Individual-level differences in infection combined with social mixing patterns lead to observed levels of male-bias for human TB

Across the world, more cases of TB are reported among men than women. Hypotheses for this pattern loosely break down into differences in social networks and/or biology. Social network trends include differences in employment, community activities, or school attendance and could lead men to have larger social networks or be more central in social networks than women, leading to higher contact rates overall or with a more diverse array of social groups. Alternatively, patterns in preferential social mixing by sex could lead men to have higher contact rates specifically with men, who are more likely to be infected themselves. Though TB has historically been thought of as a social disease, where transmission occurs between individuals with close and prolonged physical contact, more recent evidence has brought into question the importance of social networks to transmission trees suggesting that hypotheses pertaining to social behavior.

Biological mechanisms include men having less effective immunological responses and longer time before seeking care leading to higher susceptibility and longer infectious periods among men, respectively. In addition, men may be more likely to transmit disease due to larger volume and faster coughs, a phenomenon previously described in influenza.

Here, we wanted to learn the relative impact of social mixing patterns (assortativity) and individual-level differences in the infection process (susceptibility, transmissibility, and infectious period) on sex-bias in TB cases. We wanted to learn this because previous explanations for sex-bias are unsatisfying and have never been systematically compared. Additionally, understanding drivers of male-bias might improve case-finding or other public health control strategies. To determine the relative effects of mixing patterns and individual-level differences in infection, we conducted a comparative simulation study of three pathogen scenarios spreading on networks of varying assortativity. Pathogen scenarios included higher male susceptibility, transmissibility, and infectious period. We found