How human location-specific contact patterns impact spatial transmission between populations?

Supplementary Information

Lin Wang[1], **Zhen Wang**[2,3], **Yan Zhang**[1], **Xiang Li**[1*]

[1]Adaptive Networks and Control Laboratory, Department of Electronic Engineering, Fudan University, Shanghai 200433, PR China
[2]Department of Physics, Hong Kong Baptist University, Kowloon Tong, Hong Kong SAR, China
[3] Center for Nonlinear Studies and the Beijing-Hong Kong-Singapore Joint Center for Nonlinear and Complex Systems (Hong Kong), Hong Kong Baptist University, Kowloon Tong, Hong Kong SAR, China
Author for correspondence: lix@fudan.edu.cn

The population dynamics at the equilibrium

Given a diffusion rate σ and a return rate τ, we obtain a basic set of rate equations governing the population dynamics by the mean-field approximation. The rate equations describing the population evolution of subgroups N_{xx} and N_{xy} are

$$\frac{dN_{xx}}{dt} = -\sigma N_{xx}(t) + \tau N_{xy}(t), \tag{S1}$$

$$\frac{dN_{xy}}{dt} = \sigma N_{xx}(t) - \tau N_{xy}(t). \tag{S2}$$

The first equation describes the change of population in subgroup N_{xx} as the net balance of individuals departing from or returning to their own resident subpopulation x per unit time. The second equation accounts for the variation of population in subgroup N_{xy} by the net balance of residents of subpopulation x that move to or return from subpopulation y. Since the population size of residents of subpopulation x is

$$N_x^\star = N_{xx}(t) + N_{xy}(t),$$

we have

$$\frac{dN_{xx}}{dt} + (\sigma + \tau)N_{xx}(t) = N_x^\star \tau,$$

whose solution is

$$N_{xx}(t) = \frac{N_x^\star}{1 + \sigma/\tau} + C_{xx}\exp[-(\tau + \sigma)t].$$

Since the constant C_{xx} subjects to the initial condition, $N_{xx}(0) = N_x^\star$, we have

$$N_{xx}(t) = \frac{N_x^\star}{1+\sigma/\tau} + (N_{xx}(0) - \frac{N_x^\star}{1+\sigma/\tau}) \exp[-(\tau+\sigma)t].$$

Similarly, Eq. (S2) yields

$$\begin{aligned} N_{xy}(t) = & \quad \tfrac{N_x^\star}{1+\sigma/\tau}\sigma/\tau - (N_{xx}(0) - \tfrac{N_x^\star}{1+\sigma/\tau}) \exp[-(\tau+\sigma)t] \\ & + \Big[N_{xy}(0) + N_{xx}(0) - \tfrac{N_x^\star}{1+\sigma/\tau}(1+\sigma/\tau)\Big] \exp(-\tau t). \end{aligned}$$

The relaxation times of $N_{xx}(t)$ and $N_{xy}(t)$ to their equilibria are determined by $(\tau + \sigma)^{-1}$ and τ^{-1}, respectively. When $\tau \gg \sigma$, which accords with the case in reality, the characteristic relaxation time is determined by τ^{-1}. When $t \gg \tau^{-1}$, the population sizes $N_{xx}(t)$ and $N_{xy}(t)$ can be approximated by their equilibria,

$$N_{xx}^{eq} = \frac{N_x^\star}{1+\sigma/\tau}, N_{xy}^{eq} = \frac{N_x^\star}{1+\tau/\sigma}. \tag{S3}$$

Similarly, for the individuals from subpopulation y, we have

$$N_{yy}^{eq} = \frac{N_y^\star}{1+\sigma/\tau}, N_{yx}^{eq} = \frac{N_y^\star}{1+\tau/\sigma}. \tag{S4}$$

The rate equations describing the contagion process in each subgroup

With the mean-field approximation, the contagion process in subgroup N_{xx} with any of the two contact scenarios can be delineated by the rate equation:

$$\frac{dI_{xx}}{dt} = -\sigma I_{xx}(t) + (1-\sigma)\lambda_{xx}(t)[N_{xx}^{eq} - I_{xx}(t)] - (1-\sigma)\nu I_{xx}(t) + \tau I_{xy}(t), \tag{S5}$$

where the form of the force of infection $\lambda_{xx}(t)$ is based on Eq.(3) (main text) under the type-I scenario and Eq.(7) under the type-II scenario, while the first term on the right-hand side (r.h.s.) of this equation considers the diffusion of infectious individuals from subgroup N_{xx}, the second term on the r.h.s. measures the newly generated infected individuals within subgroup N_{xx}, the third term on the r.h.s. evaluates the infectious individuals that do not diffuse away from subgroup N_{xx} but experience the transition of recovery, and the last term accounts for the return of infectious individuals from subgroup N_{xy}.

Similarly, the contagion process in subgroup N_{yx} can be described by the following rate equation:

$$\frac{dI_{yx}}{dt} = -\tau I_{yx}(t) + (1-\tau)\lambda_{yx}(t)[N_{yx}^{eq} - I_{yx}(t)] - (1-\tau)\nu I_{yx}(t) + \sigma I_{yy}(t), \tag{S6}$$

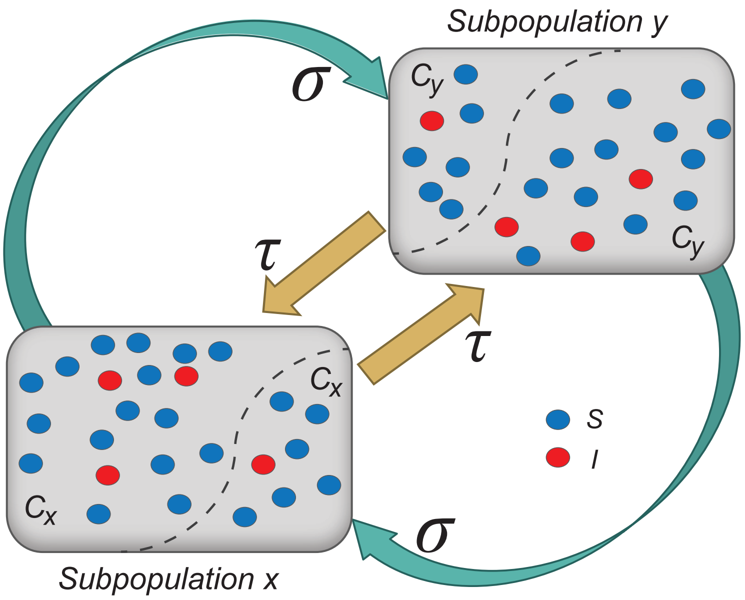
where the form of the force of infection $\lambda_{yx}(t)$ is based on Eq.(3) under the type-I scenario and Eq.(6) under the type-II scenario, while the first term on the r.h.s. of this equation refers to the return of infectious individuals from subgroup N_{yx}, the second term on the r.h.s. considers the newly generated infected individuals within subgroup N_{yx}, the third term on the r.h.s. measures the infectious individuals that do not return to subgroup N_{yy} but experience the transition of recovery, and the last term evaluates the number of infectious commuters departing from subgroup N_{yy}.

The contagion process in subgroups N_{yy}, N_{xy} with any of the two contact scenarios can be similarly delineated by the set of rate equations:

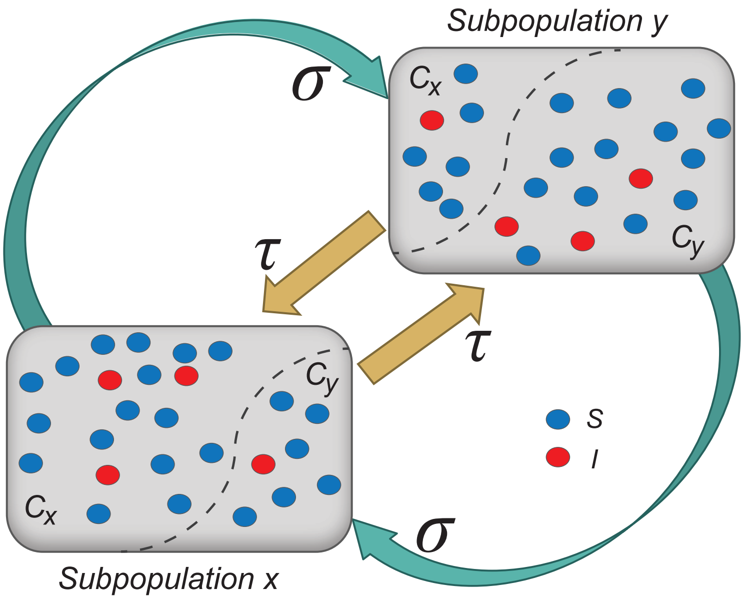
$$\frac{dI_{yy}}{dt} = -\sigma I_{yy}(t) + (1-\sigma)\lambda_{yy}(t)[N_{yy}^{eq} - I_{yy}(t)] - (1-\sigma)\nu I_{yy}(t) + \tau I_{yx}(t), \tag{S7}$$

$$\frac{dI_{xy}}{dt} = -\tau I_{xy}(t) + (1-\tau)\lambda_{xy}(t)[N_{xy}^{eq} - I_{xy}(t)] - (1-\tau)\nu I_{xy}(t) + \sigma I_{xx}(t), \tag{S8}$$

where the form of $\lambda_{yy}(t), \lambda_{xy}(t)$ is based on Eq.(2) under the type-I scenario and Eq.(5) and Eq.(4) under the type-II scenario.



(a) *Type-I (destination-driven) contact scenario*



(b) *Type-II (origin-driven) contact scenario*

Figure S1. Schematic illustrations of (a) the type-I (destination-driven) contact scenario and (b) the type-II (origin-driven) contact scenario.

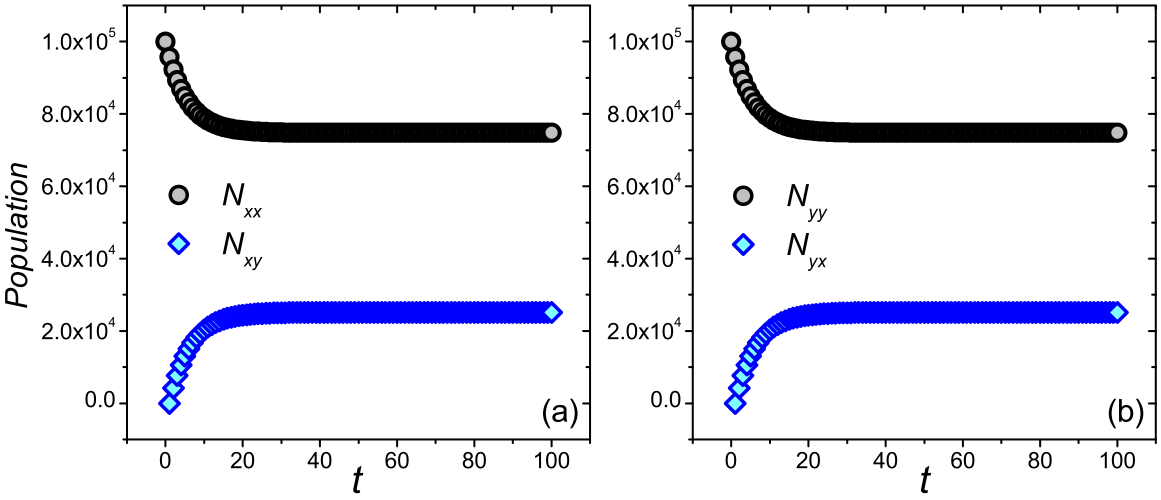


Figure S2. The time series of the population evolution in each subgroup.