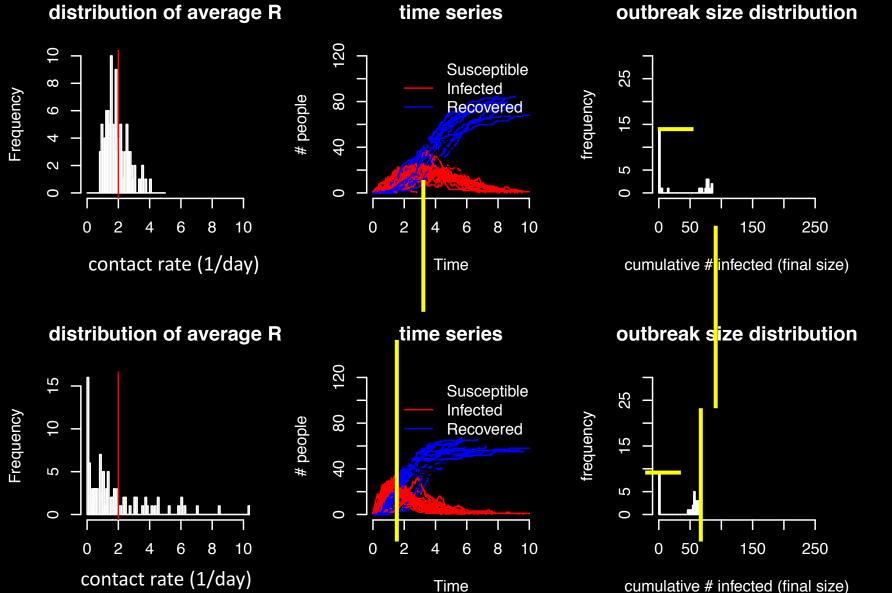
het.epidemic(beta.mean = 2, beta.var = .5, runs = 30, end.time = 10, pop.size = 100, gmma = 1) het.epidemic(beta.mean = 2, beta.var = 8, runs = 30, end.time = 10, pop.size = 100, gmma = 1)





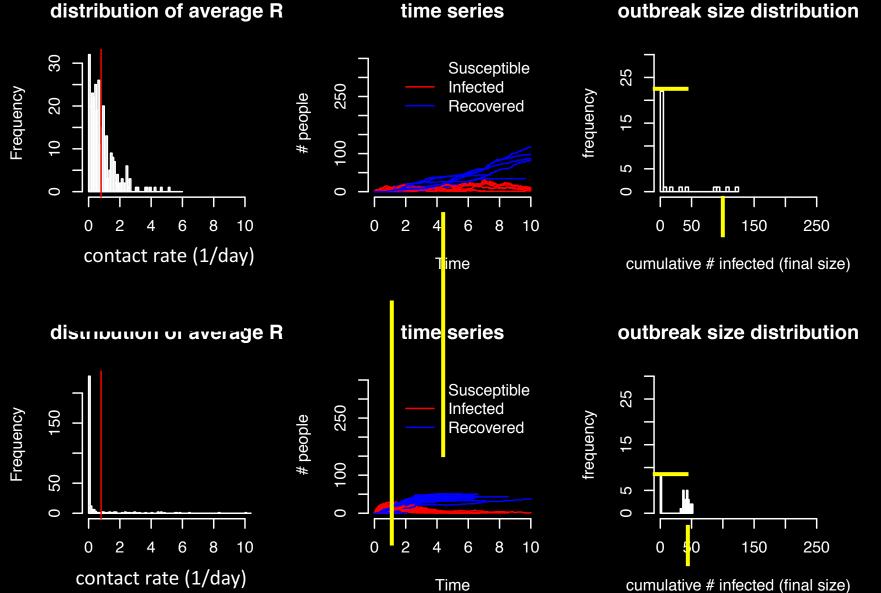
het.epidemic(beta.mean = 2, beta.var = .5, runs = 30, end.time = 10, pop.size = 300, gmma = 1) het.epidemic(beta.mean = 2, beta.var = 8, runs = 30, end.time = 10, pop.size = 300, gmma = 1) distribution of average R time series outbreak size distribution 20 Susceptible 25 Infected 250 15 Frequency frequency Recovered 15 10 100 2 5 шТит 0 0 0 0 10 50 150 250 contact rate (1/day) cumulative # infected (final size) Time outbreak size distribution distribution of average R time series Susceptible 25 Infected 250 Frequency frequency Recovered 15 20 100 2 0 0 0 8 50 250 10 10 150

Time

contact rate (1/day)



het.epidemic(beta.mean = .8, beta.var = .5, runs = 30, end.time = 10, pop.size = 300, gmma = 1) het.epidemic(beta.mean = .8, beta.var = 8, runs = 30, end.time = 10, pop.size = 300, gmma = 1) distribution of average R time series outbreak size distribution





Summary

- Heterogeneity makes pathogens
 - more likely to invade (higher R0)
 - smaller epidemics for a given R0
 - faster epidemics
 - faster initial rate of increase

