

Supplementary information for integrated extensive detection, contact tracing and dynamical social distancing interventions to prevent future epidemic waves

Xiao Hong, Yuexing Han, Bing Wang

I. MODEL PARAMETER

In this section, we list the main parameters used in the SEIQR model based on detection, contact tracing and dynamical social distancing, as shown in Supplementary Table I. Note that, all the parameters range from 0 to 1.

Supplementary Table I: The parameters used in the SEIQR model.

Parameter	Description
$C(t)$	Intensity of dynamical social distancing
α	Detection rate
δ^2	Contact tracing rate
λ	Infection rate
μ	Recovery rate of I state
κ	Cure rate of Q^I state
$\frac{1}{\beta}$	Latent period
$\frac{1}{\tau}$	Quarantine period

II. EMPIRICAL CONTACT DATA SET ANALYSIS

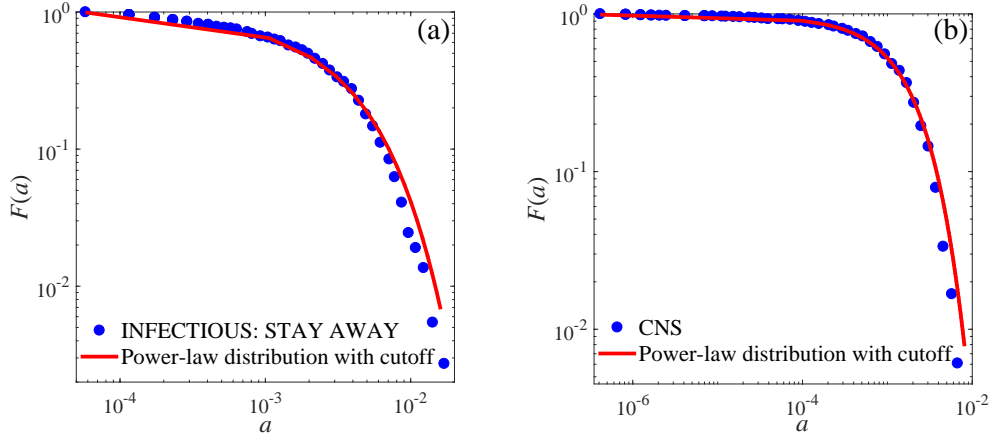
In this section, we provided more details on the two representative high-resolution empirical contact data sets used in the main text, which describe the dynamic interactions between individuals in two different scenarios. Specifically, the "INFECTIOUS: STAY AWAY" data set contains the anonymous ID and timestamp of the active contacts at one day. Unlike the "INFECTIOUS: STAY AWAY" data set, the CNS data set also contains the signal

This work was supported by the Natural Science Foundation of Shanghai under Grant No. 20ZR1419000. (Corresponding authors: Yuexing Han and Bing Wang.)

Xiao Hong, Yuexing Han, and Bing Wang are with the School of Computer Engineering and Science, Shanghai University, Shanghai 200444, P. R. China. (e-mail: hongxxss@126.com; han_yx@i.shu.edu.cn; bingbignwang@shu.edu.cn).

strength (RSSI) of the active contacts at one month. Significantly, the timestamp of active contacts represents the time sequence of real contact networks, which can be used to evaluate the contact duration, and the signal strength is usually used to assess the physical distance between individuals. Here, we assume that the first anonymous ID of each record is the active node, and the second anonymous ID is the inactive node that receives the connection from the first anonymous ID. Then, we construct the instantaneous network according to the timestamp of the active contacts. When the duration of epidemic simulation exceeds the data set duration, we simply replicate the above data sets from the beginning [1].

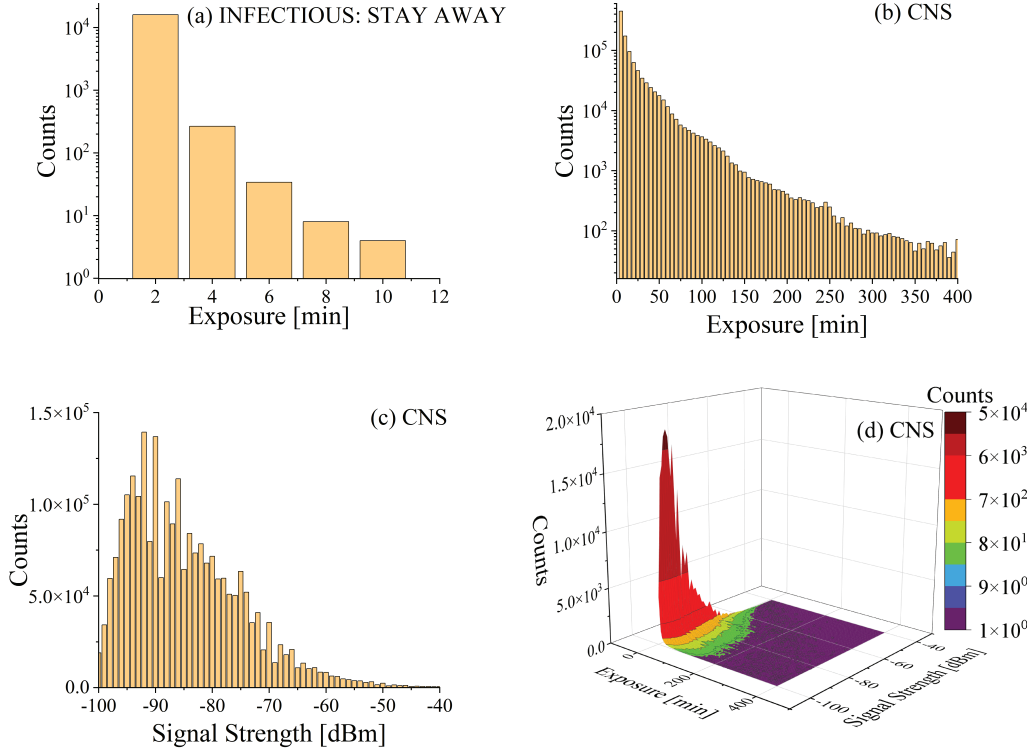
Considering that human activity patterns follow the heavy-tailed distribution in real life [2], we measure the activity a_i of the “INFECTIOUS: STAY AWAY” and CNS data sets, which describes the tendency of node i to participate in social interactions. For the sake of calculating the activity a_i of empirical contact data sets, we consider the node’s out-degree as proxy for its activity [3]. Hence, the activity of node i is estimated as $a_i = \frac{S_{i,out}}{\sum_j S_{j,out}}$ ($i = 1, 2, \dots, N$), where $S_{i,out}$ represents its out-degree in the whole time span. Since the real contact data set is difficult to strictly follow a single power-law distribution well in the whole range, the power-law distribution with exponential cutoff is usually used to evaluate [4]. In Supplementary Fig. 1, we find that the activity distribution of nodes well fits the power-law distribution with exponential cutoff. Based on this observation, the above real contact data sets well reflect the human activity patterns. Therefore, the “INFECTIOUS: STAY AWAY” and CNS data sets are suitable for exploring the effectiveness of joint interventions of detection, contact tracing and social distancing in real environments.



Supplementary Fig. 1: Activity analysis of the “INFECTIOUS: STAY AWAY” and Copenhagen Networks Study (CNS) data sets. The blue circles represent the activity distribution in the INFECTIOUS: STAY AWAY and Copenhagen Networks Study (CNS) temporal networks. The red curves represent the fitting result of the power-law distribution with exponential cutoff, $F(a) = ca^{-\xi}e^{-\eta a}$. (a): $c = 235.8$, $\xi = 0.0464$ and $\eta = 295.3$; (b): $c = 600.4$, $\xi = 0.0054$ and $\eta = 591.2$.

Since heterogeneous distributions of real contact patterns affect the epidemic spread, we calculated the distributions of contact duration of the interactions contained in the “INFECTIOUS: STAY AWAY” and CNS data sets. In particular, we also calculated the distribution of signal strength (RSSI) of the interactions contained in

the CNS data set. Supplementary Fig. 2 shows the distributions of contact duration and signal strength (RSSI) of individual interaction. In Supplementary Fig. 2(a), we find that most interactions have short contact duration in the “INFECTIOUS: STAY AWAY” data set. In the CNS data set (see Supplementary Fig. 2(b)-(d)), most interactions between individuals have low signal strength and short contact duration, but large signal strength and long-lasting contact duration are also observed. In conclusion, the broad distributions of signal strength and contact duration in the above data sets reflect the typical characteristic of human interactions.

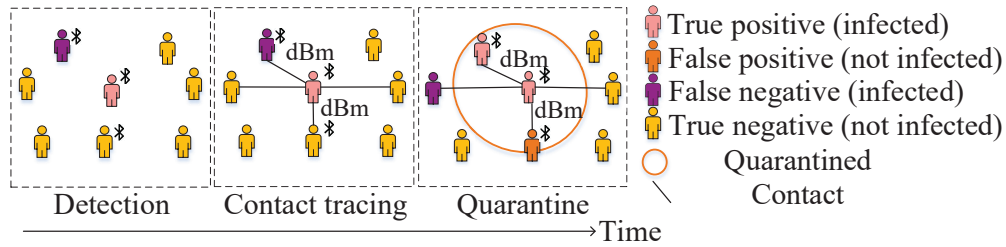


Supplementary Fig. 2: Statistical properties of the “INFECTIOUS: STAY AWAY” and Copenhagen Networks Study (CNS) data sets. (a): The distribution of contact duration of the “INFECTIOUS: STAY AWAY” data set; (b): The distribution of contact duration of the CNS data set; (c): The distribution of signal strength (RSSI) of the CNS data set; (d) The heat-maps of contact duration and signal strength (RSSI) of the CNS data set.

III. CONTAGION, DETECTION, CONTACT TRACING AND QUARANTINE PROCESS

At present, although the large-scale detection, contact tracing and dynamical social distancing interventions are effective, they have caused huge economic costs. Meanwhile, considering the wide popularity of vaccines in most countries or regions, selectively quarantining individuals at high risk of infection is more suitable for the current situation when most of the population is uninfected. In reality, infectious events are random in nature, not all “at-risk” contacts between individuals are considered to lead to infectious events. This can lead to individuals who have not been infected being quarantined, i.e., “false positives” [5]. Similarly, among contacts considered “risk-free” by contact tracing, it may actually lead to infectious events (“false negatives”), i.e., exposed or infected individuals who

are not quarantined, as shown in Supplementary Fig. 3. Thus, according to the proportions of “false positives” and “false negatives”, it is very important to quantify the ability of interventions to distinguish actual infected contacts from other contacts.



Supplementary Fig. 3: The whole process is from contagion to detection, contact tracing and quarantine. Once infected individuals (pink) who have installed the contact tracing app are detected as virus positive, their recent contacts (purple and yellow) installing the tracing app can be traced according to different tracing policies. Note also that contacts who did not install the tracing app cannot be quarantined.

REFERENCES

- [1] M. Starnini, A. Baronchelli, and Barrat A et al., “Random walks on temporal networks,” *Physical Review E*, vol. 85, no. 5, 2012, no. 056115.
- [2] A. Barabási, “The origins of bursts and heavy tails in human dynamics,” *Nature*, vol. 435, no. 7039, pp. 207-211, 2005.
- [3] L. Alessandretti, K. Sun, and A. Baronchelli et al., “Random walks on activity-driven networks with attractiveness,” *Physical Review*, vol. 95, 2017, no. 052318.
- [4] A. Clauset, C. R. Shalizi, and M. Newman, “Power-law distributions in empirical data,” *SIAM Review*, vol. 51, no. 4, pp. 661-703, 2009.
- [5] J. Ioannidis, R. Tarone, and J. K. McLaughlin, “The false-positive to false-negative ratio in epidemiologic studies,” *Epidemiology*, vol. 22, no. 4, pp. 450-456, 2011.