Life Data Epidemiology

Lect 20: epidemics in space 3

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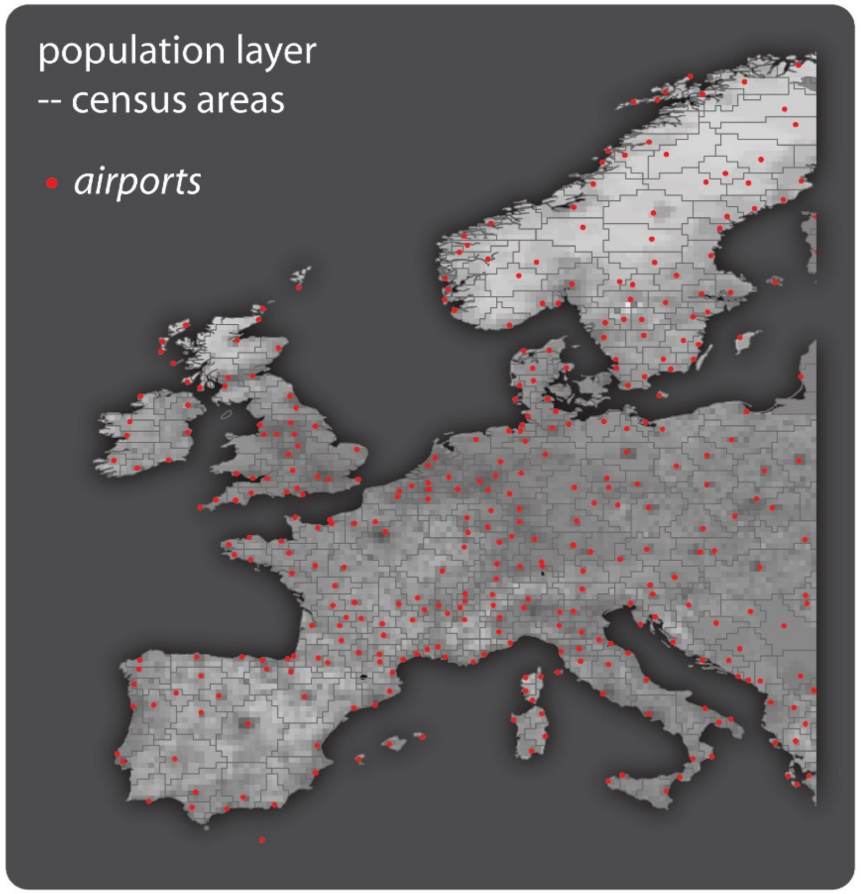
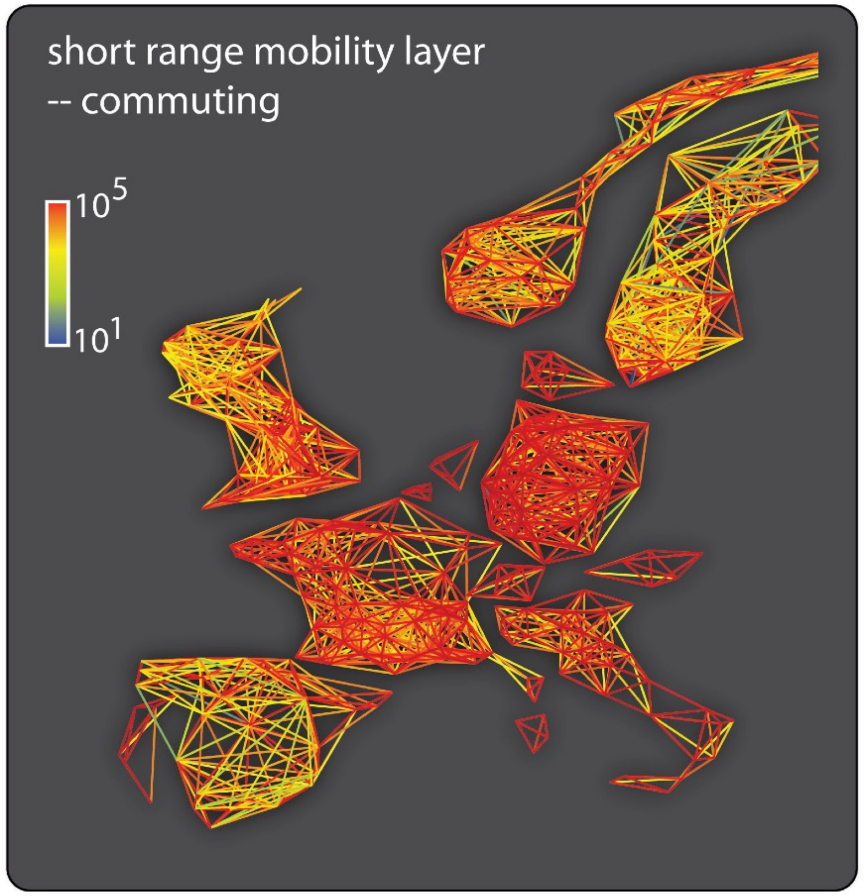
SIR metapopulation model: markovian mobility

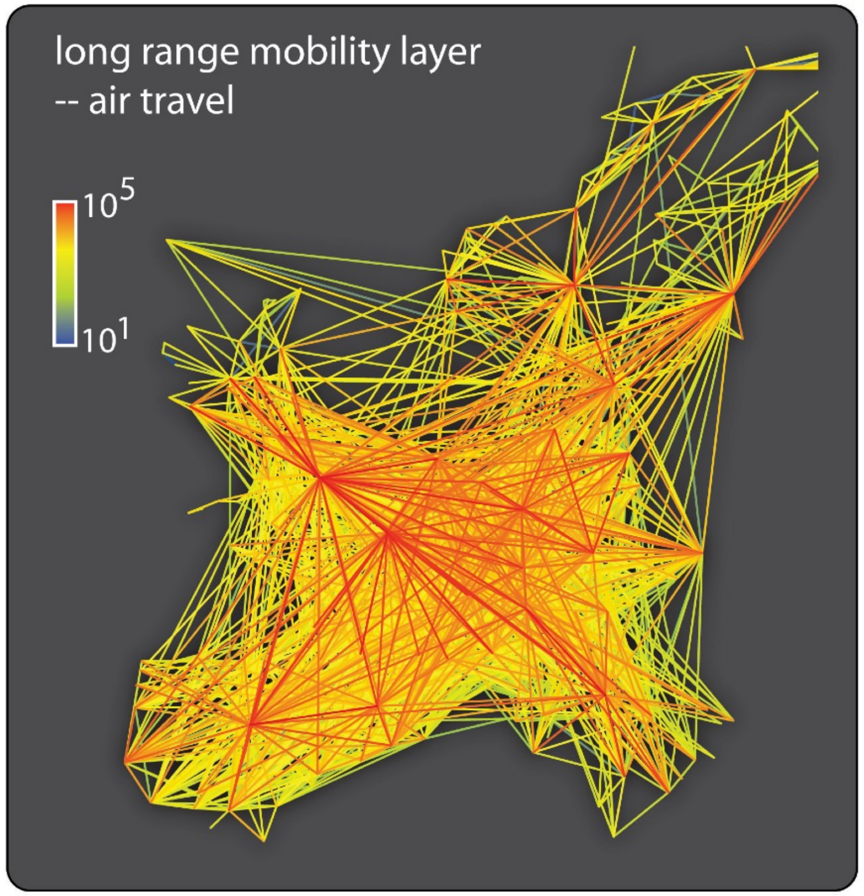
What can I do with that?

- analytical understanding
    - spatial propagation & predictability
    - global invasion threshold
- application for epidemic assessment
- **computer simulations**

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

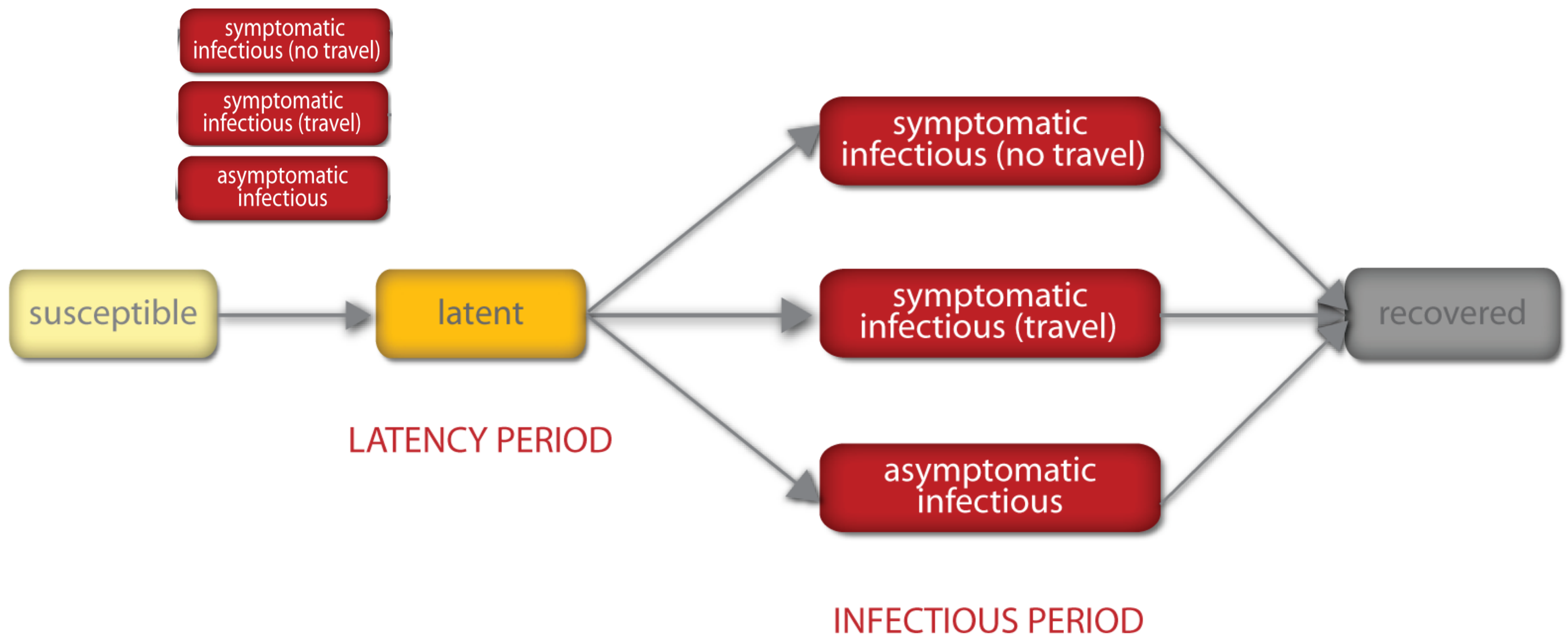
World Airport Network

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

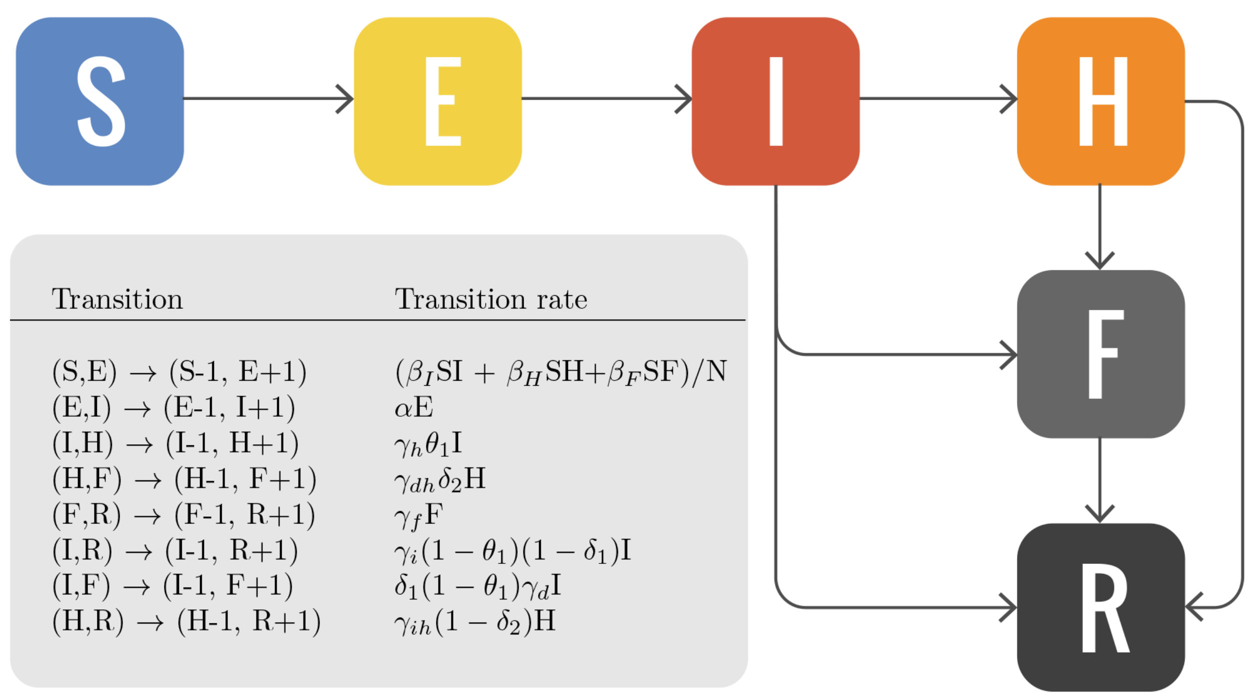
[Balcan, Colizza et al. PNAS (2009)]

GLEaM: Global epidemic and mobility model

H1N1 pandemic:



Ebola:



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

human mobility

To model epidemics in space we need information on human mobility

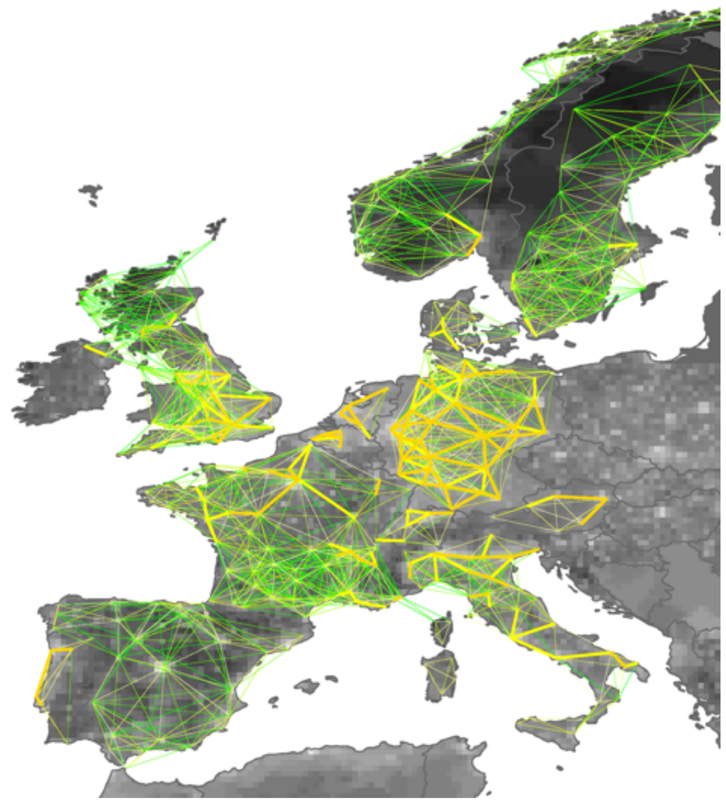
[Human mobility: Models and applications, Barbosa et al. Physics Reports 734 (2018)]

Air travel

source: Air Transport Association.

The data can be purchased. Not available for free

<u>*Global and complete!*</u>



Commuting

source: census of different countries (residence and work location)

spatial resolution (administrative level) highly variable by country

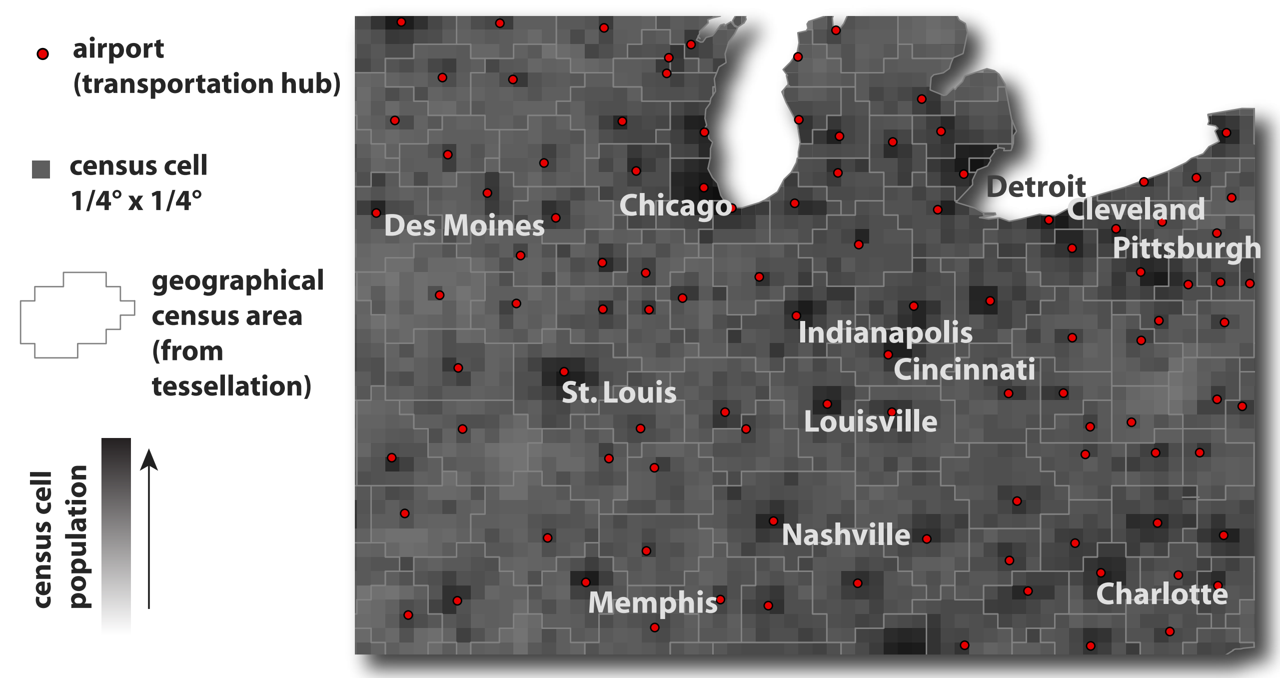
~30-40 countries

[Balcan, et al PNAS 2009]

air travelling vs. commuting

To be compared the two networks must be defined at the same spatial resolution: Balcan et al. defined macro urban areas centred around airports

- daily number of travellers
  - ~1,000 air travel
  - ~20,000 commuting
- fraction of daily travellers
  - ~10^{-3} days^{-1} air travel
  - ~10^{-2} days^{-1} commuting
- travel duration
  - days /weeks
  - hours



[Balcan, et al PNAS 2009]

Commuting faster dynamics and higher level of mixing

air travel and commuting can be combined

human mobility

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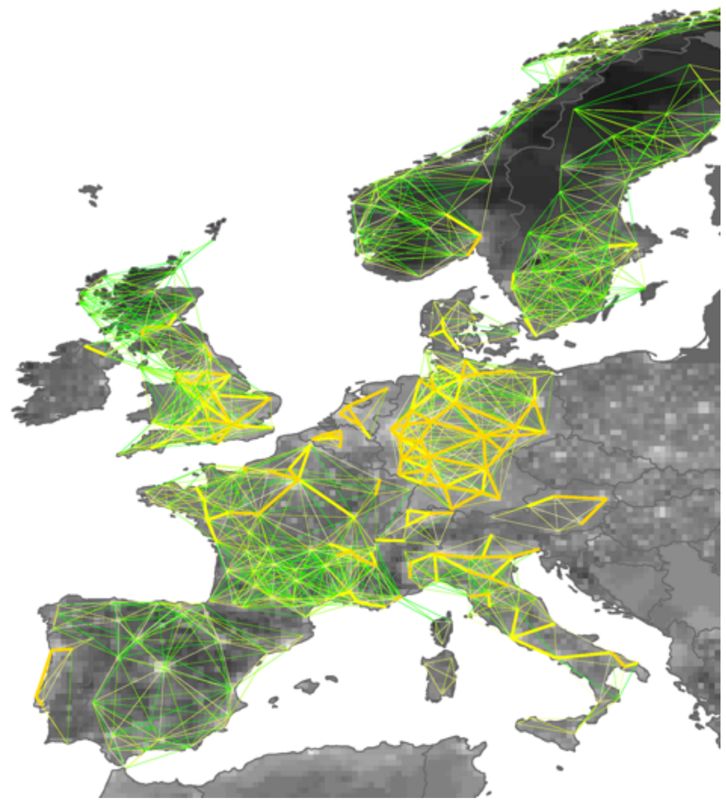

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[Balcan, et al PNAS 2009]

What about other kind of mobility?

car/trains (rarely available/hard to combine with commuting)

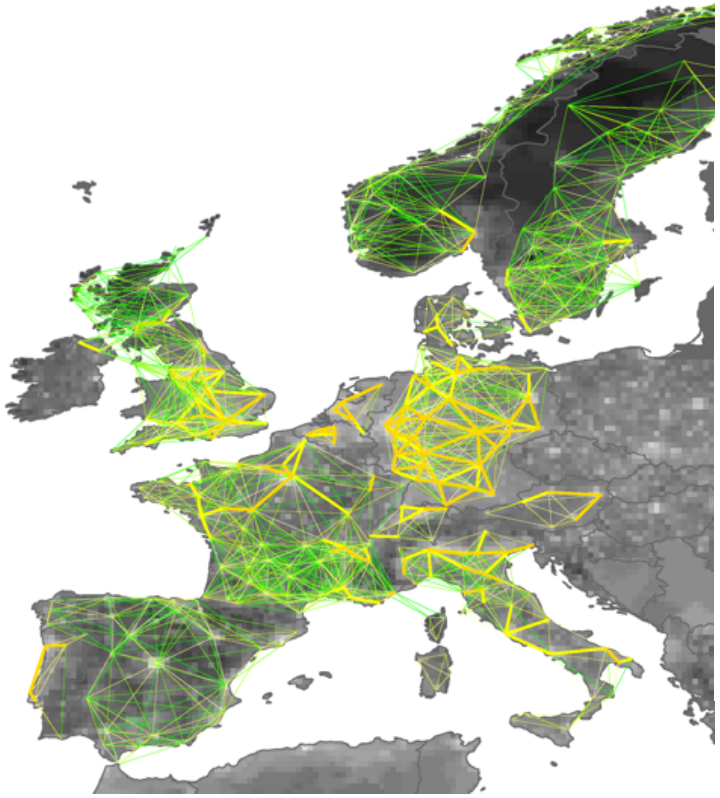
trans-border mobility (No official source)

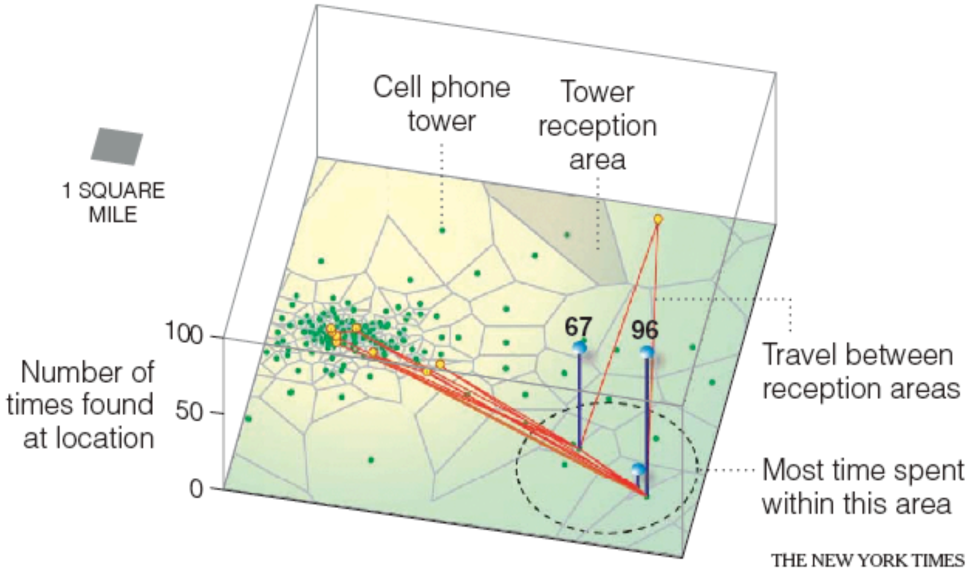
local mobility other than commuting

human mobility

To model epidemics in space we need information on human mobility

[Human mobility: Models and applications, Barbosa et al. Physics Reports 734 (2018)]





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[Balcan, et al PNAS 2009]

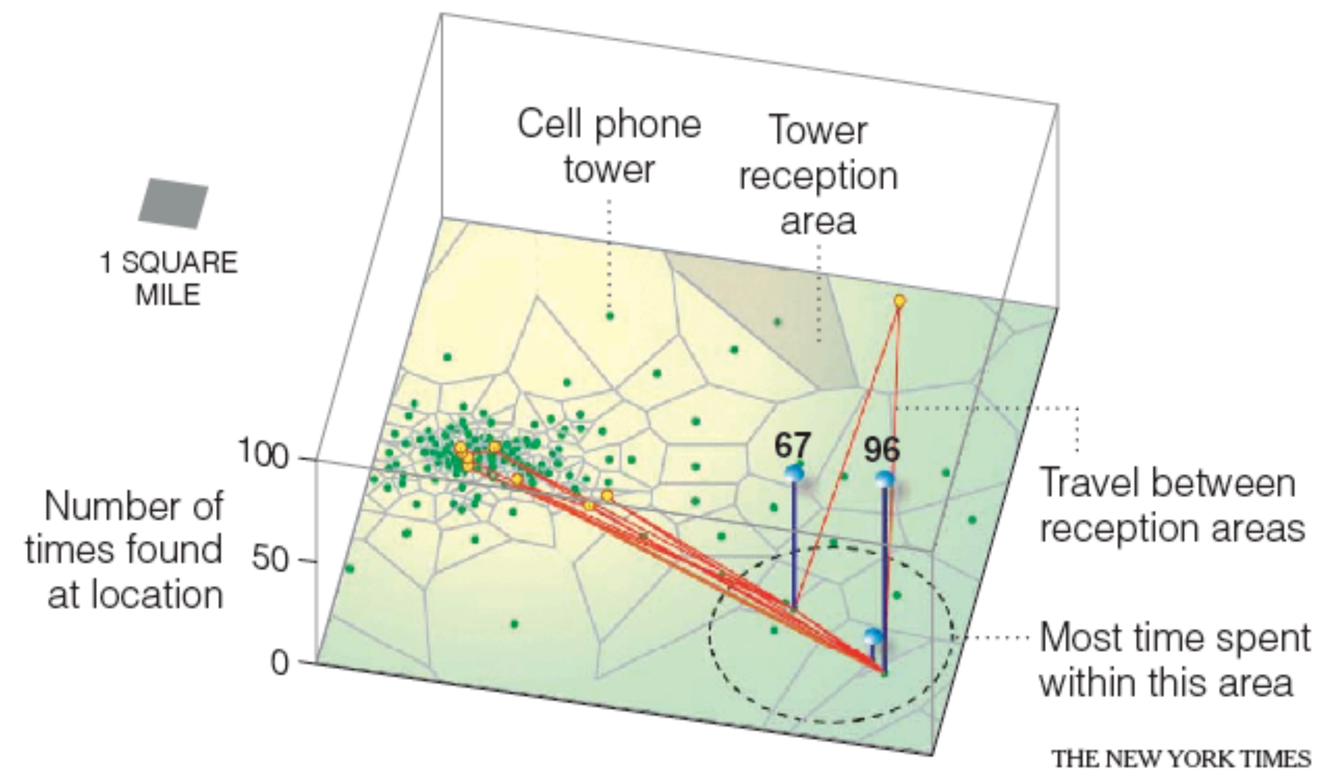
Mobile phone

data shared privately by the telephone providers

mobility network data: mobile phone

information recorded for each call & SMS:
time, caller ID, recipient ID, call duration, cellular tower

individual level trajectories (users are anonymised)



[Gonzalez et al, Nature (2008)]

PROS:

Individual trajectories combining all transportation media and purposes. Possible to infer the residence and work locations

high temporal and spatial resolution

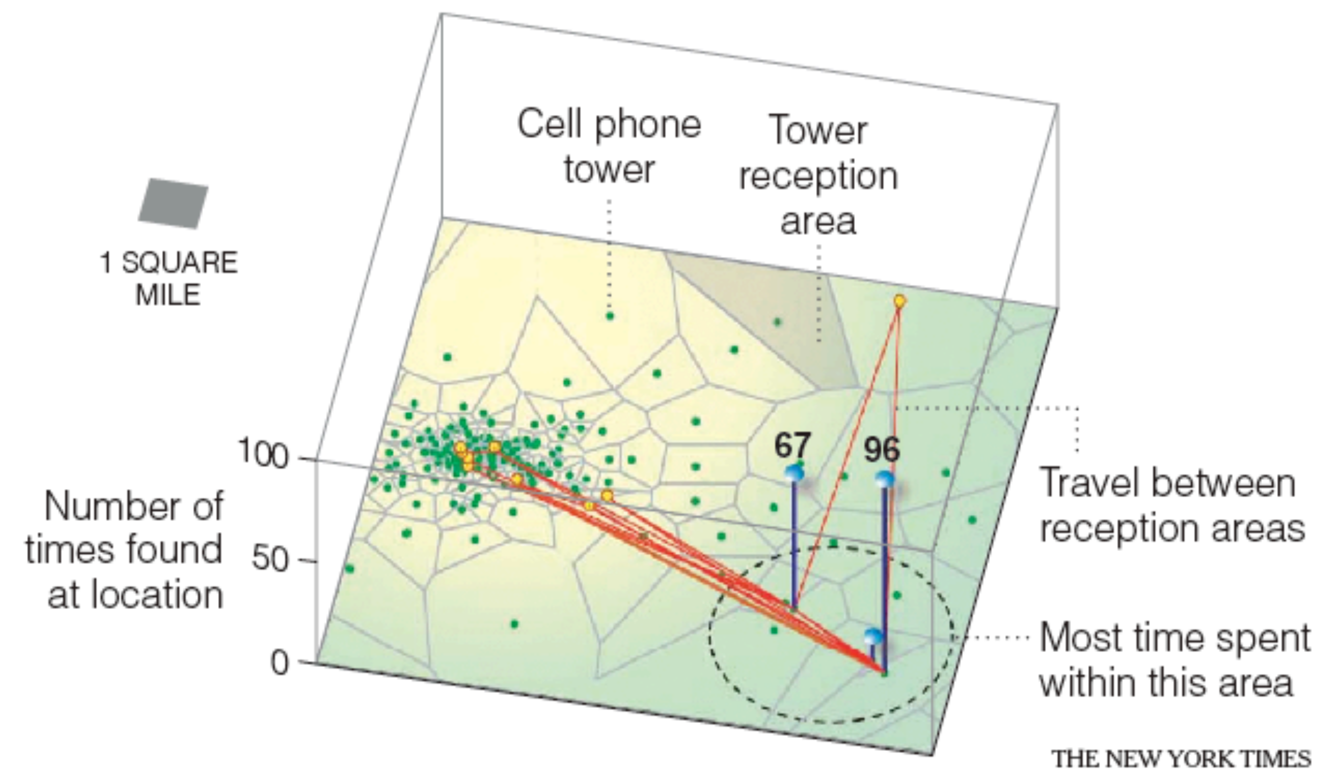
available at large geographical extent (main source of information regarding mobility for many low income countries)

mobility network data: mobile phone

information recorded for each call & SMS:
time, caller ID, recipient ID, call duration, cellular tower

individual level trajectories (users are anonymised)

CONS:



[Gonzalez et al, Nature (2008)]

for statistical reliability the analysis is restricted to users that call with high frequency (still many locations may be missed)

Area covered by the cell tower highly variable: Towers more dense in densely populated area –> spatial resolution in rural areas very poor

data cannot be shared across groups (problems with validation)

data-analysis poses statistical and numerical challenges

mobility network data: others

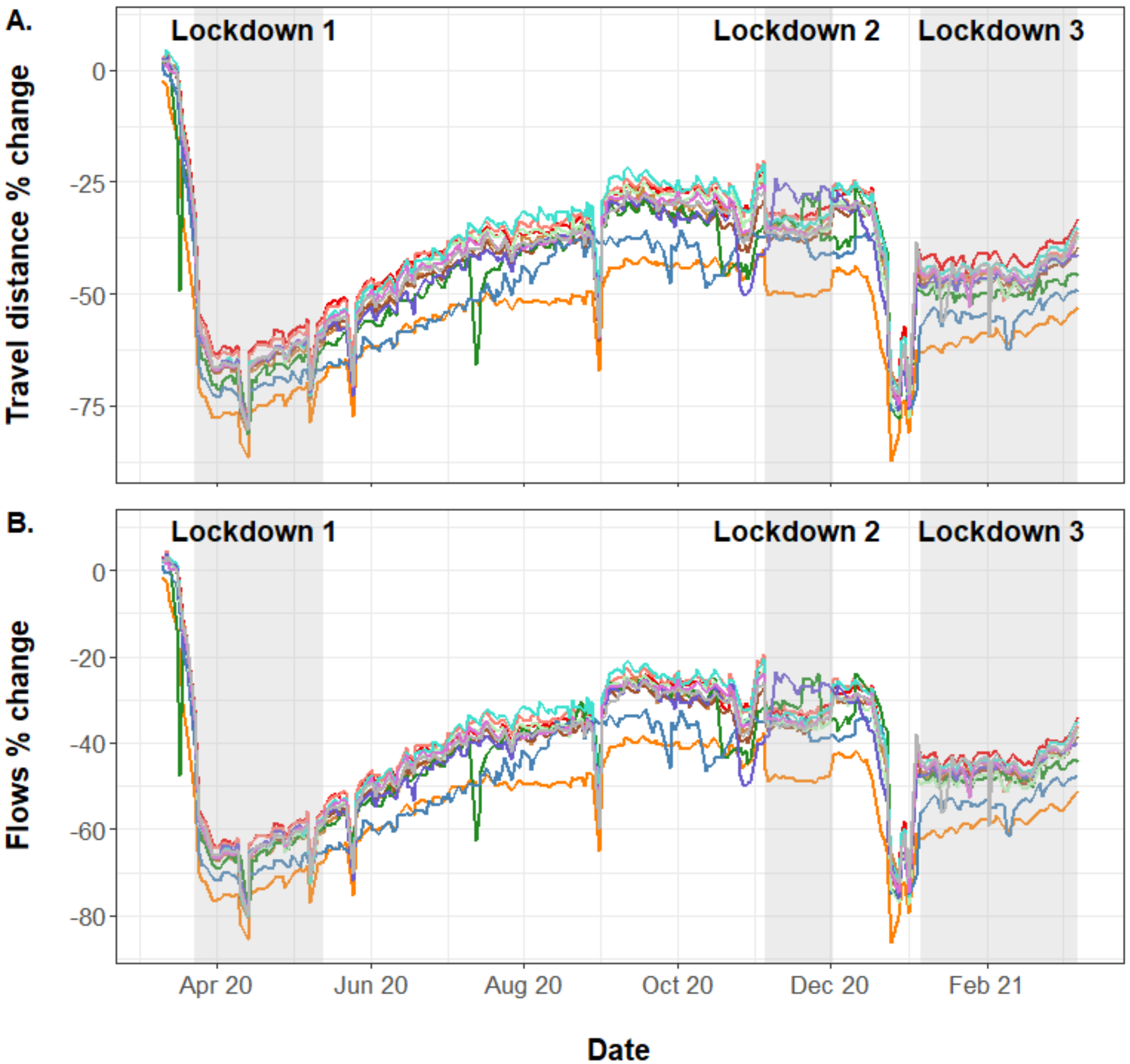
Online social network services (e.g. Google, Twitter, Facebook) … a revolution?

PROS:

high spatial resolution (based on GPS)

CONS:

the population is likely not representative



modelling human mobility

Individuals-level models

modelling trajectories of individuals: random walk, brownian motion, Levy flight, preferential return, …

Population level model

modelling fluxes, i.e. the Origin-Destination matrices.

- Two main families: gravity models, intervening opportunities models

gravity model

Introduces by G. K. Zipf (1946) . Equation to calculate mobility flows inspired by Newton's law of gravitation

$T_{ij} \propto \frac{N_i N_j}{d_{ij}}$, N_i population of i, d_{ij} distance between i and j

More general form:

$$T_{ij} = C\ M_i M_j\ F(d_{ij})$$

$$M_i = N_i^{\alpha},\ M_j = N_j^{\gamma}$$

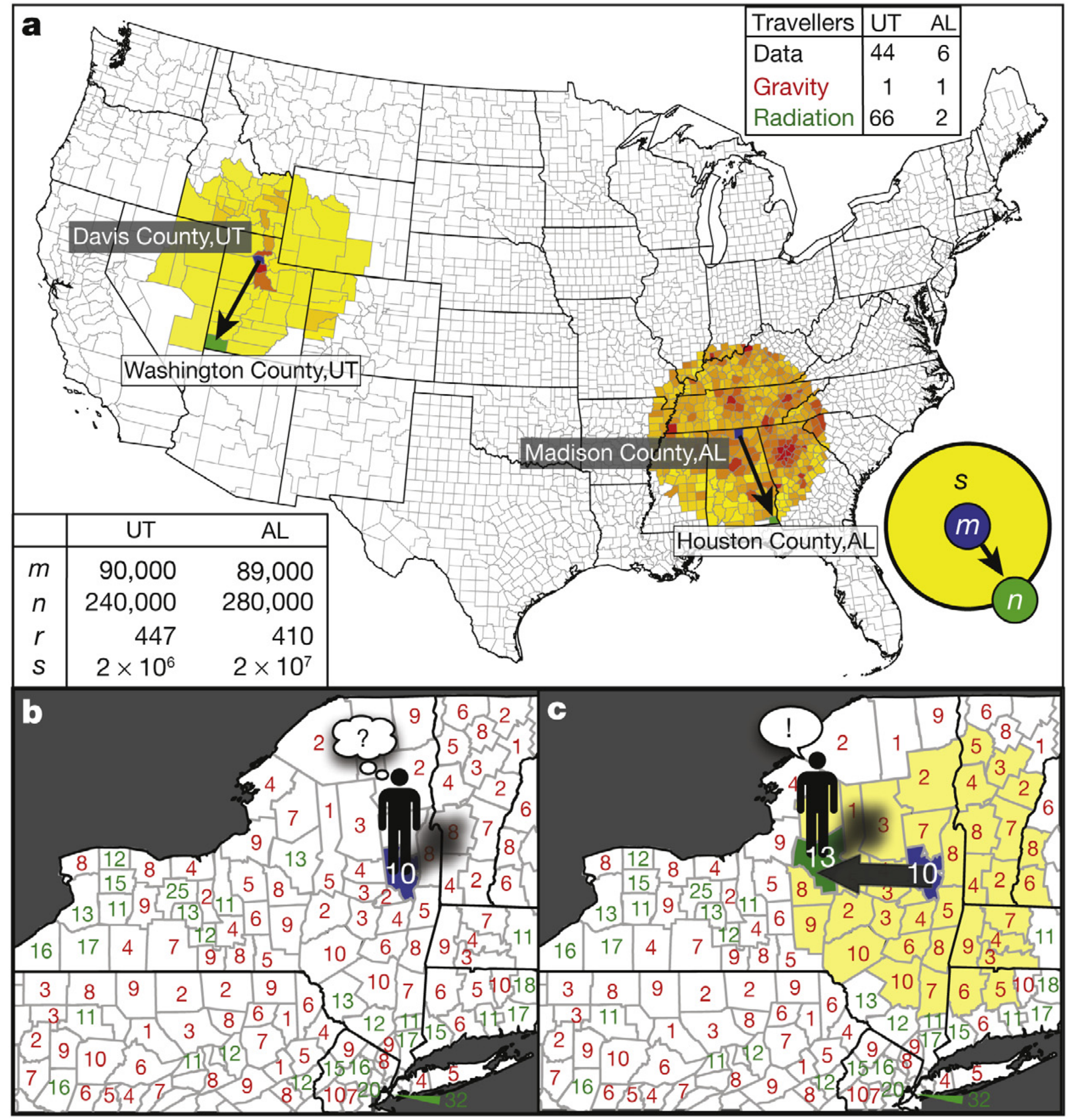
$F(d_{ij}) =$ either power low d_{ij}^{β} or exponential form $e^{-\beta\, d_{ij}}$ or combination of both

PROS: Is able to fit well the data

CONS: fitted parameters vary according to the spatial granularity

intervening opportunities models: radiation model

Introduces by Stouffer (1940). A key driver of migration is the number of intervening opportunities or the cumulative number of opportunities between the origin and the destination. Definition of "Opportunities" intentionally *vague*.



[Simini et al Nature 2012]

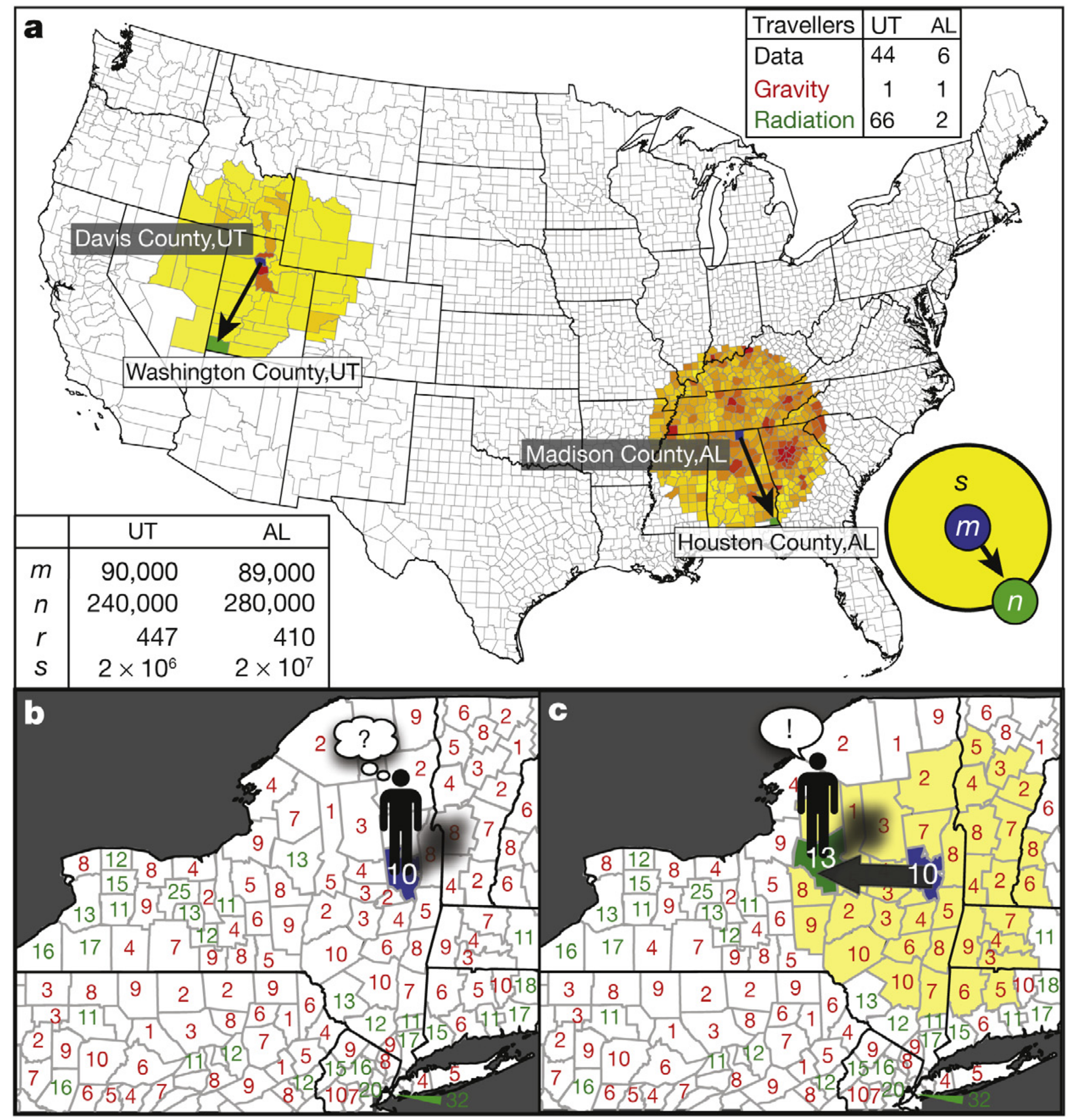
radiation model

an individual seeks a job from all counties, including his/her home county.

jobs in each county ∝ county's population n (one job opening each n_{jobs} individuals)

z = benefits (income, working hours, conditions) of a potential job opportunity, random variable with probability $p(z)$

we assign to a county n/n_{jobs} random numbers, z_1, z_2, …



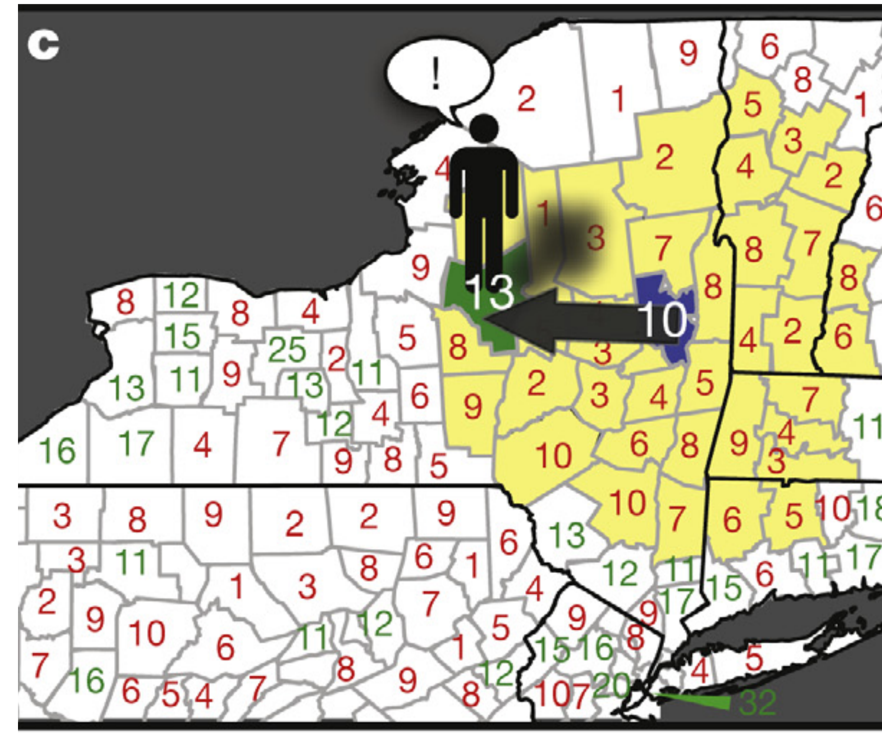
The individual chooses the closest job to his/her home, whose benefits z is higher than the best offer available in his/her home county.

[Simini et al Nature 2012]

radiation model

probability that a person living in i finds a job in j

$$P(1 \,|\, m_i, n_j, s_{ij}) = \int_0^\infty dz P_{m_i}(z) P_{s_{ij}}(<z) P_{n_j}(>z)$$



where:

m_i = source population

$P_{m_i}(z)$ probability that the maximum of $p(z)$ after m_i trials is z

s_{ij} = population in the radius r_{ij}

$$P_{s_{ij}}(<z) = p(<z)^{s_{ij}}$$

$$P_{n_j}(>z) = 1 - p(<z)^{n_j}$$

$$P_{m_i}(z) = \frac{dP_{m_i}(<z)}{dz} = m_i \, p(<z)^{m_i - 1} \frac{dp(<z)}{dz}$$

[Simini et al Nature 2012]

radiation model

probability that a person living in i finds a job in j

$$P(1 | m_i, n_j, s_{ij}) = m_j \int_0^\infty dz \frac{dp(<z)}{dz} \left[p(<z)^{m_i+s_{ij}-1} - p(<z)^{m_i+n_j+s_{ij}-1} \right]$$

Resulting fluxes are independent of $p(z)$ and parameter free

$$P(1 | m_i, n_j, s_{ij}) = \frac{m_i n_j}{(m_i + s_{ij})(m_i + n_j + s_{ij})}$$

$$T_{ij} = T_i \frac{m_i n_j}{(m_i + s_{ij})(m_i + n_j + s_{ij})}$$

[Simini et al Nature 2012]

radiation model

probability that a person living in i finds a job in j

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$$T_{ij} = T_i \frac{m_i n_j}{(m_i + s_{ij})(m_i + n_j + s_{ij})}$$ with T_i the total number of commuters in location i

(this can be approximated by $m_i N_c / N$, with N_c the total number of commuters

PROS: parameters free. Useful in epidemiology were we have only information of population distribution (low developed countries)

CONS: goodness of fit depends on the spatial resolution

[Simini et al Nature 2012]

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 & COVID-19: traveling rate= 10^{-3} days^{-1} vs. recovery rate> 0.1 days^{-1})
- early spread of COVID-19 or a flu pandemic. It does not work well if I want to model the long term continuous circulation

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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:**

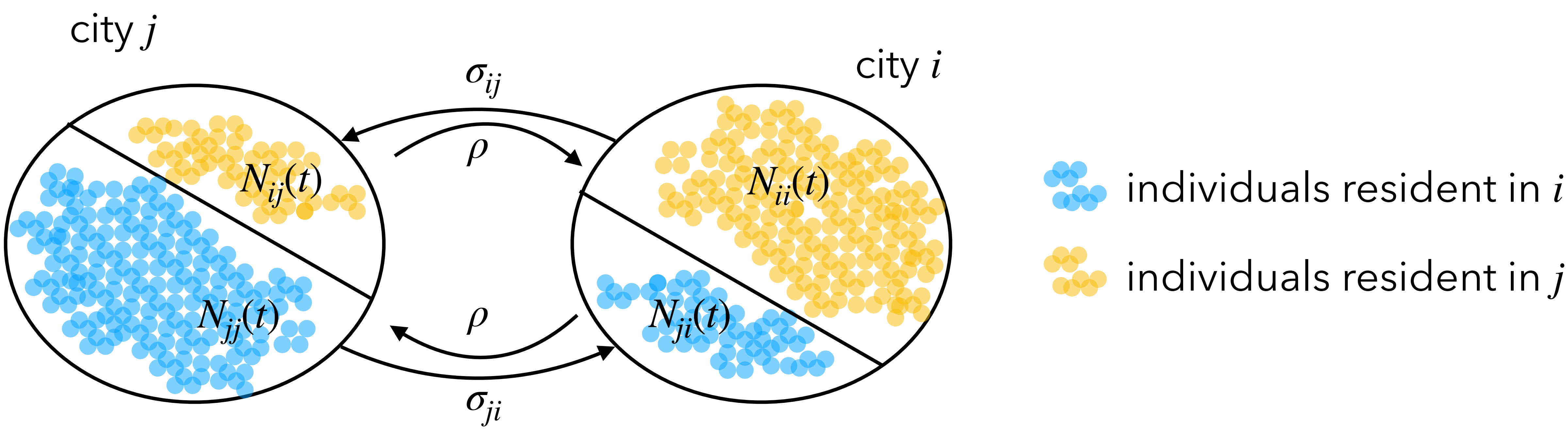
either

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 (commuting and flu: traveling rate= 3 days^{-1} (~1/8h) vs. recovery rate> ~0.1 days^{-1})

SIR metapopulation model with memory



σ_{ij} leaving rate, fraction of commuters

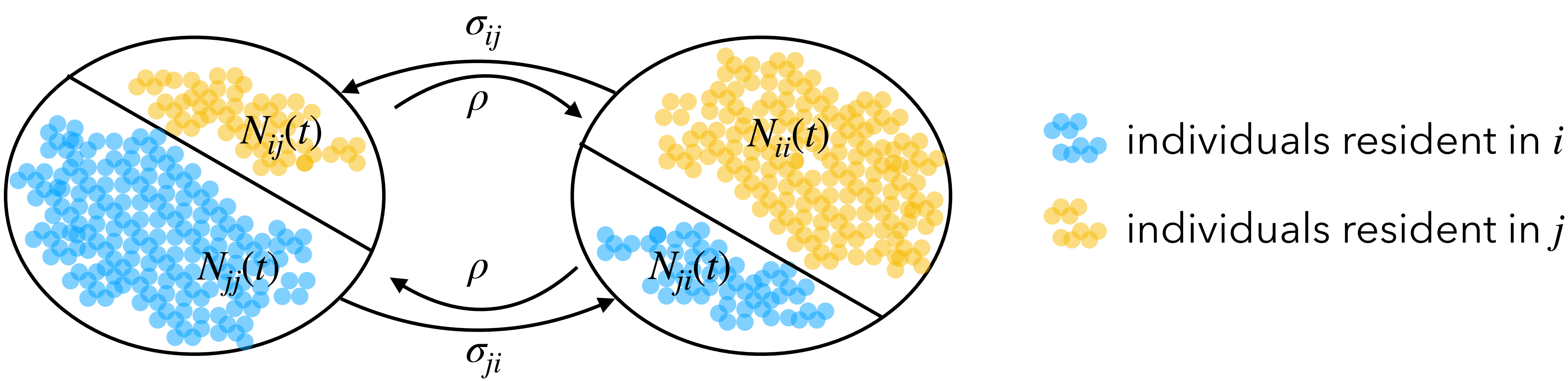
ρ returning rate ($\rho^{-1} = \tau \sim 8h$)

$N_i = N_{ii}(t) + \sum_j N_{ij}(t)$ 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 ($\rho^{-1} = \tau \sim 8h$)

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

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

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

[Sattenspiel, L. & Dietz, K. Math. Biosci. 128, 71–91 (1995);
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SIR metapopulation model with memory

differential equations

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

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

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

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

solution

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

linear ordinary differential equation of order 1

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

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

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

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

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SIR metapopulation model with memory

differential equations

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

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

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

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

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:

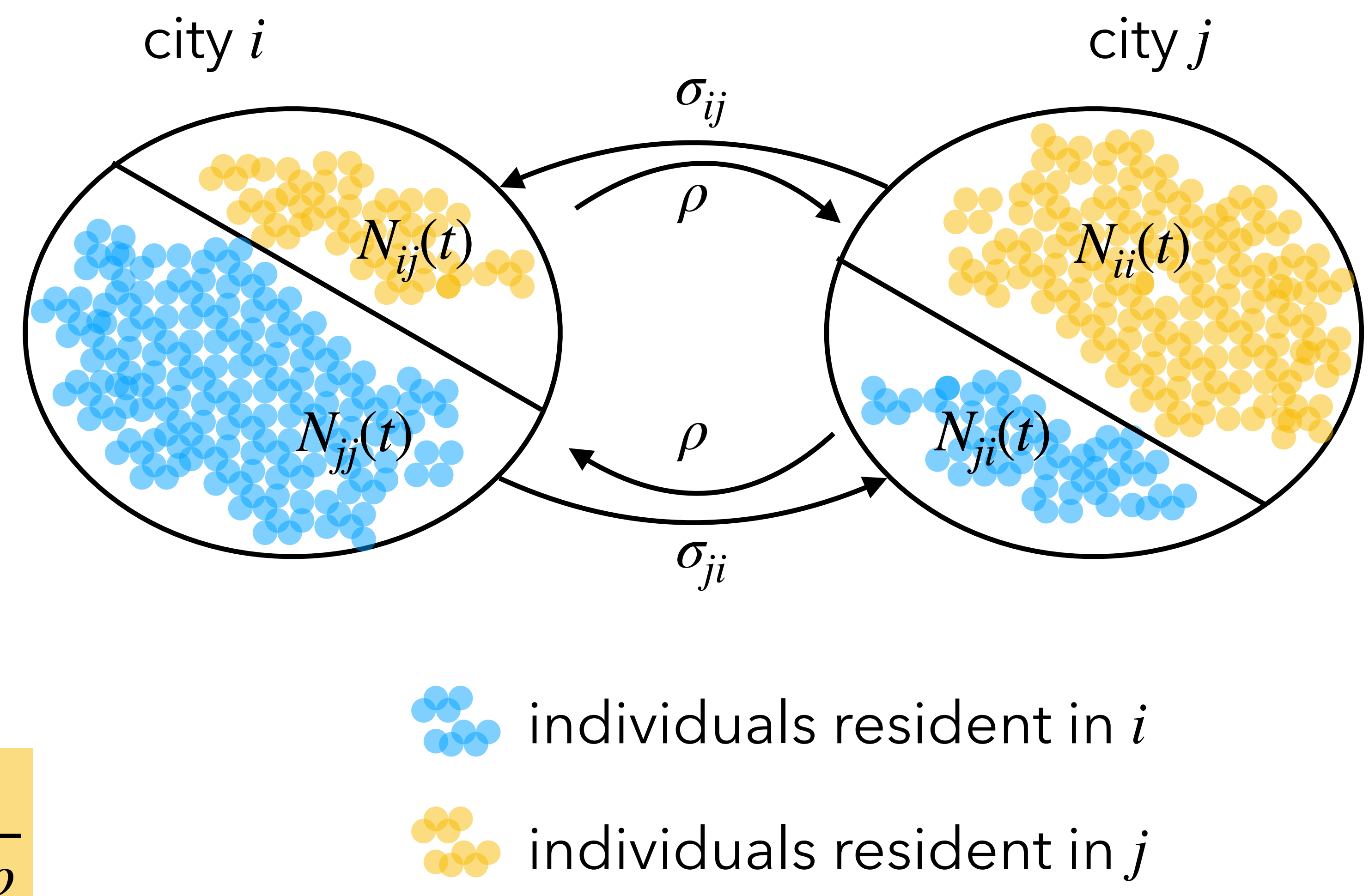
$$N_{ii}(t) = \frac{N_i}{1 + \sigma_i/\rho} \qquad N_{ij}(t) = \frac{\sigma_{ij} N_i/\rho}{1 + \sigma_i/\rho}$$

People resident in i

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

People present in i

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



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SIR metapopulation model with memory

Equilibrium solutions:

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

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

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

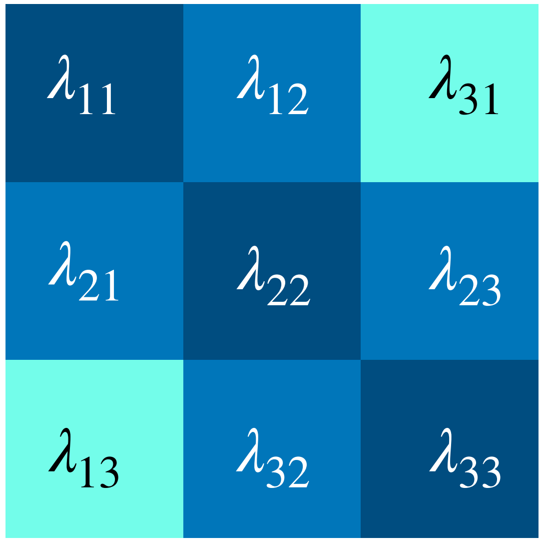
[Sattenspiel, L. & Dietz, K. Math. Biosci. 128, 71–91 (1995); Keeling, M. J. & Rohani, P. Ecol. Lett. 5, 20–29 (2002)]

SIR metapopulation model with commuting

I collapse the modelling approach to a risk matrix approach

risk of transmission across groups (fairly) realistically account for duration of travel and commuter mobility network

It enable analytical calculation - e.g. computation of the global invasion threshold in the homogenous and the heterogenous case



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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?**

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

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Time scale separation

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

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

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

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

[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

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

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

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

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

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

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

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

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

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

mathematical expressions to speed up computer simulations

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