Nonequilibrium Statistical Physics of Complex Systems

25 July (Mon.) - 28 July(Thu.), 2022. at 1503, 5th Fl.,KIAS

Agent-based model of COVID-19 transmission for location-specific risk assessment and control

Lei-Han Tang

Department of Physics
Institute of Computational and Theoretical Studies
Hong Kong Baptist University

<u>Goal</u>

Brings modelling one step closer to epidemic management in real life

Overview

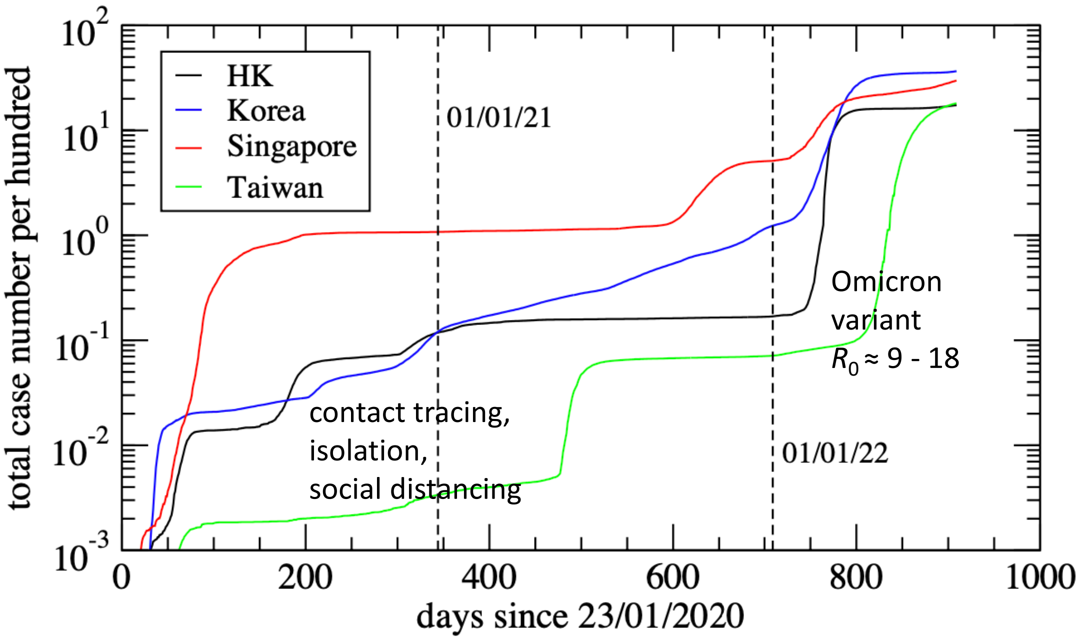
- Quick facts about COVID-19 waves in east Asia
- The SEIR model
  - Infectious period, R0, exponential growth, renewal process
  - Community-wide qPCR testing and quarantine
- A location-based transmission network model for risk evaluation and pandemic control
  - Formulation
  - Epidemic growth rate — a fundamental equation
  - Social contact: a toy model
- Conclusions

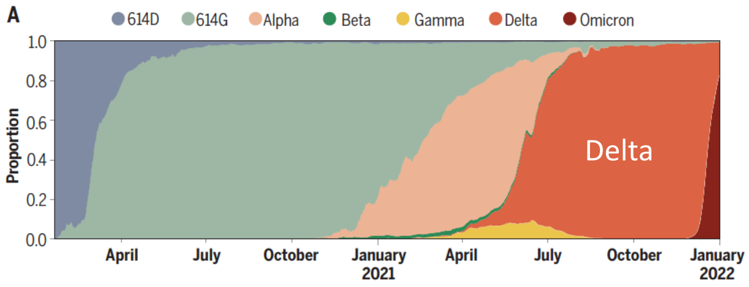
Quick facts about COVID-19 waves in east Asia

COVID-19 waves in
4-dragon countries/regions

owid/covid-19-data

Koelle et al., *Science* **375**, 1116–21 (2022)

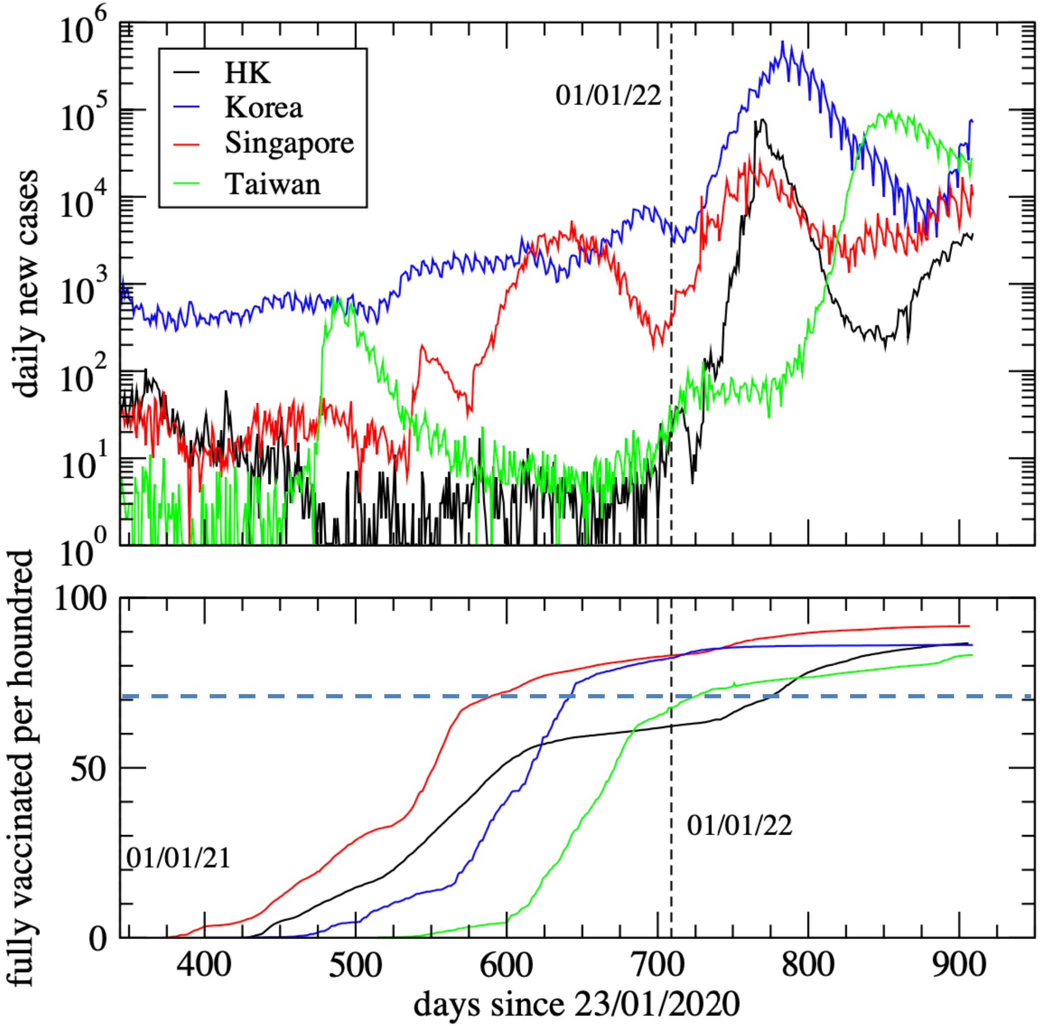




COVID-19 waves in
4-dragon countries/regions

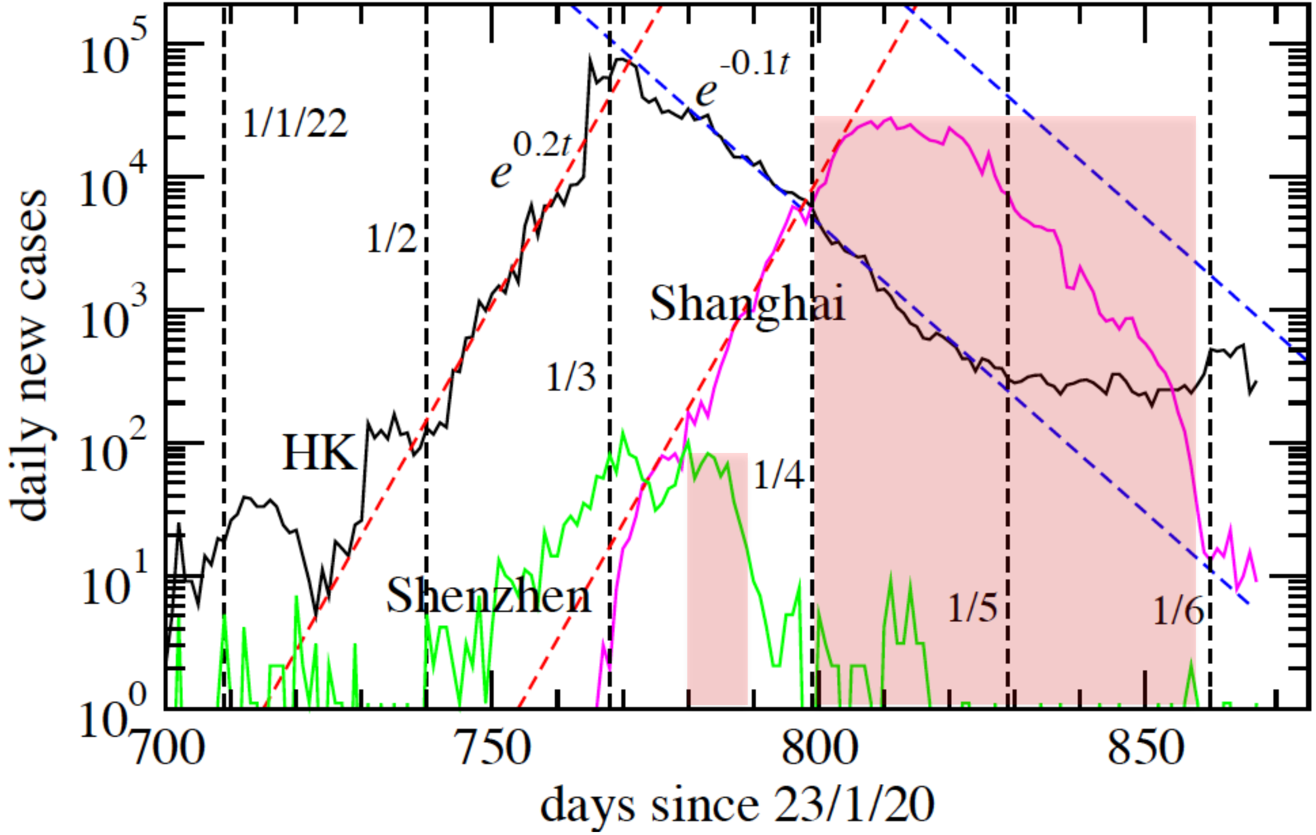
The omicron challenge

Increased vaccination (say beyond 70%) significantly slows down the growth and speeds up the decline of a new wave



Omicron waves in HK, Shenzhen and Shanghai

Growth rate
day



near lockdown

Community-wide qPCR testing implemented in Shenzhen and Shanghai on routine basis to curb hidden transmission by asymptomatic viral carriers

The SEIR model
susceptible-exposed-infected-recovered

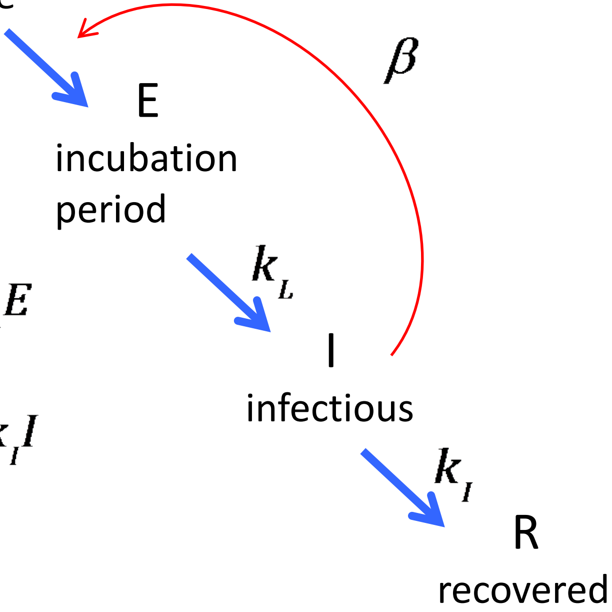
incubation-infectious-recovered/removed (this work)

Compartmentalized model for disease progression

Kermack, W.O. & McKendrick, A.G. A contribution to the mathematical theory of epidemics. Proc R Soc Lond A 115, 700-721 (1927).

Disease progression and isolation (SEIR model)

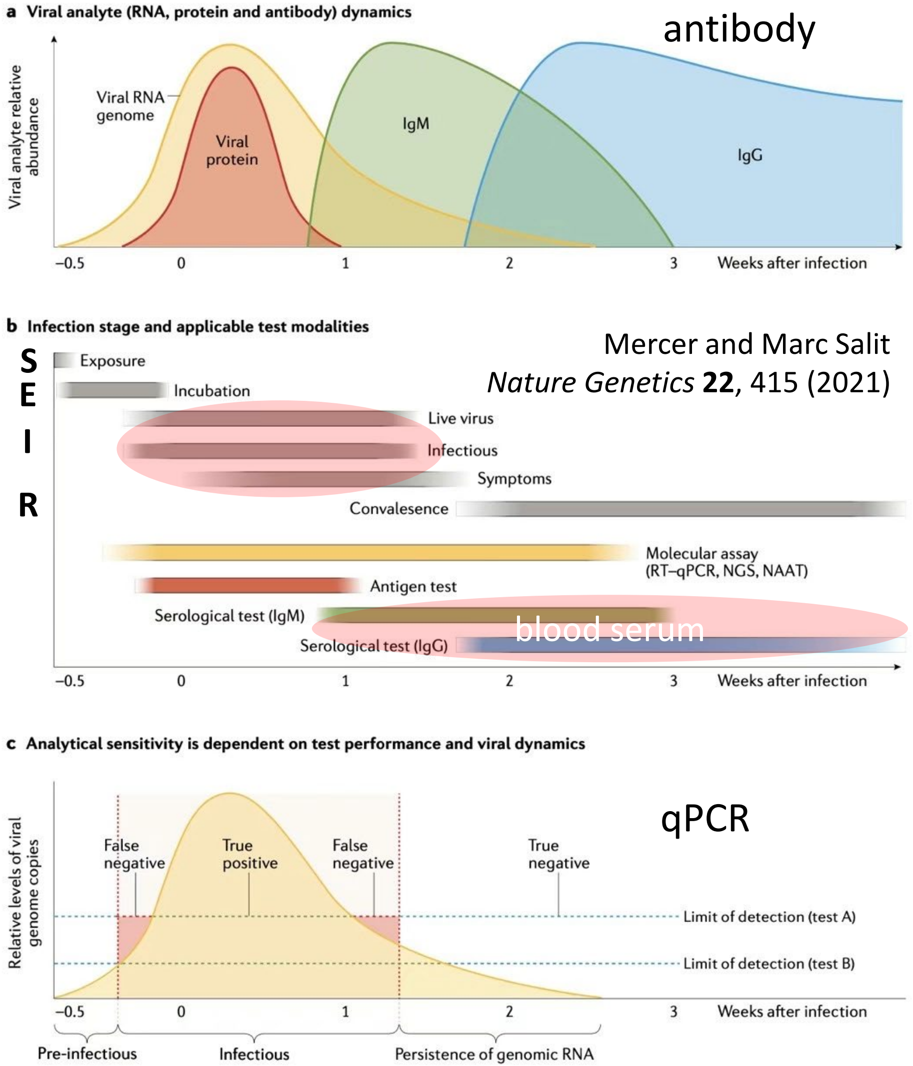
S
susceptible



$$\frac{dE}{dt} = \beta I - k_L E$$

$$\frac{dI}{dt} = k_L E - k_I I$$

$$\frac{dR}{dt} = k_I I$$



Mercer and Marc Salit
Nature Genetics **22**, 415 (2021)

Disease progression and isolation (SEIR model)

$$\begin{tikzcd}
\text{S (susceptible)} \arrow[dr] & & & \\
& \text{E (incubation period)} \arrow[dr, "k_L"] & & \\
& & \text{I (infectious)} \arrow[dr, "k_I"] \arrow[ul, bend right, "\beta"'] & \\
& & & \text{R (recovered)}
\end{tikzcd}$$

$$\frac{dE}{dt} = \beta I - k_L E$$

$$\frac{dI}{dt} = k_L E - k_I I$$

$$\frac{dR}{dt} = k_I I$$

Probability that a person infected at $t = 0$ is infectious at time t:

$$\boxed{\rho(t) = \frac{k_L}{k_I - k_L}\left(e^{-k_L t} - e^{-k_I t}\right)}$$

Laplace transform

$$\hat{\rho}(\lambda) \equiv \int_0^\infty \rho(t) e^{-\lambda t}\, dt = \frac{k_L}{(\lambda + k_L)(\lambda + k_I)}$$

Reproduction number

$$R_0 = \int_0^\infty \rho(t) \beta dt = \beta \hat{\rho}(0) = \frac{\beta}{k_I}$$

Disease progression and isolation (SEIR model)

S
susceptible

E
incubation period

I
infectious

R
recovered

β

k_L

k_I

$$\frac{dE}{dt} = \beta I - k_L E$$

$$\frac{dI}{dt} = k_L E - k_I I$$

$$\frac{dR}{dt} = k_I I$$

Renewal process

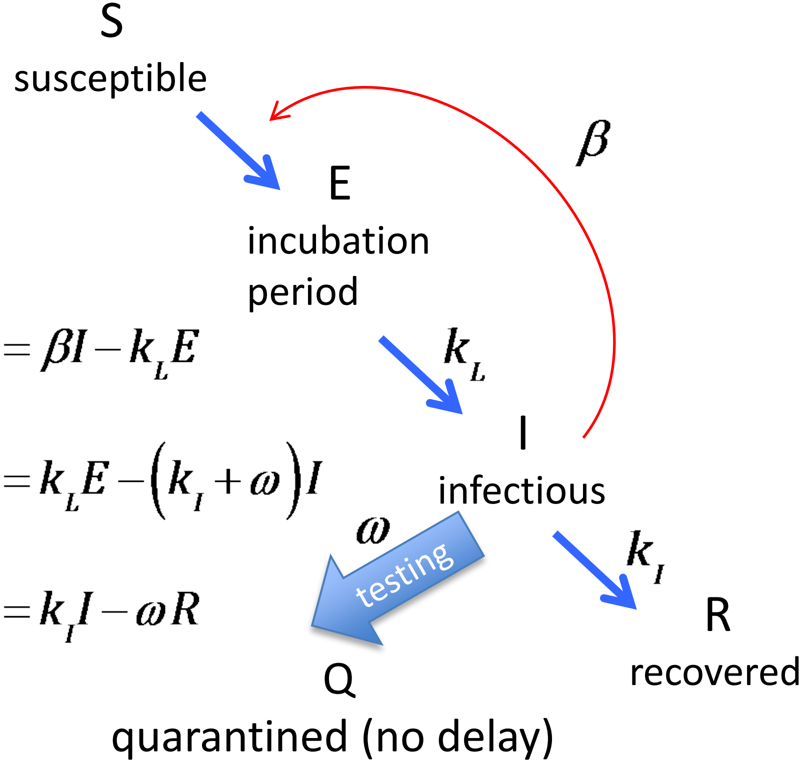
$$\boxed{E(t) = \int_{-\infty}^{t} \rho(t - t_1) E(t_1) \beta \, dt_1}$$

Exponential growth

$$\boxed{E(t) = E_0 e^{\lambda t} \quad \Rightarrow \quad \beta \hat{\rho}(\lambda) = 1}$$

$$\lambda = -\frac{k_L + k_I}{2} + \sqrt{\left(\frac{k_L + k_I}{2}\right)^2 + (R_0 - 1) k_L k_I}$$

Testing



$$\frac{dE}{dt} = \beta I - k_L E$$

$$\frac{dI}{dt} = k_L E - (k_I + \omega) I$$

$$\frac{dR}{dt} = k_I I - \omega R$$

Probability that a person infected at $t = 0$
Is infectious at time t:

$$\rho_E(t) = \frac{k_L}{k_I + \omega - k_L}\left(e^{-k_L t} - e^{-(k_I+\omega)t}\right)$$

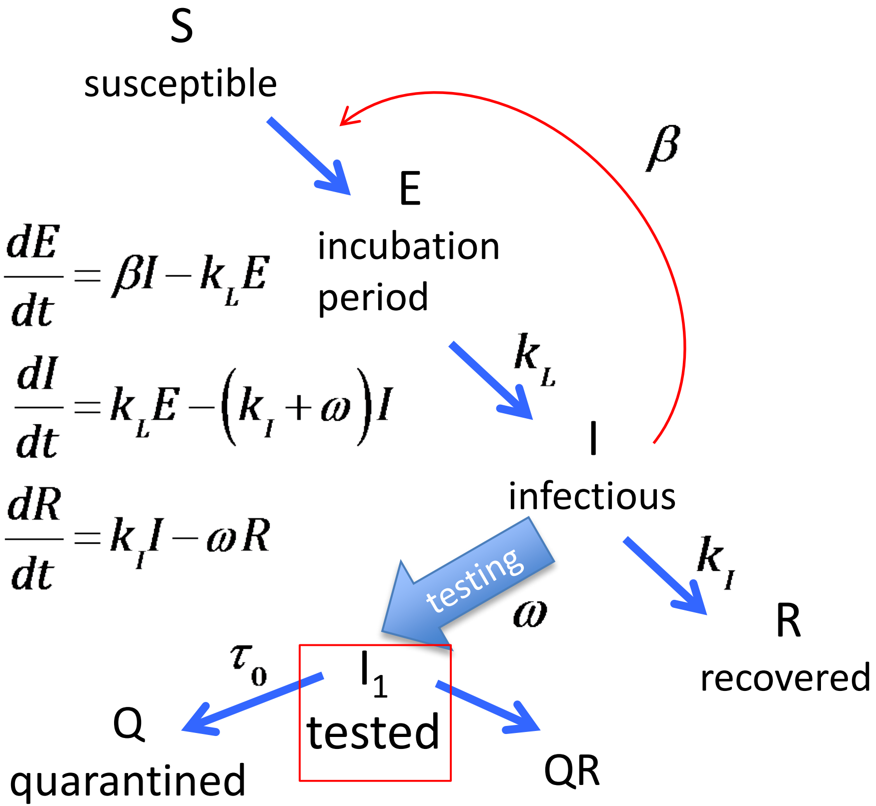
$$\hat{\rho}_E(\lambda) = \frac{k_L}{(\lambda + k_L)(\lambda + k_I + \omega)}$$

Reproduction number: $R_E = \beta \hat{\rho}_E(0) = \dfrac{\beta}{k_I + \omega}$

Rate of exponential growth:

$$\lambda_E = -\frac{k_L + k_I + \omega}{2} + \sqrt{\left(\frac{k_L + k_I + \omega}{2}\right)^2 + (R_E - 1) k_L (k_I + \omega)}$$

Testing with reporting delay



$$\frac{dE}{dt}=\beta I-k_L E$$

$$\frac{dI}{dt}=k_L E-(k_I+\omega)I$$

$$\frac{dR}{dt}=k_I I-\omega R$$

$$\boxed{I_1(t)=\int_0^{\tau_0} d\tau\,\omega I(t-\tau)e^{-k_I\tau}}$$

Probability that a person infected at t = 0
Is infectious at time t:

$$\rho_E(t,\tau_0)=\rho_E(t,\tau_0=0)+\int_0^{\tau_0} d\tau\,\omega\rho_E(t-\tau,\tau_0=0)e^{-k_I\tau}$$

$$\hat{\rho}_E(\lambda)=\left(1+\omega\frac{1-e^{-(\lambda+k_I)\tau_0}}{\lambda+k_I}\right)\hat{\rho}_E(\lambda,\tau_0=0)$$

Reproduction number:

$$R_E=\beta\hat{\rho}_E(0)=R_0\left(1-\frac{\omega}{k_I+\omega}e^{-k_I\tau_0}\right)$$

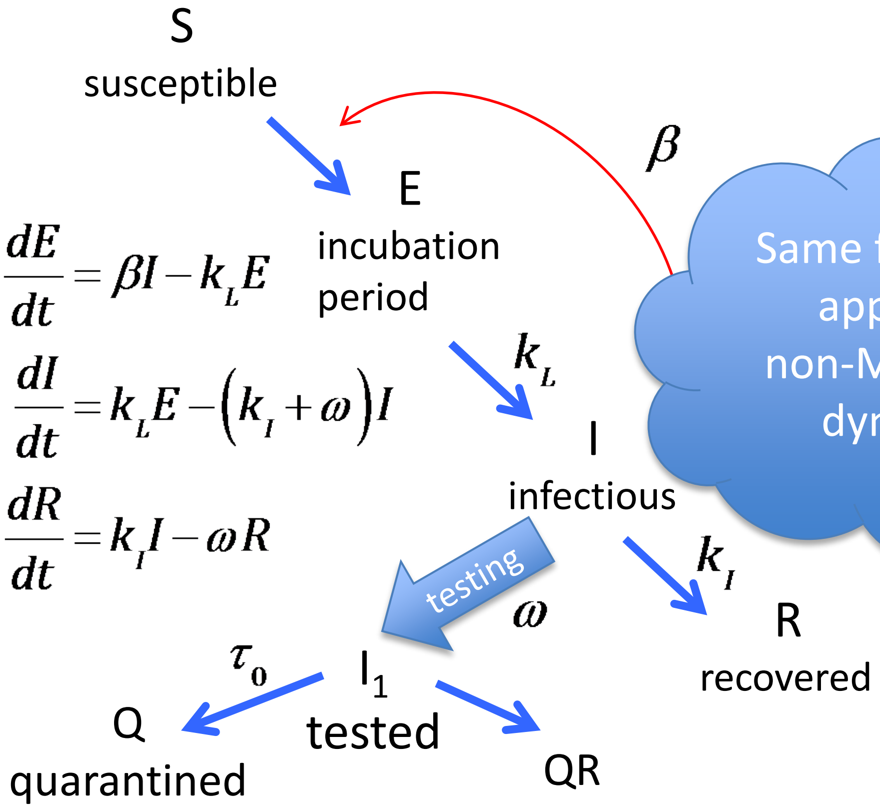
Testing with reporting delay

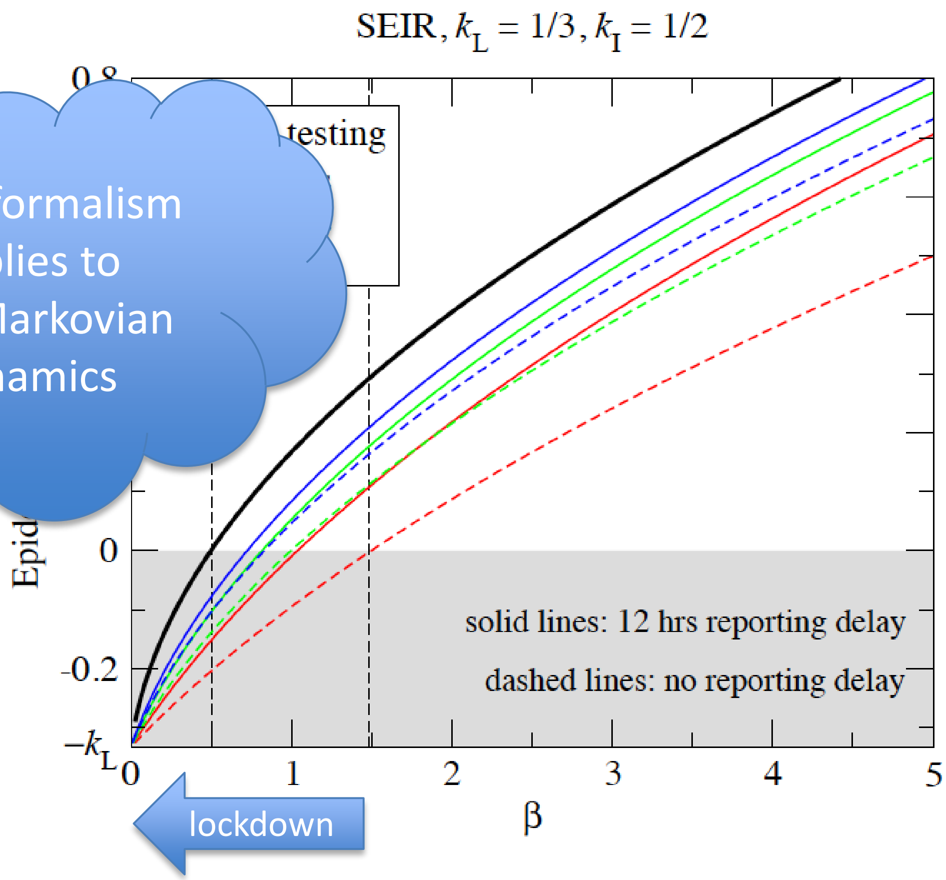
Exponential growth: $\boxed{\beta\hat{\rho}_E(\lambda)=1}$

$$\frac{dE}{dt}=\beta I-k_L E$$

$$\frac{dI}{dt}=k_L E-\left(k_I+\omega\right)I$$

$$\frac{dR}{dt}=k_I I-\omega R$$





Same formalism applies to non-Markovian dynamics

Tian L *et al.*, Nat Comm **12**, 1147 (2021)

But… what determines β ?

Challenges for precision epidemic control:

- Transmission likely to take place at “high-risk” venues and among “high-risk groups”.
- Omicron is much more transmissible than earlier variants, and a large percentage of infections are asymptomatic or with very mild symptoms.
- To be resource-efficient, control measures need to focus more on high-risk venues their roles in a complex network setting.

A location-based transmission network model for risk evaluation and pandemic control

Agent-based Model

Individual *i*

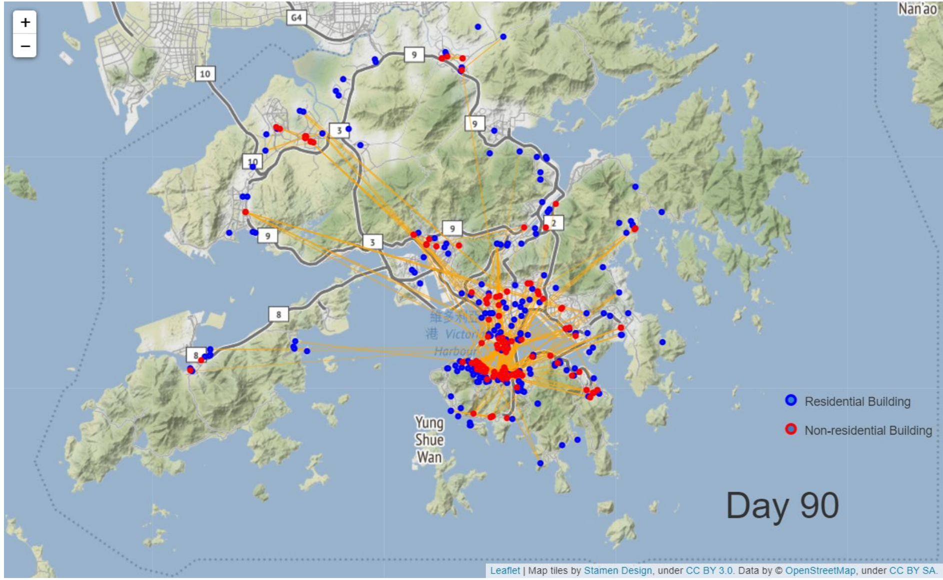
Trajectory: $\Gamma_i(t) \in$ set of locations $\{\alpha\}$

Infection rate at α: $\mu_{i\alpha}(t) r_\alpha(t)$

Total infection rate:

$$p_i(t) = p_{i,ext}(t) + \sum_\alpha \mu_{i\alpha}(t) r_\alpha(t) \delta_{\alpha,\Gamma_i(t)}$$

Risk increment if infectious: $\nu_{i\alpha}(t)$



Location α

Risk factor: $r_\alpha(t) = \sum_i \nu_{i\alpha} q_i(t) \delta_{\alpha,\Gamma_i(t)}$

Prob being infectious: $q_i(t) = \int_0^\infty \rho_E(\tau) p_i(t-\tau) d\tau$

Network formulation of transmission risk

$$r_\alpha(t) = \sum_i v_{i\alpha} q_i(t) \delta_{\alpha,\Gamma_i(t)} = \sum_i v_{i\alpha} \delta_{\alpha,\Gamma_i(t)} \int_0^\infty d\tau \rho_E(\tau) p_i(t-\tau)$$

Hence $\boxed{r_\alpha(t) = r_{\alpha,ext}(t) + \sum_\beta \int_0^\infty d\tau h(\tau) K_{\alpha\beta}(t, t-\tau) r_\beta(t-\tau)}$

with the **risk propagation matrix**

$$\boxed{K_{\alpha\beta}(t, t_1) = \sum_i v_{i\alpha}(t) \mu_{i\beta}(t_1) \delta_{\alpha,\Gamma_i(t)} \delta_{\beta,\Gamma_i(t_1)}}$$

i.e., individuals serve as agents to transfer risk from one location to another.

- Has the capacity to model a variety of behavioral and mitigation scenarios
- Delay dynamics on complex networks, analogy to excitable systems such as the human brain
- Nonlinearity can be introduced through risk aversion etc.

Exponential growth

Well-mixed: $\boxed{\beta\hat{\rho}_E(\lambda)=1}$

Under a constant transmission matrix $K_{\alpha\beta}$,

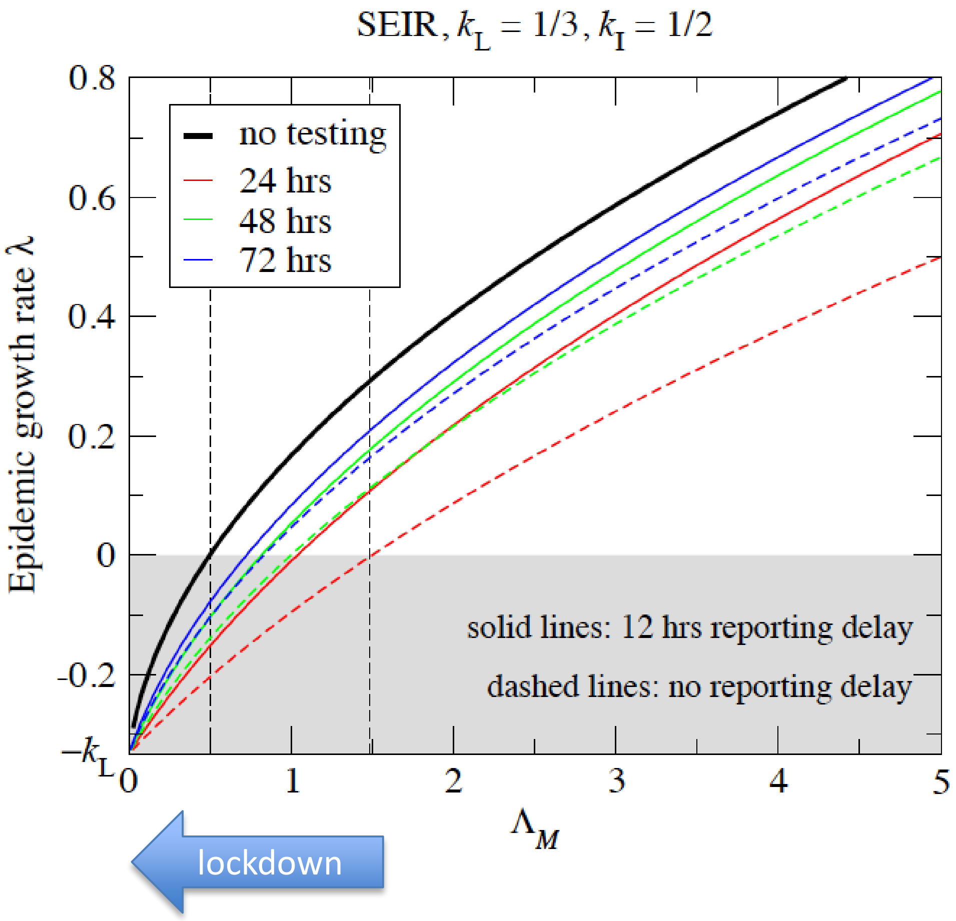
let $\quad r_\alpha(t)=a_\alpha e^{\lambda t}$

$$a_\alpha e^{\lambda t}=\sum_\beta\int_0^\infty d\tau\rho_E(\tau)K_{\alpha\beta}a_\beta e^{\lambda(t-\tau)}$$

$$=e^{\lambda t}\hat{\rho}_E(\lambda)\sum_\beta K_{\alpha\beta}a_\beta$$

$$\mathbf{K}\mathbf{a}_M=\Lambda_M\mathbf{a}_M$$

network control $\quad \boxed{\Lambda_M=\frac{1}{\hat{\rho}_E(\lambda)}} \quad$ testing contact-tracing

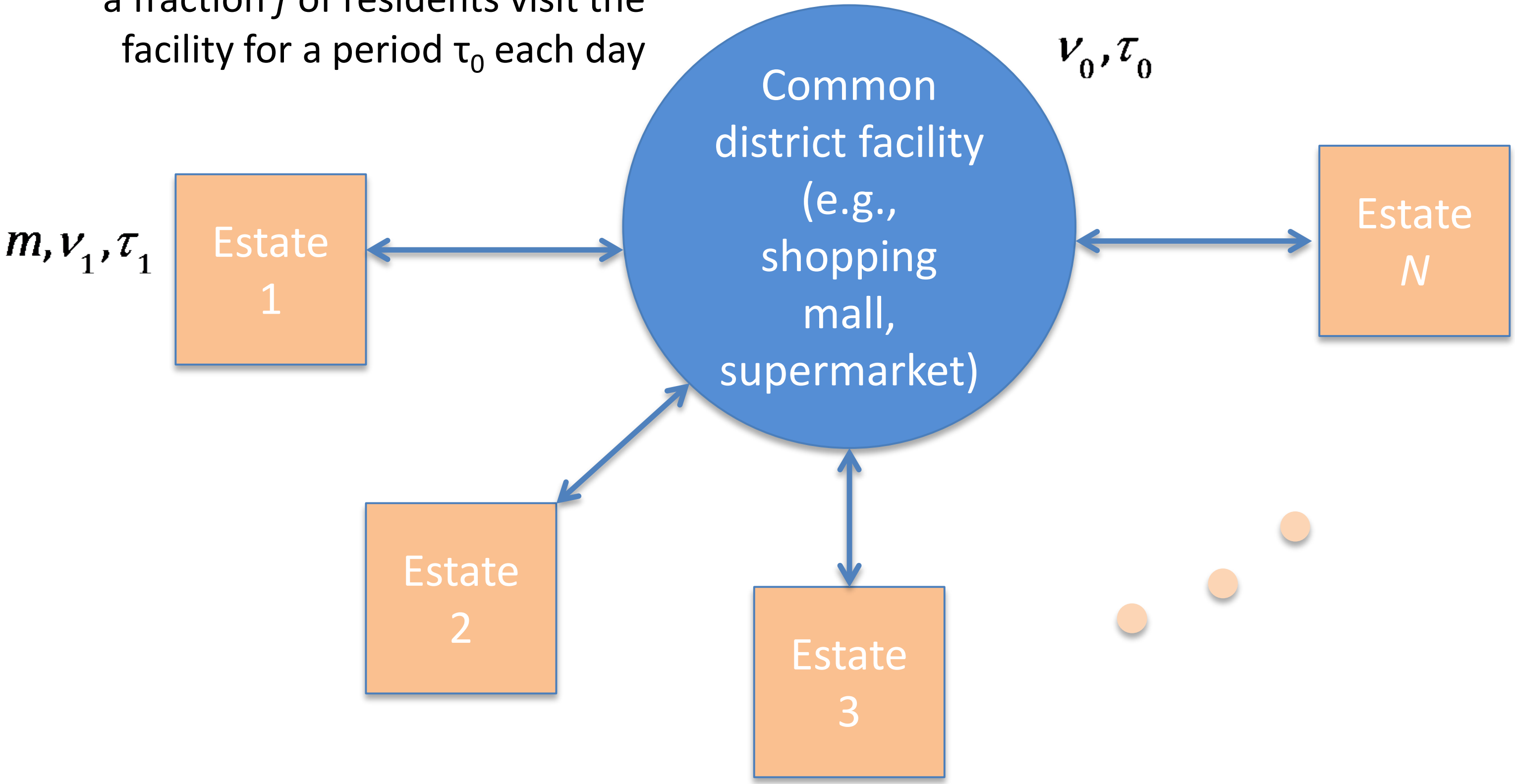


Social contact: a toy model

$$\mu_{i\alpha} = 1 \text{ day}^{-1}$$

m = # active individuals

a fraction *f* of residents visit the facility for a period τ_0 each day



Social contact: a toy model

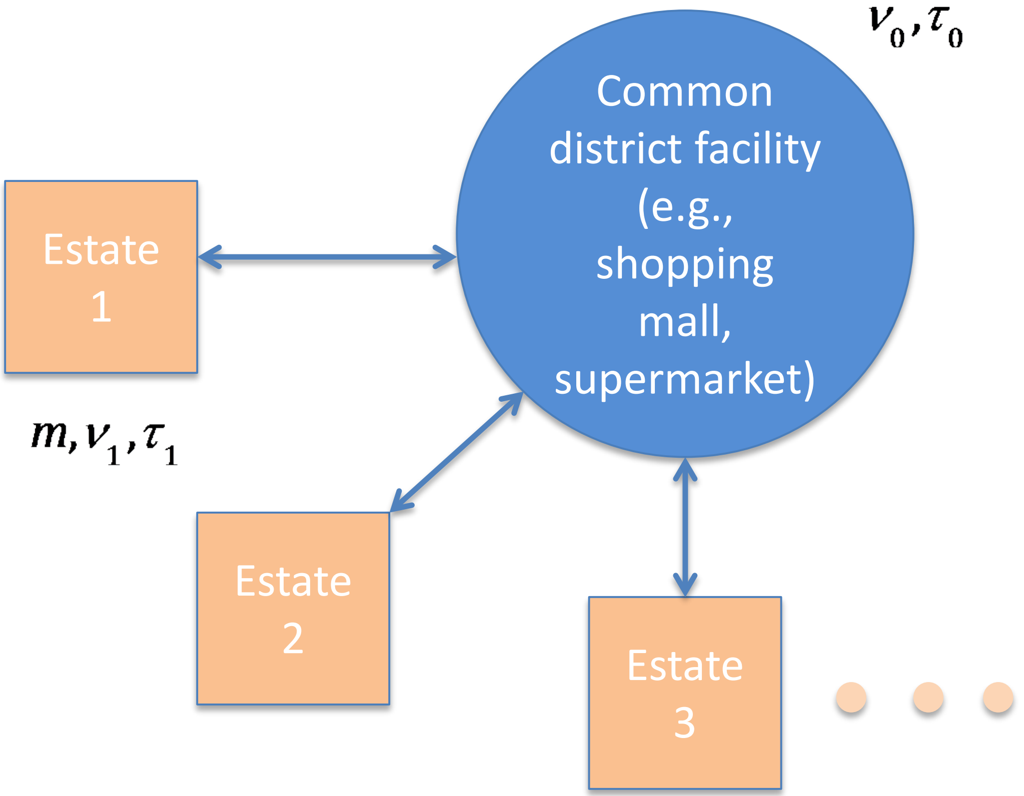
Propagation matrix:

$$K_{\alpha\beta}(t,t_1)=\sum_i v_{i\alpha}(t)\mu_{i\beta}(t_1)\delta_{\alpha,\Gamma_i(t)}\delta_{\beta,\Gamma_i(t_1)}$$

Temporal correlation of repeated visits to the common facility:

$$\left\langle \delta_{0,\Gamma_i(t)}\delta_{0,\Gamma_i(t_1)} \right\rangle = \begin{cases} f\tau_0^2, & \text{same group} \\ f^2\tau_0^2, & \text{random} \\ 0, & \left|t-t_1\right| > k_L^{-1}+k_I^{-1} \end{cases}$$

a fraction f of residents visit the facility for a period τ_0 each day



Social contact: a toy model

K_{11} = infection rate within each estate

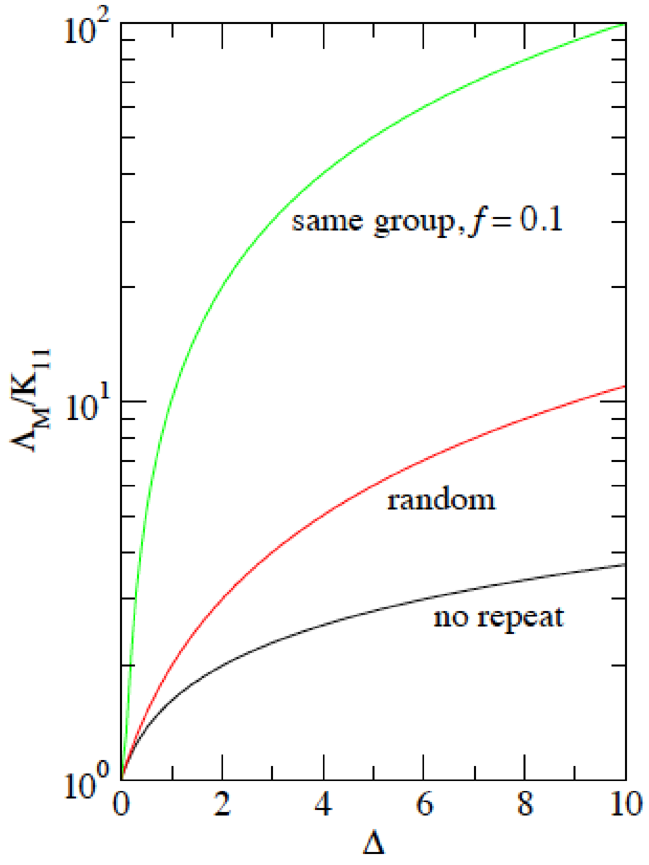
Assuming identical occupation and management of the *N* estates,

$$\begin{pmatrix} K_{00} & NK_{01} \\ K_{10} & K_{11} \end{pmatrix}\begin{pmatrix} a_0 \\ a_1 \end{pmatrix} = \Lambda_M \begin{pmatrix} a_0 \\ a_1 \end{pmatrix}$$

$$\Lambda_M = \frac{K_{11}}{2}\left[1+\gamma\Delta+\sqrt{(1-\gamma\Delta)^2+4\Delta}\right]$$

$$\Delta = Nf^2\frac{\nu_0\tau_0^2}{\nu_1\tau_1^2}, \qquad \gamma = \begin{cases} f^{-1}, & \text{same group} \\ 1, & \text{random} \\ 0, & |t-t_1| > k_L^{-1}+k_I^{-1} \end{cases}$$

Network transmission can be much reduced when successive visits are separated by an interval longer than the recovery time.



Covasim

IDM

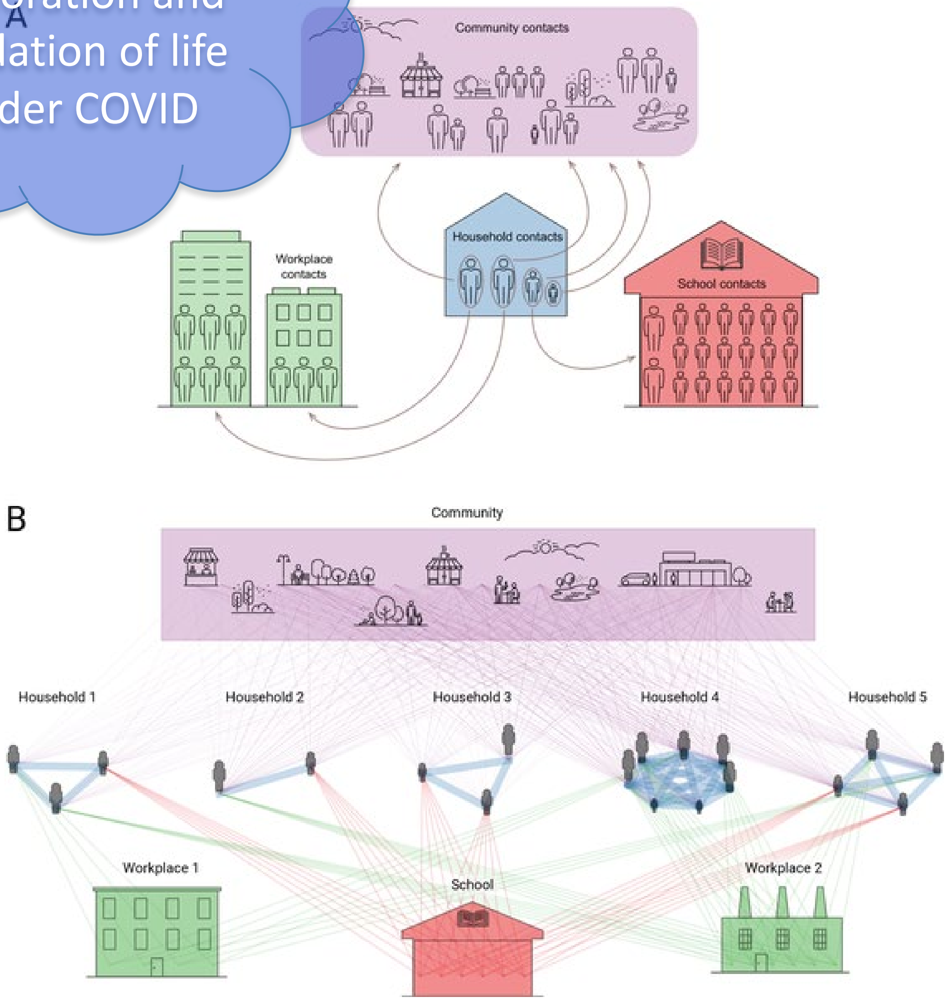
Exploration and validation of life under COVID

Covasim is a stochastic agent-based simulator, written in Python, for exploring and analyzing the COVID-19 epidemic.

Illustration of contact networks with multiple layers in Covasim.

Kerr CC, Stuart RM, Mistry D, Abeysuriya RG, Rosenfeld K, et al. (2021)

Covasim: An agent-based model of COVID-19 dynamics and interventions. PLOS Computational Biology 17(7): e1009149.



Concluding remarks

- Omicron set the bar much higher for pandemic control.

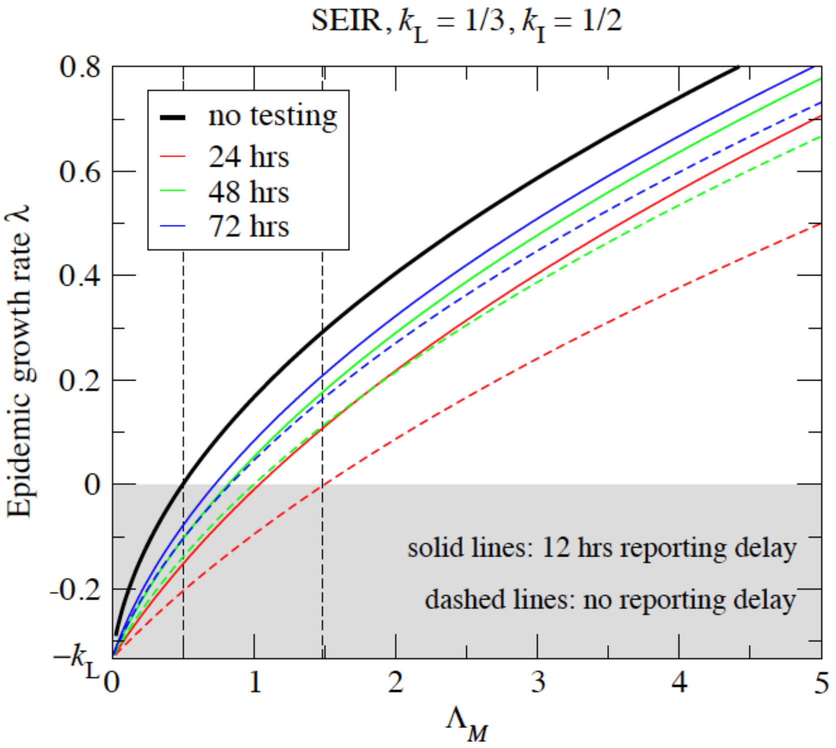
- Complex network dynamics study can offer novel strategies to manage risk based on the fundamental relation:

network control

$$\boxed{\Lambda_M = \frac{1}{\hat{\rho}_E(\lambda)}}$$

testing contact-tracing

- Exploration of clever network motifs to bring down Λ_M



Thank you for your attention!

COVID-19 Modelling Group, HKBU
Spring 2020