Advanced modeling hands-on session:

meta-population models

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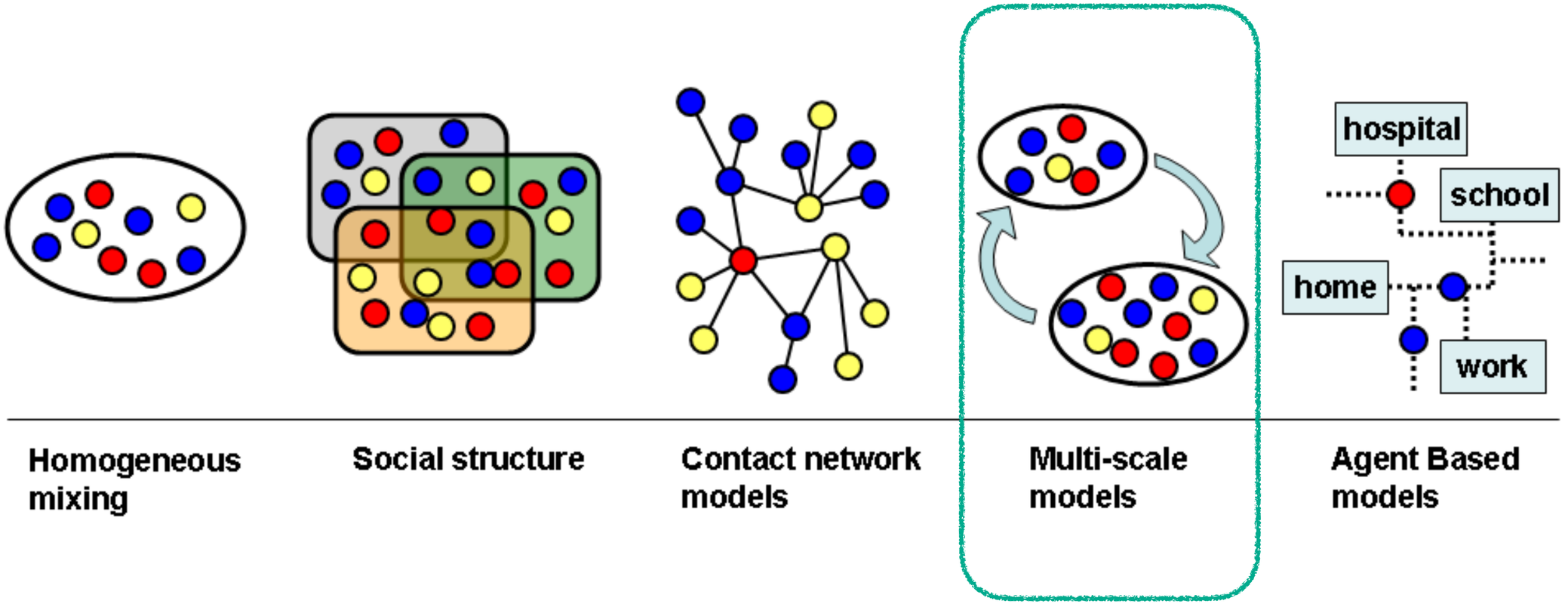
July 2 2025, Mahidol University, Bangkok

ISI Foundation

The metapopulation scheme



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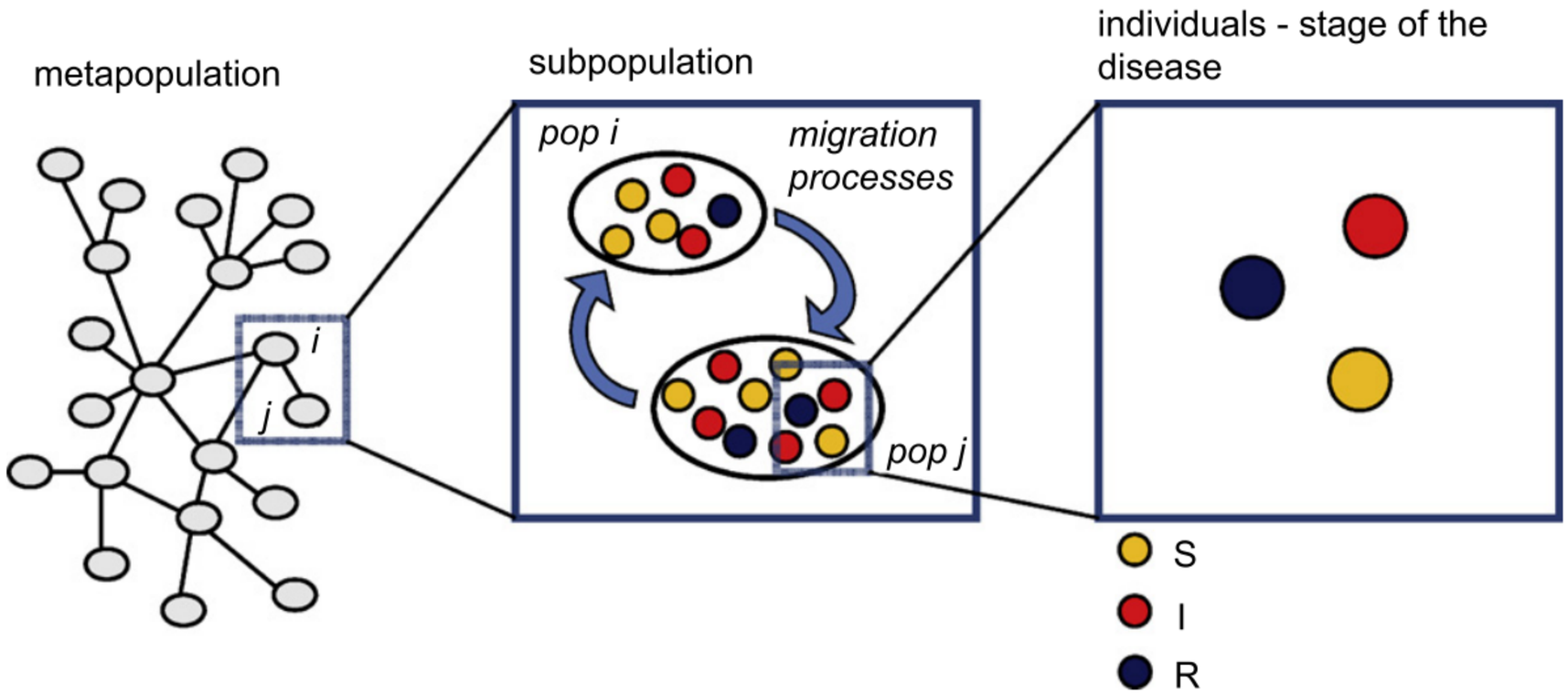


Spatially structured subpopulations (city, regions, etc).

Epidemic dynamic in each subpopulation is the same as in the single population scheme, but individuals travel

Colizza, Vespignani. Journal of Theoretical Biology 251 (2008) 450–467

Reaction-diffusion analogy for mobility

We consider a network of V populations (nodes), where each node hosts N_i individuals, which can be in state S, I or R

The total population is preserved as: $N = \sum_i N_i$

each individual moves from i to j with a diffusion rate $d_{ij} \sim$ node degree or population size or mobility matrix

Diffusion: individuals travel from one node to another

d_{ij}: rate at which an individual is moving from subpopulation i to subpopulation j

$d_{ij} = \frac{w_{ij}}{N_i}$ where w_{ij} is known real-world mobility between subpopulations

Reaction: in each subpopulation, individuals interact according to an epidemic compartmental model in homogenous mixing (mass action principle)

Colizza, Vespignani. Journal of Theoretical Biology 251 (2008) 450–467

Recap on the mass-action principle

Force of infection: the rate at which susceptible individuals become infectious

$\lambda = \beta i = \beta \frac{I}{N}$ force of infection acting within the population at each subpopulation

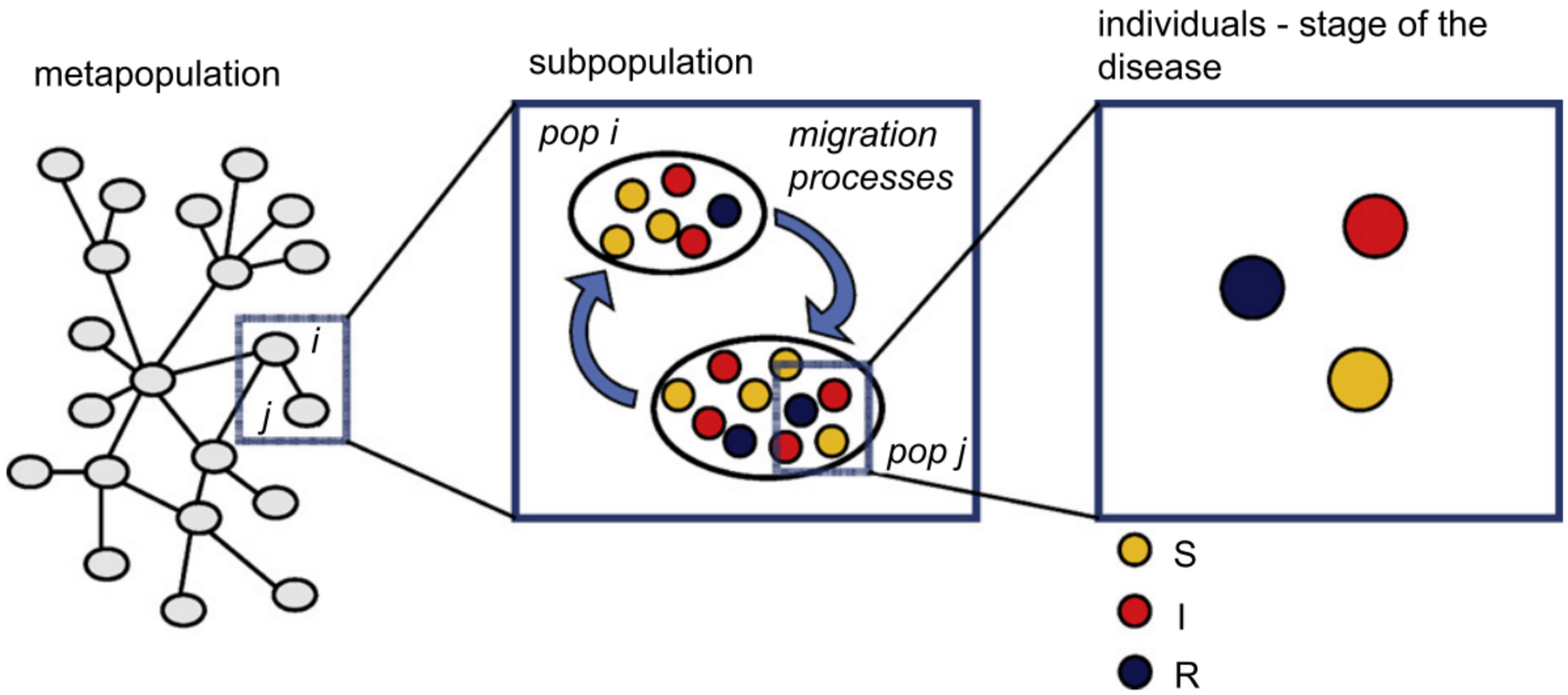
Mass-action: within each population, new infections are produced by the density of contacts of susceptible and infected individuals

$S + I \rightarrow 2I$ principle of mass-action: chemical reagents amount determines the product amount

Homogenous mixing: all individuals interact with the same rate, like particles in a box at given temperature T

$$\frac{dI}{dt} = \lambda S - \mu I = \beta S \frac{I}{N} - \mu I$$

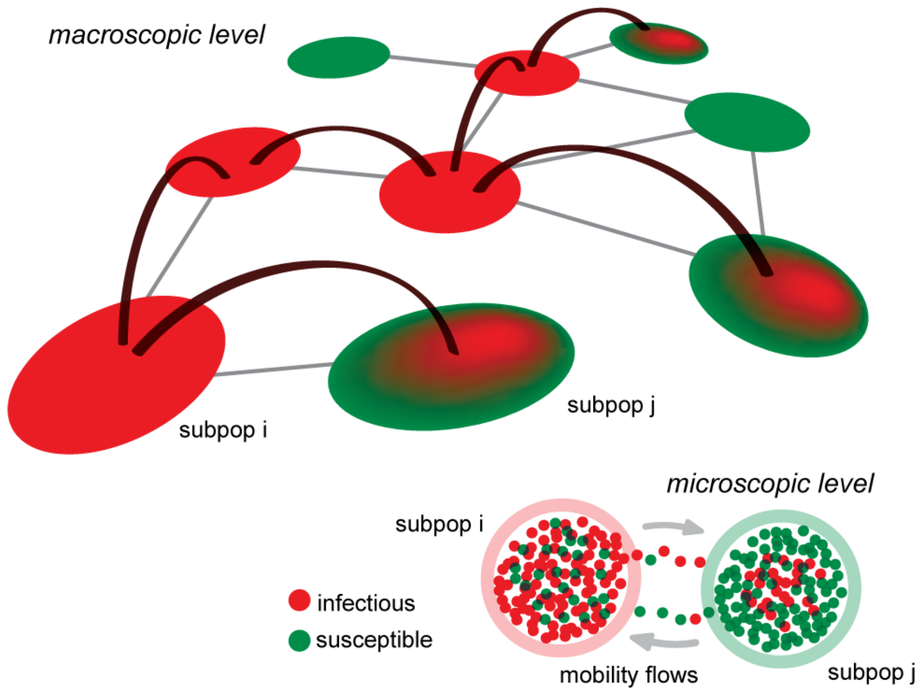
Reaction-diffusion wrap-up

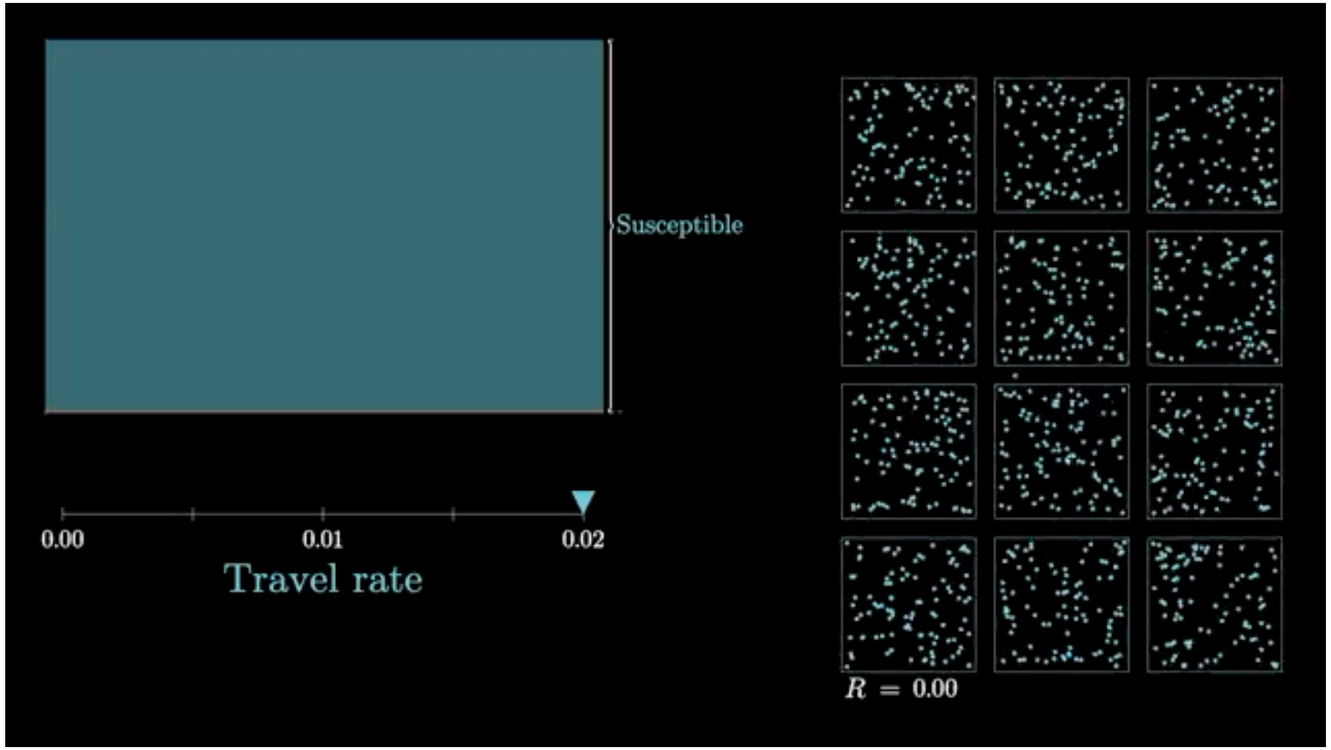


Reaction within all subpopulations
Diffusion between subpopulations

Colizza, Vespignani. Journal of Theoretical Biology 251 (2008) 450–467

The metapopulation scheme



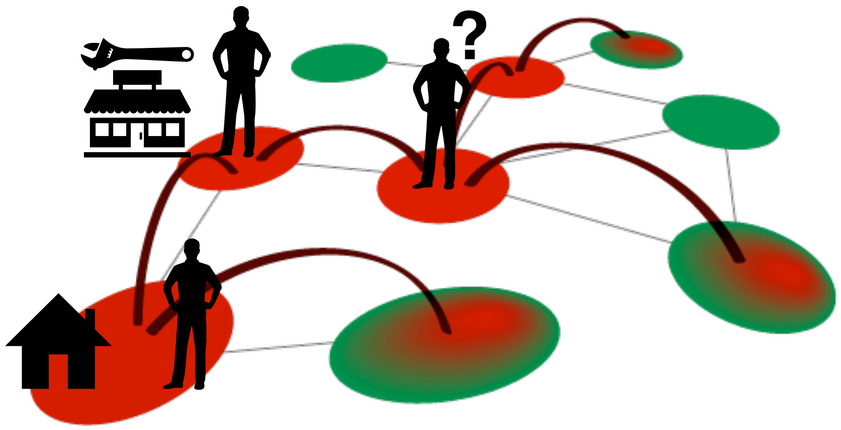


Colizza, Vespignani. Journal of Theoretical Biology 251 (2008) 450–467

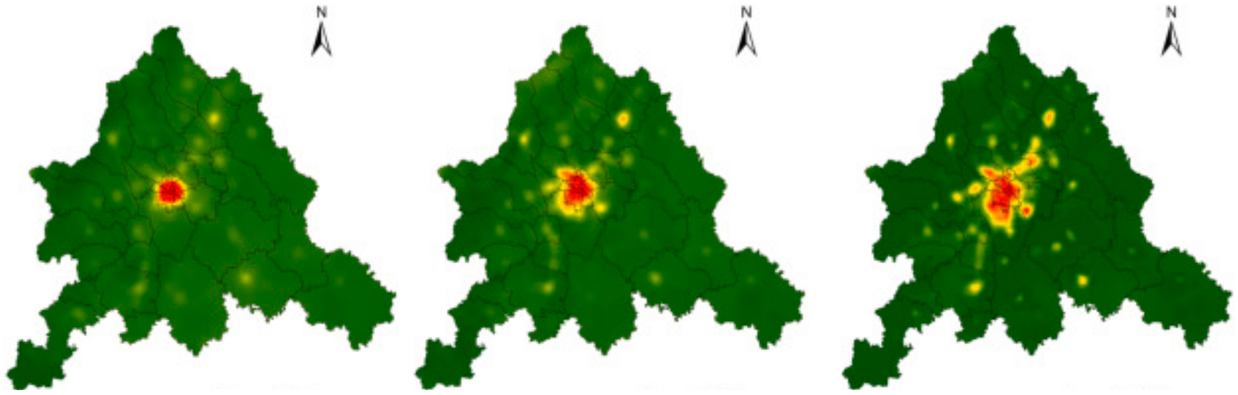
Metapopulation models with markovian mobility

Markovian mobility: individuals move among populations without memory, the probability of moving from i to j depends only on the average flows between i and j

Indistinguishability: individuals are not distinguishable, i.e. not labelled, they do not belong to a patch.
A susceptible in i moving in j might come from anywhere



non-markovianity of mobility impacts invasion threshold



Balcan D, Vespignani A. Invasion threshold in structured populations with recurrent mobility patterns. J Theor Biol. 2012

Rvachev-Longini model

Rvachev-Longini model (1985):
first model of global spread using diffusion rates in compartmental models

$x_i(t)$: number of susceptibles in i at time t

$u_i(\tau, t)$: n of exposed in i at time t who were infected at t-tau

$y_i(\tau, t)$: n of infected in i at time who were infected at t-tau

$z_i(t)$: n of recovered in i at time t

$\gamma(\tau)$: incubation period distribution

τ_1 : max of incubation period

$\delta(\tau)$: infectious period distribution

τ_2 : max of infectious period

n : n of populations $p_i(t)$: population of i, preserved

$n[1 + (\tau_1 + 1) + (\tau_2 + 1)]$ ODEs

Rvachev, Leonid A., and Ira M. Longini Jr. "A mathematical model for the global spread of influenza." Mathematical biosciences 75.1 (1985): 3-22.

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n : n of populations $p_i(t)$: population of i, preserved

$n[1 + (\tau_1 + 1) + (\tau_2 + 1)]$ ODEs

$$x_i(t) + \sum_{\tau=0}^{\tau_1} u_i(\tau, t) + \sum_{\tau=0}^{\tau_2} y_i(\tau, t) + z_i(t) = p_i, \ \forall t$$

$$x_i(t+1) = \Omega[x_i(t)] - u_i(0, t), \tag{9}$$

$$u_i(\tau+1, t+1) = [1 - \gamma(\tau)]\,\Omega[u_i(\tau, t)], \qquad \tau = 0, 1, \ldots, \tau_1 - 1, \tag{10}$$

$$y_i(\tau+1, t+1) = \begin{cases} \gamma(\tau)\,\Omega[u_i(\tau, t)] + [1 - \delta(\tau)]\,y_i(\tau, t), & \tau = 0, 1, \ldots, \tau_1, \\ [1 - \delta(\tau)]\,y_i(\tau, t), & \tau = \tau_1 + 1, \tau_1 + 2, \ldots, \tau_2 - 1, \end{cases} \tag{11}$$

$$w_i(t+1) = \sum_{\tau=0}^{\tau_1} \gamma(\tau)\,\Omega[u_i(\tau, t)], \tag{12}$$

Output
$w_i(t)$: new infected on time t

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Rvachev-Longini model

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first model of global spread using diffusion rates in compartmental models

σ_{ij} : n x n matrix of trips from i to j (symmetric!)

$p_i(t)$: population of i, preserved

Transport operator

$$\Omega[A_i(t)] = A_i(t) + \sum_{j=1}^{n} \left[A_j \frac{\sigma_{ji}}{p_j} - A_i \frac{\sigma_{ij}}{p_i} \right]$$

travel rates

$$x_i(t+1) = \Omega[x_i(t)] - u_i(0,t), \tag{9}$$

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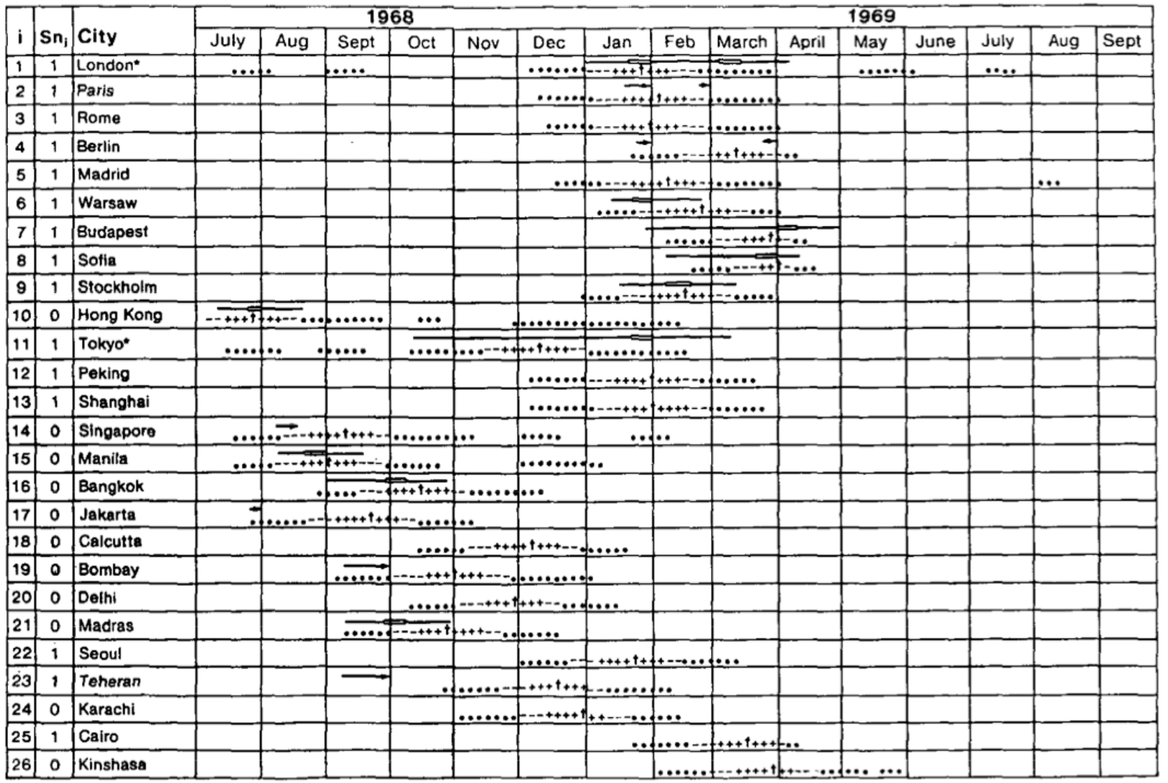
Rvachev-Longini model

Rvachev-Longini model (1985):
first model to introduce diffusion rates in compartmental models

Very complex model, high n of ODEs

Fitted very well the intensity of influenza pandemic of 1968-69 from Hong Kong in 52 cities of the world



* *Empirical data are joint with the surrounding region.*

FIG. 1. A schematic plot of the forecasted $b(t)$ and actual $a(t)$ course of the 1968–1969 influenza pandemic. Each of the following symbols represents the daily forecasted morbidity incidence per 10^5 over four calendar days: ● for $b_i(t) < 10$, - for $10 \le b_i(t) \le 100$, + for $100 > b_i(t)$, and † when the peak in morbidity occurred during the four days indicated. When a symbol falls directly on a border between months, this indicates two days in each month.

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Simpler deterministic approach

$$\begin{cases} \dfrac{dS_i}{dt} = -\beta \dfrac{S_i I_i}{N_i} + \langle \Omega_i(S) \rangle \\ \dfrac{dI_i}{dt} = \beta \dfrac{S_i I_i}{N_i} - \mu I_i + \langle \Omega_i(S) \rangle \\ \dfrac{dR_i}{dt} = \mu I_i + \langle \Omega_i(S) \rangle \end{cases}$$

Encodes the average behavior
Transport operator is averaged

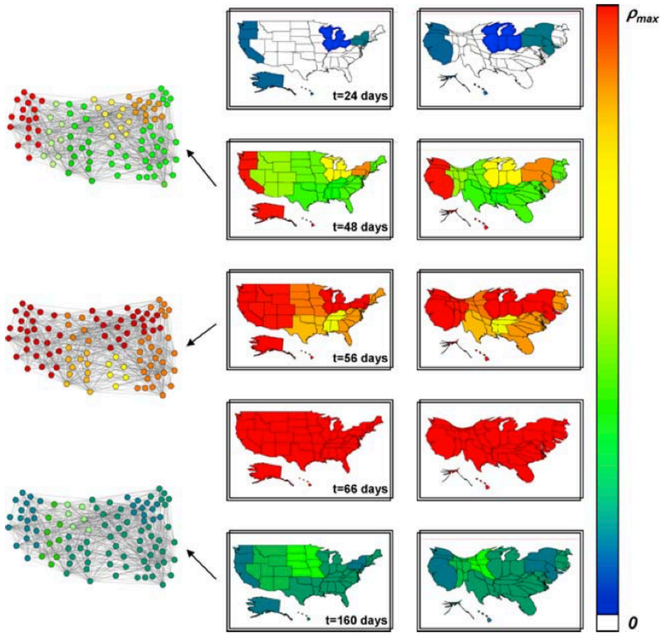

Fig. 4 Geographical representation of the evolution in the US of the SIR epidemic specified in the text with Hong Kong as initial seed. States are grouped according to the nine influenza surveillance regions. The color code corresponds to the prevalence in each region, from 0 to the maximum value reached (ρ_{max}). The first set of maps provides the original US maps, while the second shows the corresponding cartograms obtained by rescaling each region according to its population (Gastner and Newman, 2004). Three representations of the airport network restricted to the United States are also shown, corresponding to three different snapshots of the epidemic diffusion. For the sake of visualization, only the 100 airports with largest traffic in the US are shown, however the data have been obtained by using the full data set including 3100 airports. The color code is the same adopted for the maps.

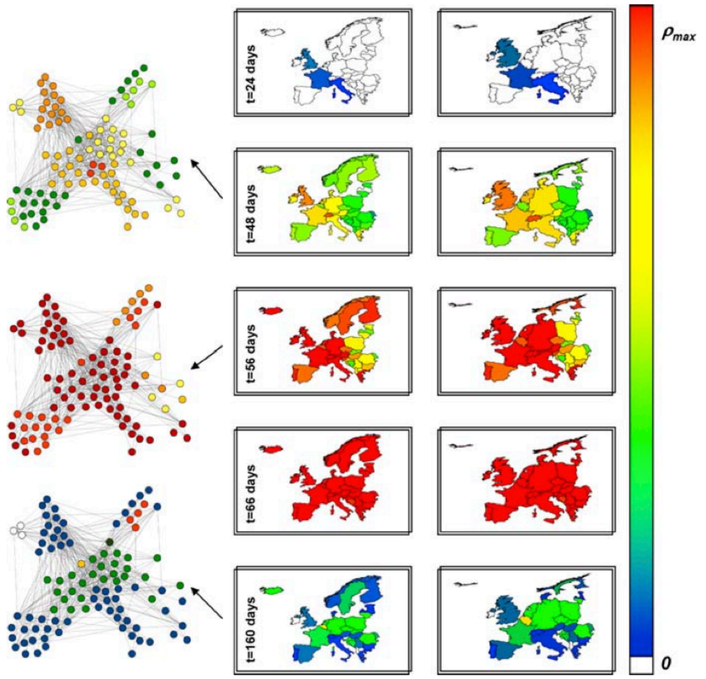

Fig. 5 Geographical representation of the evolution in Europe of the SIR epidemics starting in Hong Kong. The color code corresponds to the prevalence in each European country, from 0 to the maximum value reached (ρ_{max}). The first set of maps provides the original maps of Europe, while the second shows the corresponding cartograms obtained by rescaling each country according to its population (Gastner and Newman, 2004). Three representations of the airport network restricted to Europe are also shown, corresponding to three different snapshots of the epidemic diffusion. For the sake of visualization, only the 100 airports with largest traffic in Europe are shown, however the data have been obtained by using the full data set including 3100 airports. The color code is the same adopted for the maps.

Colizza, V., Barrat, A., Barthélemy, M., & Vespignani, A. (2006). The Modeling of Global Epidemics: Stochastic Dynamics and Predictability. Bulletin of Mathematical Biology, 68(8), 1893–1921. doi:10.1007/s11538-006-9077-9

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Hands on session
Go to https://github.com/mattiamazzoli/workshop/
Click on *metapop*
Open the *mobility modeling.ipynb* notebook

Notebook:
metapop_deterministic.ipynb

Colizza, V., Barrat, A., Barthélemy, M., & Vespignani, A. (2006). The Modeling of Global Epidemics: Stochastic Dynamics and Predictability. Bulletin of Mathematical Biology, 68(8), 1893–1921. doi:10.1007/s11538-006-9077-9

Non-markovian metapopulation models

Non-Markovian mobility: individuals move to destination j and come back to i with returning rate tau

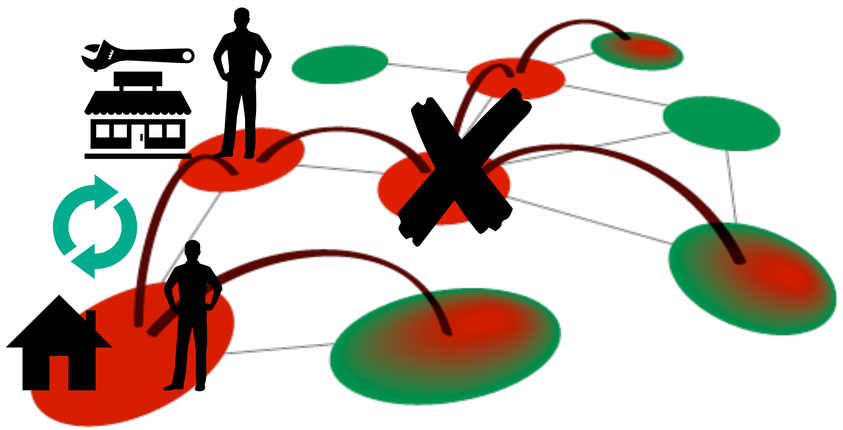
Distinguishability: individuals are distinguishable, compartments populations are labelled, they belong to a patch => i can divide between infected of i staying in i and infected of j staying in i.

$$\begin{cases} X_{ii}^m = \dfrac{X_i^m}{1+\sigma_i/\tau} \\ X_{ij}^m = \dfrac{X_i^m}{1+\sigma_i/\tau}\sigma_{ij}/\tau \end{cases}$$

σ_{ij} travel rate from i to j

σ_i total rate of travel of individuals of i

τ returning rate: 8 hours per day ~ 1/3 days-1



where X is the population of the compartment m at equilibrium

$$N_i^* = \frac{N_i}{1+\sigma_i/\tau} + \Sigma_j \frac{N_j}{1+\sigma_j/\tau}\sigma_{ji}/\tau$$

Non-markovian metapopulation models

$$\lambda_i = \frac{\lambda_{ii}}{1 + \sigma_i/\tau} + \sum_j \frac{\lambda_{ij}\sigma_{ij}/\tau}{1 + \sigma_i/\tau}$$

λ_{ii} force of infection felt by i in i

λ_{ij} force of infection on susceptibles of i when they travel to infected places j

σ_{ij} travel rate from i to j

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λ_{ii} force of infection felt by i in i

λ_{ij} force of infection on susceptibles of i when they travel to infected places j

σ_{ij} travel rate from i to j

σ_i total rate of travel of individuals of i

τ returning rate: 8 hours per day ~ 1/3 days-1

$$\lambda_{ii} = \frac{\beta}{N_i^*}\left(\frac{I_{ii}}{1+\sigma_i/\tau} + \sum_j \frac{I_j\sigma_{ji}/\tau}{1+\sigma_j/\tau}\right)$$

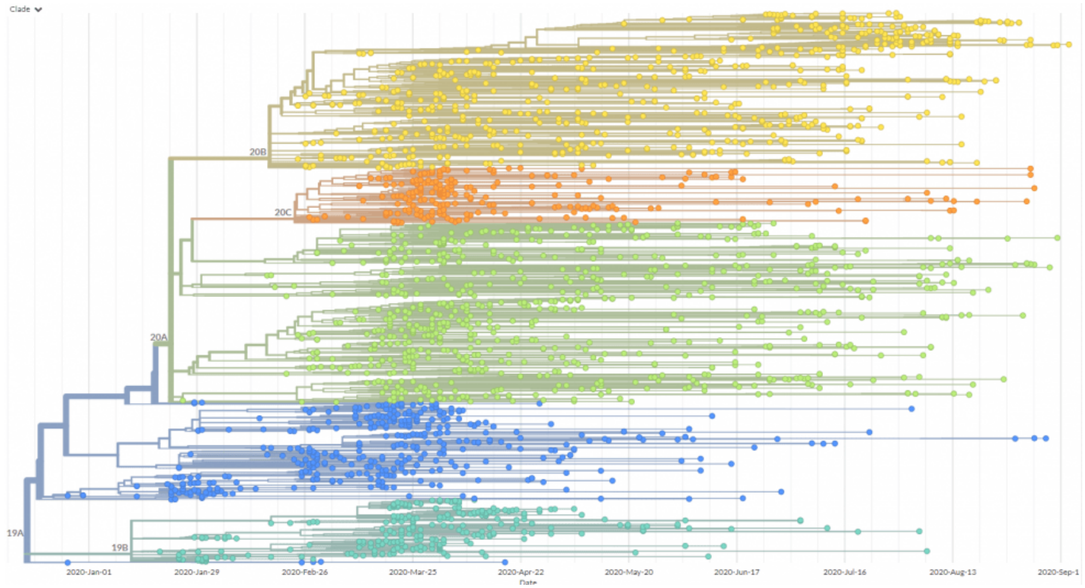
$$\lambda_{ij} = \frac{\beta}{N_j^*}\left(\frac{I_j}{1+\sigma_j/\tau} + \sum_l \frac{I_l\sigma_{lj}/\tau}{1+\sigma_l/\tau}\right)$$

Mobility and phylogeographic analyses

Phylogenetic analyses

Uses genomic data as sequenced cases of a pathogen with location and date of specimen

Make associations between sequences by minimising sequences mutations (genomic proximity) and distance (space-time proximity)



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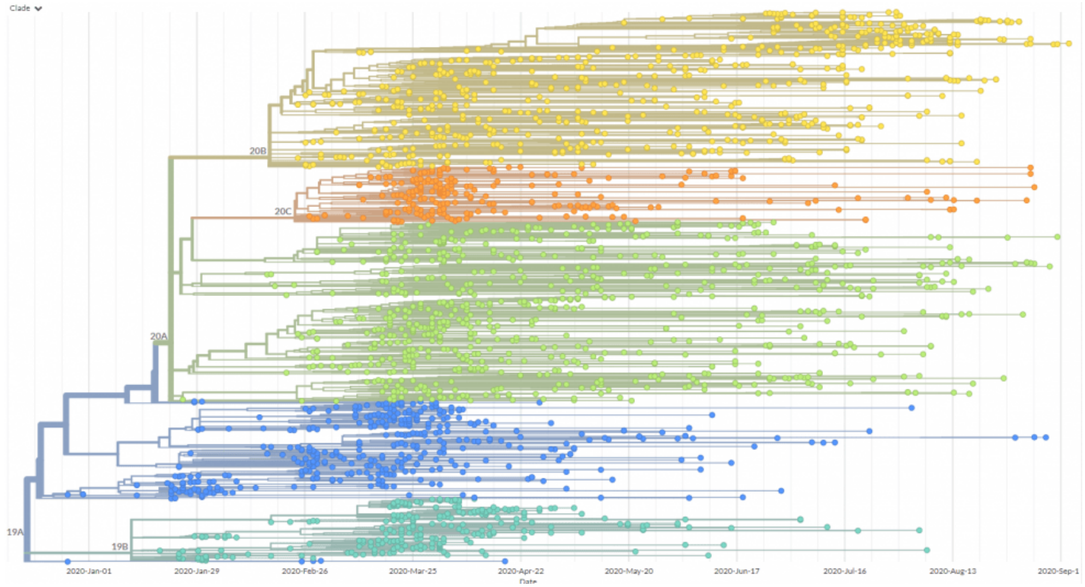
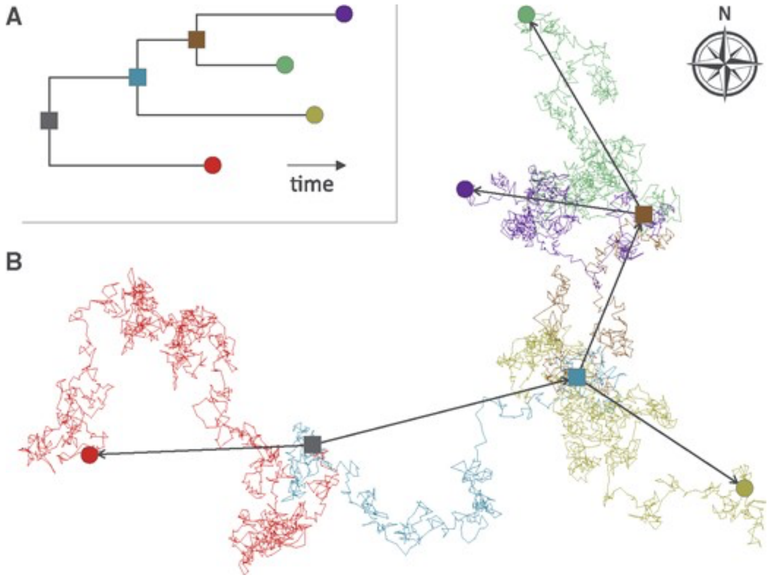
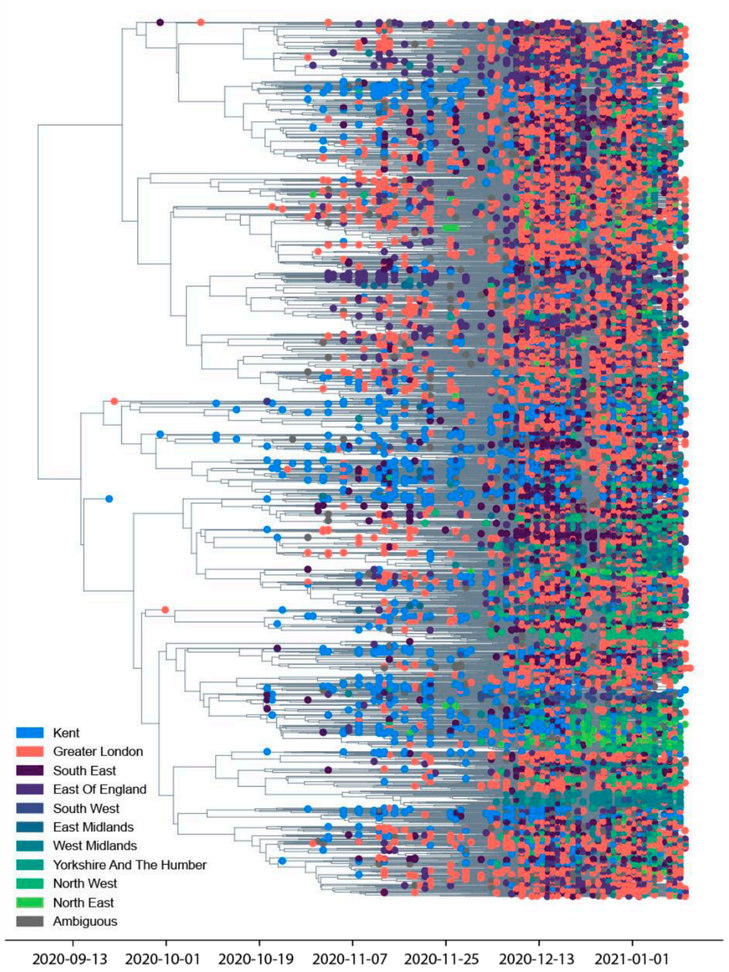
BEAST is the reference model, uses random walks instead of geographic distance to add stochasticity to estimated routes of seeding

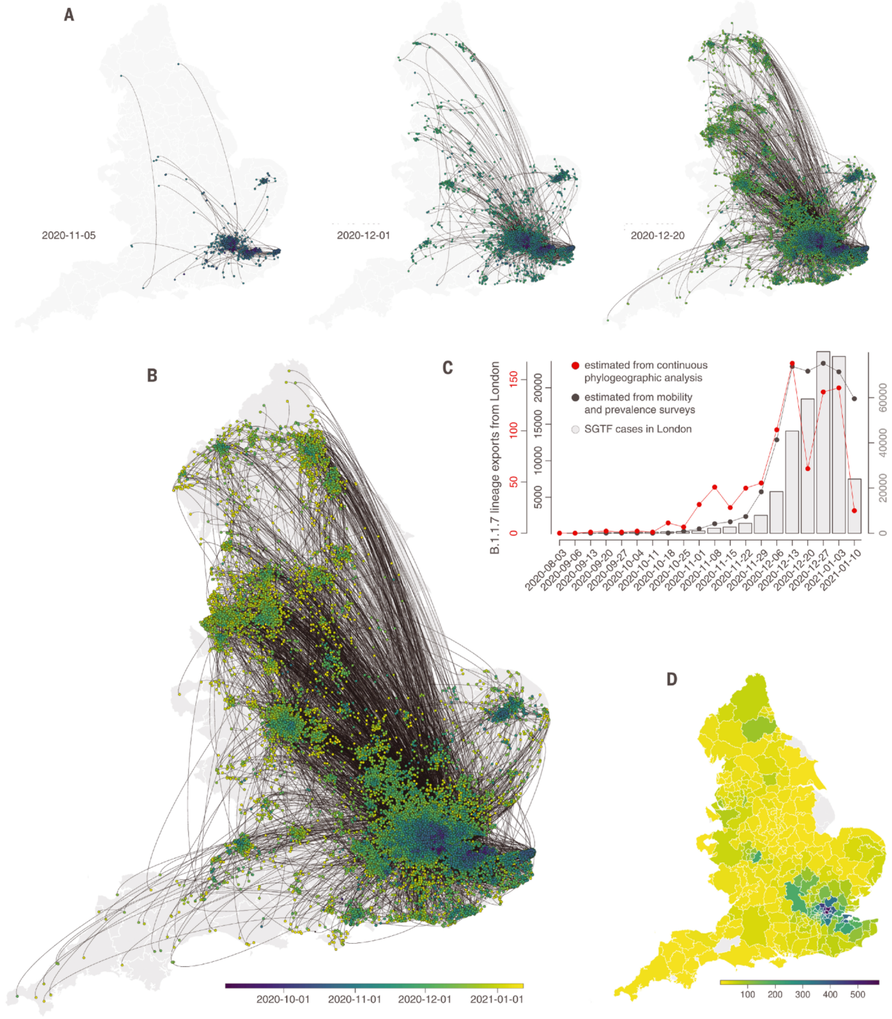




Mobility and phylogeographic analyses



spatial visualization of genomic introductions resulting from phylogenetic model

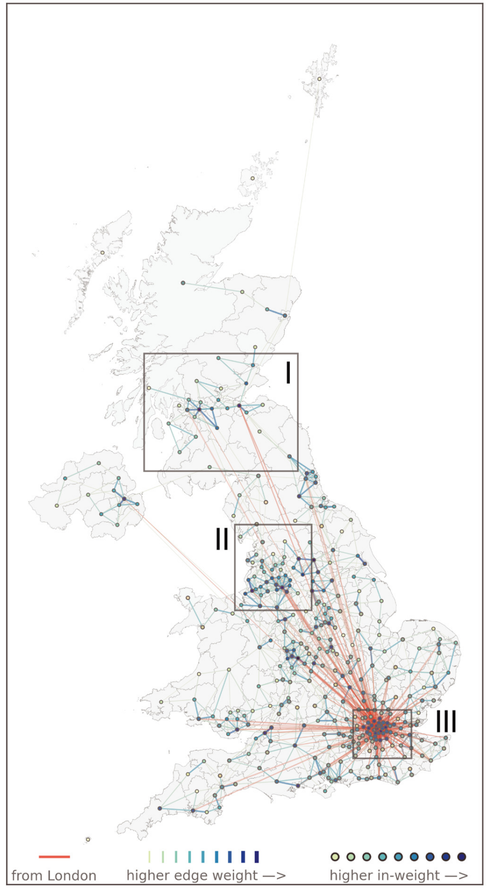


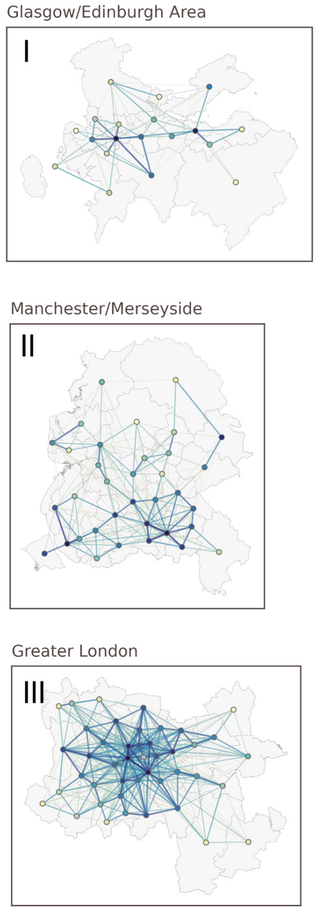
Moritz U. G. Kraemer et al. Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence.Science 373,889-895 (2021)

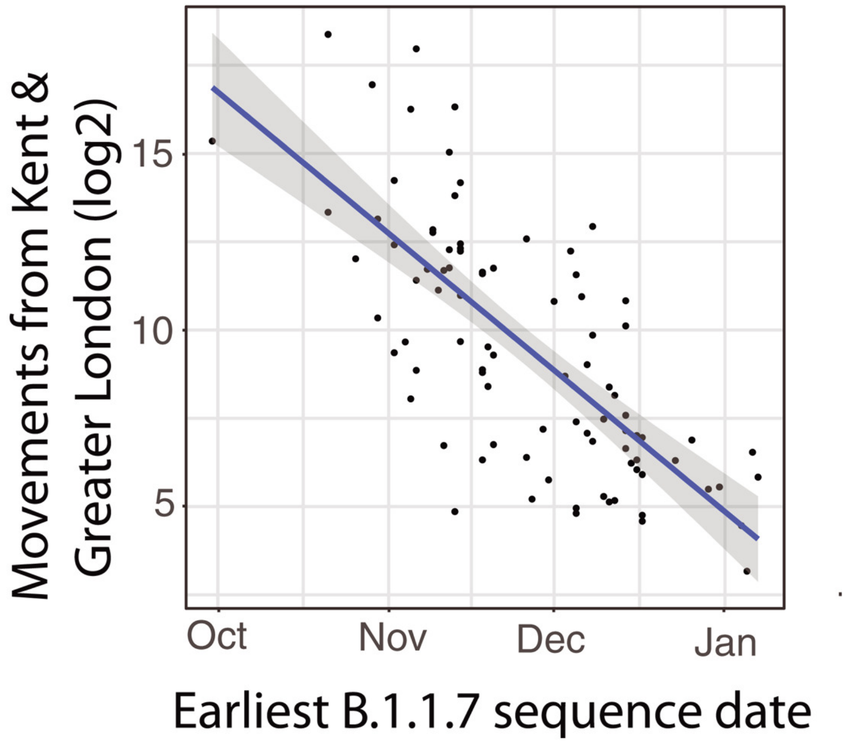
Mobility and phylogeographic analyses

relationship with mobility

mobility network of trips originating from phylogenetic identified sources in the same period







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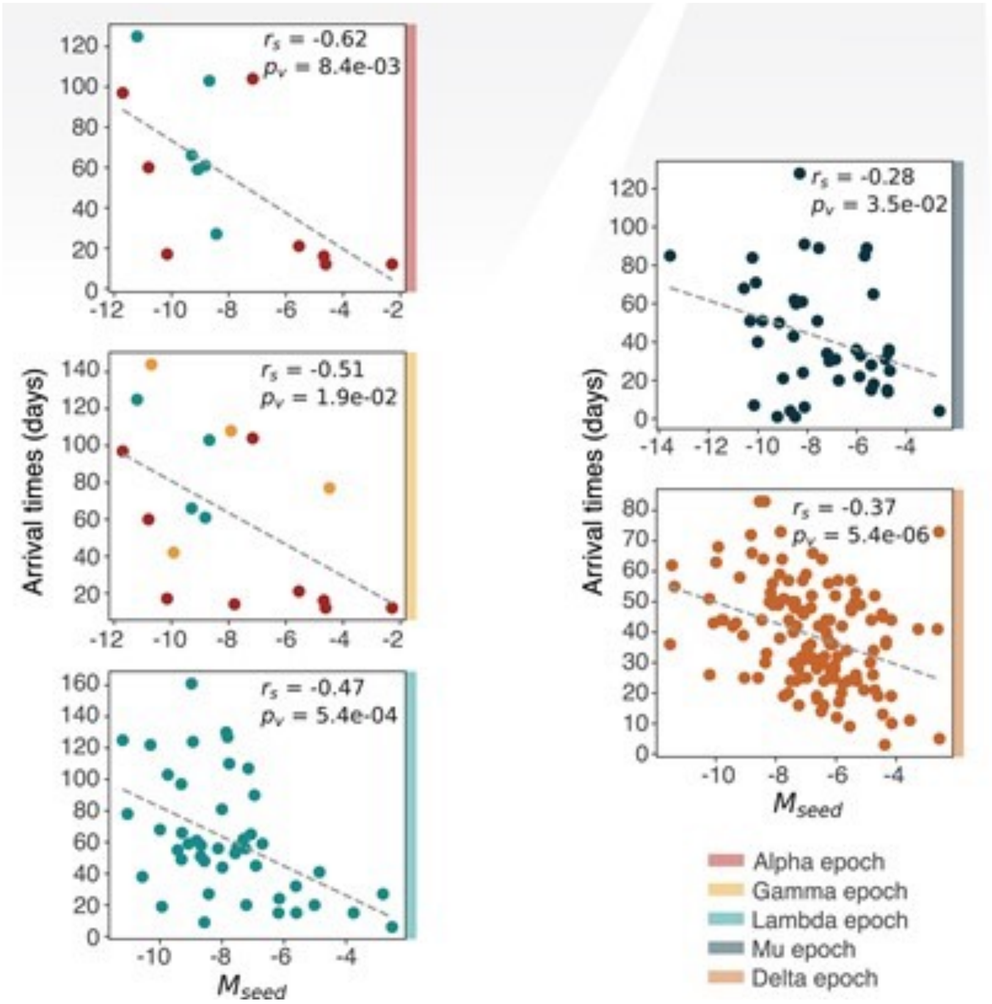
Mobility and phylogeographic analyses

Brought this to next level using municipality resolution in Chile

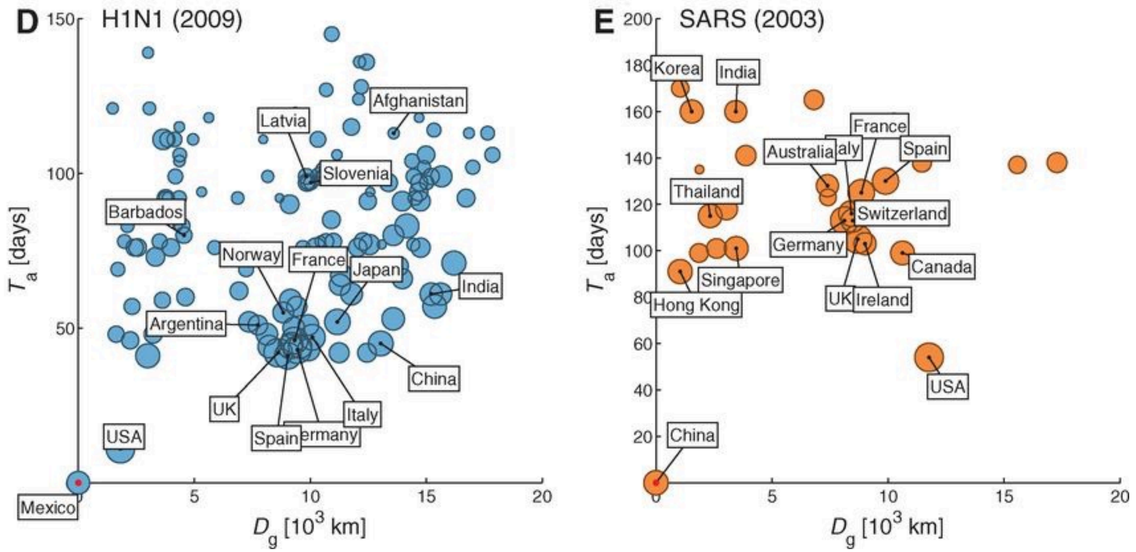
Association between first lineage introduction and mobility from the lineage source identified from phylogenetic analysis



Gutierrez, B. et al. Routes of importation and spatial dynamics of SARS-CoV-2 variants during localized interventions in Chile, *PNAS Nexus*, Volume 3, Issue 11, November 2024

The hidden geometry of epidemic spread, predicting arrival times

Predicting disease arrival times at country scale
From distance to the effective distance



Geographic distance

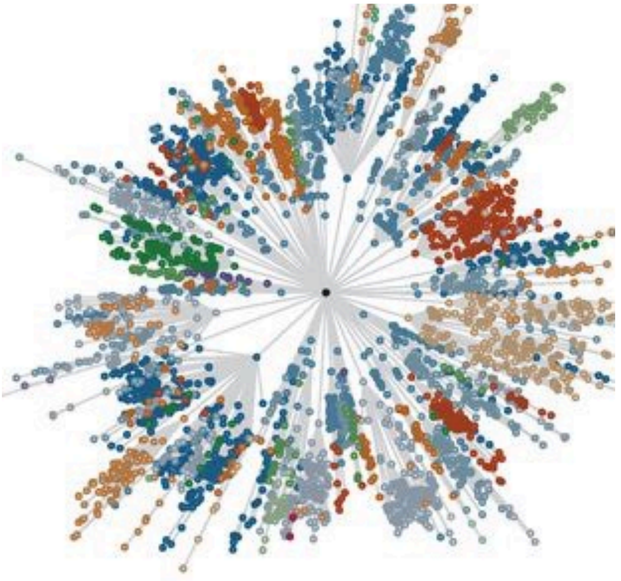
Dirk Brockmann, Dirk Helbing ,The Hidden Geometry of Complex, Network-Driven Contagion Phenomena.Science342,1337-1342(2013)

The hidden geometry of epidemic spread, predicting arrival times

$$d_{mn} = (1 - logP_{mn})$$

Flow fraction

$$D_{mn} = min_{\Gamma}\lambda(\Gamma)$$



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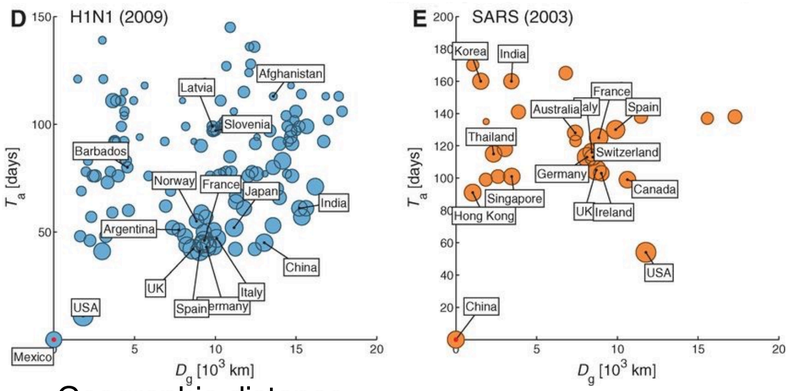

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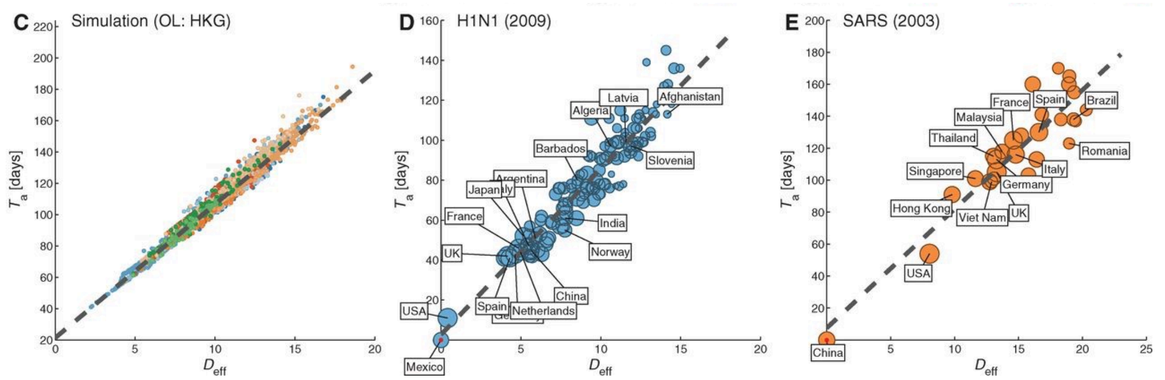


Effective distance

$$d_{mn} = (1 - logP_{mn})$$

Flow fraction

$$D_{mn} = min_{\Gamma}\lambda(\Gamma)$$

Dirk Brockmann, Dirk Helbing ,The Hidden Geometry of Complex, Network-Driven Contagion Phenomena.Science342,1337-1342(2013).DOI:10.1126/science.1245200

The hidden geometry of epidemic spread, predicting arrival times

Dirk Brockmann, YouTube

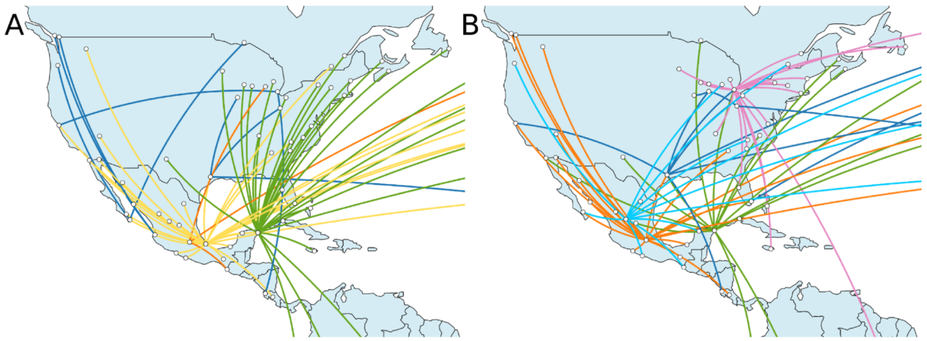
Wave-like diffusion is still there, but now it is projected in another space!

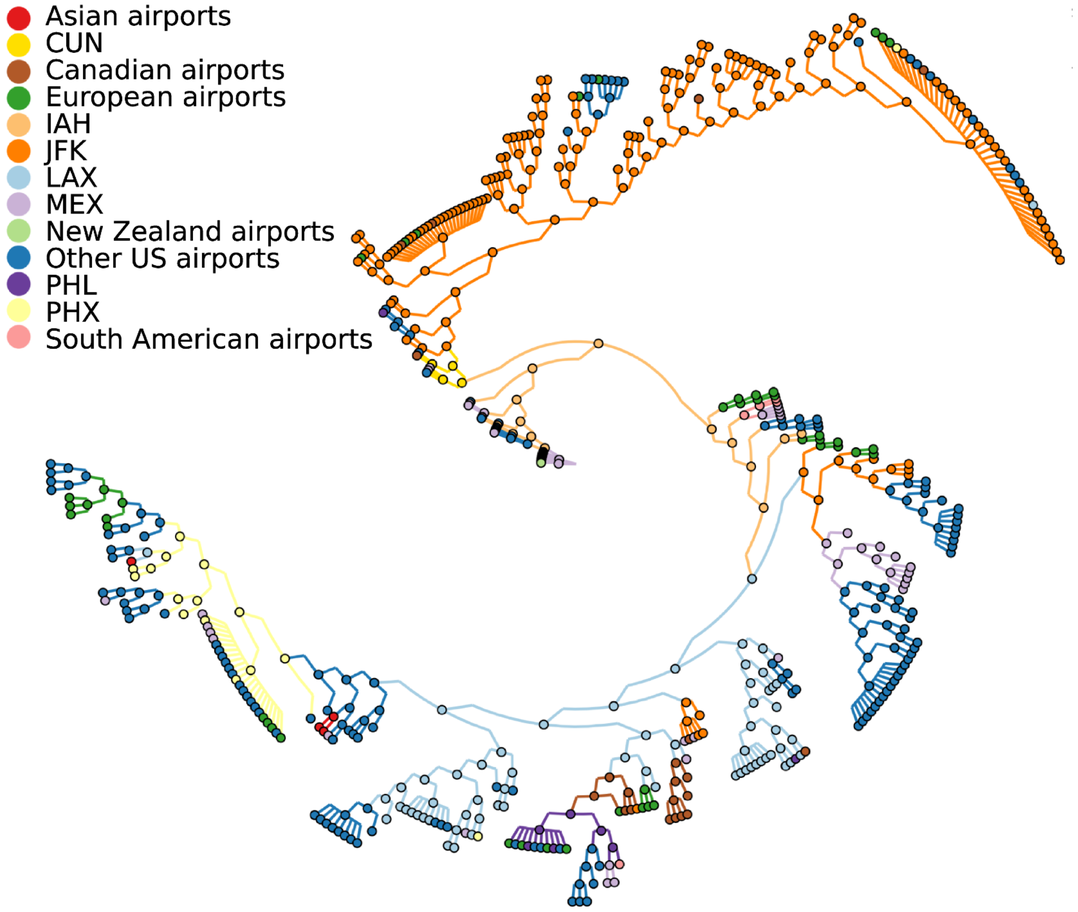
Using mobility data to inform phylogenetic models

Use phylogenetic trees on genetic sequences from H1N1 Influenza A in 2009

Phylogenetic model informed with from mobility data (air traffic data) playing as an effective distance

Performed better than informing the model with geographic distances only or BEAST that assume random walks





Reimering, S et al. "Phylogeographic reconstruction using air transportation data and its application to the 2009 H1N1 influenza A pandemic." *PLoS computational biology* 16.2 (2020): e1007101.