LIFE DATA EPIDEMIOLOGY

lect. 3: application of metapopulation models

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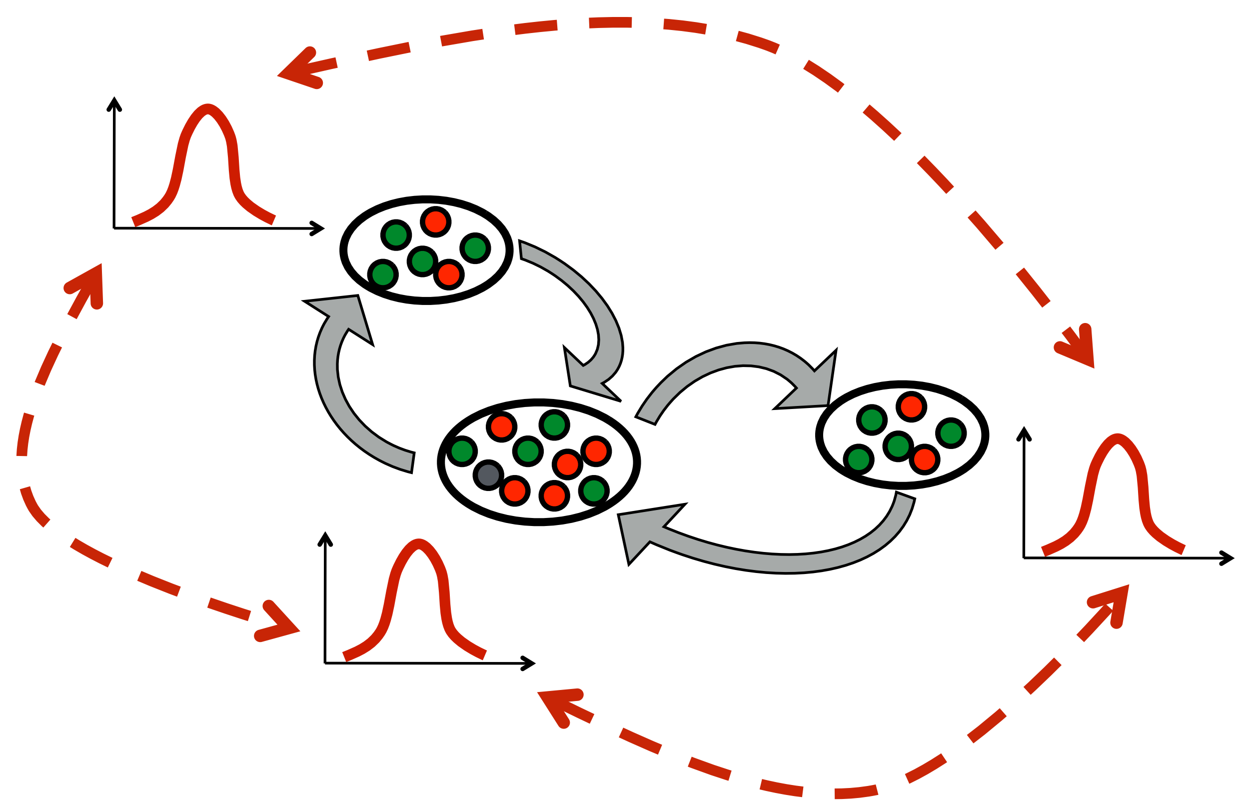
SIR metapopulation model: markovian mobility

$$\frac{dS_i}{dt} = -\beta \frac{I_i(t)S_i(t)}{N_i} + \Omega_i^S$$

$$\frac{dI_i}{dt} = \beta \frac{I_i(t)S_i(t)}{N_i} - \mu I_i(t) + \Omega_i^I$$

$$\frac{dR_i}{dt} = \mu I_i(t) + \Omega_i^R$$

$$\Omega_i^X = \sum_j \frac{w_{ji}}{N_j} X_j - \frac{w_{ij}}{N_i} X_i$$



SIR metapopulation model: markovian mobility

What can I do with that?

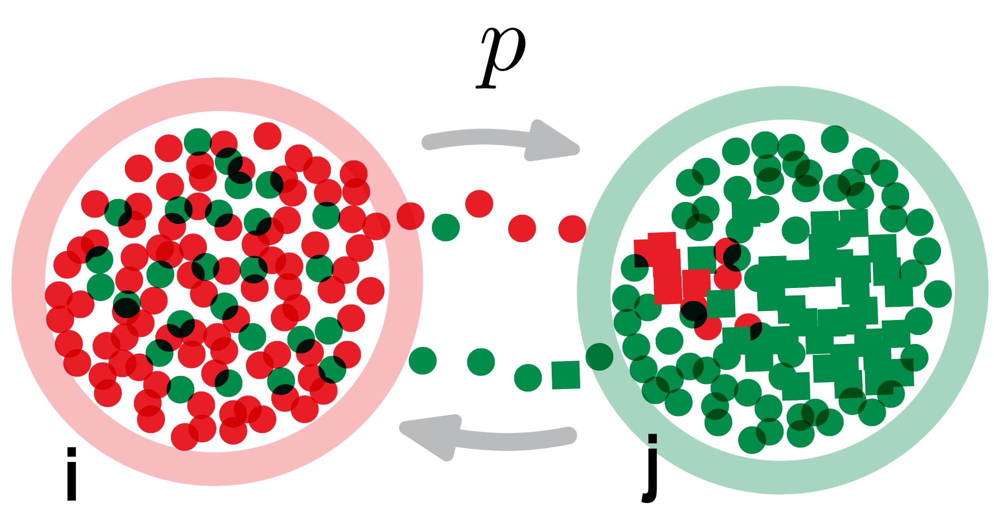
- analytical understanding
  - **spatial propagation & predictability**
  - global invasion threshold
- computer simulations

spatial propagation

Dynamics of spatial spread above the epidemic threshold

An epidemic starts in a given city i how does it spread to j, h, etc.?

seeding time (o arrival time), t_{seeding}**:** time of arrival of the first case in patch j



p traveling probability from i to j

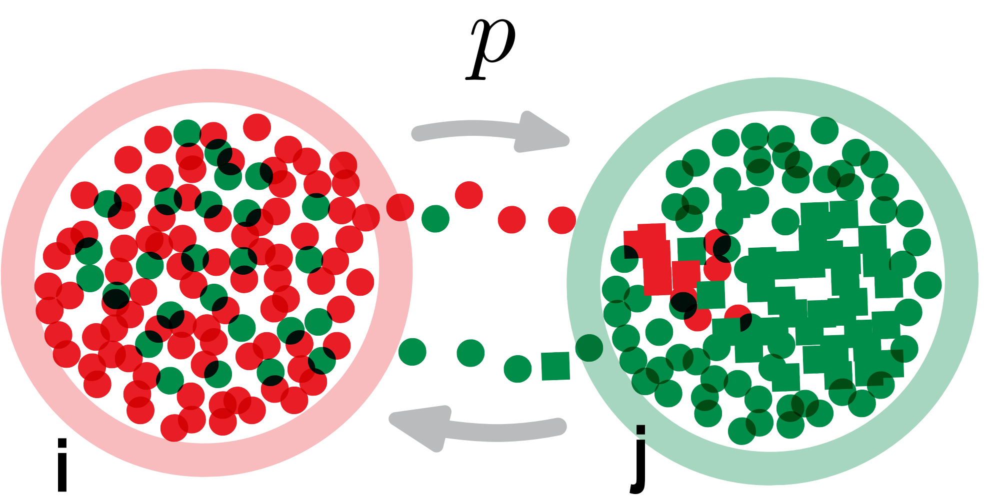
$I(t)$ infectious in i

probability that an infectious arrives in j at time t:

$$\left[1-(1-p)^{I(t\,dt)}\right]$$

[Gautreau et al JTB 2008]

spatial propagation



probability that an infectious arrives in *j* at time *t*: $\left[1-(1-p)^{I(t\,dt)}\right]$

probability that the **first** infectious arrives in *j* at time *t*:

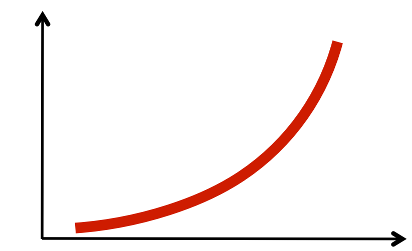
$$P\left(t_{\text{seeding}}=t\,dt\right)=\prod_{s=1}^{t-1}(1-p)^{I(s\,dt)}\times\left[1-(1-p)^{I(t\,dt)}\right]$$

$$\Big\downarrow\; p\rightarrow 0$$

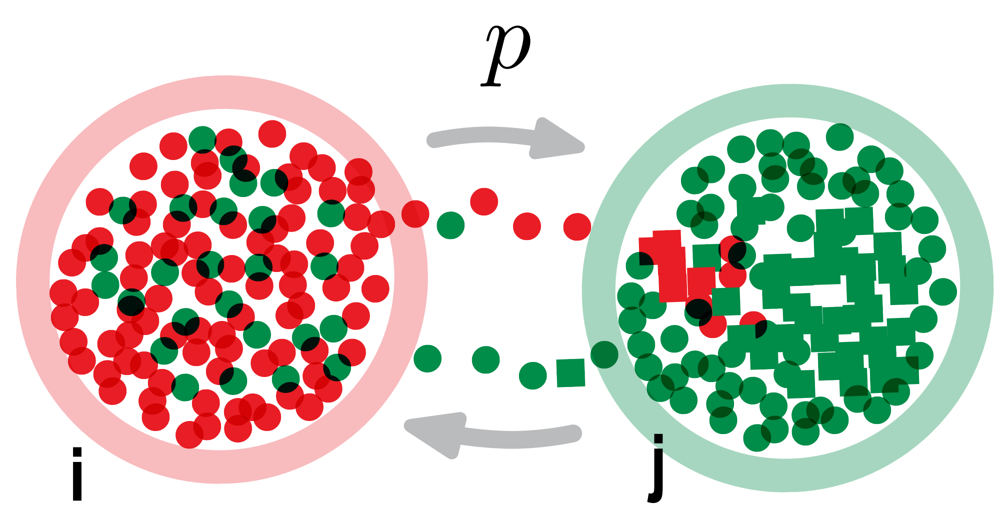
$$P\left(t_{\text{seeding}}=t\right)=p\,I(t)e^{-p\int_0^t I(s)ds}$$

[Gautreau et al JTB 2008]

spatial propagation



$$I(t) \sim e^{\mu(R_0-1)t}$$



$$P\left(t_{\text{seeding}} = t\right) = p\, I(t) e^{-p \int_0^t I(s)ds}$$

$$a = \mu(R_0 - 1)$$

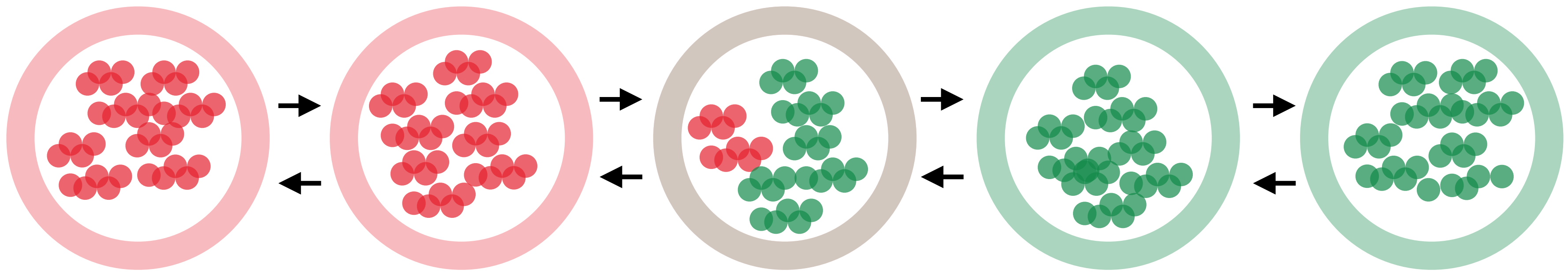
$$P\left(t_{\text{seeding}} = t\right) = p\, e^{at} e^{-pae^{at}}$$

Gumbel distribution

$$\langle t_{\text{seeding}} \rangle \simeq \frac{1}{a} \ln(p\, a)$$

[Gautreau et al JTB 2008]

spatial propagation



chain of identical cities (population N traveling weight p):

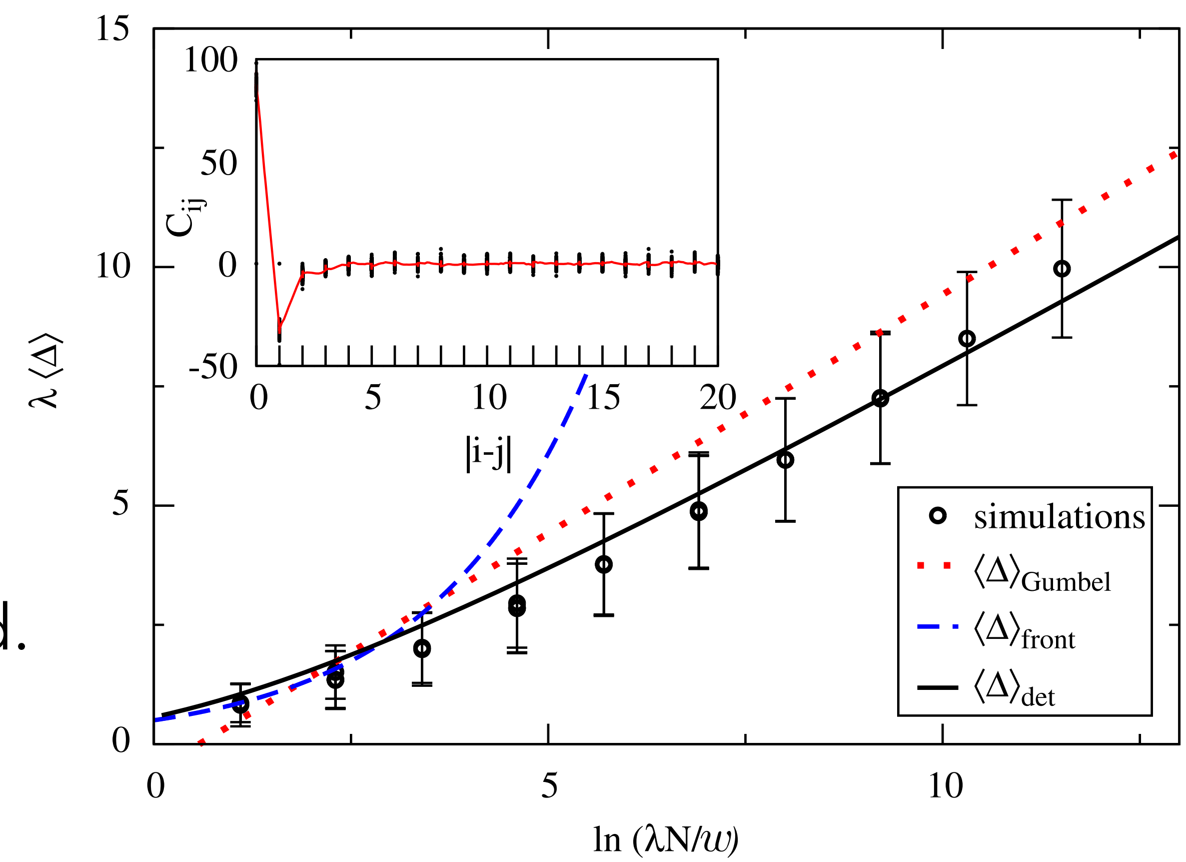
$$\langle t_{\text{seeding},i}\rangle - \langle t_{\text{seeding},i-1}\rangle = \Delta_i$$

$$\langle t_{\text{seeding},n}\rangle = \sum_{i=1}^{n} \Delta_n$$

Δ_i are correlated and not identically distributed.

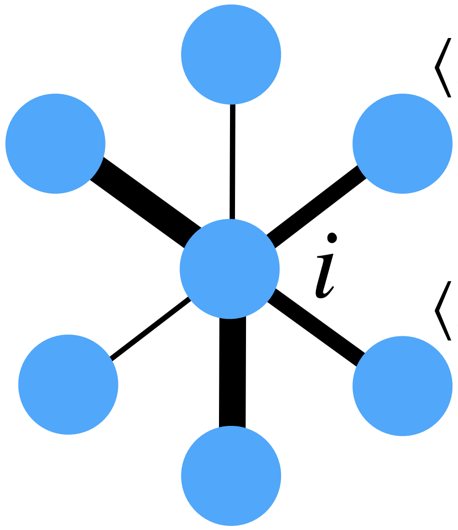
Dimensional analysis: $a\Delta = F\left[\frac{p}{a}\right]$

The simple approximation $\langle \Delta \rangle = \langle t_{\text{seeding},1}\rangle$ is not so bad!



[Gautreau et al JTB 2008]

spatial propagation: spreading pathways



$$\langle t_{\text{seeding}, j} \rangle \simeq \frac{1}{a} \ln(p_{ij} a)$$

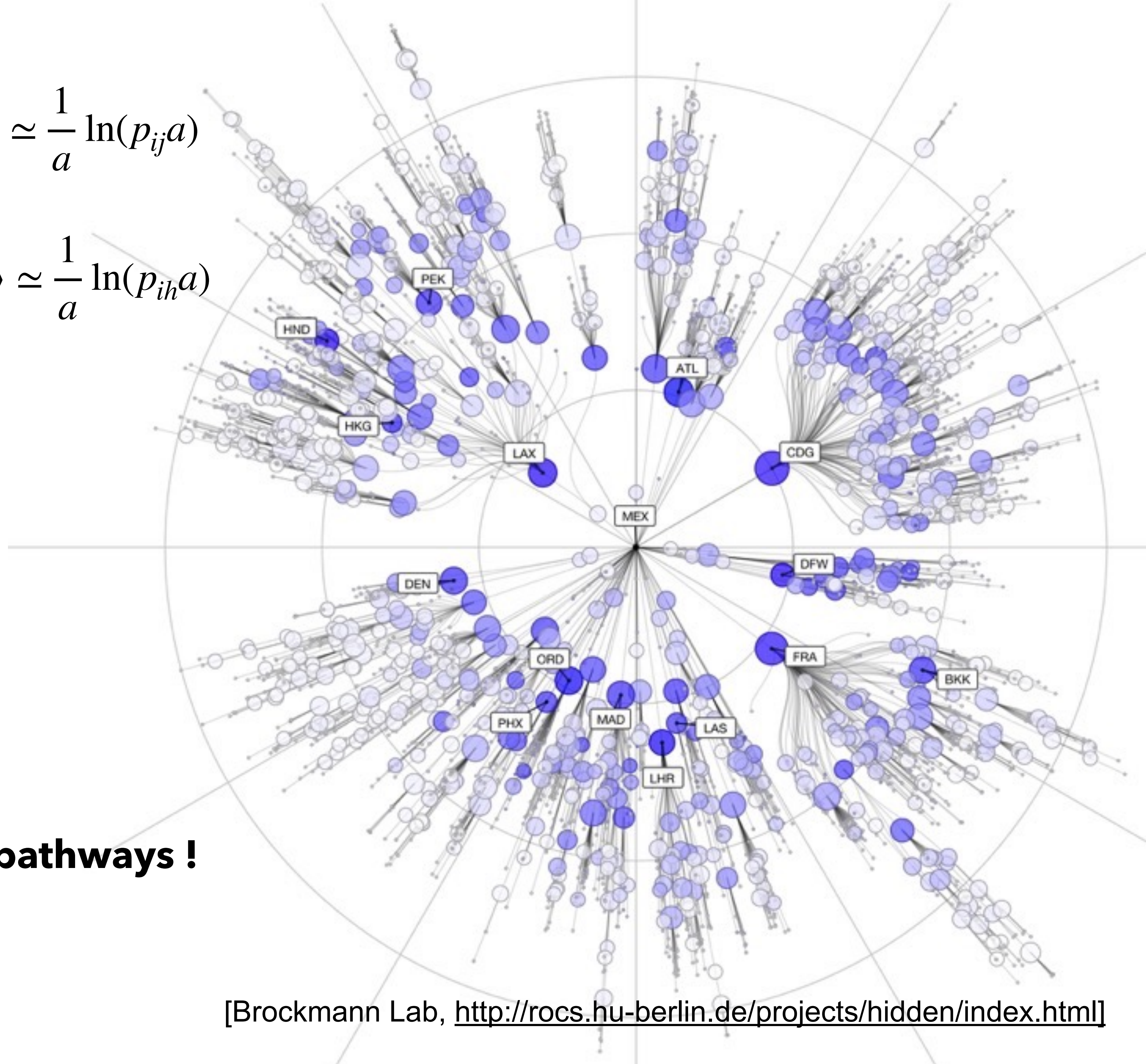
$$\langle t_{\text{seeding}, h} \rangle \simeq \frac{1}{a} \ln(p_{ih} a)$$

effective distance

between i and j

$$\ln(p_{ij})$$

[Brockmann, Helbing, Science 2013]



good news: existence of pathways !

risk assessment analysis, ...

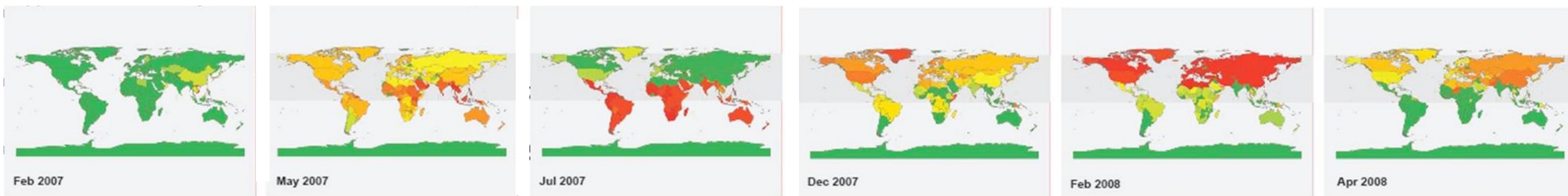
[Colizza, et al PNAS (2006)]

[Brockmann Lab, http://rocs.hu-berlin.de/projects/hidden/index.html]

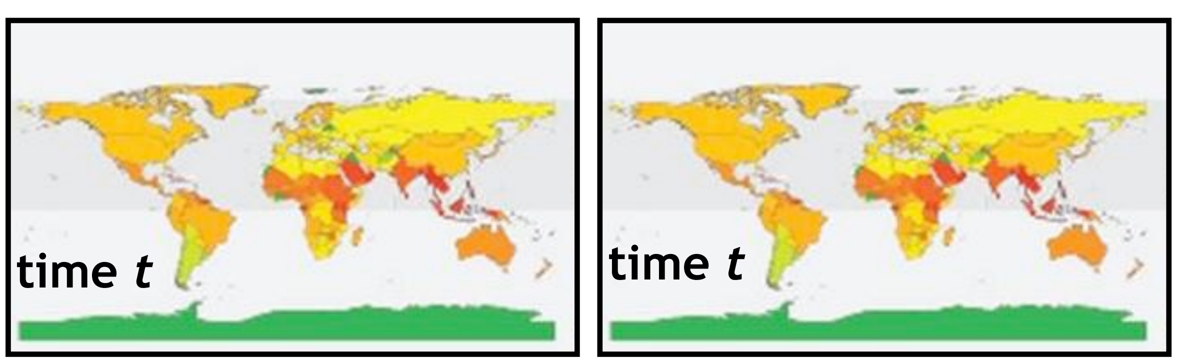
spatial propagation: spreading pathways

numerical simulation of a global outbreak

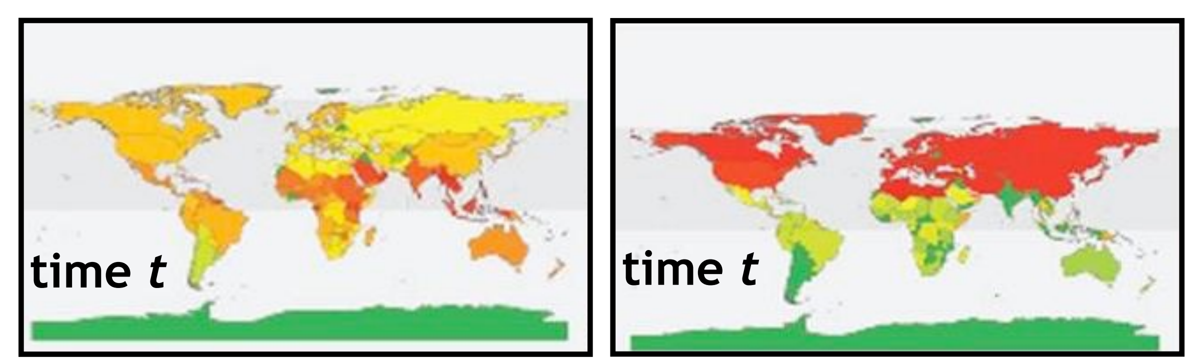
1 stochastic simulation:



similarity between 2 outbreak realizations: overlap function $\Theta(t)$



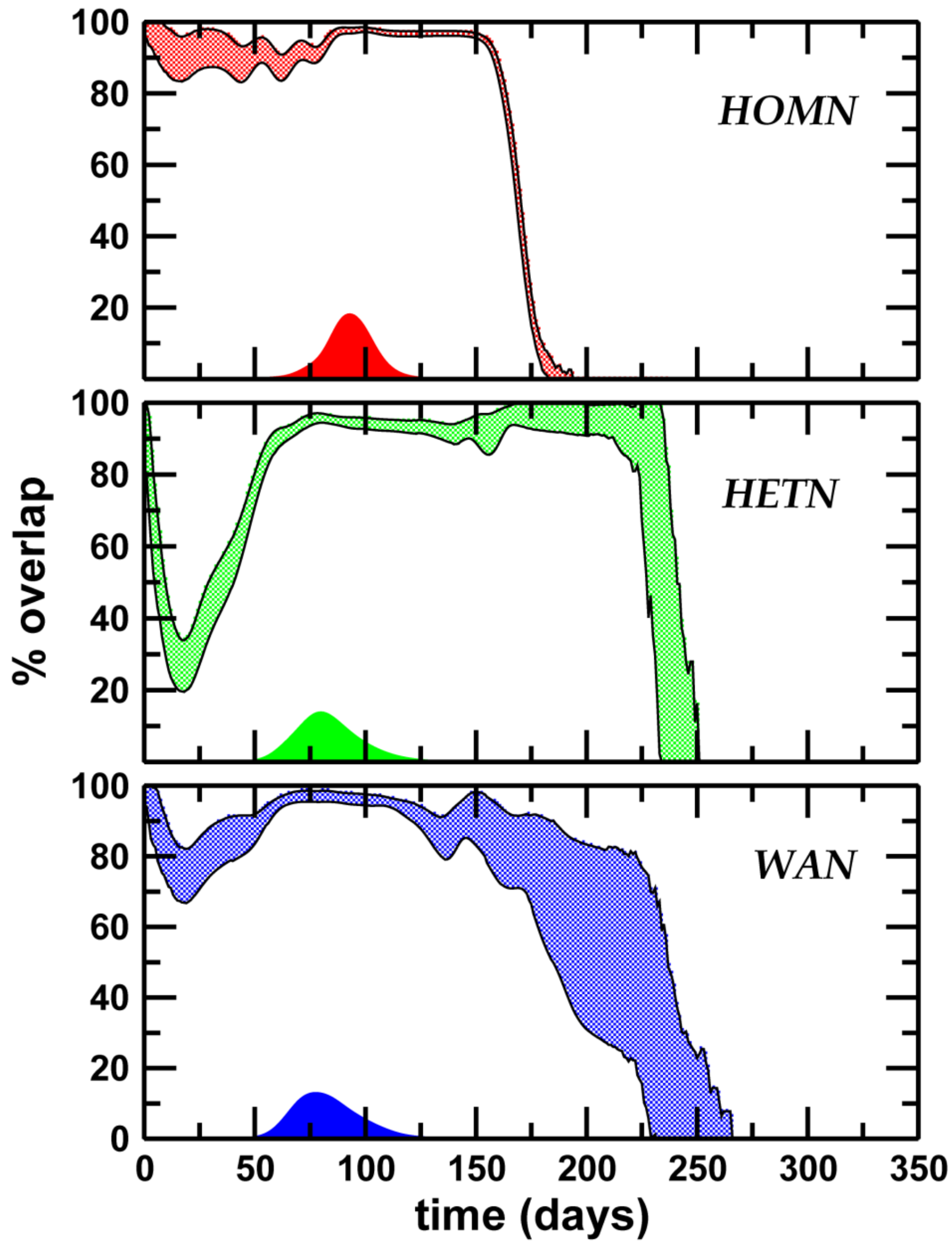
$$\Theta(t) = 1$$



$$\Theta(t) < 1$$

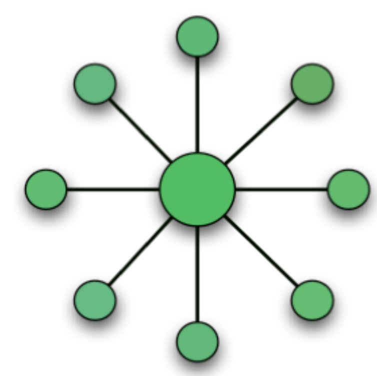
[Colizza, Barrat, Barthelemy & Vespignani, PNAS (2006)]

spatial propagation: spreading pathways



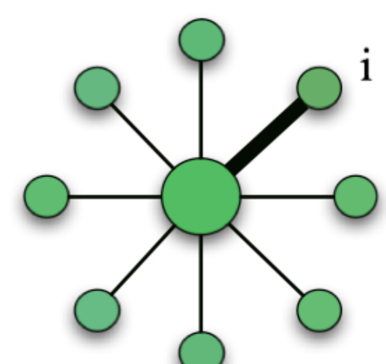
no degree fluctuations
no weight fluctuations

+ degree heterogeneity



- degree heterogeneity: decreases predictability

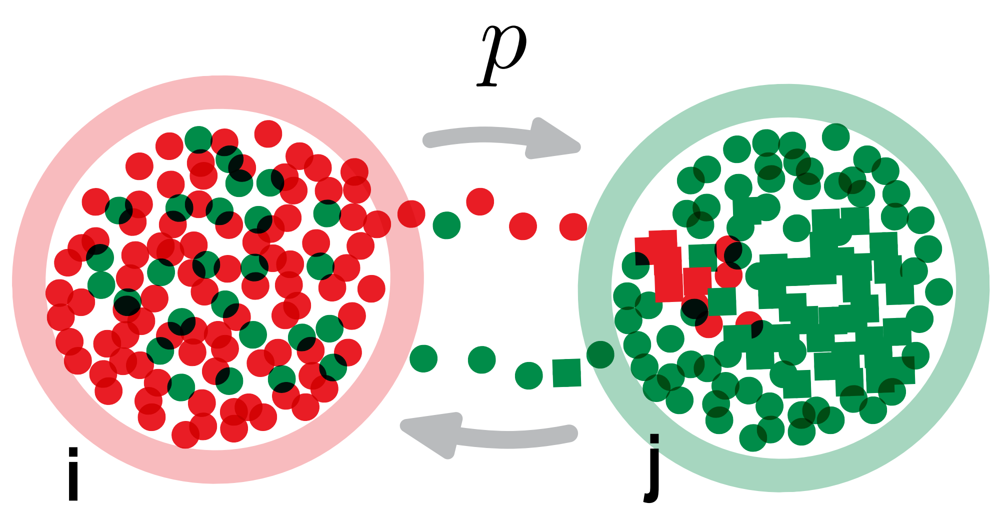
+ weight heterogeneity



- weight heterogeneity: increases predictability

[Colizza, Barrat, Barthelemy & Vespignani, PNAS (2006)]

spatial propagation: travel restrictions



I reduce the traffic with the epidemic origin: is it effecting in containing or delaying the propagation?

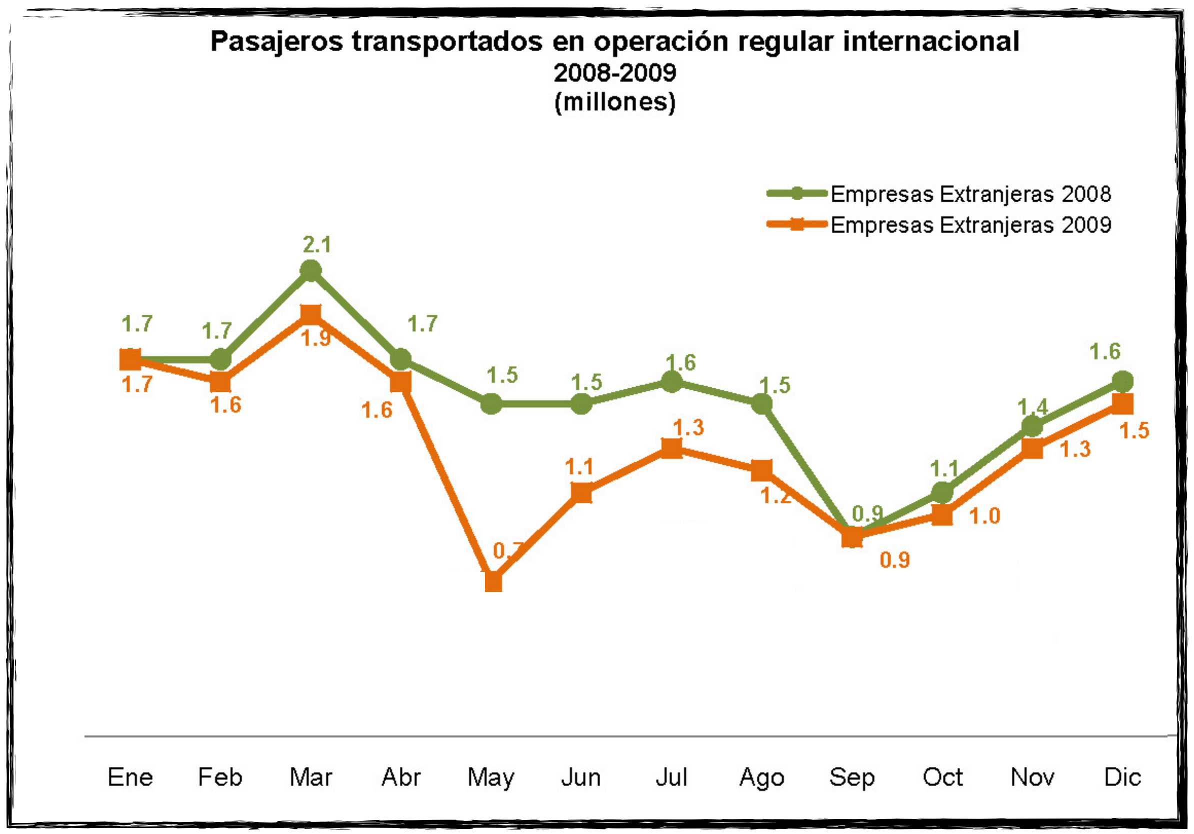
I rescale the traveling probability of a factor ω

$$\langle t_{\text{seeding, T.R.}} \rangle \simeq \frac{1}{a}\ln(\omega p a)$$

$$\begin{aligned}
\langle t_{\text{seeding, T.R.}} \rangle - \langle t_{\text{seeding}} \rangle &\simeq \frac{1}{a}\ln(\omega p a) - \frac{1}{a}\ln(pa) \\
&= \frac{1}{a}\ln(\omega) + \frac{1}{a}\ln(pa) - \frac{1}{a}\ln(pa) \\
&= \frac{1}{a}\ln(\omega)
\end{aligned}$$

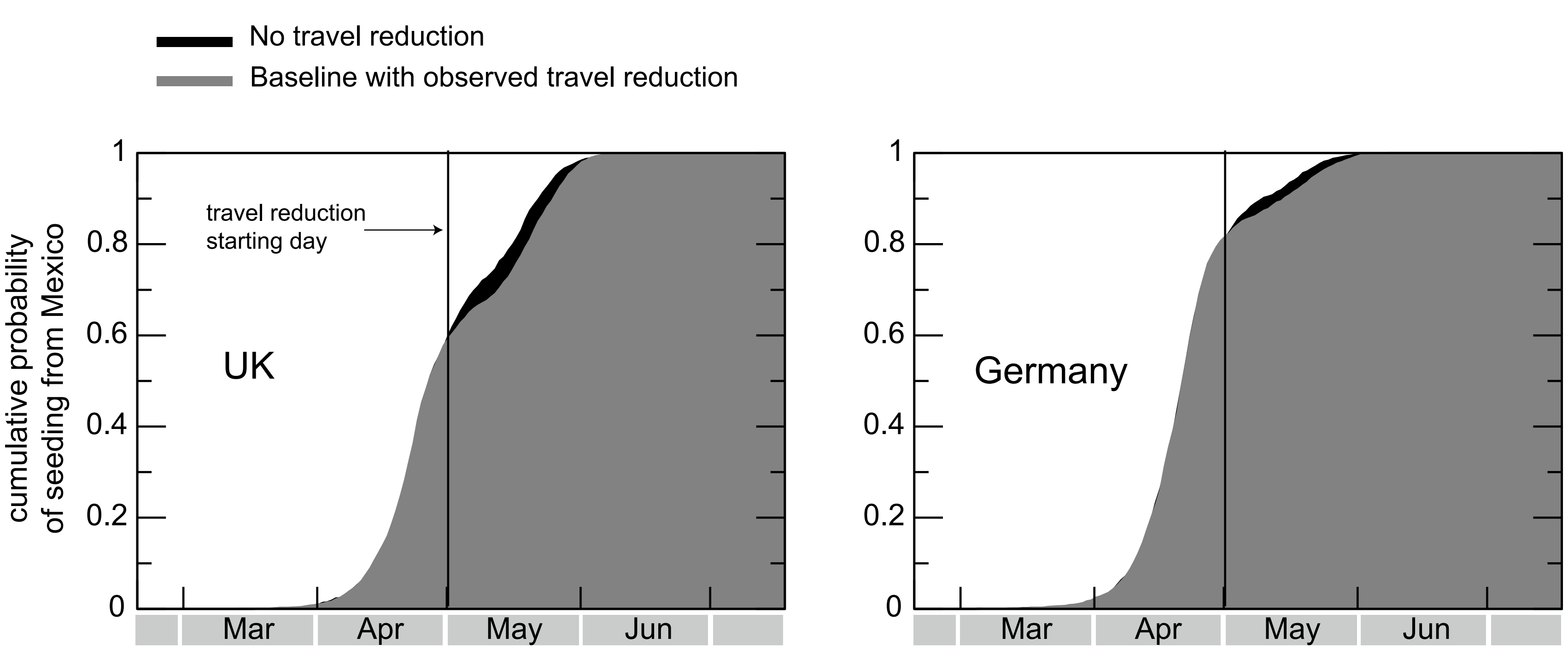
[Gautreau et al JTB 2008; Hollingsworth et al Nature Med 2006; Scalia Tomba et al Math Biosci 2008]

spatial propagation: travel restrictions



H1N1 pandemic 2009

- drop of 40% in the air-travel to/from Mexico
- simulations with a global spreading model for influenza show negligible delay



[Bajardi et al, PLoS ONE 2011]

SIR metapopulation model: markovian mobility

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  - global invasion threshold
- **computer simulations**

modelling worldwide spread of epidemics

TABLE 1

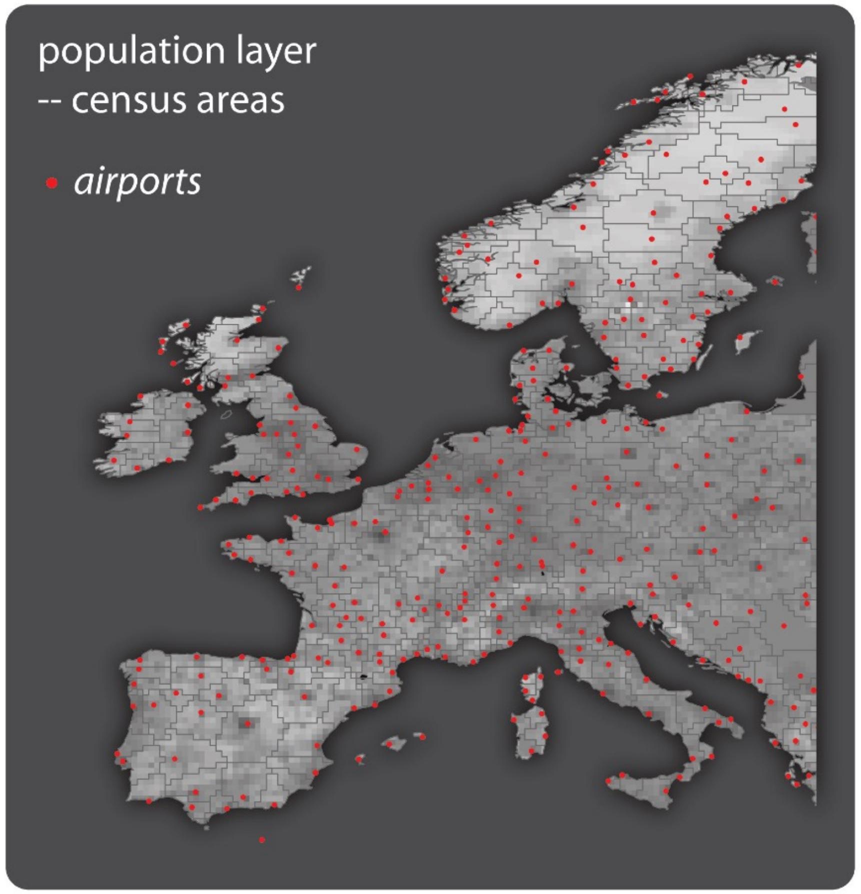
Mean Daily Number of Airline Passengers between Modeled Cities during the 1968–1969 Influenza Pandemic

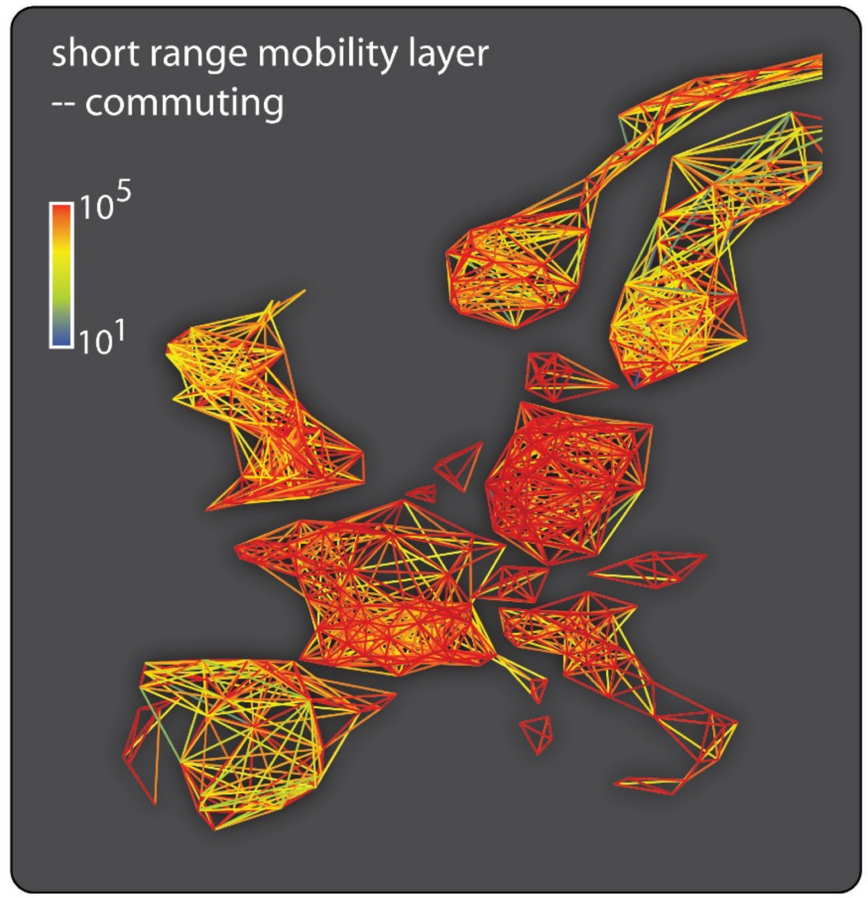
Pop. × 10^3	City	Passengers (as printed, left to right)
7379	London	377 110 38 171 32 6 1 117 69 10 7 50 7 5 5 3 5 7 12 5 24 152 7 23 1 6 1 4 6 10 1 5 68 7 19 105 413 127 94 37 81 6 37 14 12
8197	Paris	150 32 198 30 1 1 52 12 10 5 8 4 8 3 5 7 4 8 3 20 5 14 100 48 11 12 13 5 20 34 7 10 127 223 31 29 7 20 6 18
2800	Rome	2 71 9 7 5 11 4 8 3 6 2 6 3 1 7 3 7 1 45 13 18 8 28 2 10 9 6 7 2 2 45 119 52 93 55 21
3249	Berlin	5 51 133 38 8 3 3 4 10 10 5 4
2936	Madrid	3 8 4 14 2 3 6 3 13 18 49 14 9 37 10 10 48 18 2 63 143 45 20
1356	Warsaw	22 22 7 2 1 1 7 24
2039	Budapest	24 5 3
910	Sofia	6 1 4 1 4
973	Stockholm	40
3900	Hong Kong	140 9 18 53 100 15 24 3 6 7 13 15 4 15 16 2 2 37 9 54
11410	Tokyo	5 15 34 42 8 8 1 2 4 95 4 4 3 2 12 6 3 3 31 13 4 60 108 21 26 58 108
7570	Peking	72 1 12 4 1 6 5 26
7000	Shanghai	6 6 11
2017	Singapore	48 101 74 2 27 5 25 3 2 6 21 8 15 9 7 12
1582	Manila	19 2 1 1 7 4 2 21 5 4 5 10 7 8 28
2027	Bangkok	6 8 8 21 2 7 4 12 1 7 5
4915	Jakarta	1 2 3 2 1 1
3141	Calcutta	100 125 65 3
5970	Bombay	435 115 37 19 3 6 1 5 3 1 3
3647	Delhi	96 2 4 12 10
2470	Madras	
5536	Seoul	8 5 17 1
3400	Teheran	70
3469	Karachi	2 2 2 2
5384	Cairo	4 7 3
1404	Kinshasa	36 22
1433	Johannesburg	13 4 25 7 18 590
1506	Casablanca	12 6 17
3026	Mexico City	8 7 8 15 7 5 5 18 21 84 168 12 71 78 42 50
2818	Bogota	28 15 4 5 4 2 9 9 3
1755	Havana	1 2
1035	Caracas	10 11 14 3 43 4 8
2541	Lima	28 21 10 4 25 25 10 8
2556	Santiago	85 9 7 11 4 3 7
2972	Buenos Aires	55 61 2 30 7 1 6 25
4316	Rio de Janeiro	1060 5 66 8 8 2 6
5187	Sao Paulo	2 2 1 1 6
628	Honolulu	34 2 10 13 10 10 38 10
2780	Sydney	1604 75 24 4 13 3 36
2425	Melbourne	152 3 2 1 5
725	Perth	
136	Wellington	
1214	Montreal	438 49 15 18 354 10 50
11572	New York	1779 729 450 1345 1068 1020 8
7000	Los Angeles	348 342 1912 3504 1367
2836	Washington	116 952 436 1104
1231	Houston	451 216 790
7800	Chicago	1522 1237
3700	San Francisco	909
1258	Atlanta	
901	Lagos	
691	Capetown	

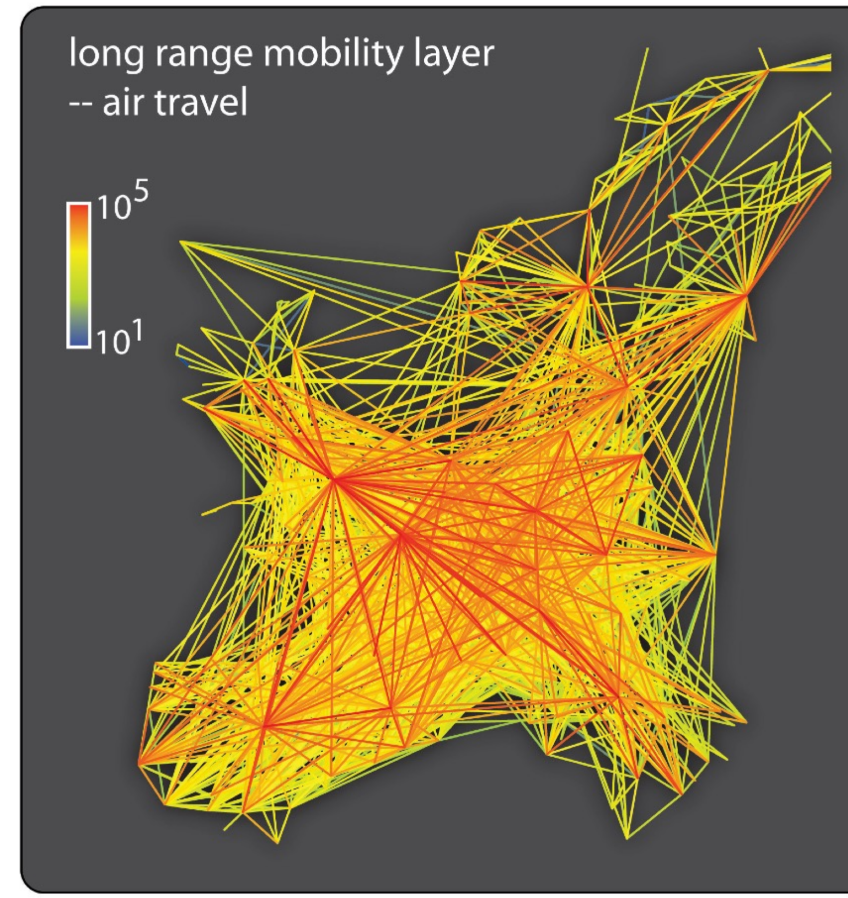
52 major cities: spread of 1968 -1969 H3N2 pandemic from Hong Kong

[Rvachev, Longini, Math. Biosci. 1985]

GLEaM: Global epidemic and mobility model







Population Distribution

- resolution 15′x15′ arc
- data source: SEDAC (Columbia University)
- tessellation: geographical census areas

Commuting Network

- census data for >40 countries in 5 continents
- different admin levels
- change of resolution scale: from admin boundaries to geo census areas

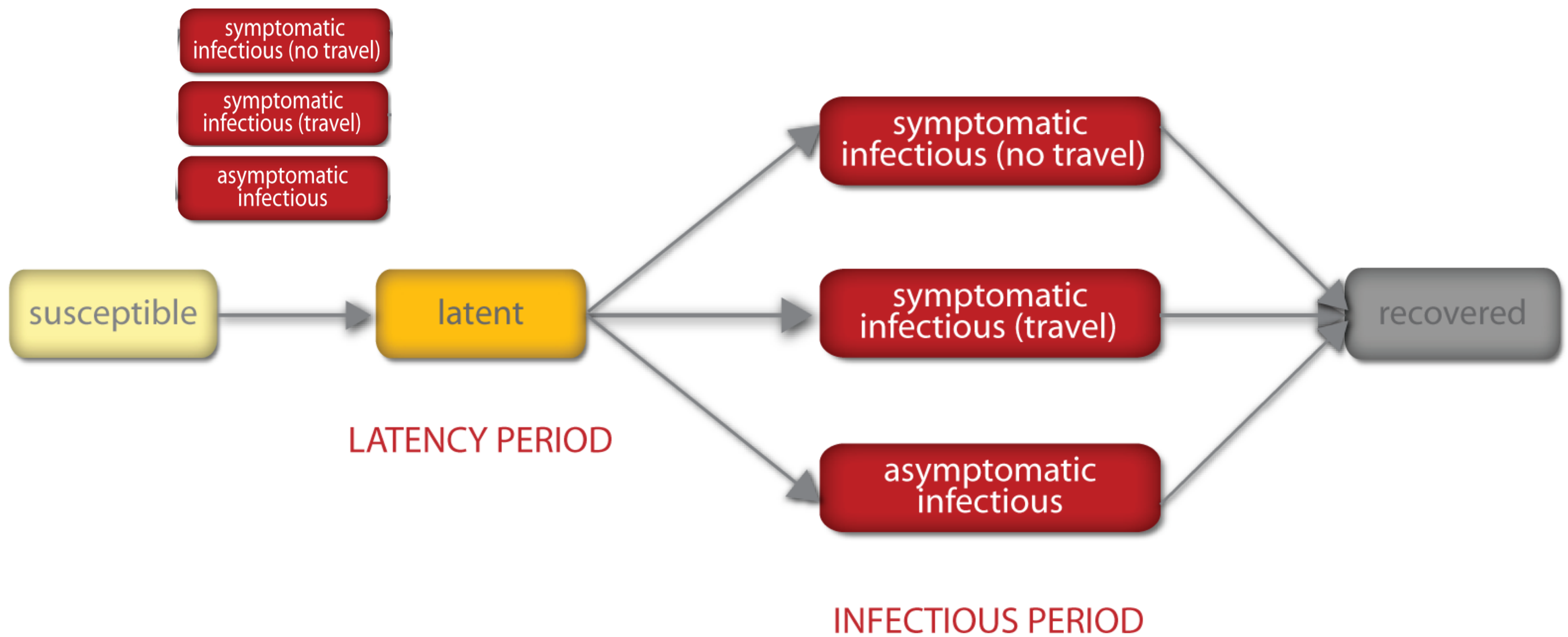
World Airport Network

- 3362 airports in 220 countries
- 16842 connections with travel flows
- more than 99 % of the global commercial traffic
- data source: IATA, OAG

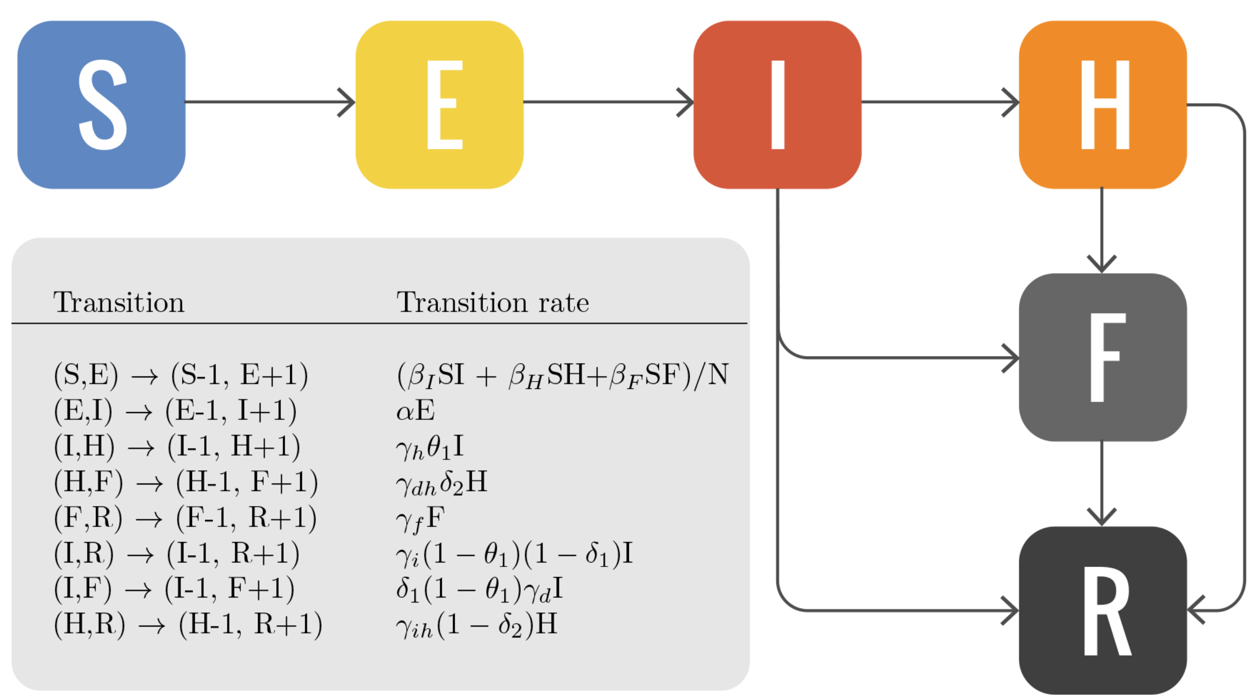
[Balcan, Colizza et al. PNAS (2009)]

GLEaM: Global epidemic and mobility model

H1N1 pandemic:



Ebola:



Transition	Transition rate
(S,E) $\rightarrow$ (S-1, E+1)	$(\beta_I SI + \beta_H SH + \beta_F SF)/N$
(E,I) $\rightarrow$ (E-1, I+1)	αE
(I,H) $\rightarrow$ (I-1, H+1)	$\gamma_h \theta_1 I$
(H,F) $\rightarrow$ (H-1, F+1)	$\gamma_{dh} \delta_2 H$
(F,R) $\rightarrow$ (F-1, R+1)	$\gamma_f F$
(I,R) $\rightarrow$ (I-1, R+1)	$\gamma_i (1-\theta_1)(1-\delta_1) I$
(I,F) $\rightarrow$ (I-1, F+1)	$\delta_1 (1-\theta_1) \gamma_d I$
(H,R) $\rightarrow$ (H-1, R+1)	$\gamma_{ih} (1-\delta_2) H$

SIR metapopulation model in a different regime: commuting

The Markovian assumption works well as long as

- travels are not frequent, i.e. traveling rate negligible with respect to the epidemic time scales $p_{ij} \ll \mu$
- we want to model the short term dynamics of an epidemic

Situations for which this holds in first approximation:

- air-travel and acute infections. E.g. for flu: traveling rate= 10^{-3} days^{-1} vs. recovery rate> 0.1 days^{-1})
- early spread of a flu pandemic. It does not work well if I want to model the long term continuous circulation

SIR metapopulation model in a different regime: commuting

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Situations for which this holds in first approximation:

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- early spread of a flu pandemic. It does not work well if I want to model the long term continuous circulation

SIR metapopulation model in a different regime: commuting

In general treating mathematically the interplay between mobility and transmission is very difficult. The problem can be solved in **time scale separation:**

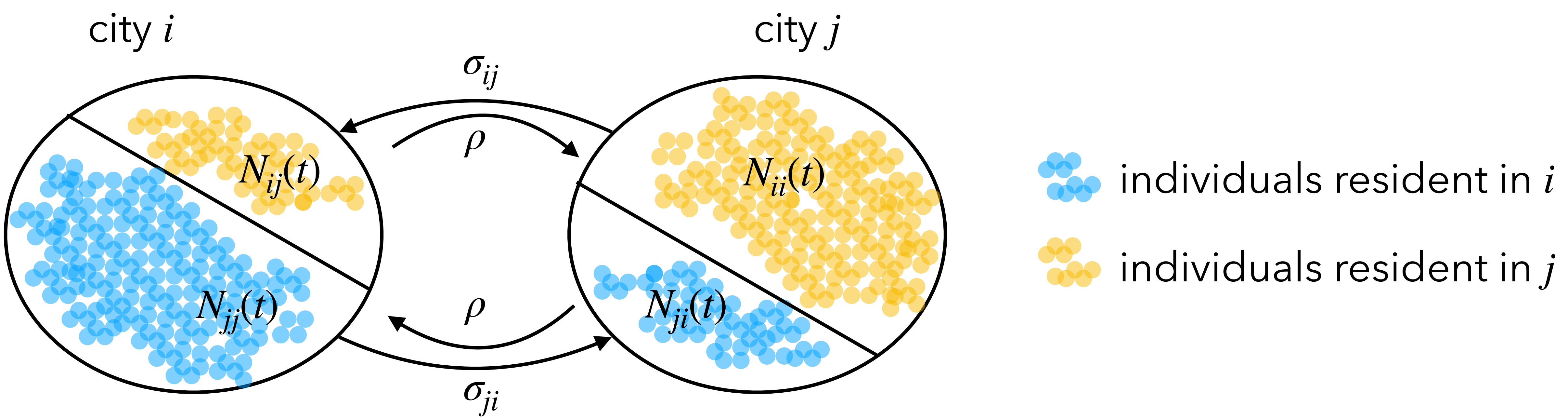
either

the epidemic unfolds faster than mobility (air-travel and flu: traveling rate= 10^{-3} days^{-1} vs. recovery rate> ~0.1 days^{-1})

or

mobility faster than the epidemic (air-travel and flu: traveling rate= 10^{-3} days^{-1} vs. recovery rate= ~0.5 days^{-1})

SIR metapopulation model with memory



σ_{ij} leaving rate, fraction of commuters

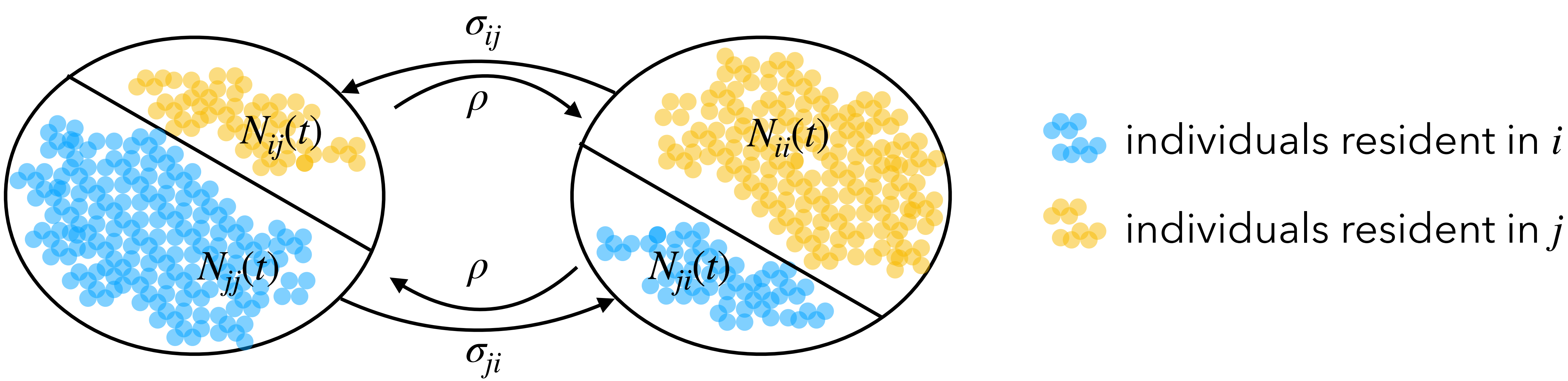
ρ returning rate ($\rho^{-1} = \tau \sim 8h$)

$N_i = N_{ii}(t) + \sum_j N_{ij}(t)$ resident in i, constant

$N_{ij}(t)$ individuals resident in i and traveling to j

[Sattenspiel, L. & Dietz, K. Math. Biosci. 128, 71–91 (1995);
Keeling, M. J. & Rohani, P. Ecol. Lett. 5, 20–29 (2002)]

SIR metapopulation model with memory



σ_{ij} leaving rate, fraction of commuters

ρ returning rate ($\rho^{-1} = \tau \sim 8h$)

$$N_i = N_{ii}(t) + \sum_j N_{ij}(t)$$

$$\partial_t N_{ii} = -\sum_j \sigma_{ij} N_{ii}(t) + \rho \sum_j N_{ij}(t)$$

$$\partial_t N_{ij} = \sum_j \sigma_{ij} N_{ii}(t) - \rho N_{ij}(t)$$

[Sattenspiel, L. & Dietz, K. Math. Biosci. 128, 71–91 (1995); Keeling, M. J. & Rohani, P. Ecol. Lett. 5, 20–29 (2002)]

SIR metapopulation model with memory

differential equations

$$\partial_t N_{ii} = -\sum_j \sigma_{ij} N_{ii}(t) + \rho \sum_j N_{ij}(t)$$

$$\partial_t N_{ij} = \sum_j \sigma_{ij} N_{ii}(t) - \rho N_{ij}(t)$$

$$N_i = N_{ii}(t) + \sum_j N_{ij}(t)$$

$$\sigma_i = \sum_j \sigma_{ij}$$

solution

$$\partial N_{ii}(t) + (\rho + \sigma_i) N_{ii}(t) = N_i \rho$$

$$N_{ii}(t) = e^{-(\sigma_i+\rho)t} \left(C_{ii} + N_i \rho \int_0^t e^{(\sigma_i+\rho)s}\, ds \right)$$

$$N_{ii}(t) = \frac{N_i}{1+\sigma_i/\rho} + \left(N_{ii}(0) - \frac{N_i}{1+\sigma_i/\rho} \right) e^{-\rho(1+\sigma_i/\rho)t}$$

$$N_{ij}(t) = \frac{\sigma_{ij} N_i/\rho}{1+\sigma_i/\rho} - \frac{\sigma_{ij}}{\sigma_i} \left(N_{ii}(0) - \frac{N_i}{1+\sigma_i/\rho} \right) e^{-\rho(1+\sigma_i/\rho)t} +$$

$$+ \left[N_{ij}(0) - \frac{\sigma_{ij} N_i/\rho}{1+\sigma_i/\rho} - \frac{\sigma_{ij}}{\sigma_i} \left(N_{ii}(0) - \frac{N_i}{1+\sigma_i/\rho} \right) \right] e^{-\rho t}$$

[Sattenspiel, L. & Dietz, K. Math. Biosci. 128, 71–91 (1995);
Keeling, M. J. & Rohani, P. Ecol. Lett. 5, 20–29 (2002)]

SIR metapopulation model with memory

differential equations

$$\partial_t N_{ii} = -\sum_j \sigma_{ij} N_{ii}(t) + \rho \sum_j N_{ij}(t)$$

$$\partial_t N_{ij} = \sum_j \sigma_{ij} N_{ii}(t) - \rho N_{ij}(t)$$

$$N_i = N_{ii}(t) + \sum_j N_{ij}(t)$$

$$\sigma_i = \sum_j \sigma_{ij}$$

solution

$$N_{ii}(t) = \frac{N_i}{1+\sigma_i/\rho} + \left(N_{ii}(0) - \frac{N_i}{1+\sigma_i/\rho}\right) e^{-\rho(1+\sigma_i/\rho)t}$$

$$N_{ij}(t) = \frac{\sigma_{ij} N_i/\rho}{1+\sigma_i/\rho} - \frac{\sigma_{ij}}{\sigma_i}\left(N_{ii}(0) - \frac{N_i}{1+\sigma_i/\rho}\right) e^{-\rho(1+\sigma_i/\rho)t} +$$

$$+ \left[N_{ij}(0) - \frac{\sigma_{ij} N_i/\rho}{1+\sigma_i/\rho} - \frac{\sigma_{ij}}{\sigma_i}\left(N_{ii}(0) - \frac{N_i}{1+\sigma_i/\rho}\right)\right] e^{-\rho t}$$

time of relaxation to the equilibrium dominated by

$\left[\rho(1+\sigma_i/\rho)\right]^{-1} \sim \rho^{-1} = \tau,$ since $\rho \gg \sigma_i$

Equilibrium solutions:

$$N_{ii}(t) = \frac{N_i}{1+\sigma_i/\rho} \qquad N_{ij}(t) = \frac{\sigma_{ij} N_i/\rho}{1+\sigma_i/\rho}$$

[Sattenspiel, L. & Dietz, K. Math. Biosci. 128, 71–91 (1995);
Keeling, M. J. & Rohani, P. Ecol. Lett. 5, 20–29 (2002)]

SIR metapopulation model with memory

Equilibrium solutions:

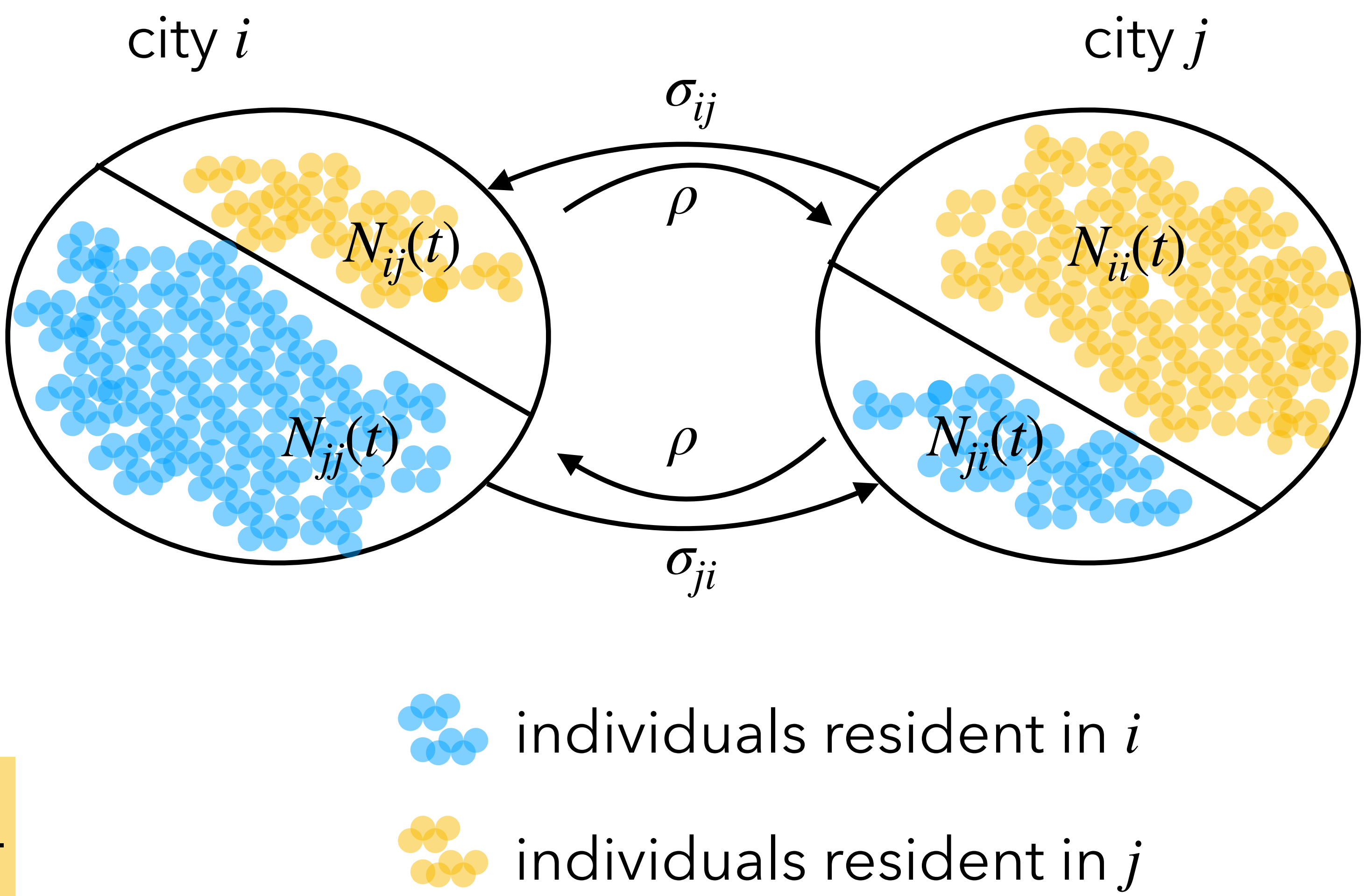
$$N_{ii}(t) = \frac{N_i}{1 + \sigma_i/\rho} \qquad N_{ij}(t) = \frac{\sigma_{ij} N_i/\rho}{1 + \sigma_i/\rho}$$

People resident in i

$$N_i = N_{ii}(t) + \sum_j N_{ij}(t)$$

People present in i

$$N_i^* = N_{ii} + \sum_j N_{ji} = \frac{N_i}{1 - \sigma_i/\rho} + \sum_j \frac{N_j \sigma_{ji}/\rho}{1 - \sigma_j/\rho}$$



[Sattenspiel, L. & Dietz, K. Math. Biosci. 128, 71–91 (1995); Keeling, M. J. & Rohani, P. Ecol. Lett. 5, 20–29 (2002)]

SIR metapopulation model with memory

Equilibrium solutions:

$$N_{ii}(t) = \frac{N_i}{1+\sigma_i/\rho} \qquad N_{ij}(t) = \frac{\sigma_{ij} N_i/\rho}{1+\sigma_i/\rho}$$

$$N_i = N_{ii}(t) + \sum_j N_{ij}(t)$$

$$N_i^* = \frac{N_i}{1-\sigma_i/\rho} + \sum_j \frac{N_j \sigma_{ji}/\rho}{1-\sigma_j/\rho}$$

σ_i/ρ quantify the ratio of time spent outside and in the residence population

Simple limit cases:

$\sigma_i \to 0 \quad \Rightarrow \quad N_{ii}(t) \to N_i;\ N_{ij}(t) \to 0;\ N_i^* \to N_i$ people rarely leave their residence thus the population of non traveling approaches the population of resident

$\rho \to \infty \quad \Rightarrow \quad N_{ii}(t) \to N_i;\ N_{ij}(t) \to 0;\ N_i^* \to N_i$ people return home immediately thus the population of non traveling approaches the population of resident

$\rho \to 0 \quad \Rightarrow \quad N_{ii}(t) \to 0;\ N_{ij}(t) \to \frac{\sigma_{ij}}{\sigma_i} N_i;\ N_i^* \to \sum_j \frac{\sigma_{ji}}{\sigma_j} N_j$ <u>migration</u>: people never get back and the population of resident in i is distributed among the neighbouring destinations j

[Sattenspiel, L. & Dietz, K. Math. Biosci. 128, 71–91 (1995);
Keeling, M. J. & Rohani, P. Ecol. Lett. 5, 20–29 (2002)]

SIR metapopulation model with memory

Time scale separation

time of relaxation to the equilibrium dominated by
$\left[\rho(1+\sigma_i/\rho)\right]^{-1} \sim \rho^{-1} = \tau$, since $\rho \gg \sigma_i$

commuting: $\tau \sim 8h$

duration of an acute infection (e.g. flu): $\mu^{-1} \simeq [1-3]$ days

transmission dynamics slower than mobility: we can assume that compartments occupations numbers is at the equilibrium with respect to mobility dynamics

$$X_{ii}^{[m]} = \frac{X_i^{[m]}}{1+\sigma_i/\rho} \qquad X_{ij}^{[m]} = \frac{\sigma_{ij} X_i^{[m]}/\rho}{1+\sigma_i/\rho} \qquad X^{[m]} = S, I, R$$

[Sattenspiel, L. & Dietz, K. Math. Biosci. 128, 71–91 (1995); Keeling, M. J. & Rohani, P. Ecol. Lett. 5, 20–29 (2002)]

SIR metapopulation model with memory

Time scale separation

force of infection:

$$\partial_t I = \lambda S(t) - \mu I(t),\ \ \lambda = \beta \frac{I(t)}{N(t)}$$

$$\partial_t S = -\beta \frac{I(t)}{N_i(t)} S(t)$$
$$\partial_t I = \beta \frac{I(t)}{N_i(t)} S(t) - \mu I(t)$$
$$\partial_t R = \mu I(t)$$

instead of explicitly modelling mobility, I directly compute the effect of the other patches on the risk of infection, i.e. I break down the force of infection in its contributions. **How many infectious individuals a susceptible person resident in i is exposed to?**

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Time scale separation

instead of explicitly modelling mobility, I directly compute the effect of the other patches on the risk of infection, i.e. I break down the force of infection in its contributions. **How many infectious individuals a susceptible person resident in i is exposed to?**

S_i distributed among patch i and all possible destinations j in proportion

$$\{\frac{1}{1+\sigma_i/\rho}, \dots \frac{\sigma_{ij}/\rho}{1+\sigma_i/\rho}, \dots\}$$

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

[Sattenspiel, L. & Dietz, K. Math. Biosci. 128, 71–91 (1995); Keeling, M. J. & Rohani, P. Ecol. Lett. 5, 20–29 (2002)]

SIR metapopulation model with commuting

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

$$\lambda_{ii} = \frac{\beta_i}{N_i^*}\left[I_{ii} + \sum_j I_{ji}\right] \quad \lambda_{ii} = \frac{\beta_i}{N_i^*}\left[\frac{I_i}{1 - \sigma_i/\rho} + \sum_j \frac{I_j\sigma_{ji}/\rho}{1 - \sigma_j/\rho}\right]$$

$$\lambda_{ij} = \frac{\beta_j}{N_j^*}\left[I_{jj} + \sum_l I_{lj}\right] \quad \lambda_{ij} = \frac{\beta_j}{N_j^*}\left[\frac{I_j}{1 - \sigma_j/\rho} + \sum_l \frac{I_l\sigma_{li}/\rho}{1 - \sigma_{lj}/\rho}\right]$$

$$N_i^* = \frac{N_i}{1 - \sigma_i/\rho} + \sum_j \frac{N_j\sigma_{ji}/\rho}{1 - \sigma_j/\rho}$$

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understanding the relative role of mobility and infection parameters on the epidemic dynamics

mathematical expressions to speed up computer simulations

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