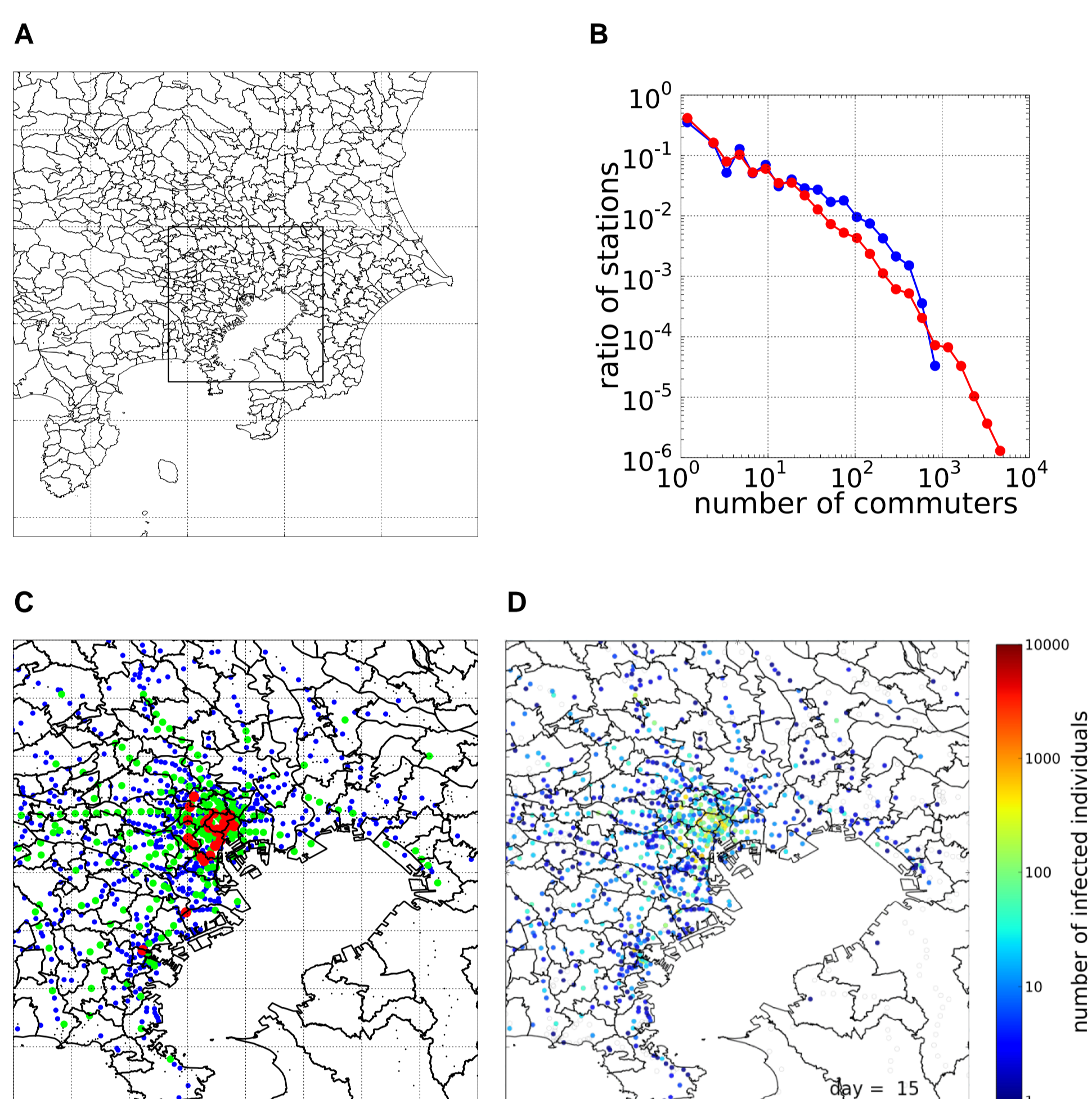


Introduction

We analyze the epidemiological dynamics of an infectious disease spreading across the commuter network of the Tokyo metropolitan area. We assume that each person commutes from home to work and back by trains connecting local populations. The Urban Transportation Census of the Japanese Ministry of Land, Infrastructure, and Transport is used to simulate the movements of commuters. In addition to extensive individual-based simulations, we have developed a random-network model that retains the connectivity structure among local populations only to the extent captured by the empirically observed average connectedness of local populations according to their size classes.

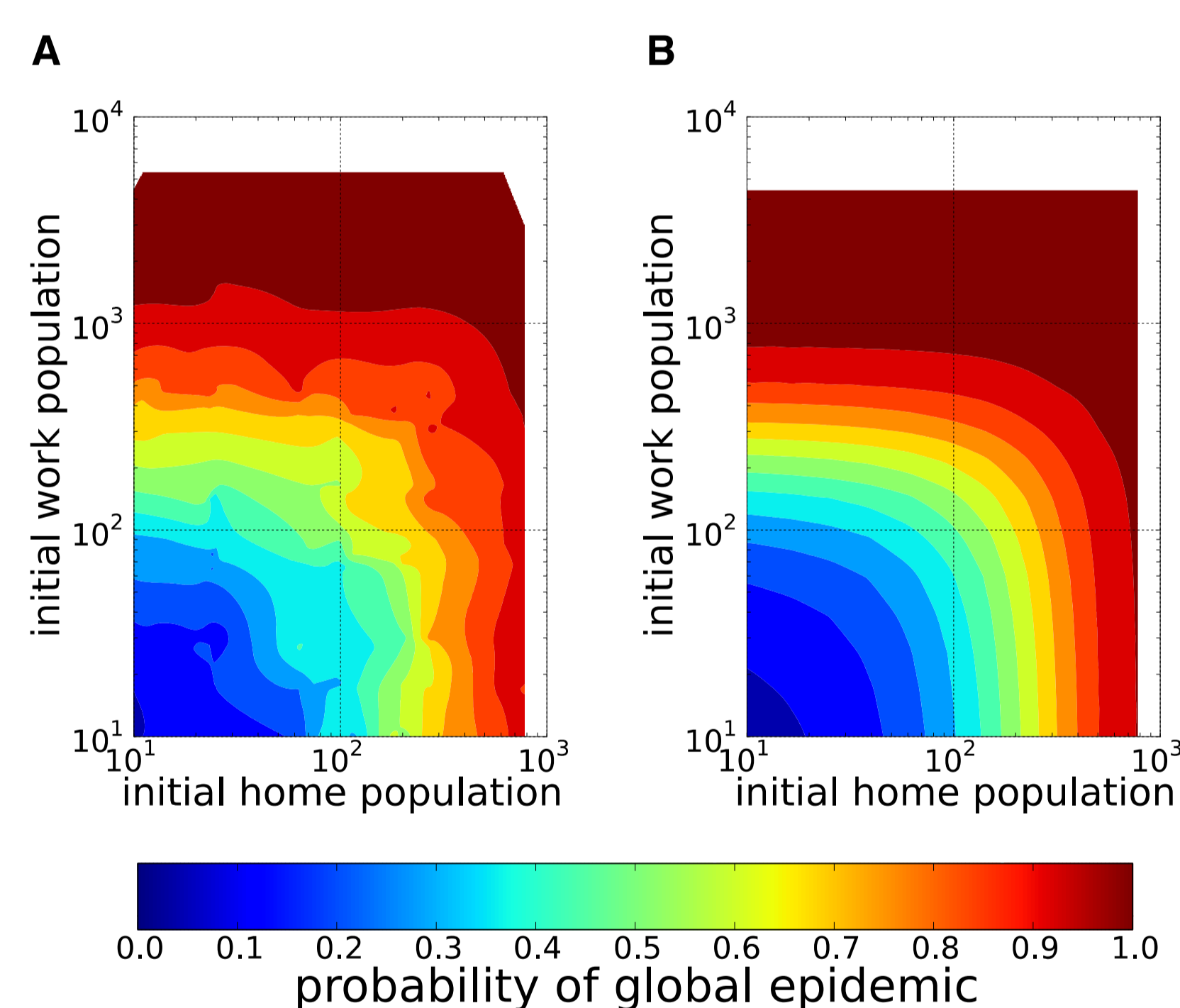


Commute network of Tokyo metropolitan area

A Map of Tokyo metropolitan area in Kanto region, Japan. Framed rectangle shows the central part we show in C and D. **B** Distribution for the station size, the numbers of incoming and outgoing passengers of railway stations, in the Tokyo metropolitan area. Blue: the stations as "home-node" (those stations the passengers take from their homes), red: the stations as "work-node" (those taken from their workplaces). **C** Geographical distribution of station sizes in the central part of Tokyo metropolitan area. **D** The distribution for the number of infected hosts 15 days after the introduction of an emerging infectious disease (a Monte Carlo simulation run, in which an initially infected host commuted between "Tsunashima" station and "Hongo-sanchoume" station).

Epidemics on commute network: Global epidemics

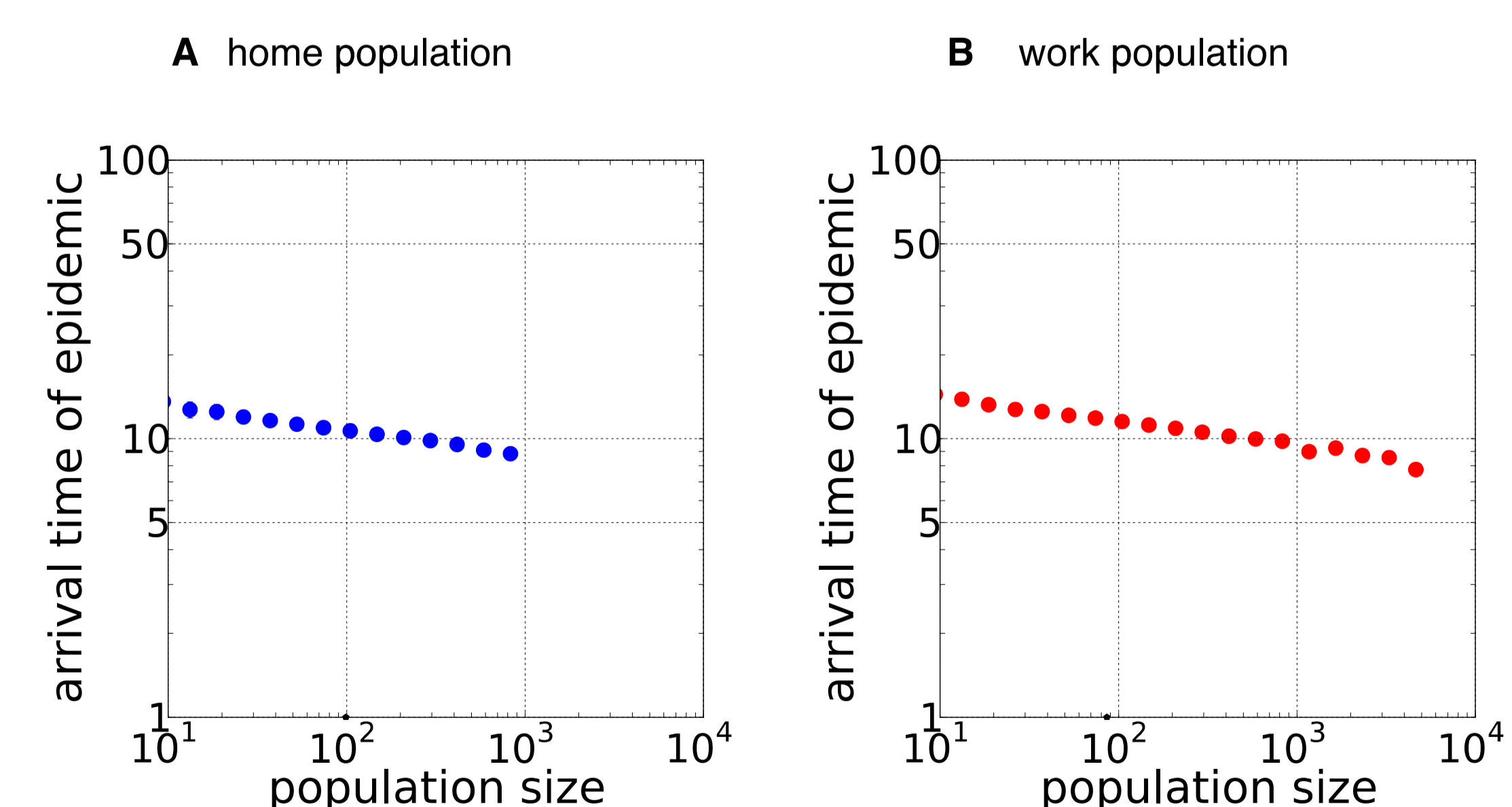
A standard Susceptible-Infected-Recovered (SIR) model is assumed for epidemic dynamics through daytime transmission at work place and nighttime transmission at home place of commuters. **A** The probability of global epidemic (epidemic spreading over the whole system), PG , observed in the IBM simulations for the commute network of Tokyo metropolitan area. PG is plotted as a function of the size of home population of an initially infected host (horizontal axis) and that of work population (vertical axis). **B** The *analytical* results for the probability of global epidemic obtained by using branching process in random reconnection network retaining the size correlation of home and work place stations observed in Tokyo metropolitan commute data.



Power law for first-arriving time

Average time t (days) until an infectious disease arrives at each home (**A**) and work population (**B**), plotted as a function of the size N of local populations. Both approximately obey power law: $t \sim N^{0.1}$

Reference: Yashima K and Sasaki A, in press



Conclusion

We find that, when an initially infected person is randomly chosen among the commuters, the probability of an epidemic outbreak depends mostly on the population sizes at that person's home and work, but not on the corresponding geographical locations. The final size of an epidemic outbreak in a local population is mostly determined by the size of that population, being little influenced by that population's distance from the initially infected population or from hub stations. We also find that the mean time until an epidemic outbreak arrives at a local population is well predicted by a simple power law: it geometrically decreases with local population size.