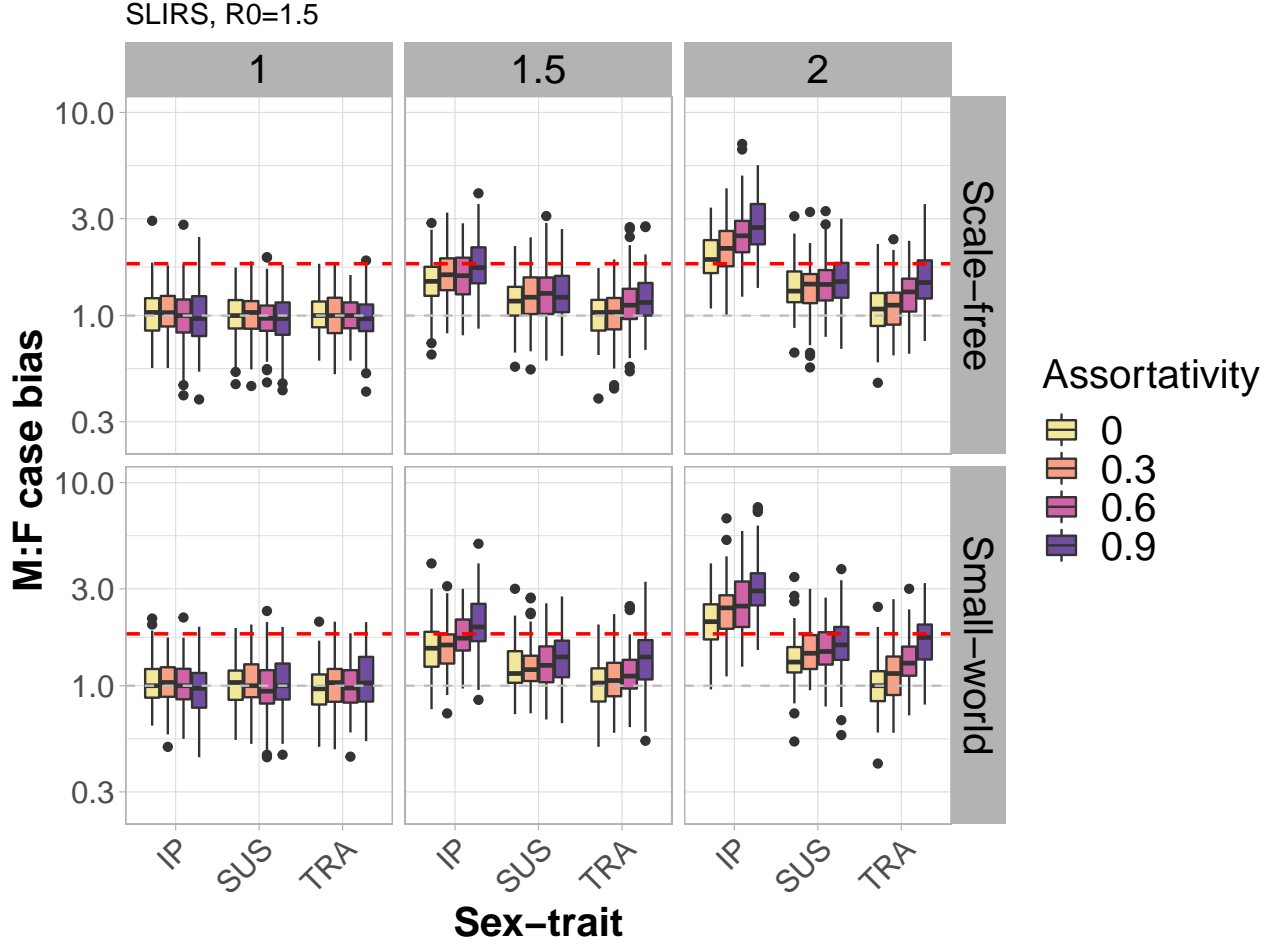


Figure 4: The effects of assortativity on male-bias in SLIRS model. Vertical panels show sex-trait ratios (α) for sex-traits shown at the bottom including male:female infectious period (IP), susceptibility (SUS), and transmissibility (TRA). Horizontal panels show different network types (scale-free and small-world). The red dashed line shows the observed ratio of male:female cases globally and the grey dashed line represents even distribution of cases between men and women. Results for $\tau = 0.075$ shown.

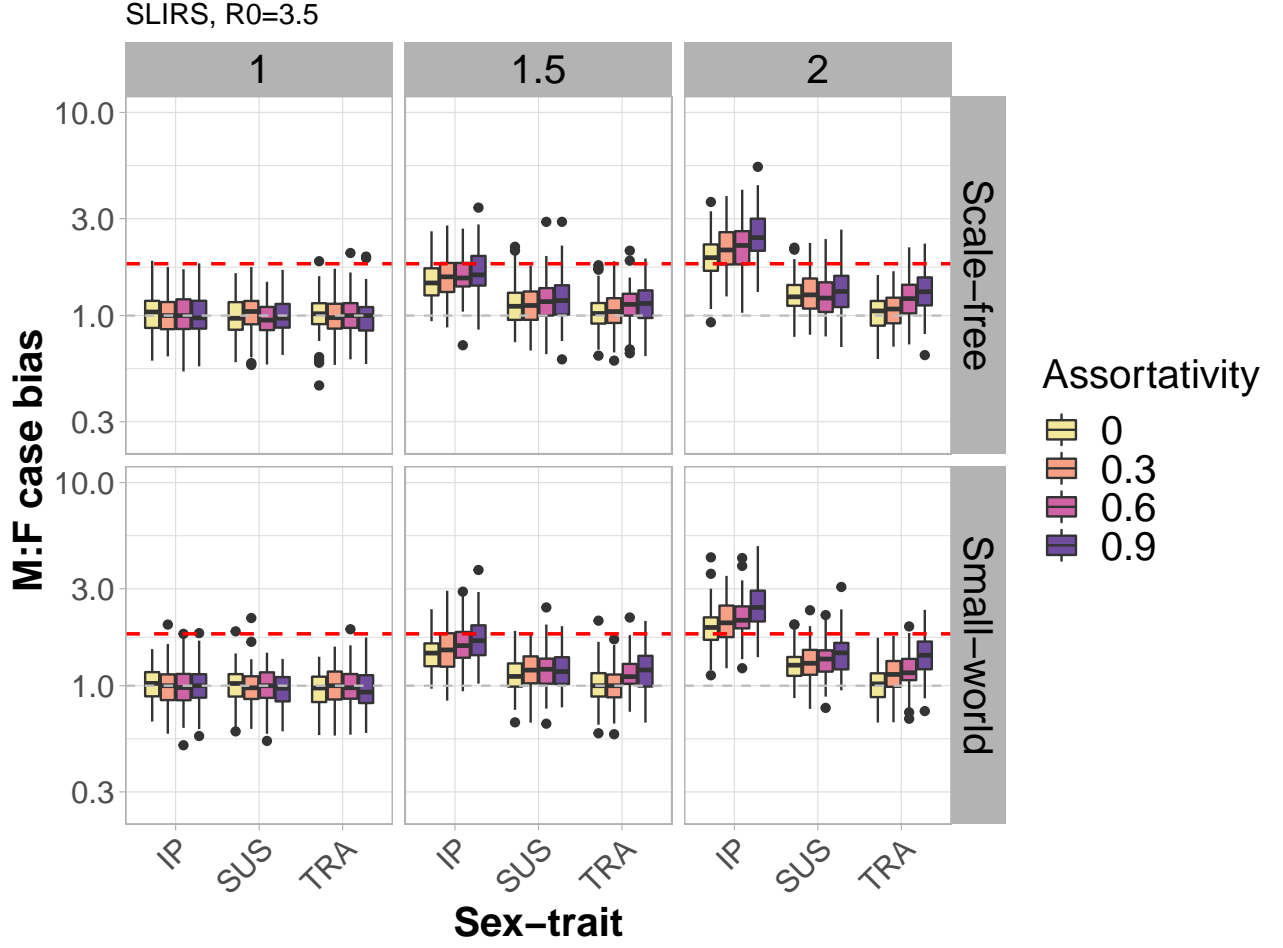


Figure 5: The effects of assortativity on male-bias in SLIRS model. Vertical panels show sex-trait ratios (α) for sex-traits shown at the bottom including male:female infectious period (IP), susceptibility (SUS), and transmissibility (TRA). Horizontal panels show different network types (scale-free and small-world). The red dashed line shows the observed ratio of male:female cases globally and the grey dashed line represents even distribution of cases between men and women. Results for $\tau = 0.15$ shown.

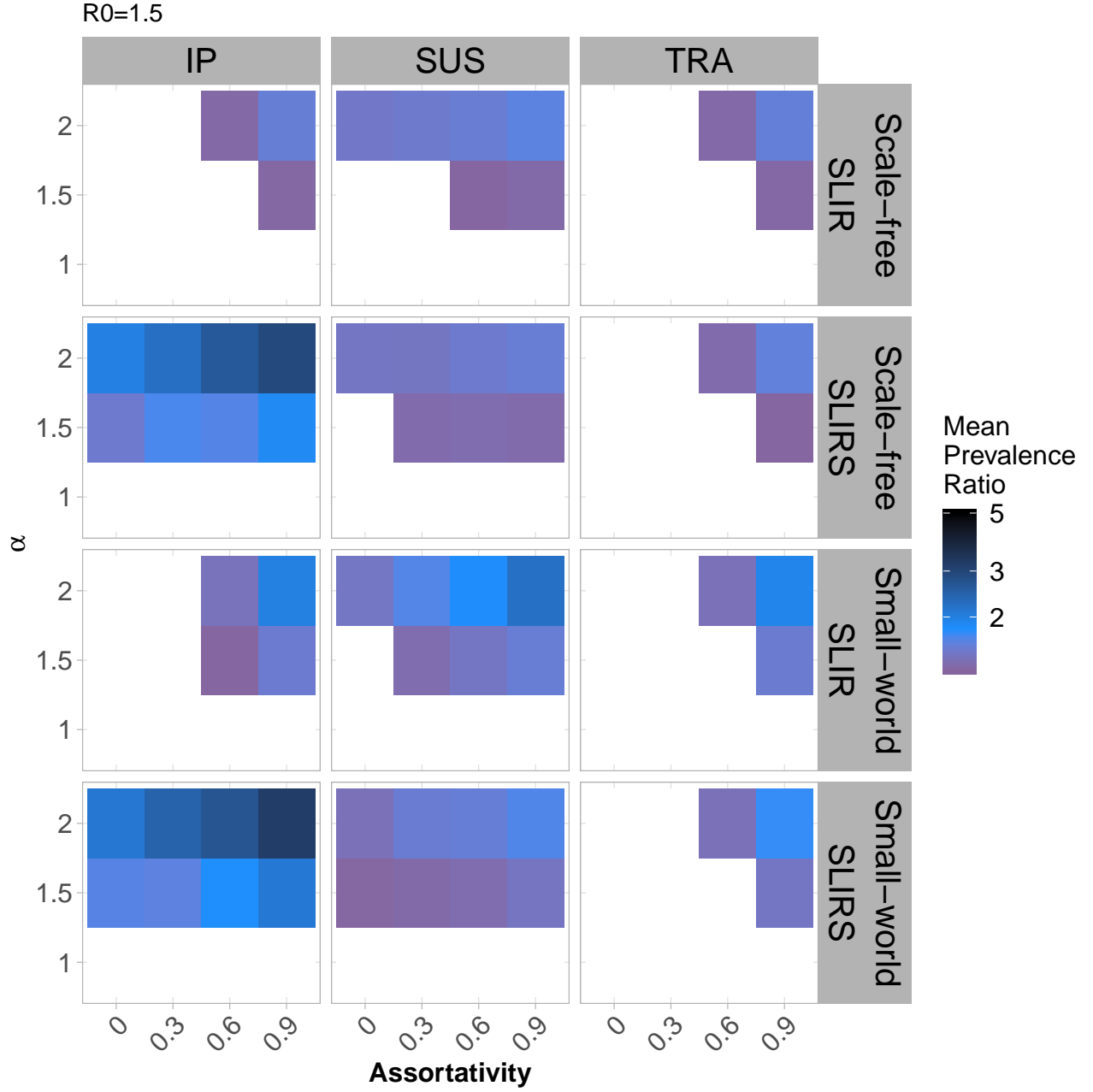


Figure 6: The combined effects of assortativity and individual-level variation on male-bias across different sex-traits and network types. Vertical panels show type of sex-traits: Infectious period (IP), Susceptibility (SUS), and Transmissibility (TRA). Horizontal panels show model types (SLIR and SLIRS) and network type (scale-free and small-world). Color shows mean value of male:female prevalence for that parameter combination (only values above 1.25 are shown). In general, higher male susceptibility can lead to some amount of male-bias, but for SLIRS models, longer male infectious periods is a striking driver of male-bias.

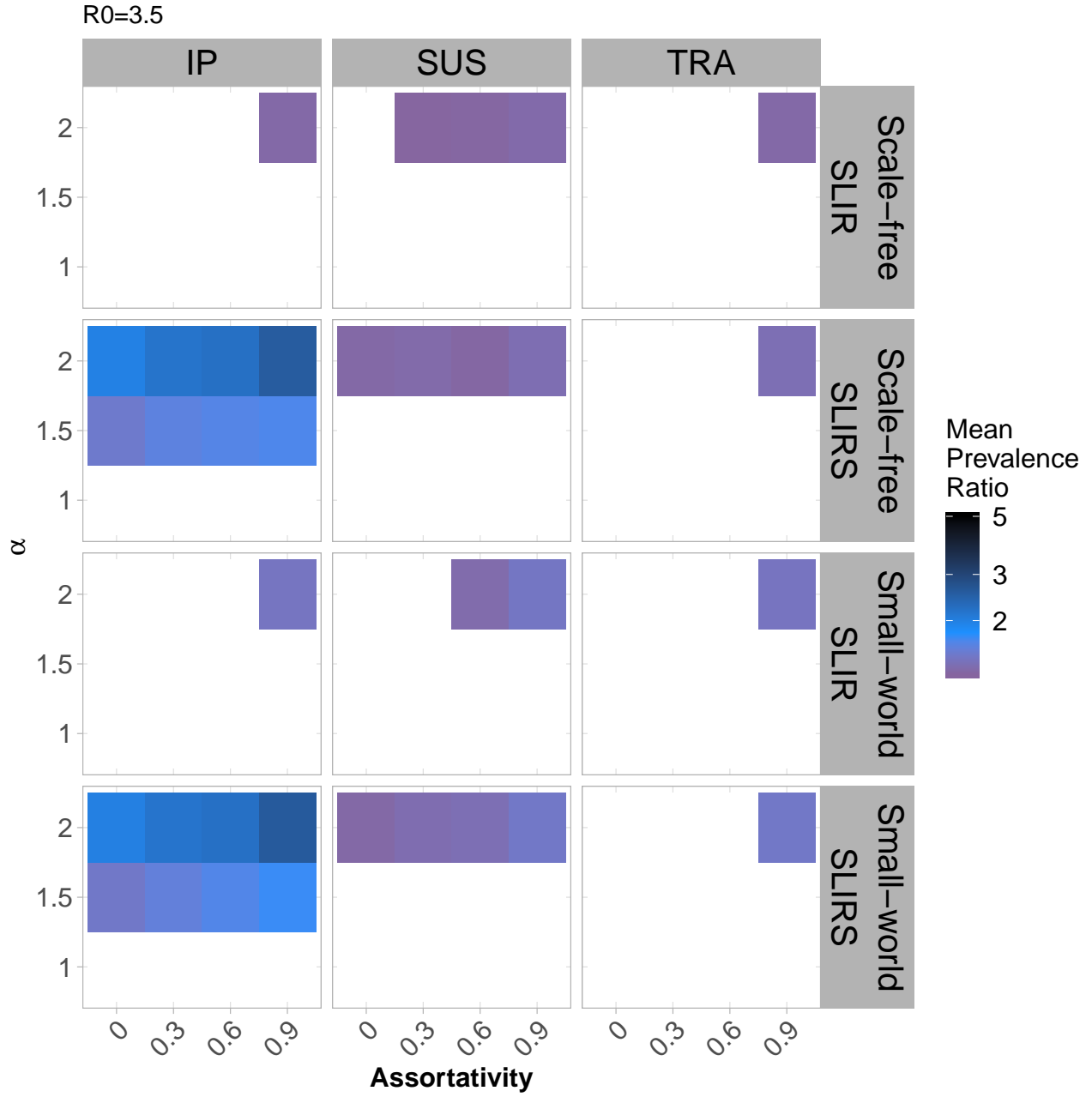


Figure 7: The combined effects of assortativity and individual-level variation on male-bias across different sex-traits and network types. Vertical panels show type of sex-traits: Infectious period (IP), Susceptibility (SUS), and Transmissibility (TRA). Horizontal panels show model types (SLIR and SLIRS) and network type (scale-free and small-world). Color shows mean value of male:female prevalence for that parameter combination (only values above 1.25 are shown). In general, higher male susceptibility can lead to some amount of male-bias, but for SLIRS models, longer male infectious periods is a striking driver of male-bias.

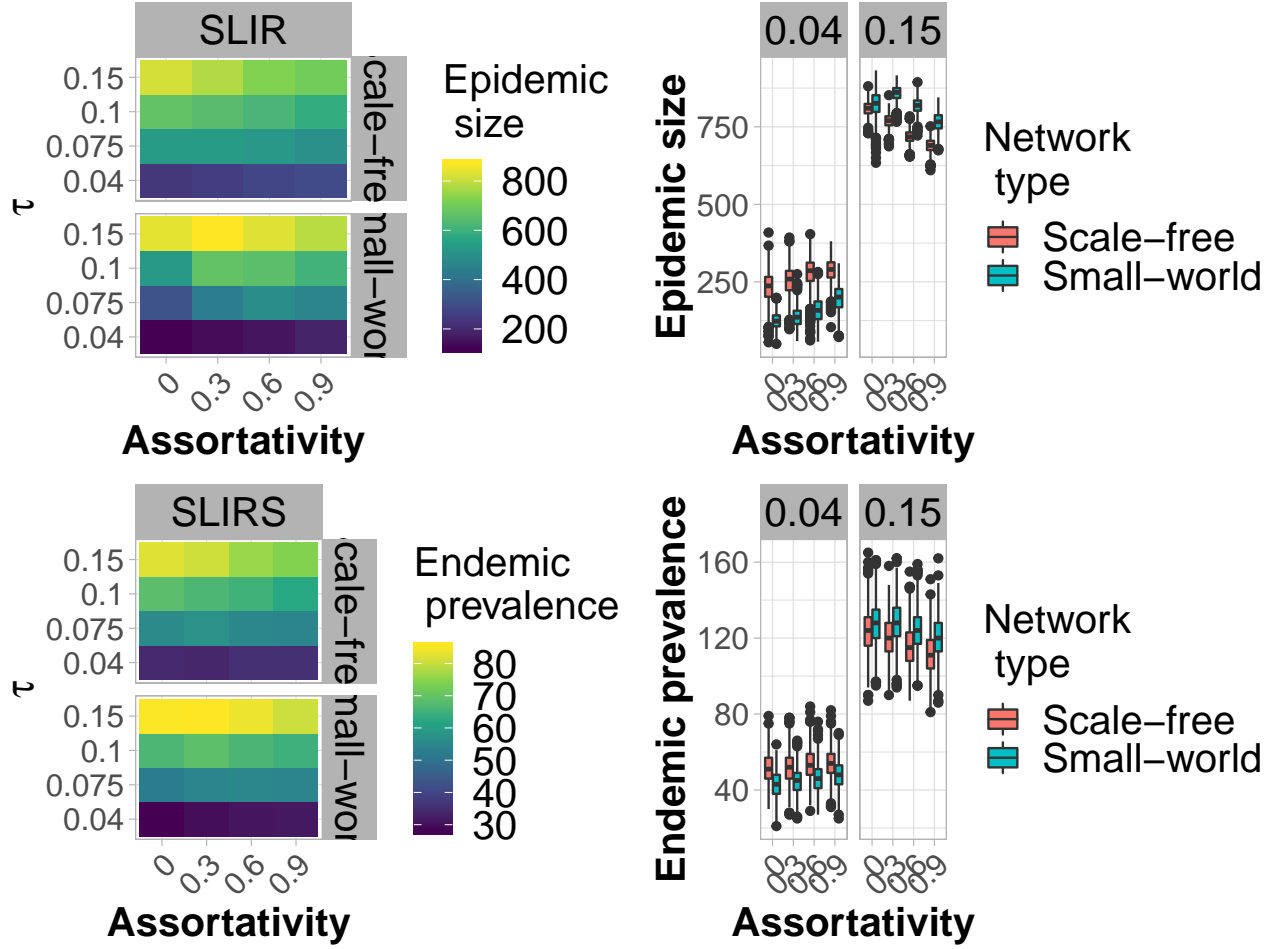


Figure 8: Effects of network structure on endemic prevalence in SLIRS model. Horizontal panels show different network types (scale-free and small-world).