The Physics Society of Iran

Shahid Beheshti University

Tehran school on Theory and Applications
of
COMPLEX NETWORKS

Introduction to network epidemiology

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Inserm

MÉDECINE
SORBONNE
UNIVERSITÉ

Outline

-modeling an epidemic

-epidemics on networks

-epidemics in space

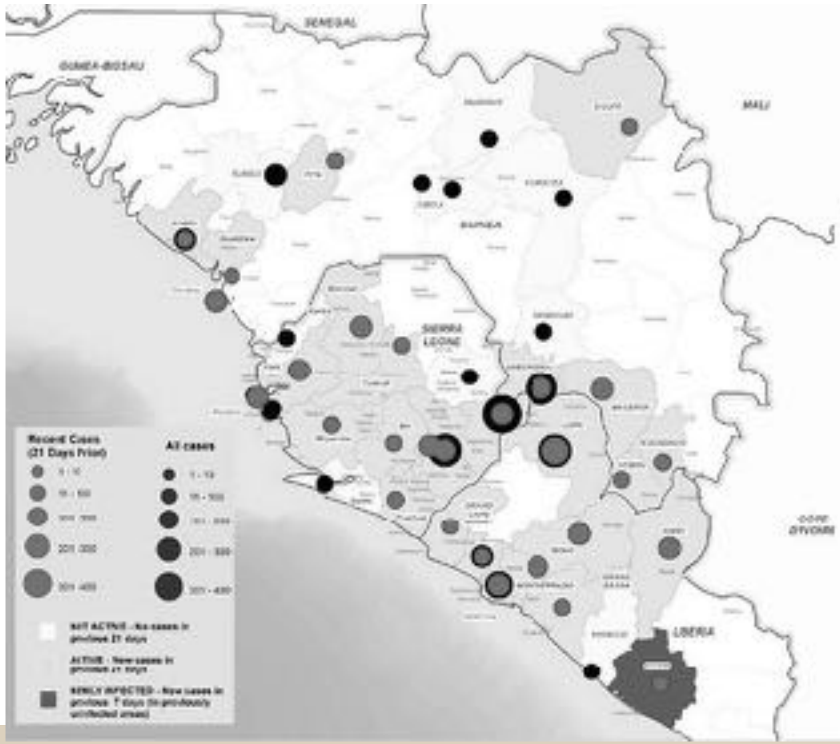
-interacting epidemics

-computer simulations

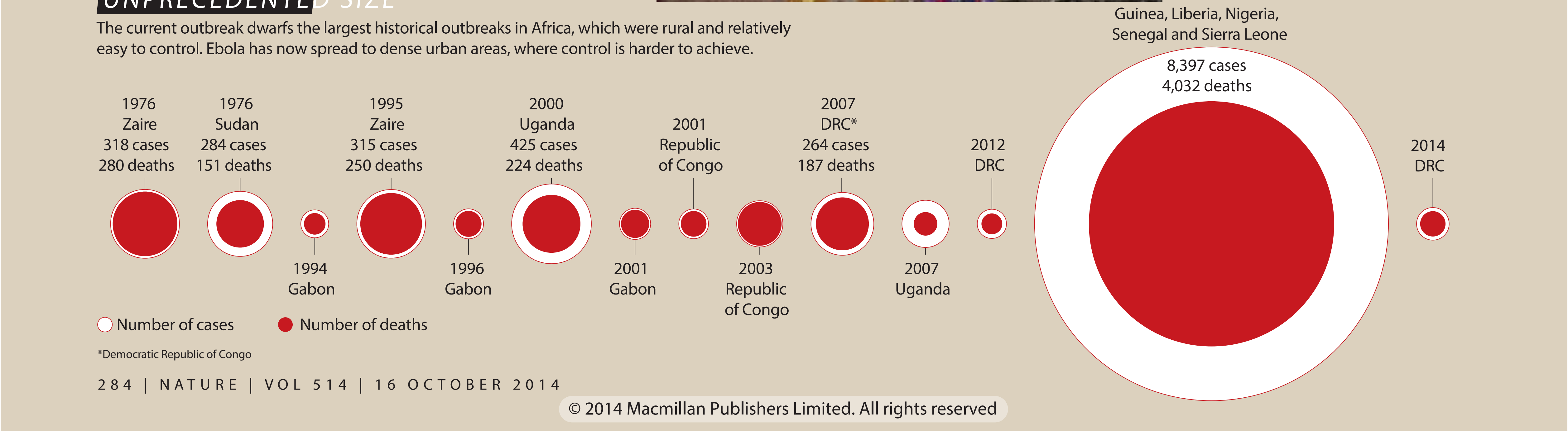
Outline

- **-modeling an epidemic**
- -epidemics on networks
- -epidemics in space
- -interacting epidemics
- -computer simulations

Western Africa ebola outbreak, 2014



28 646 cases
11 323 death



UNPRECEDENTED SIZE

The current outbreak dwarfs the largest historical outbreaks in Africa, which were rural and relatively easy to control. Ebola has now spread to dense urban areas, where control is harder to achieve.

*Democratic Republic of Congo

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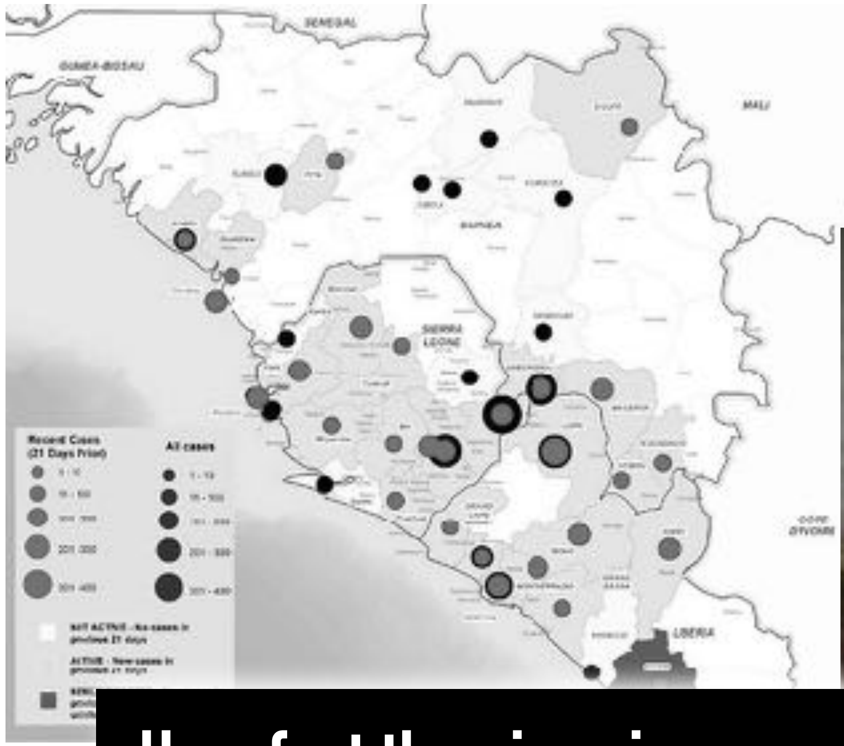
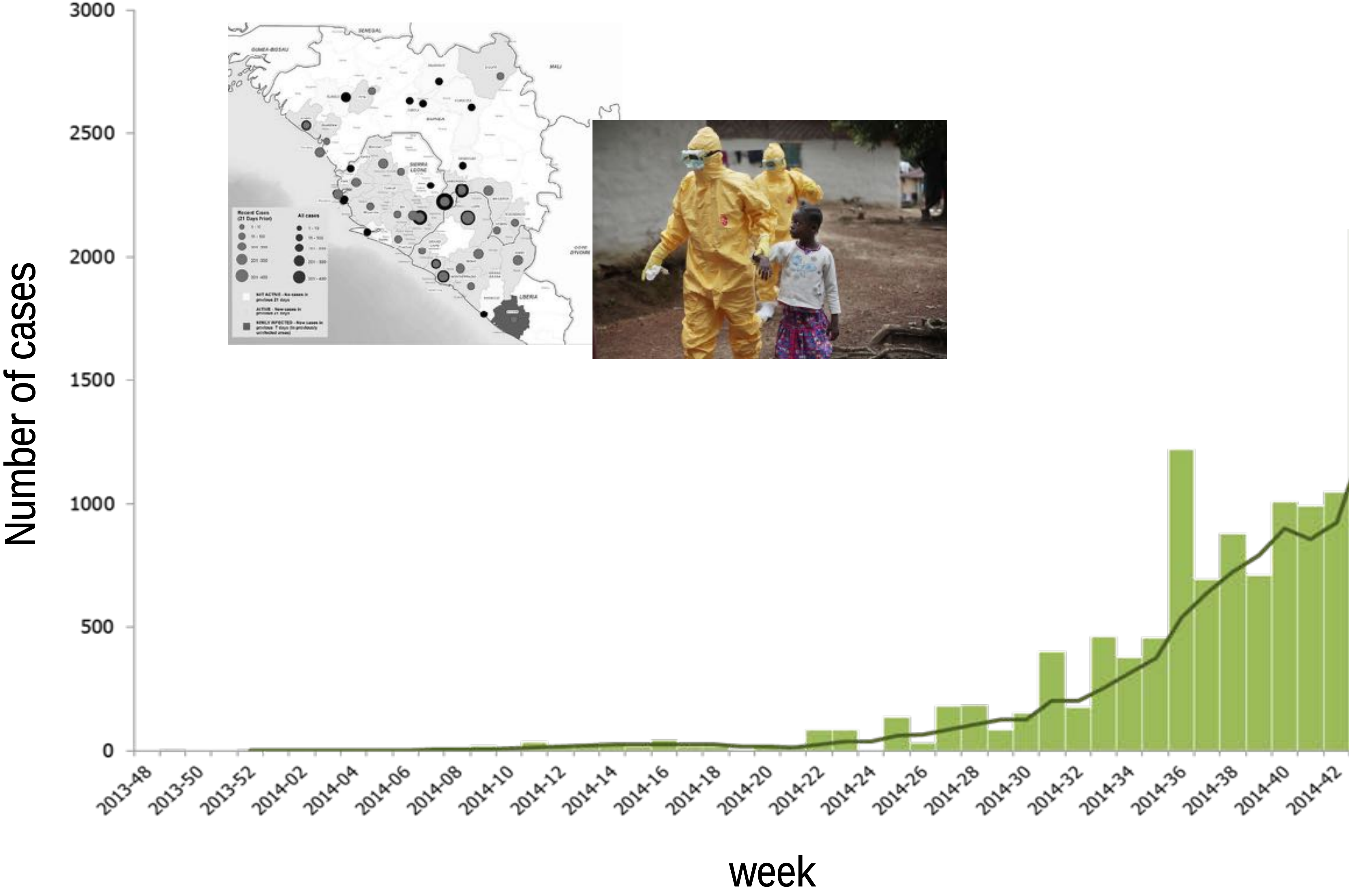
Western Africa ebola outbreak, 2014

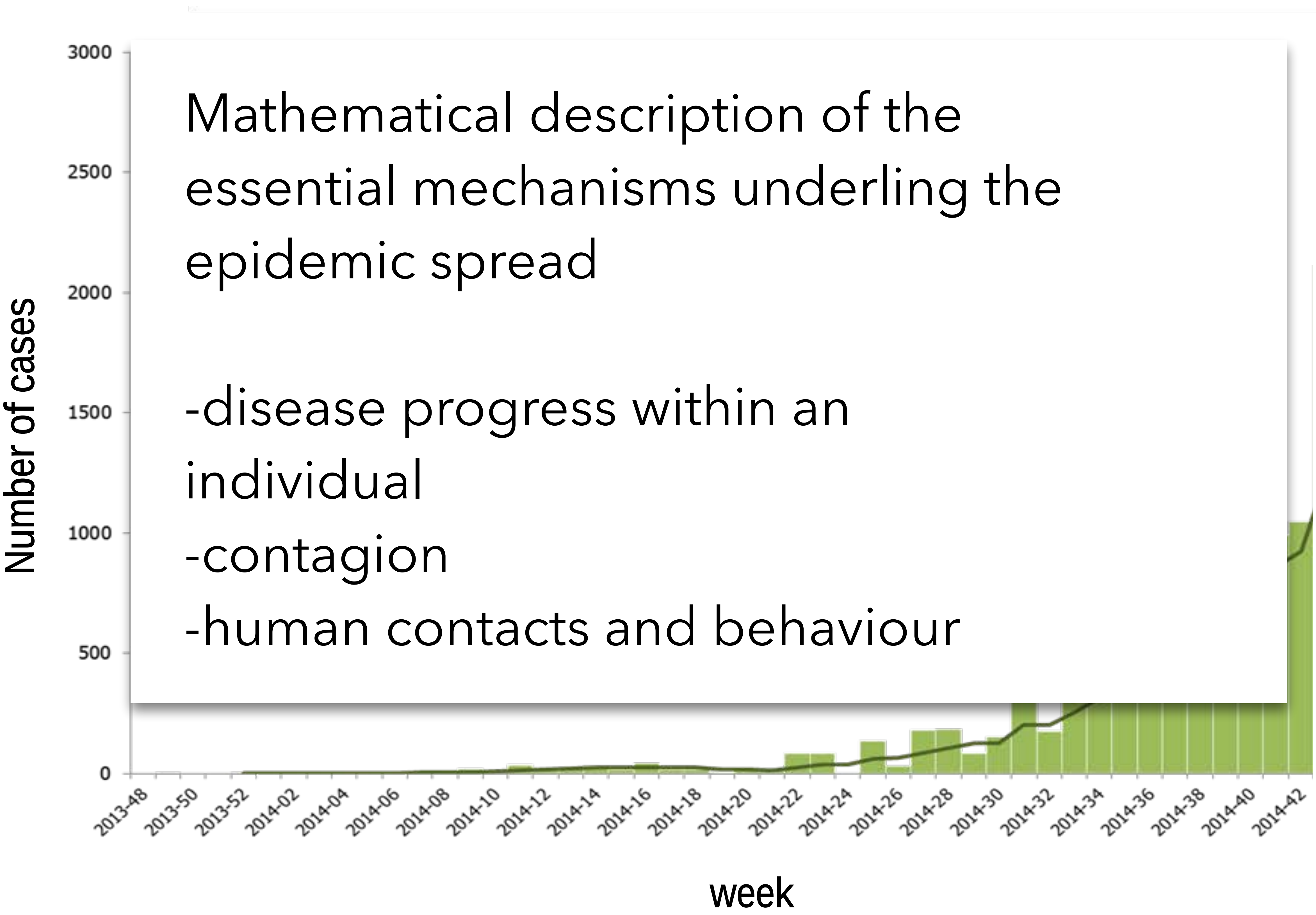


How fast the virus is spreading ?
What can we do to stop the epidemic?

quantitative description



mechanistic modelling



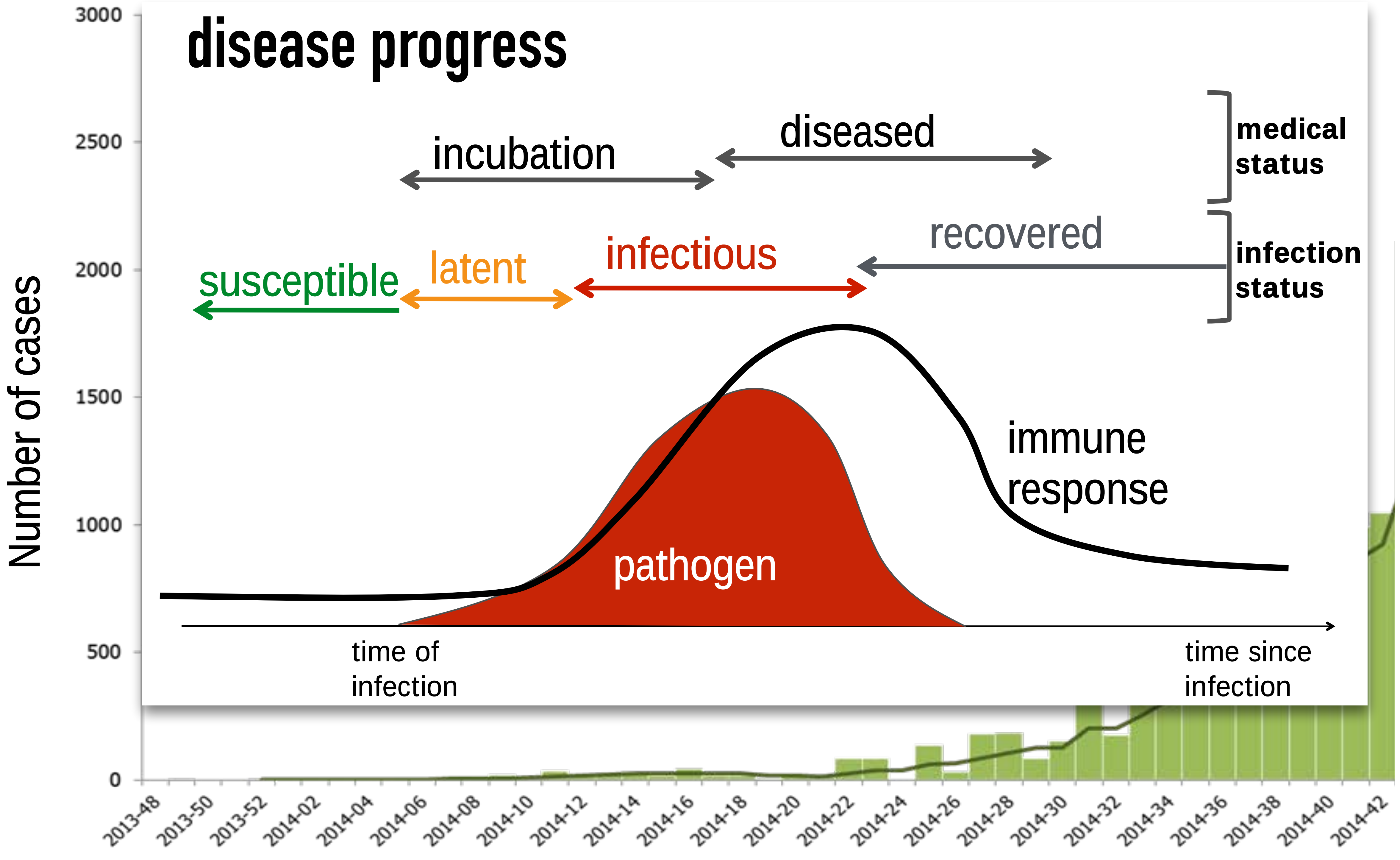
Mathematical description of the essential mechanisms underling the epidemic spread

-disease progress within an individual

-contagion

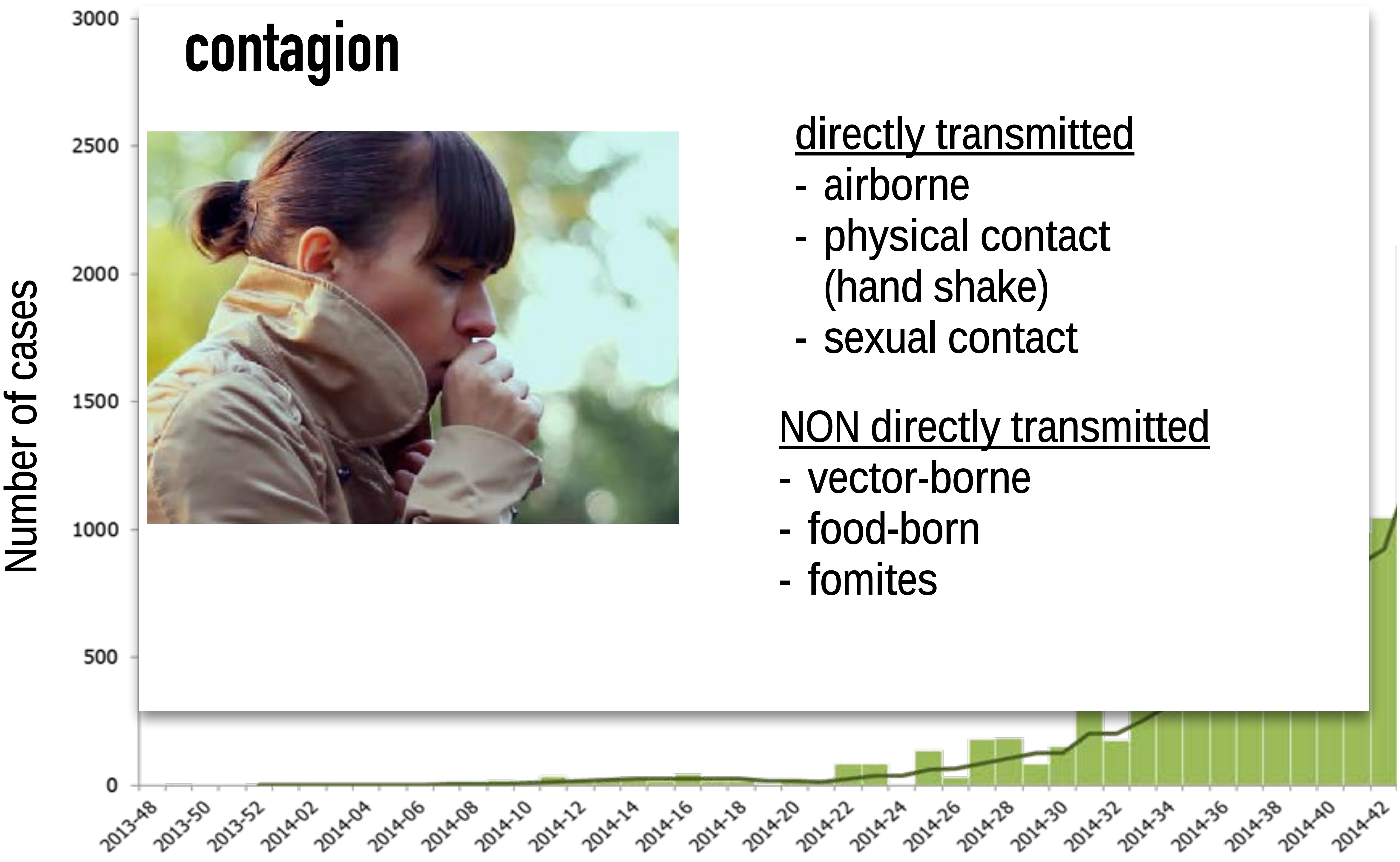
-human contacts and behaviour

mechanistic modelling



[Keeling & Rohani, Modeling Infectious Diseases (2008)]

mechanistic modelling



contagion

<u>directly transmitted</u>

- airborne
- physical contact (hand shake)
- sexual contact

<u>NON directly transmitted</u>

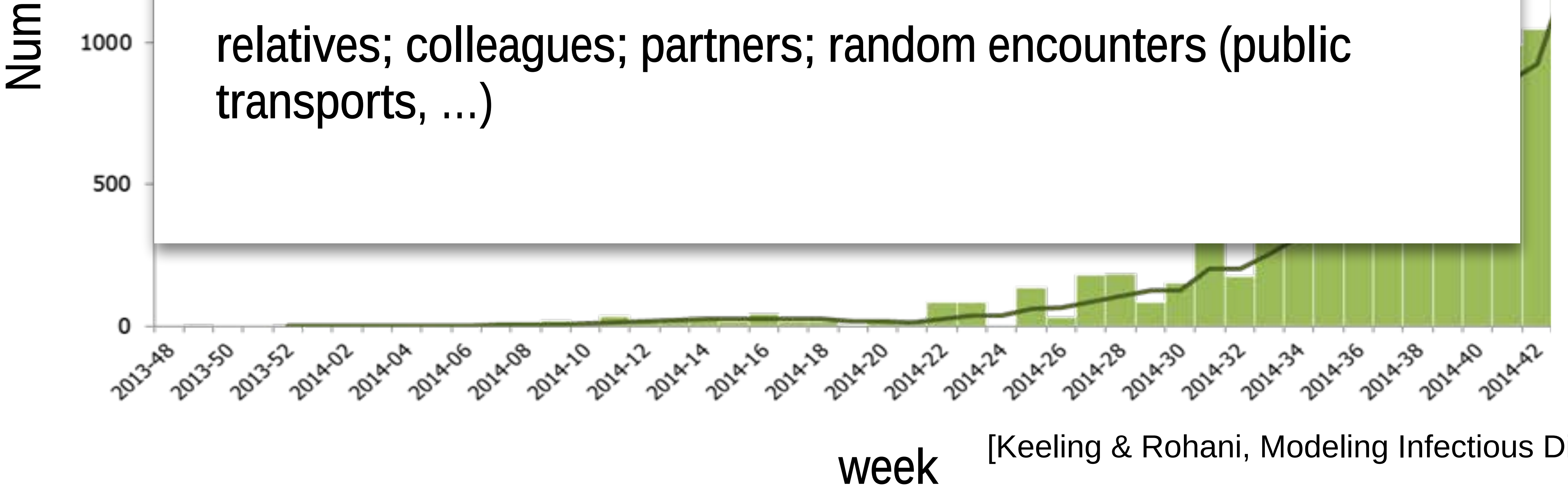
- vector-borne
- food-born
- fomites

week

[Keeling & Rohani, Modeling Infectious Diseases (2008)]

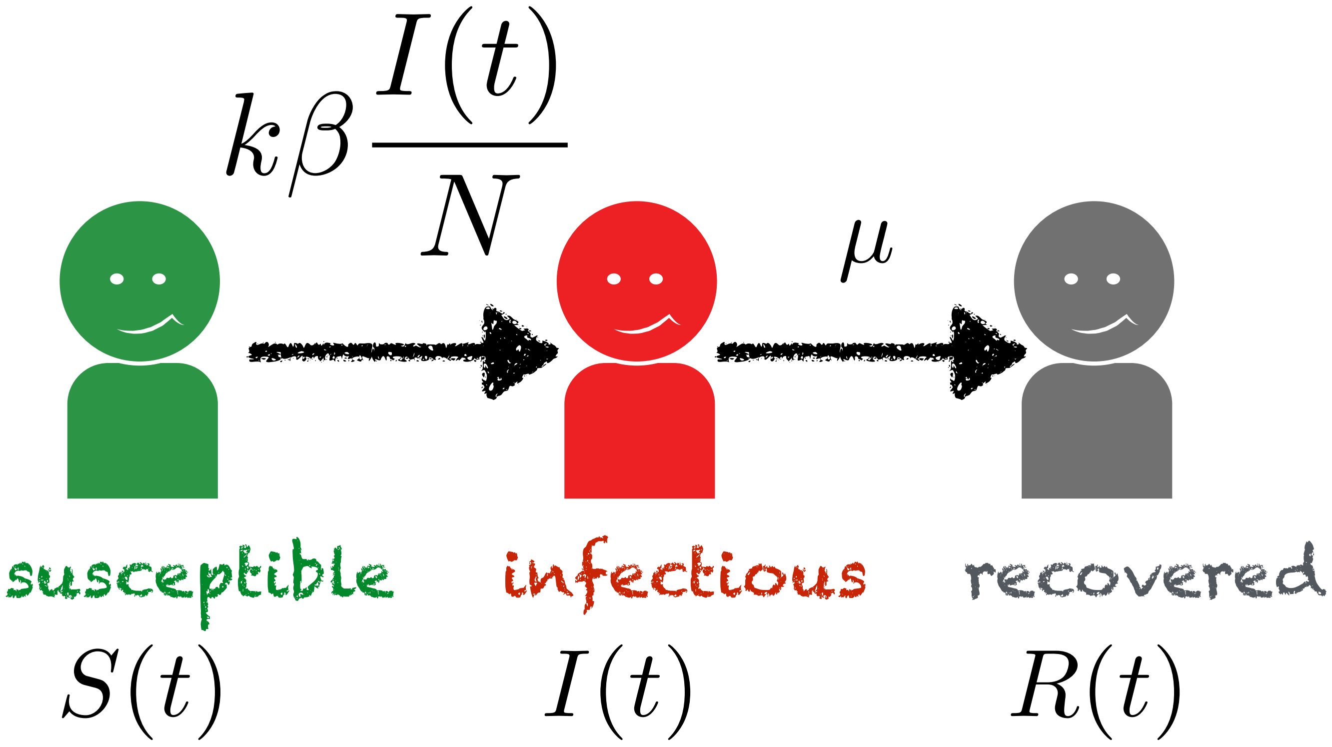
mechanistic modelling

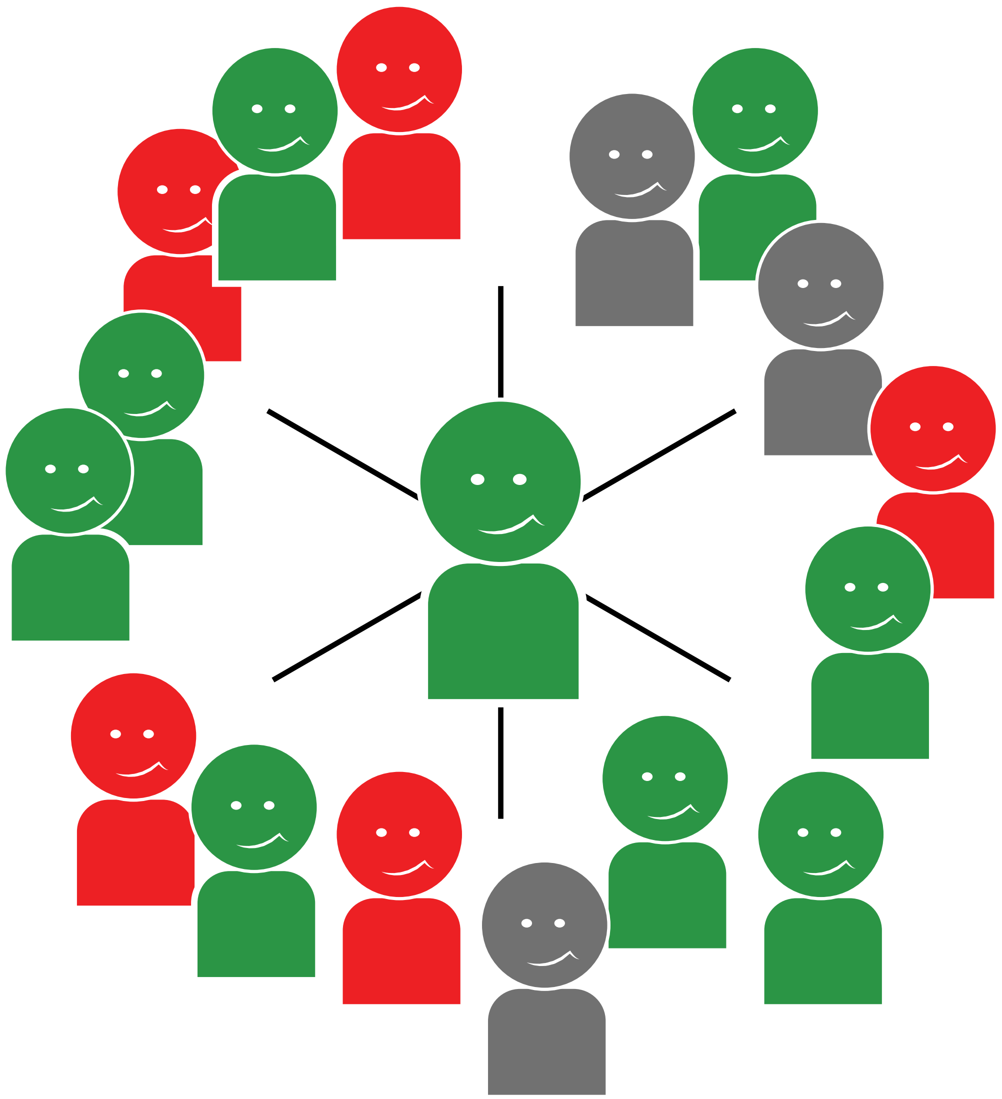
relatives; colleagues; partners; random encounters (public transports, ...)



[Keeling & Rohani, Modeling Infectious Diseases (2008)]

Kermack & McKendrick model



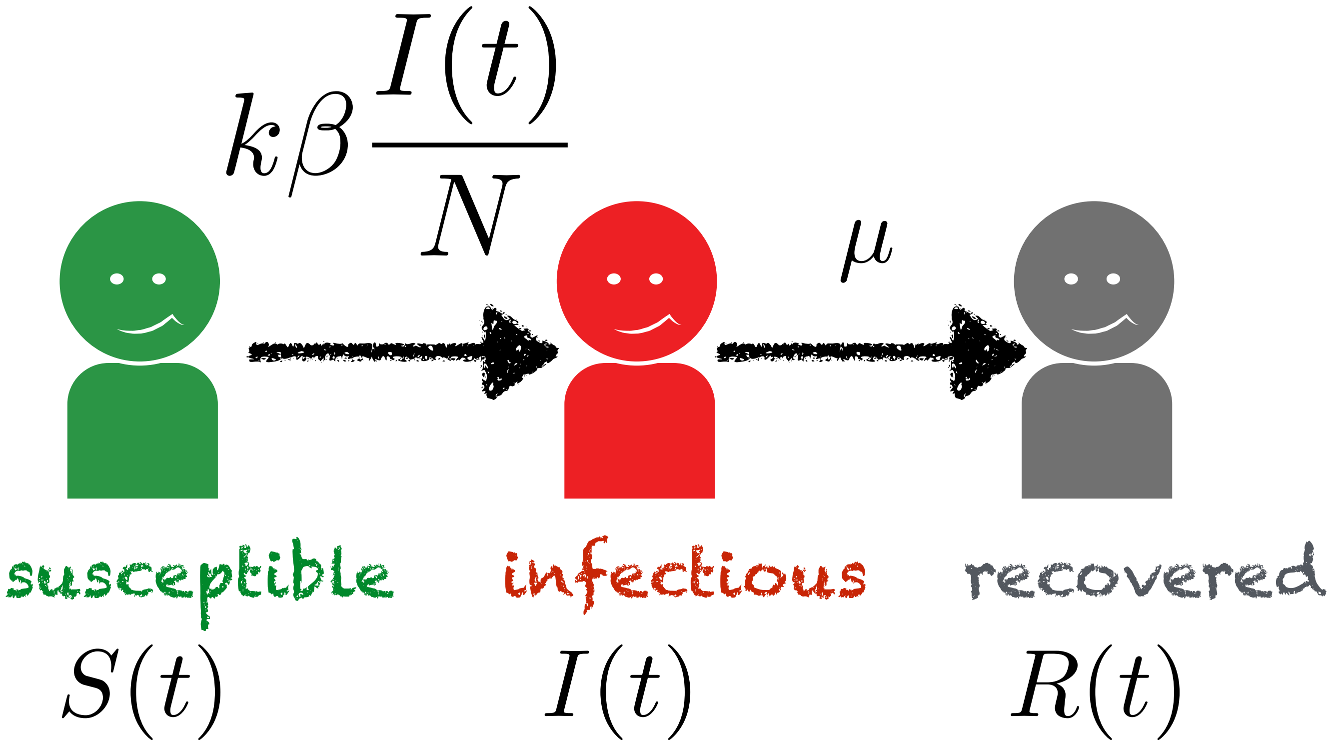


k contacts

β transmission per contact

[Kermack & McKendrick Proc Roy Soc A 1927, Keeling & Rohani, Modeling Infectious Diseases (2008)]

Kermack & McKendrick model



$$k\beta \frac{I(t)}{N}$$

$$\mu$$

susceptible

$S(t)$

infectious

$I(t)$

recovered

$R(t)$

$$d_t S(t) = -k\beta \frac{I(t)}{N} S(t)$$

$$d_t I(t) = k\beta \frac{I(t)}{N} S(t) - \mu I(t)$$

$$d_t R(t) = \mu I(t)$$

$$S(t) + I(t) + R(t) = N$$

[Kermack & McKendrick Proc Roy Soc A 1927, Keeling & Rohani, Modeling Infectious Diseases (2008)]

Kermack & McKendrick model

$$d_t S(t) = -k\beta \frac{I(t)}{\cancel{N}} \cancel{S(t)} \quad {\sim}N$$

$$d_t I(t) = k\beta \frac{I(t)}{\cancel{N}} \cancel{S(t)} - \mu I(t)$$

$$d_t R(t) = \mu I(t)$$

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

[Kermack & McKendrick Proc Roy Soc A 1927, Keeling & Rohani, Modeling Infectious Diseases (2008)]

Kermack & McKendrick model

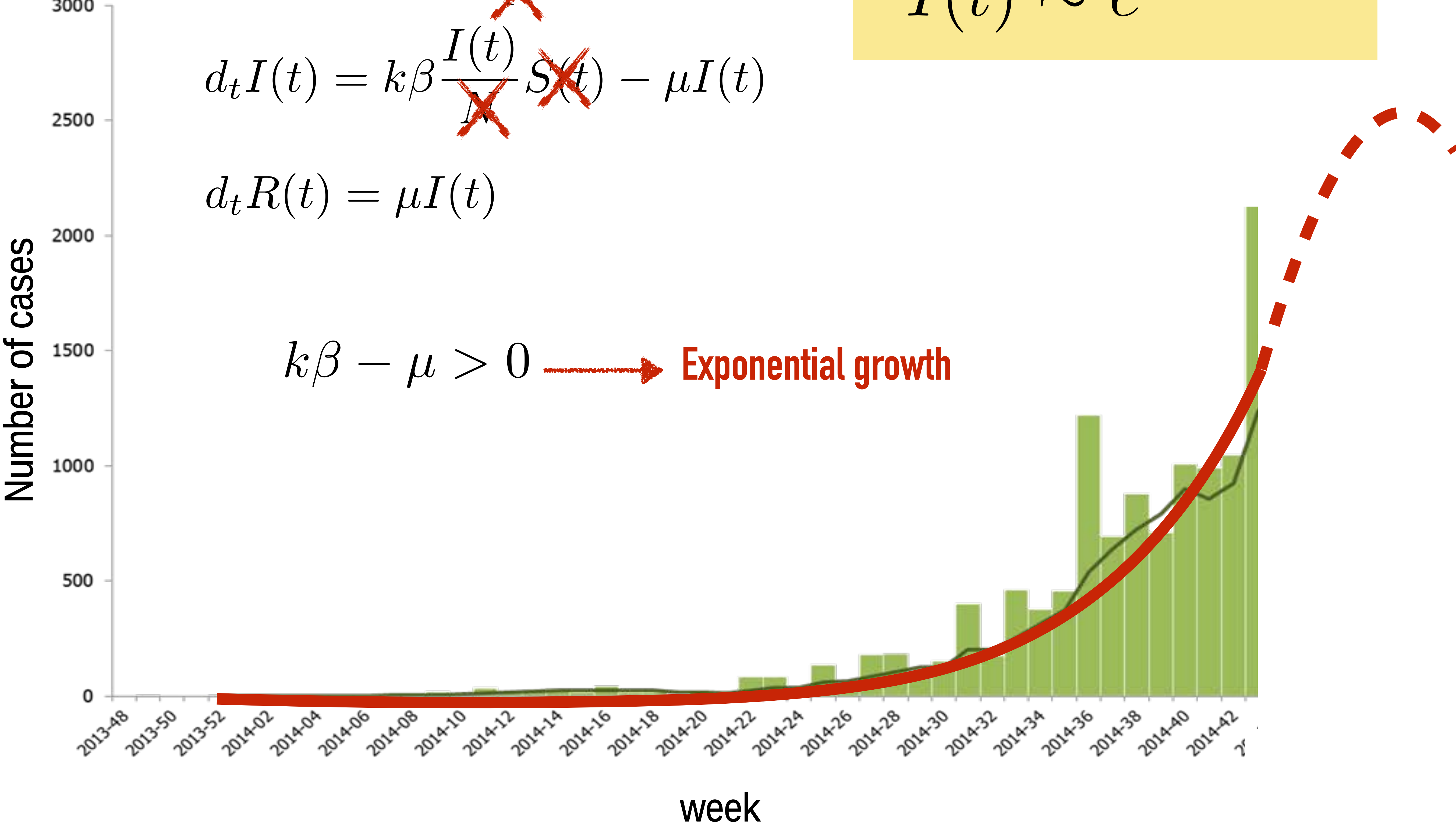
$$d_t S(t) = -k\beta \frac{I(t)}{\cancel{N}} \cancel{S(t)} \quad {}^{\sim N}$$

$$d_t I(t) = k\beta \frac{I(t)}{\cancel{N}} \cancel{S(t)} - \mu I(t)$$

$$d_t R(t) = \mu I(t)$$

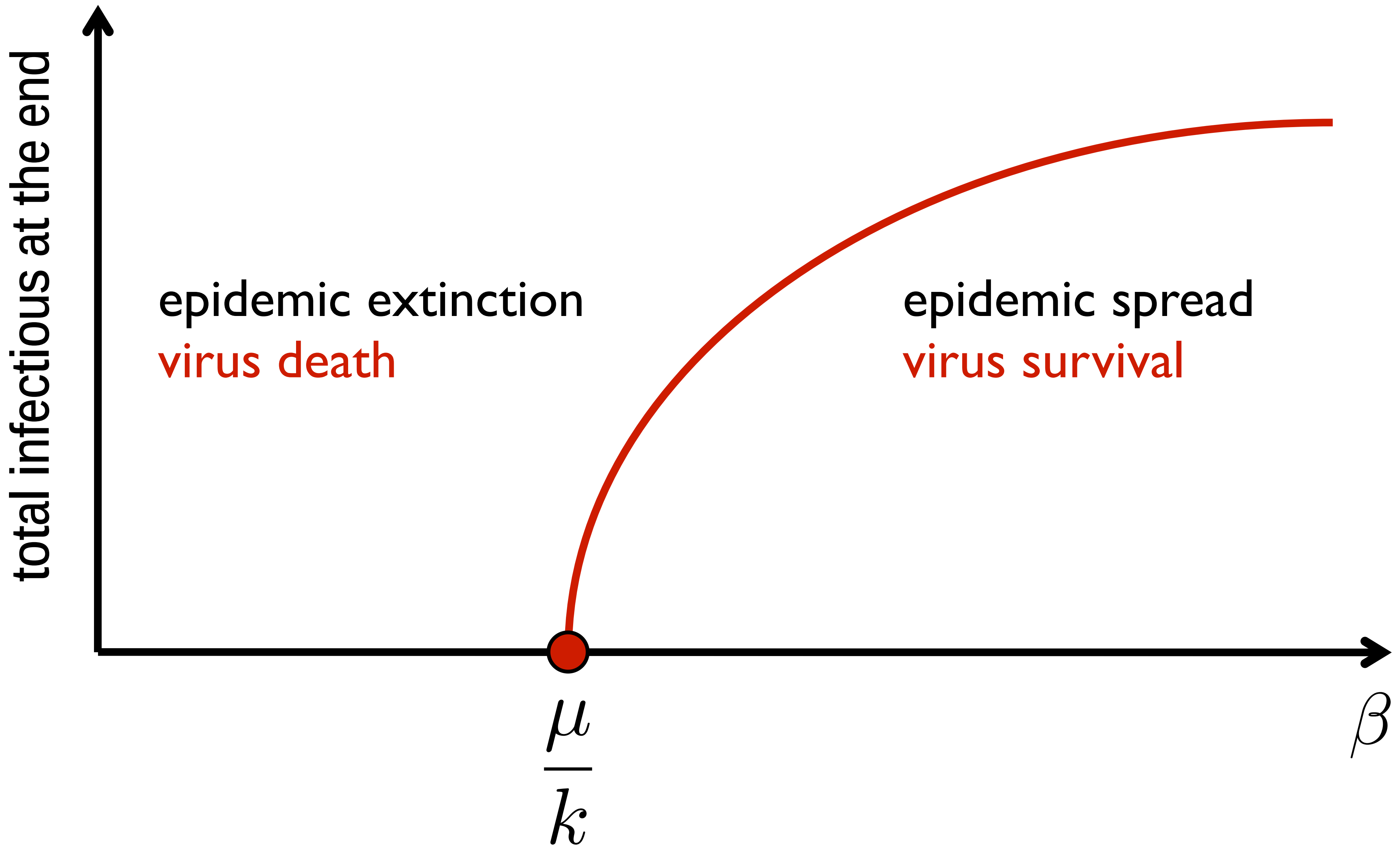
$$I(t) \sim e^{(k\beta-\mu)t}$$

$$k\beta - \mu > 0 \longrightarrow$$ **Exponential growth**



epidemic threshold

$k\beta - \mu > 0 \longrightarrow$ **Exponential growth**



basic reproductive ratio

$k\beta - \mu > 0$ → **Exponential growth**

$$\boxed{\frac{k\beta}{\mu} > 1} \quad R_0$$

average number of individuals infected by an infected individual during her/his infectious period in a fully susceptible population.

basic reproductive ratio

$$k\beta - \mu > 0 \longrightarrow \text{Exponential growth}$$

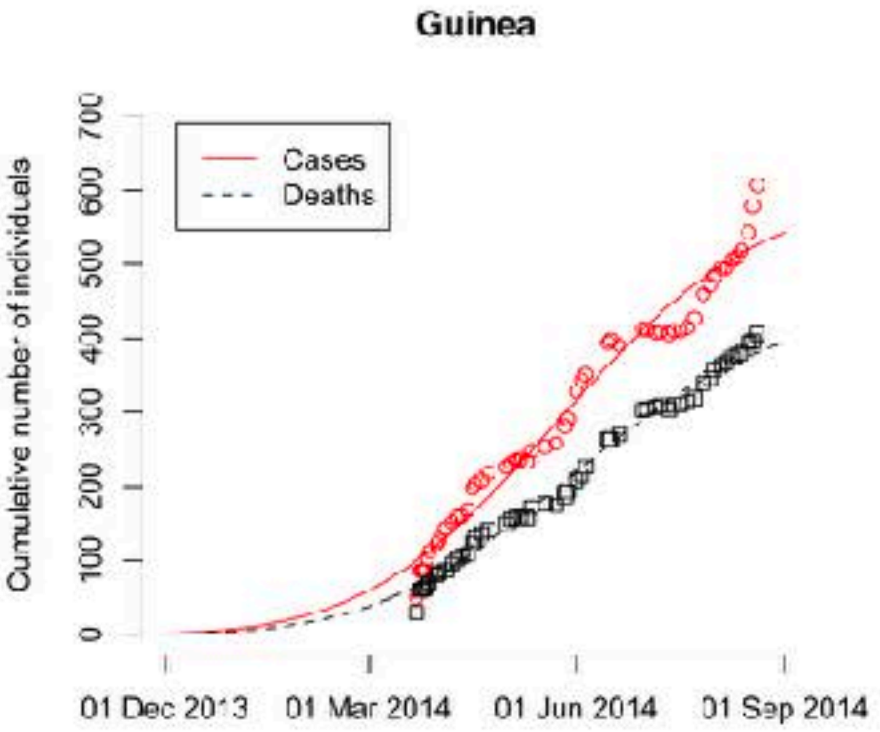
$$\boxed{\frac{k\beta}{\mu} > 1} \; R_0$$

outbreak	R_0	Ref
H1N1 pandemic (2009)	1.2 - 2.0	[Fraser et al. Science 2009]
Zika (2015)	2.6 - 4.0	[Kucharski et al. PLoS Negl Trop Dis 2016]
smallpox	3.5 - 6.0	[Gani et al. Nature 2001]
Measles	16 - 18	[Anderson & May et al. Science 1982]

basic reproductive ratio

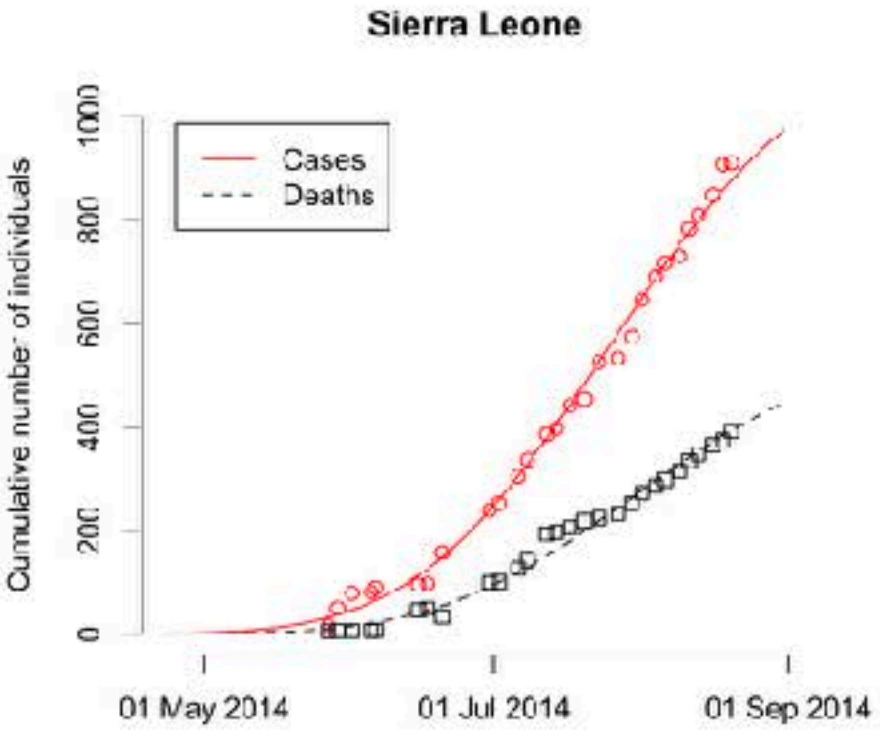
$$k\beta - \mu > 0 \longrightarrow \text{Exponential growth}$$

$$\boxed{\frac{k\beta}{\mu} > 1}\ R_0$$

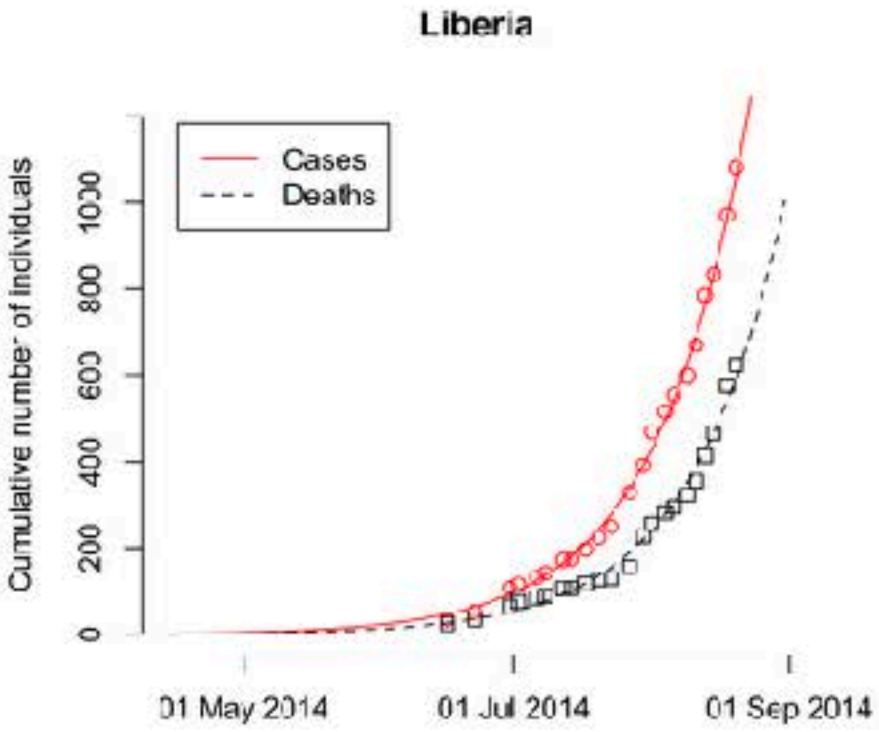


R_0= 1.51 (1.50-1.52)

[Althaus PLoS Curr. 2014]



R_0= 2.53 (2.41-2.67)

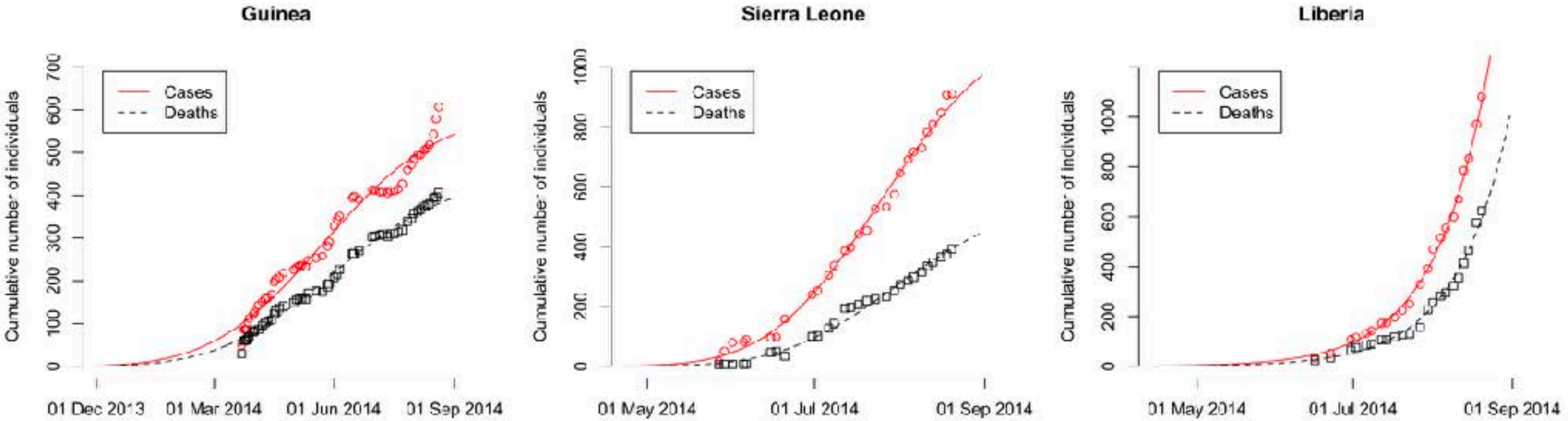


R_0= 1.59 (1.57-1.60)

epidemic forecast

$k\beta - \mu > 0$ ⟶ **Exponential growth**

$$\boxed{\frac{k\beta}{\mu} > 1} \quad R_0$$



R_0= 1.51 (1.50-1.52) R_0= 2.53 (2.41-2.67) R_0= 1.59 (1.57-1.60)

[Althaus PLoS Curr. 2014]

Projected 1.4 million cases by January 20, 2015

[Meltzer, MMWR Suppl., 65 2016]

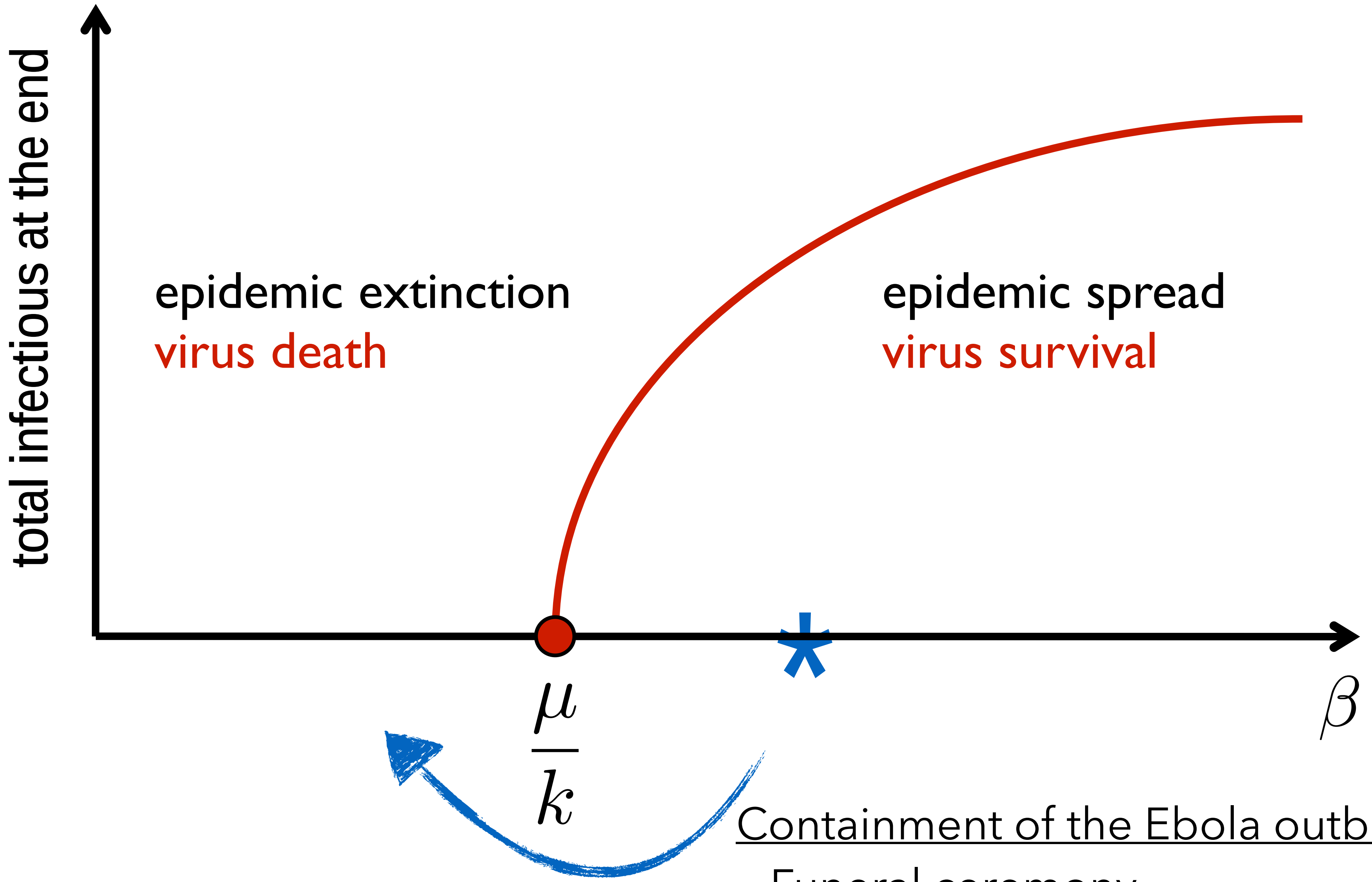
epidemic forecast

Projected 1.4 million cases by January 20, 2015

[Meltzer, MMWR Suppl., 65 2016]

- disregarding contact structure yields a larger number of cases
- prediction based on the hypothesis of no-interventions

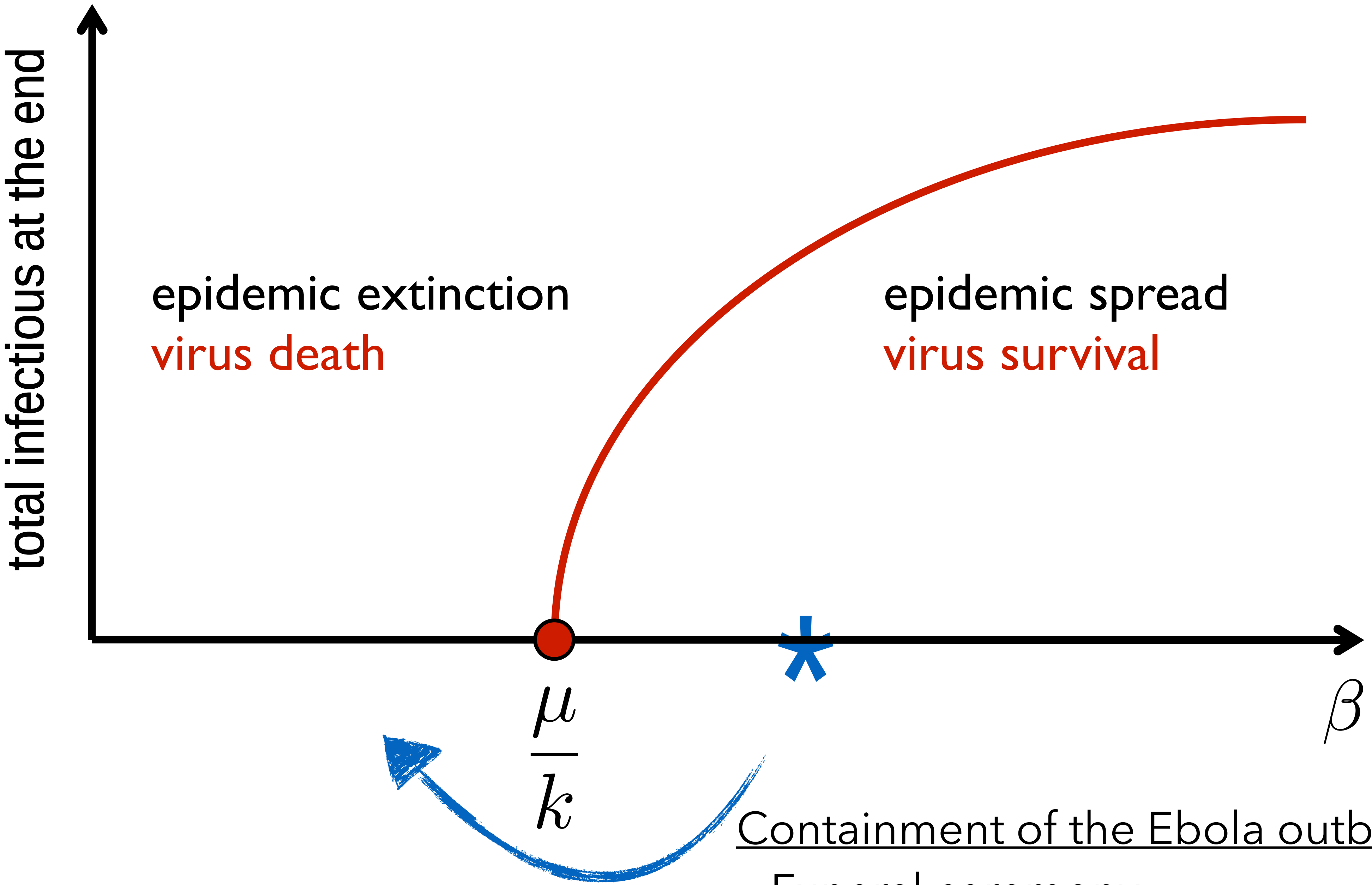
epidemic containment



Containment of the Ebola outbreak

- Funeral ceremony
- Contact tracing
- Quarantine
- Ring vaccination

epidemic containment



Containment of the Ebola outbreak

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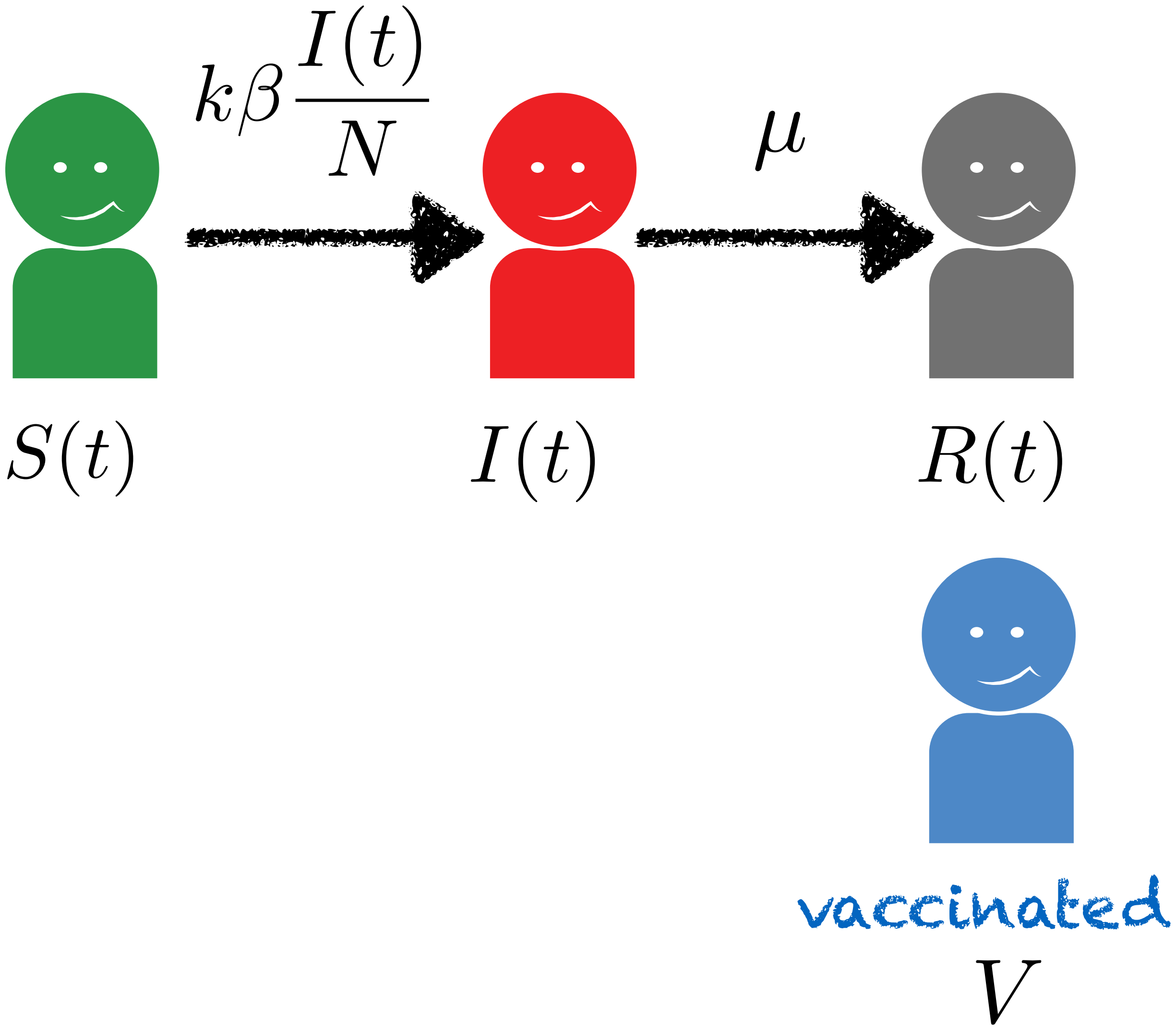
modeling vaccination



$k\beta\frac{I(t)}{N}$

μ

$S(t)$

$I(t)$

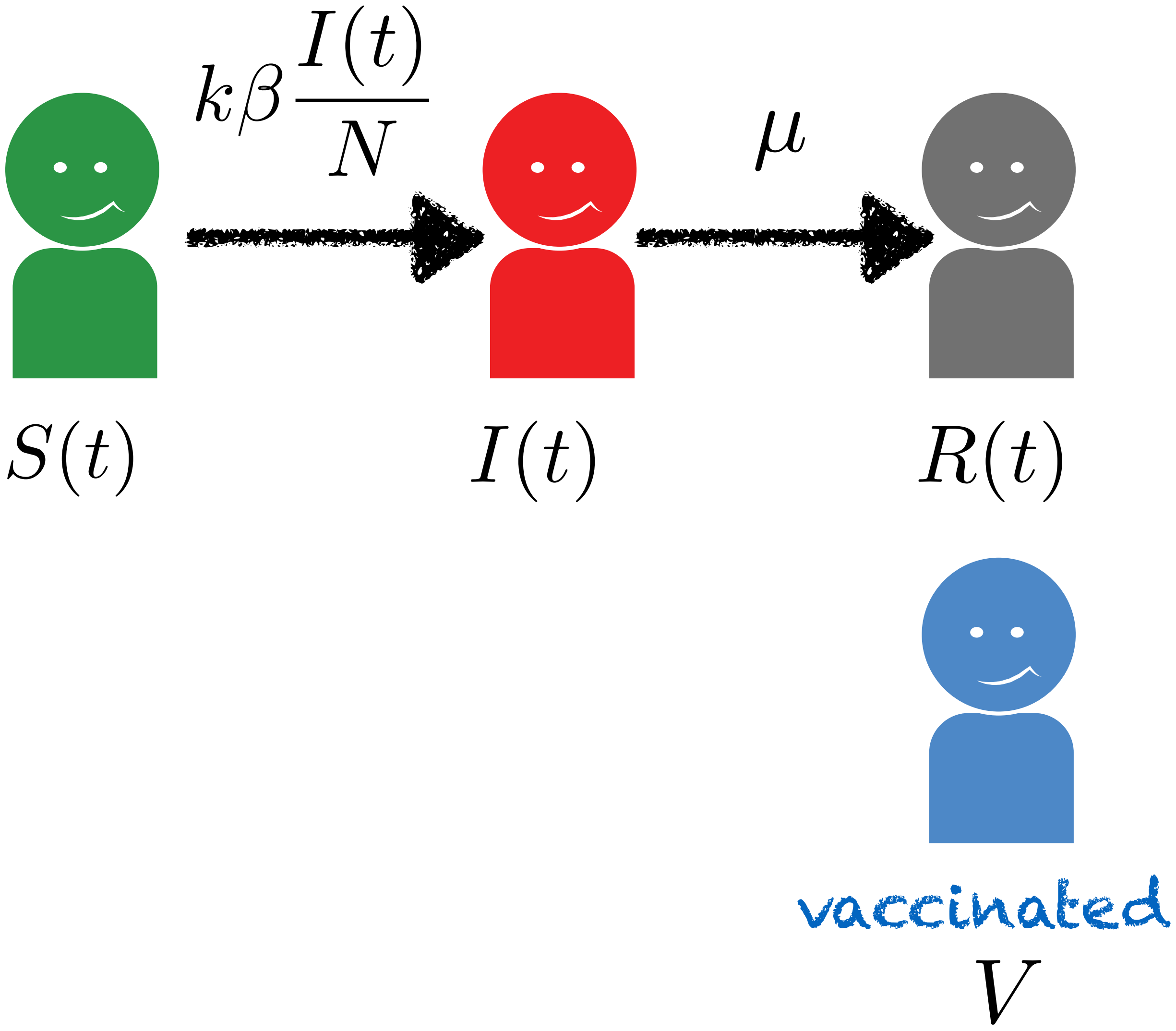
$R(t)$

vaccinated

V

$$N = S(t) + I(t) + R(t) + V \;\rightarrow\; S(t) = N - I(t) - R(t) - V$$

modeling vaccination



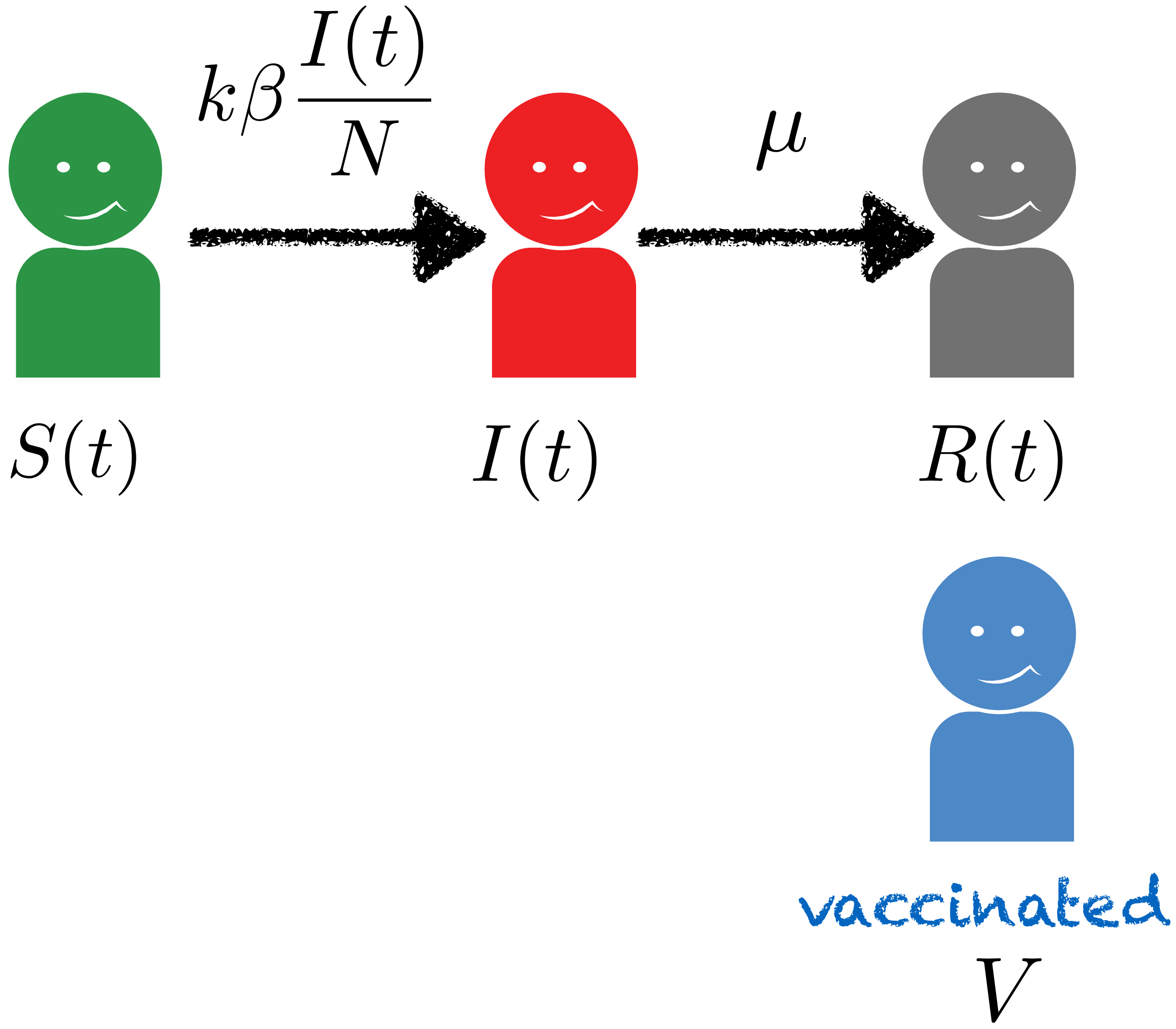
$$d_t I(t) = k\beta\frac{I(t)}{N}\left(S(t) - V\right) - \mu I(t)$$

$$d_t I(t) = k\beta\frac{I(t)}{N}\left(1 - v\right) - \mu I(t)$$

$$v = \frac{V}{N}$$

$$N = S(t) + I(t) + R(t) + V \;\rightarrow\; S(t) = N - I(t) - R(t) - V$$

modeling vaccination



$$d_t I(t) = k\beta\frac{I(t)}{N}\left(S(t) - V\right) - \mu I(t)$$

$$d_t I(t) = k\beta\frac{I(t)}{N}\left(1 - v\right) - \mu I(t)$$

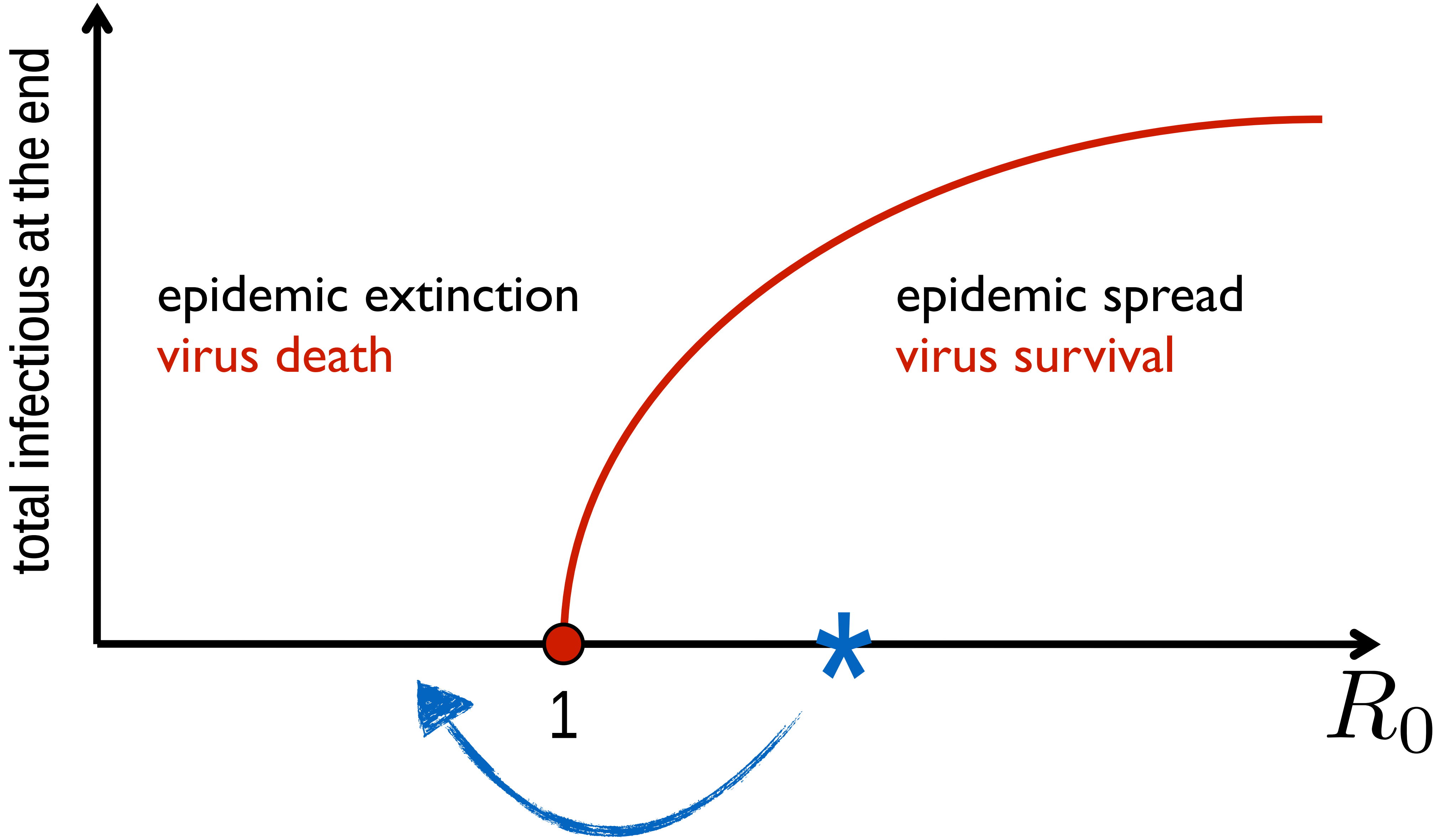
$$v = \frac{V}{N}$$

$$I(t) = e^{[\beta(1-v)-\mu]t}$$

$$R_{\text{eff}} = R_0(1 - v)$$

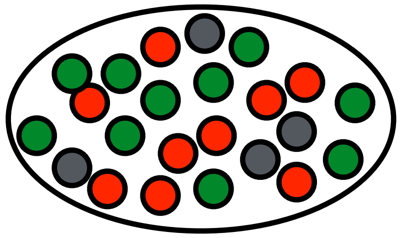
modeling vaccination

$$v_c = \frac{R_0 - 1}{R_0}$$

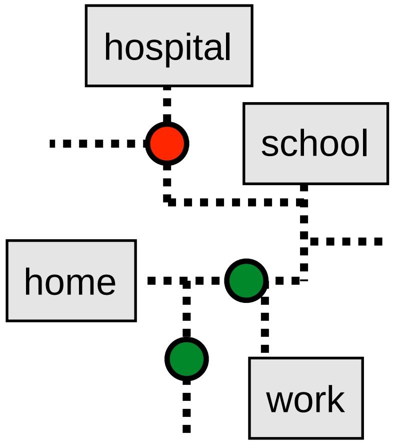


epidemic extinction
virus death

epidemic spread
virus survival



homogeneous
mixing



agent based

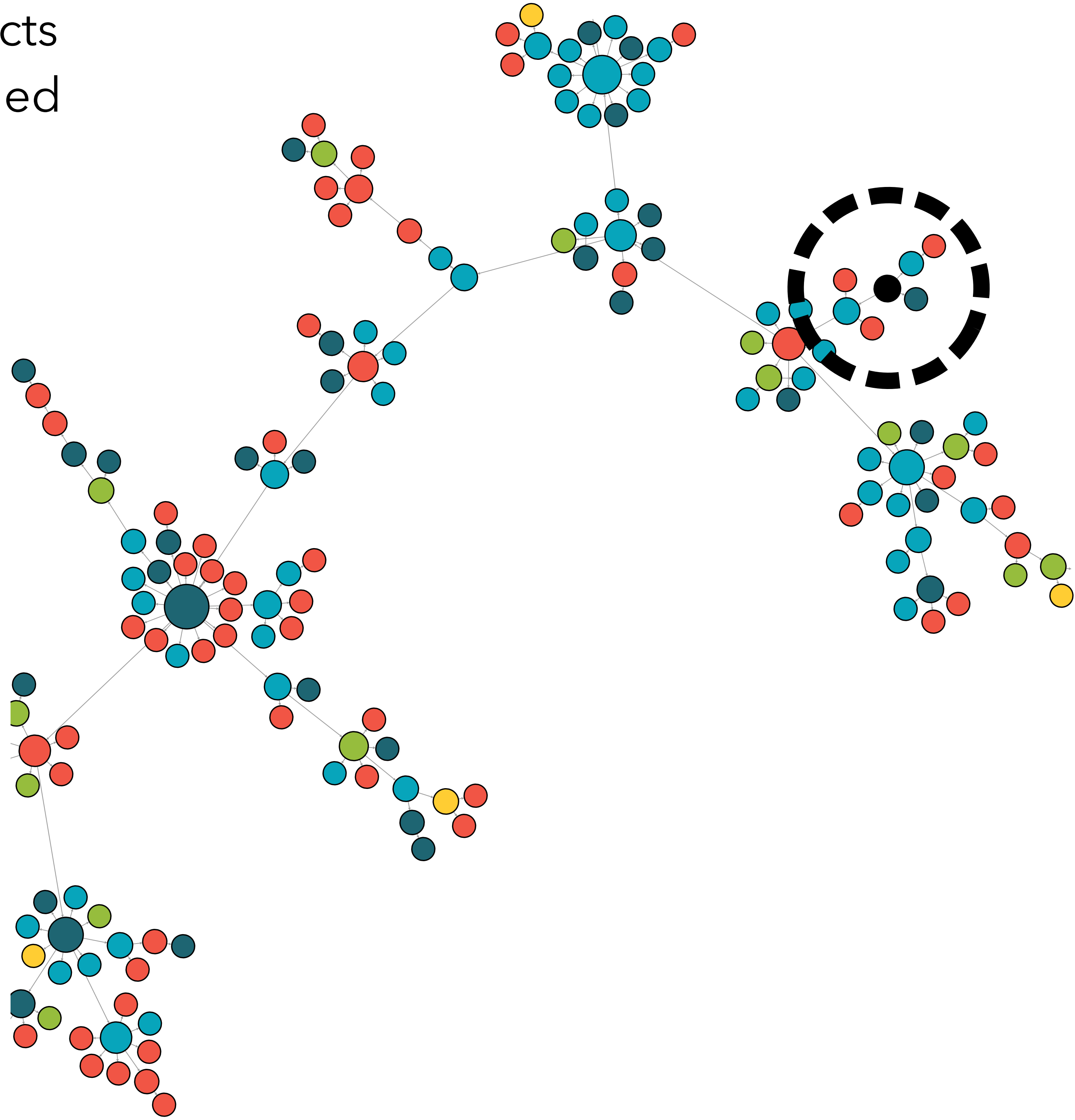
COMPLEXITY

epidemic containment

ring vaccination: the contacts and contacts of contacts of each index case are identified and vaccinated

<u>agent based model for Pujehun district of Sierra Leone</u>

- creation of a synthetic population
- individual spatial distribution
- demography
- household compositions
- link among households as typical in rural Africa



[Aielli et al, BMC med 2016; Merler et al PLOS NTD 2016]

epidemic containment

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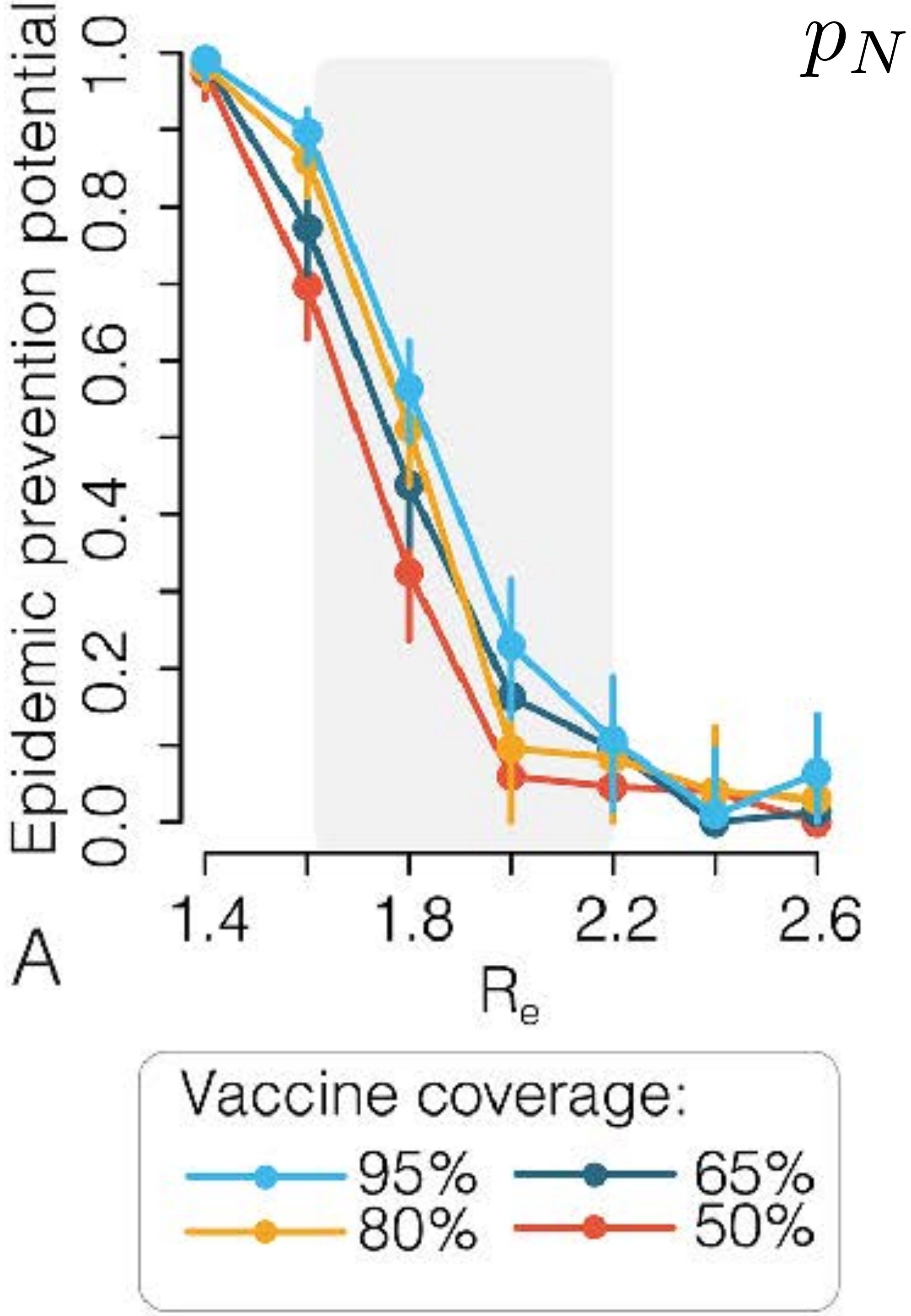
<u>agent based model for Pujehun district of Sierra Leone</u>

- creation of a synthetic population
- individual spatial distribution
- demography
- household compositions
- link among households as typical in rural Africa

- 2 days identify the contacts and obtain consent and administer vaccine
- 4 days to develop immunity

$$\mathrm{EPP} = 1 - \frac{p_I}{p_{NI}}$$



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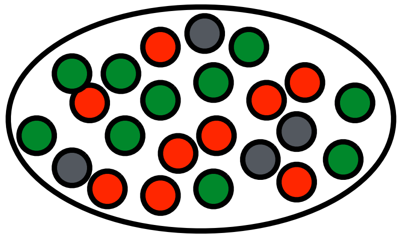
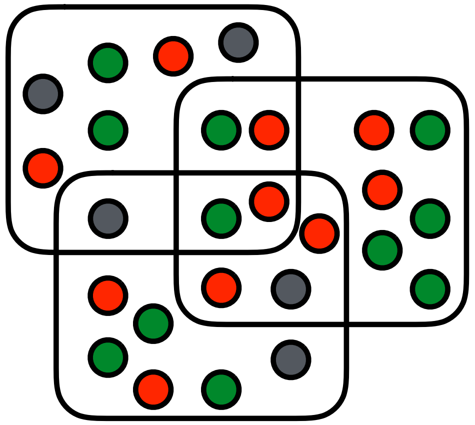
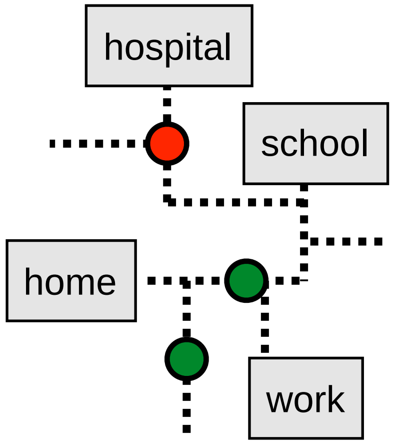


homogeneous mixing



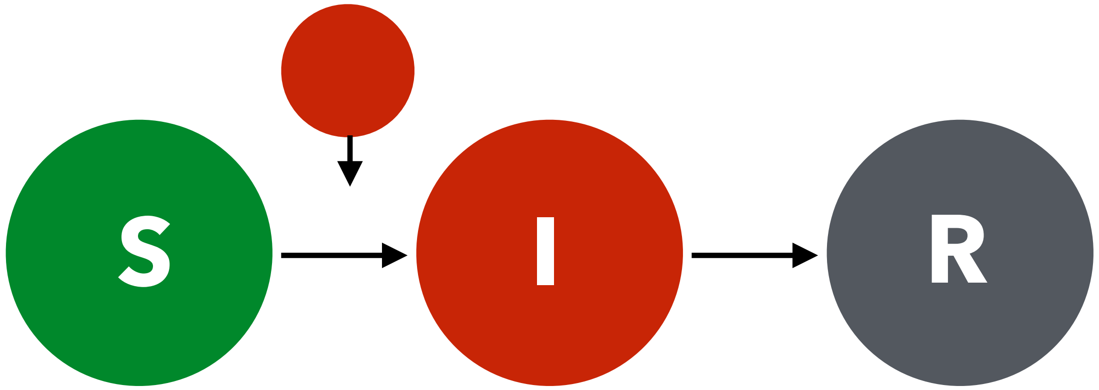
population structure

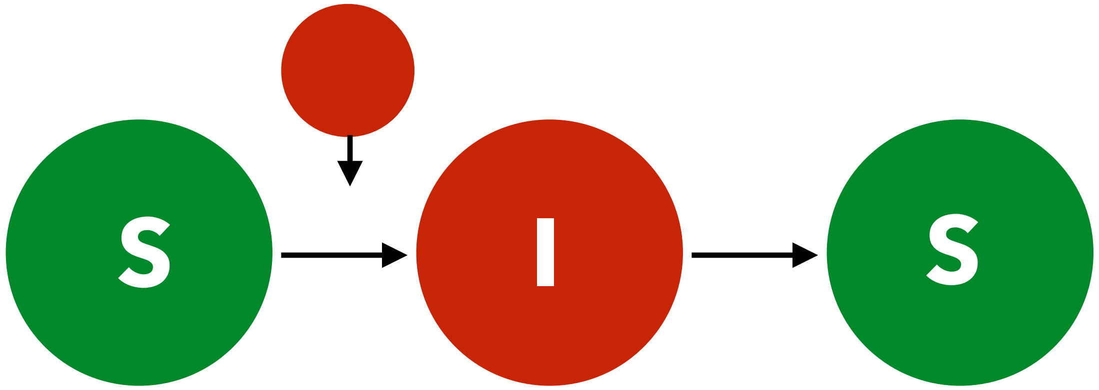


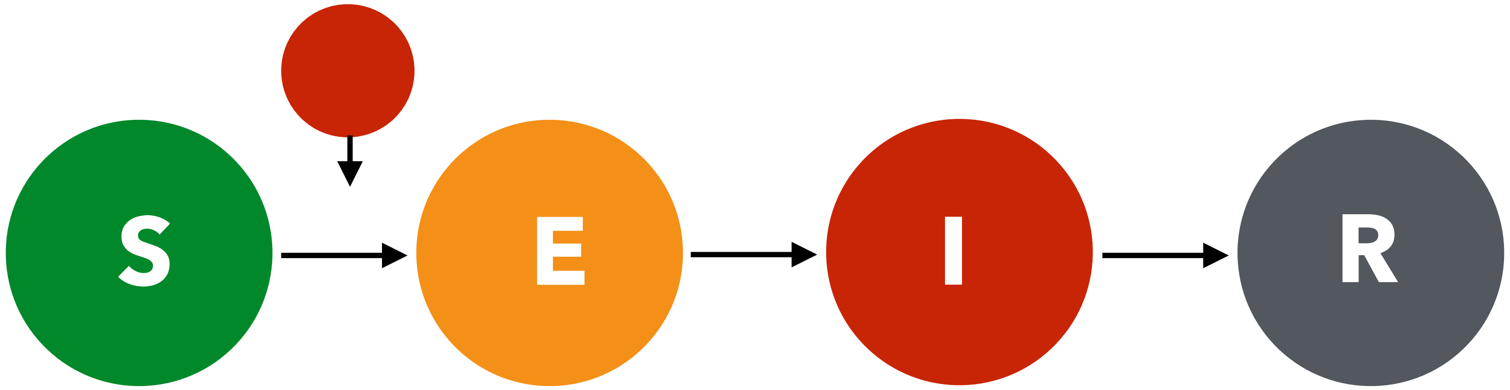
agent based

compartmental models

complex disease unfolding: the population is divided in classes according to diseases stages







compartmental models

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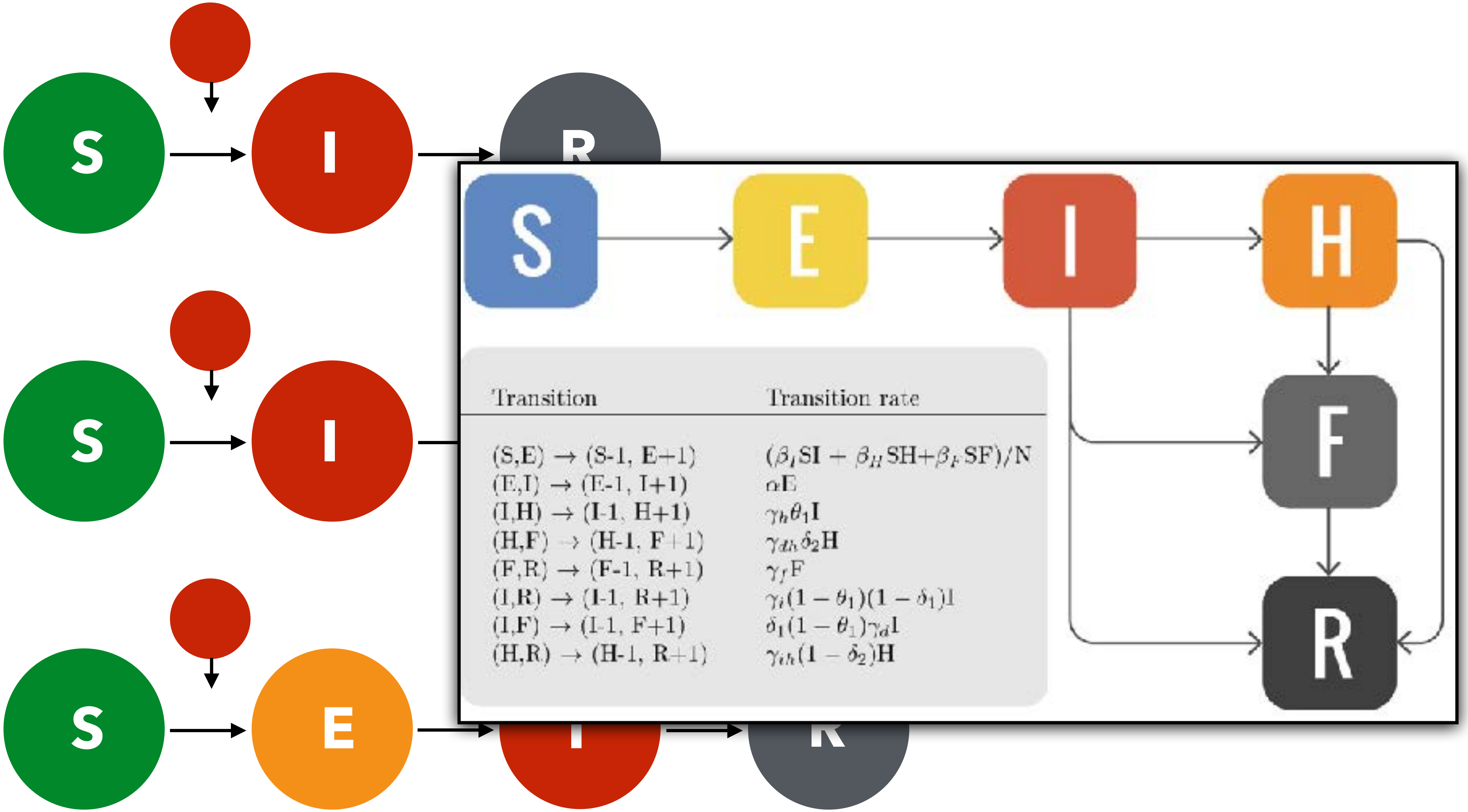
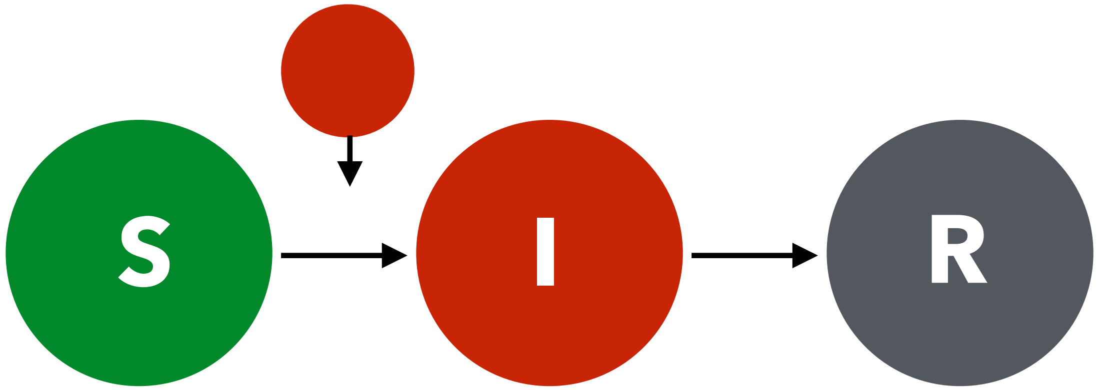
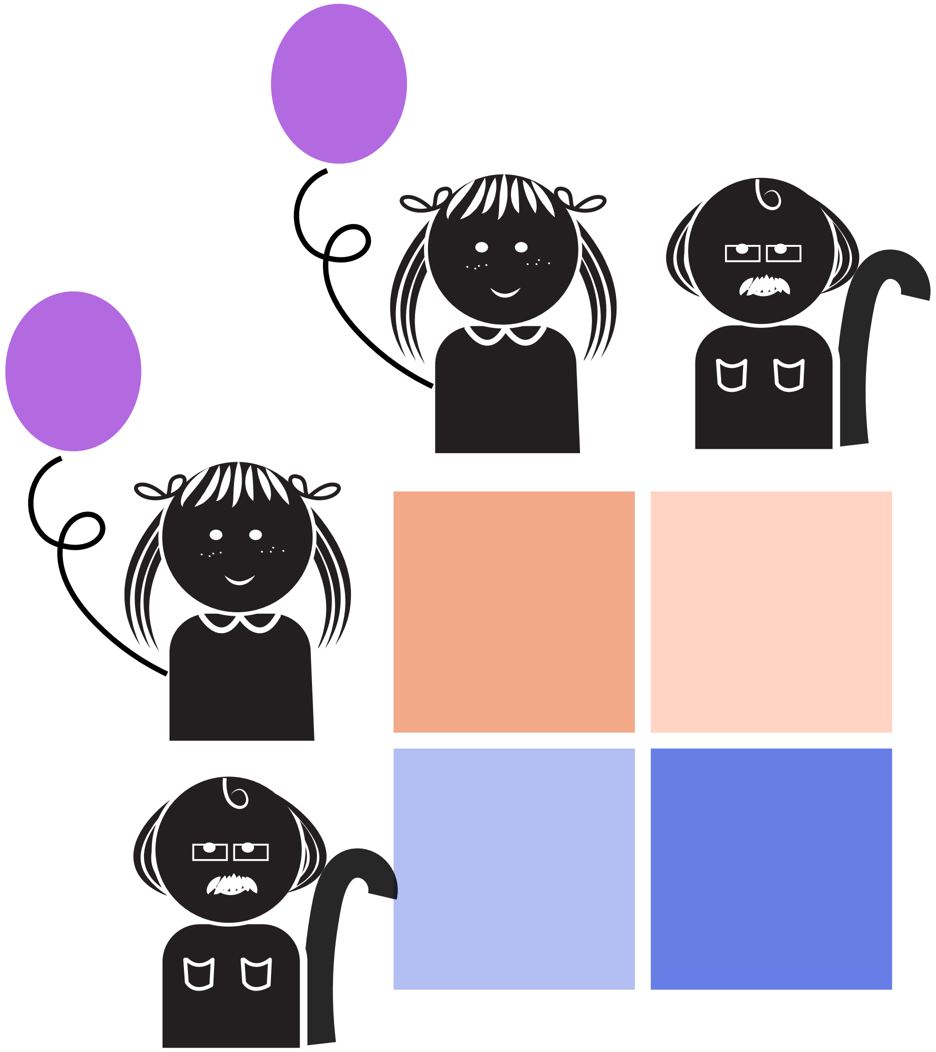


Transition	Transition rate
(S,E) → (S-1, E+1)	$(\beta_I SI + \beta_H SH + \beta_F SF)/N$
(E,I) → (E-1, I+1)	αE
(I,H) → (I-1, H+1)	$\gamma_h \theta_1 I$
(H,F) → (H-1, F+1)	$\gamma_{dh} \delta_2 H$
(F,R) → (F-1, R+1)	$\gamma_f F$
(I,R) → (I-1, R+1)	$\gamma_i (1-\theta_1)(1-\delta_1) I$
(I,F) → (I-1, F+1)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

compartmental models

complex population structure: further division in classes based on host characteristic of epidemiological relevance





different contacts rates within/across age classes → different infections rates

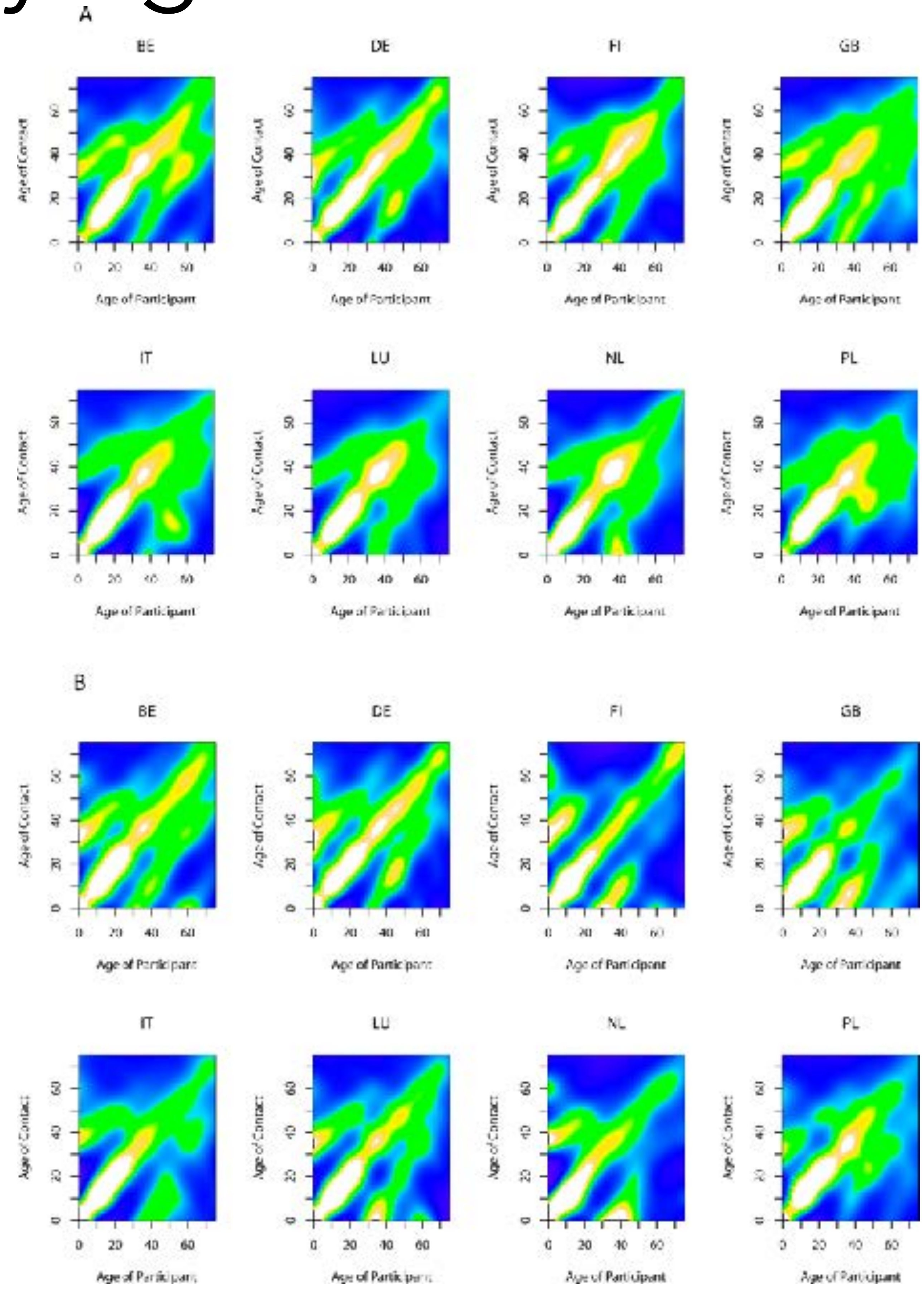
social contacts by age

University, UK ~ 100 participant
[Edmund et al Pro R Soc Lond B (1997)]

8 countries in Europe ~ 7000 participants
[Mossong et al PLoS Med (2008)]

All contacts

physical contacts



conclusion

- simple models can be useful
- key concepts: epidemic threshold and R_0
- agent based models: 😊 most realistic, allow the exploration of possible intervention scenarios, 😞 data & computational intensive
- in some cases complex compartmental models can be a good compromise

Outline

-modeling an epidemic

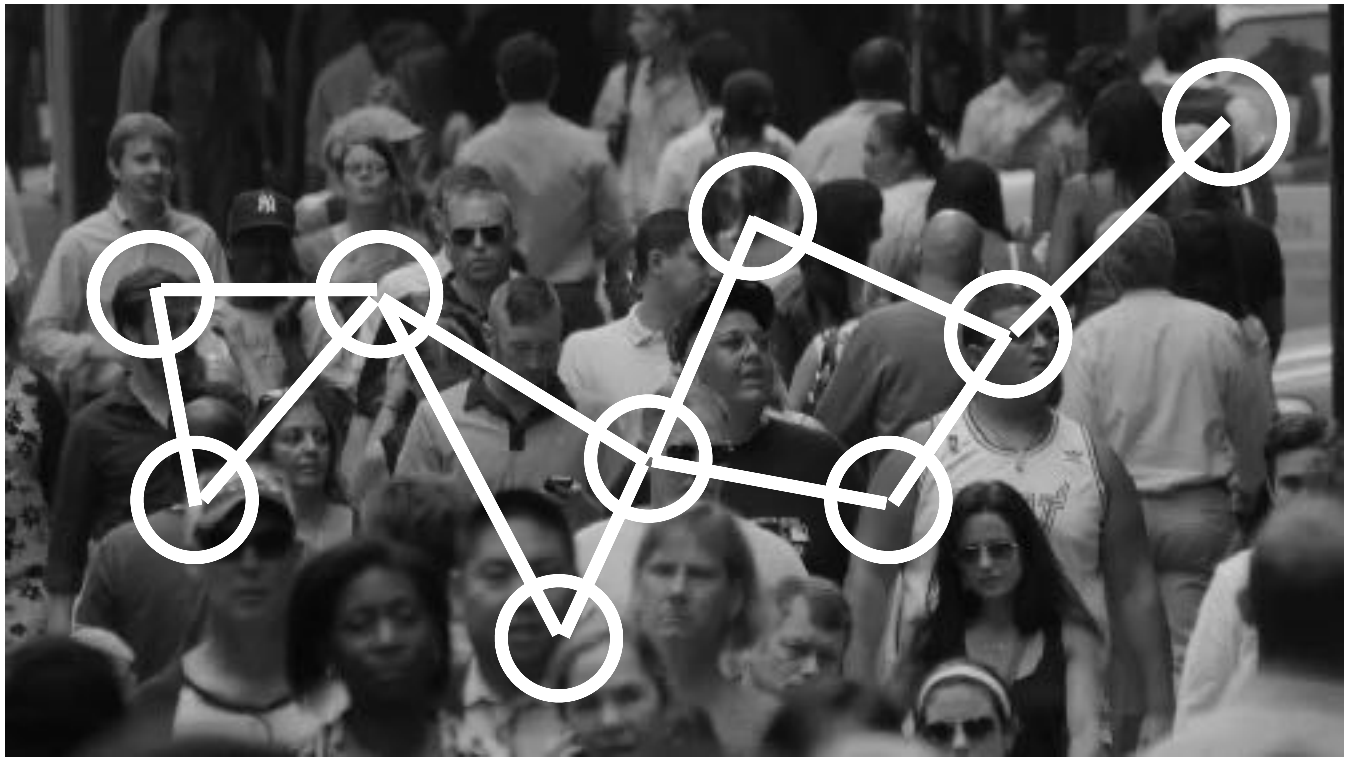
-epidemics on networks

-epidemics in space

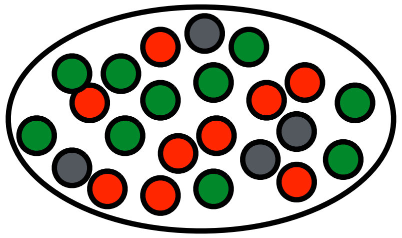
-interacting epidemics

-computer simulations

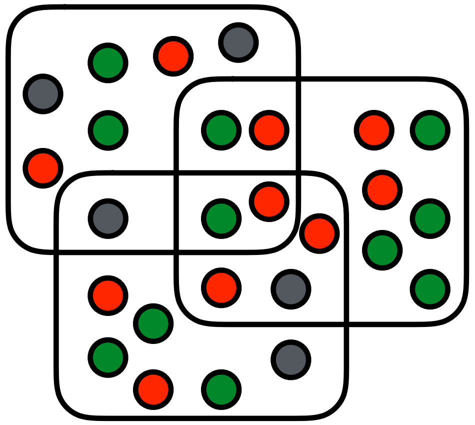
key ingredient:
human to human contacts



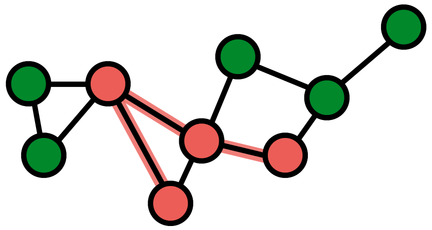
relatives; colleagues; partners; random encounters (public transports, ...)



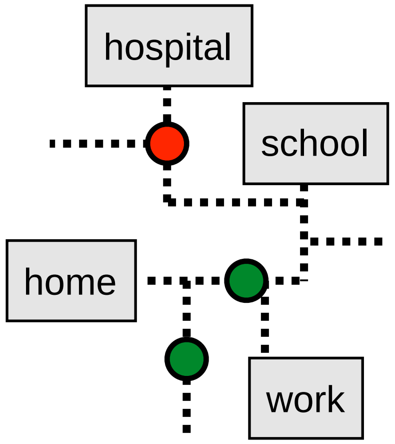
homogeneous
mixing



population
structure



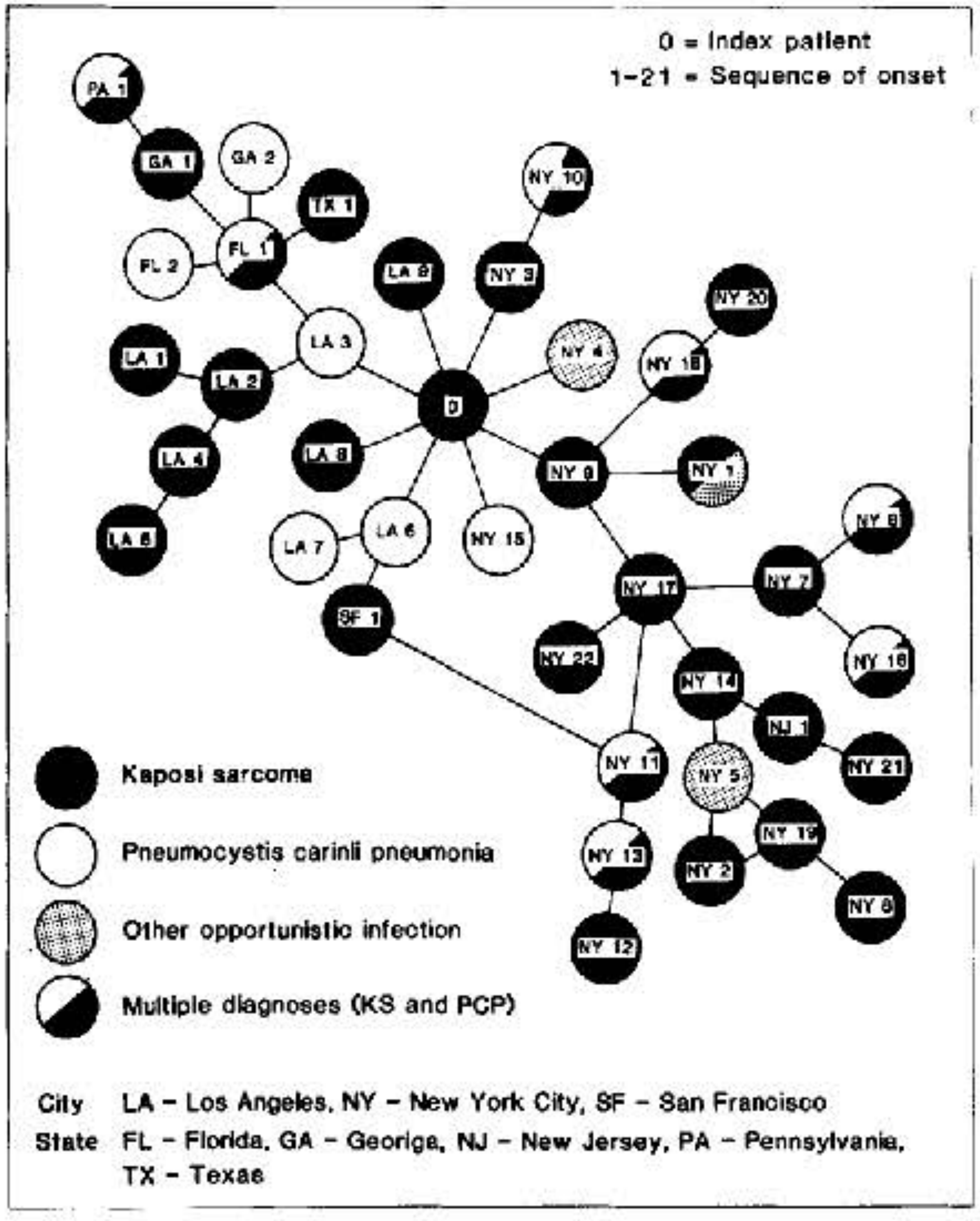
network



agent based

COMPLEXITY

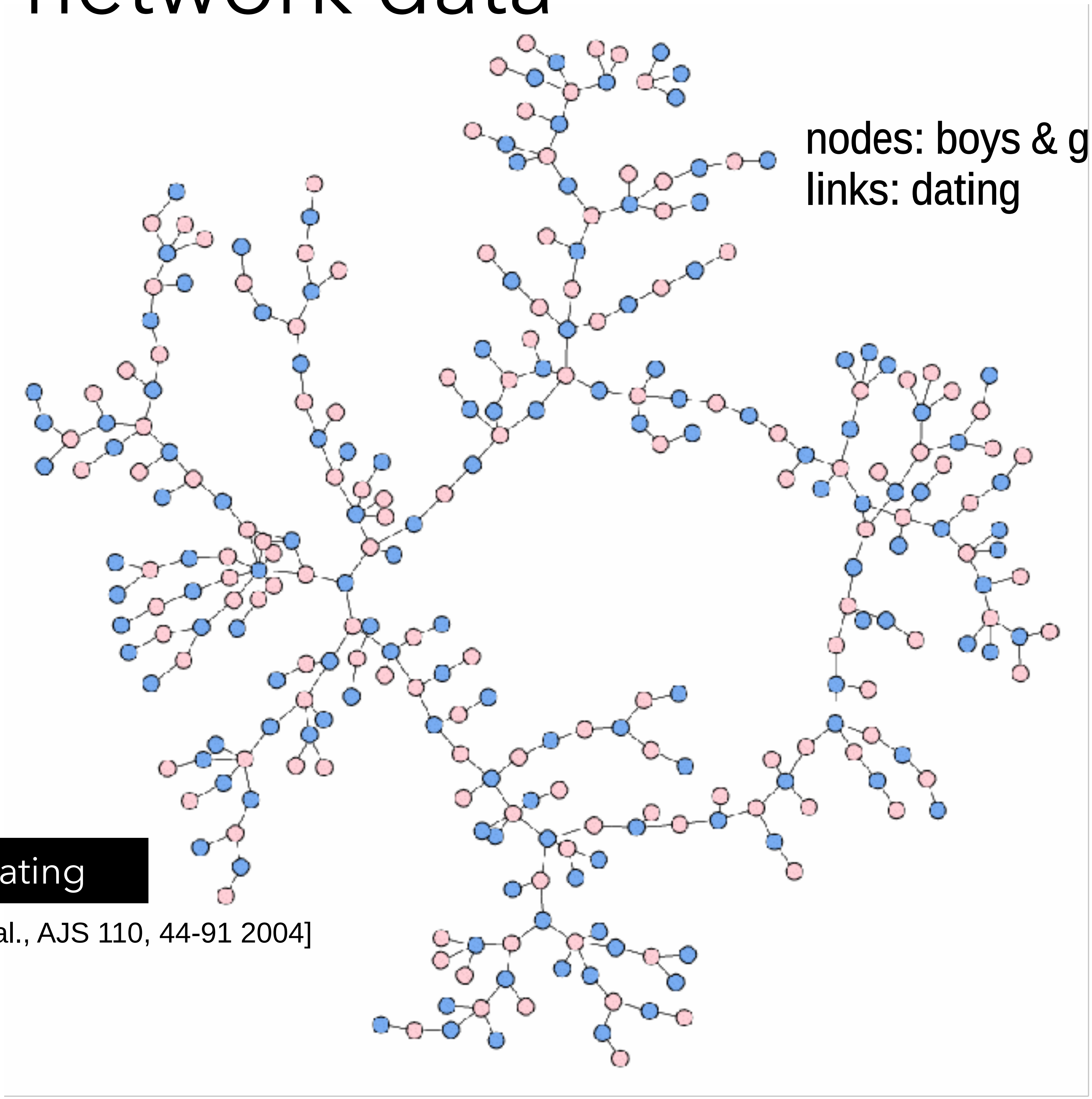
early network data



HIV spread

[Auerbach, et al the American Journal of medicine 76, 487 1984]

early network data



nodes: boys & girls
links: dating

high school dating

[P. S. Bearman, et al., AJS 110, 44-91 2004]

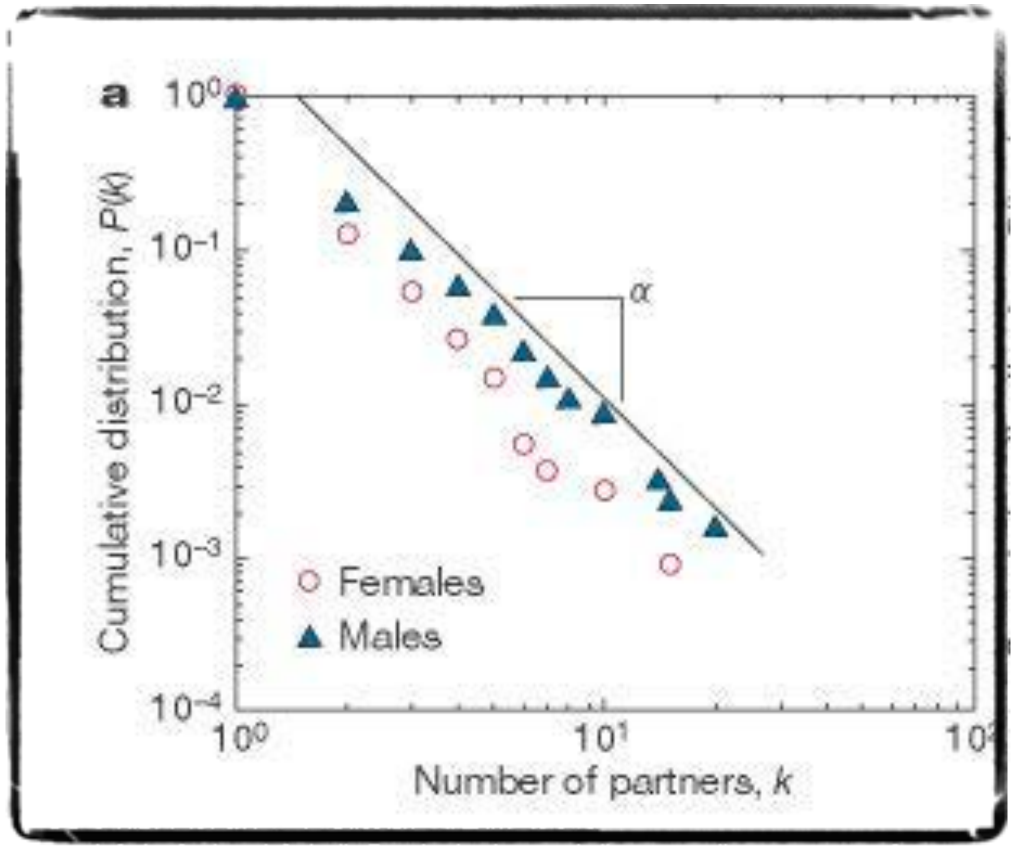
network properties

- small world
- high clustering
- heterogeneous contact behaviours
- presence of communities
- degree-degree correlations

network properties: heterogeneous connectivity

Swedish survey with 2810 respondents

#partners in the last year



[Liljeros et al, Nature 411 2001]

$$P(k) \propto k^{-\alpha}, \quad \alpha \simeq 2.3$$

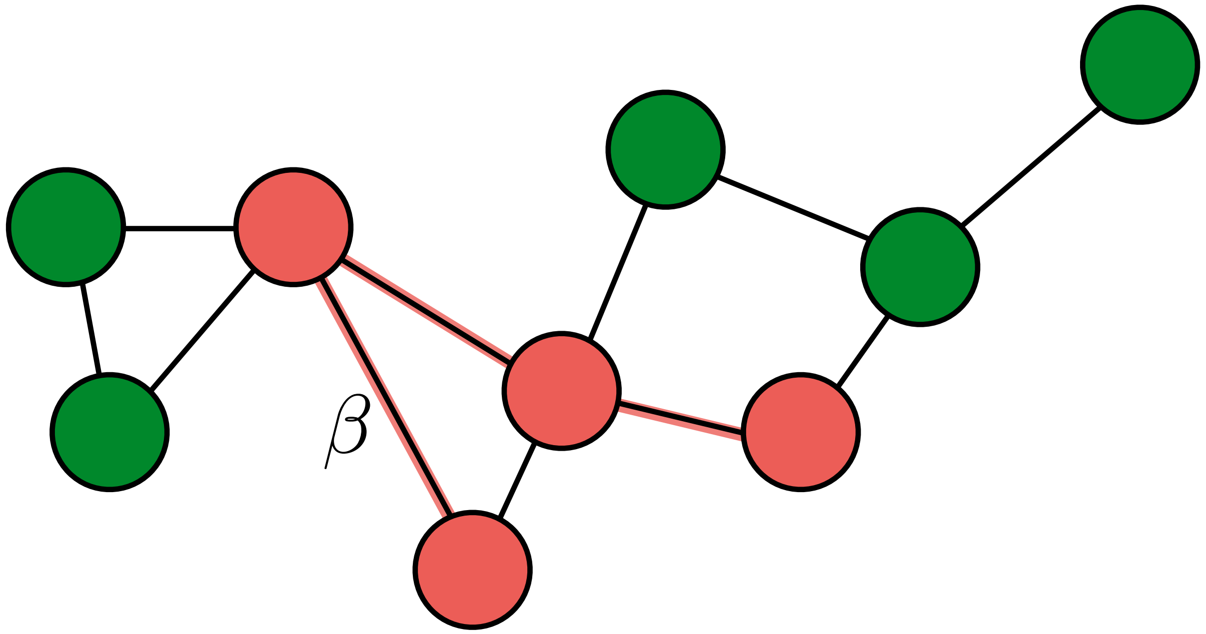
$$2 < \alpha < 3 \quad \Rightarrow \langle k^2 \rangle \to \infty$$

power law distribution

-variance is big

-existence of hubs

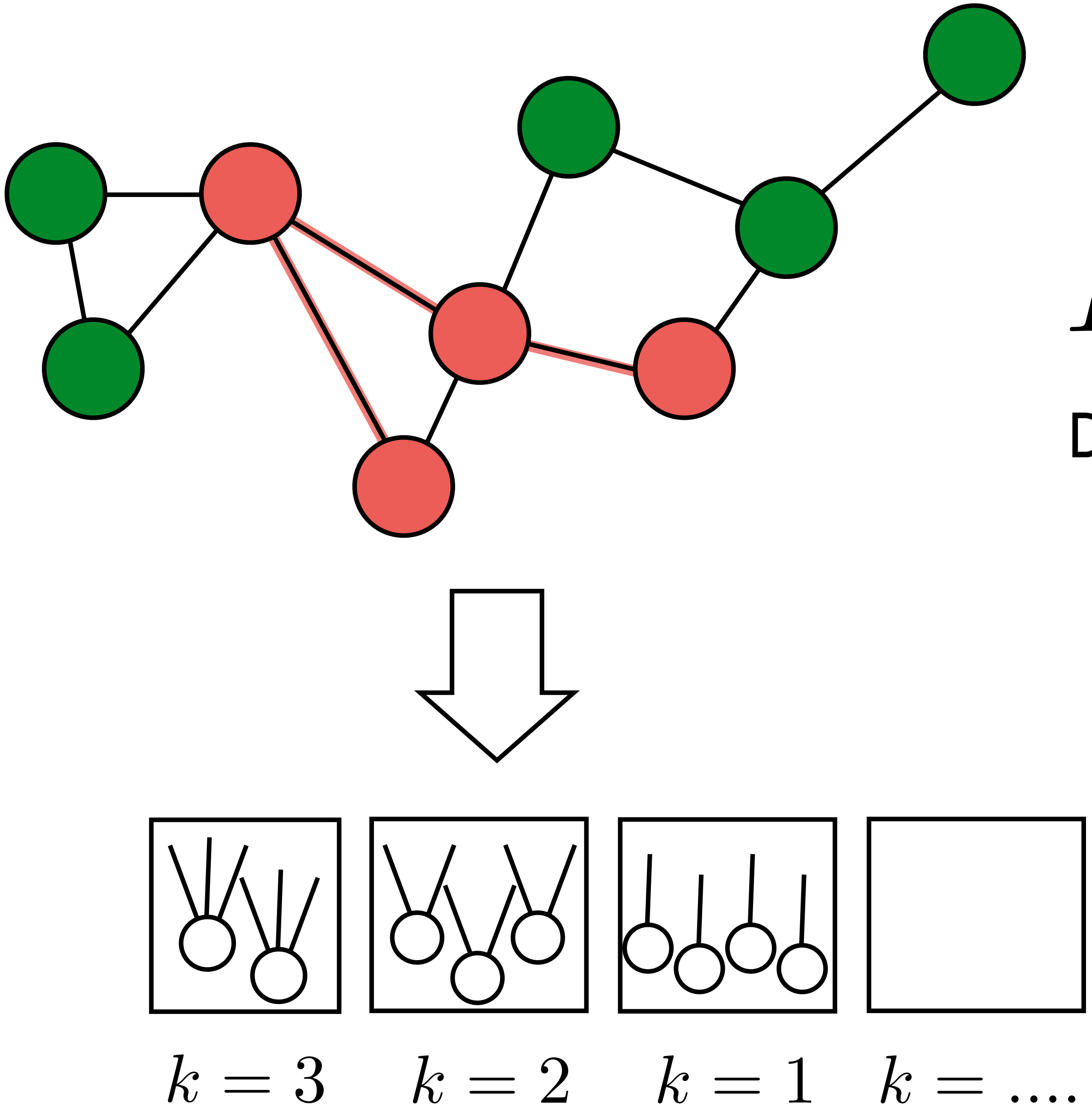
modelling epidemic on networks



$$S \xrightarrow{\beta} I \xrightarrow{\mu} S$$

$$S \xrightarrow{\beta} I \xrightarrow{\mu} R$$

heterogeneous mean field approach

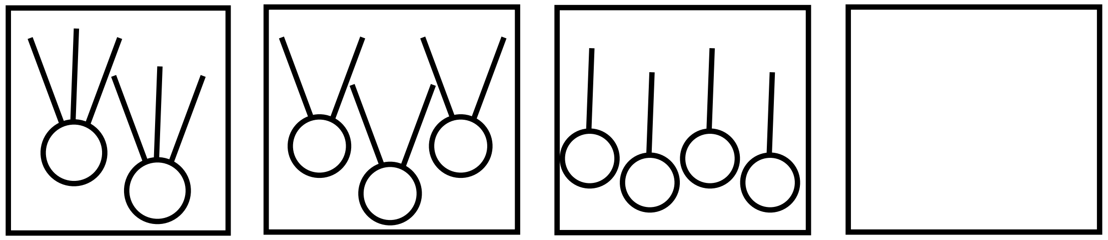


$$P(k)$$

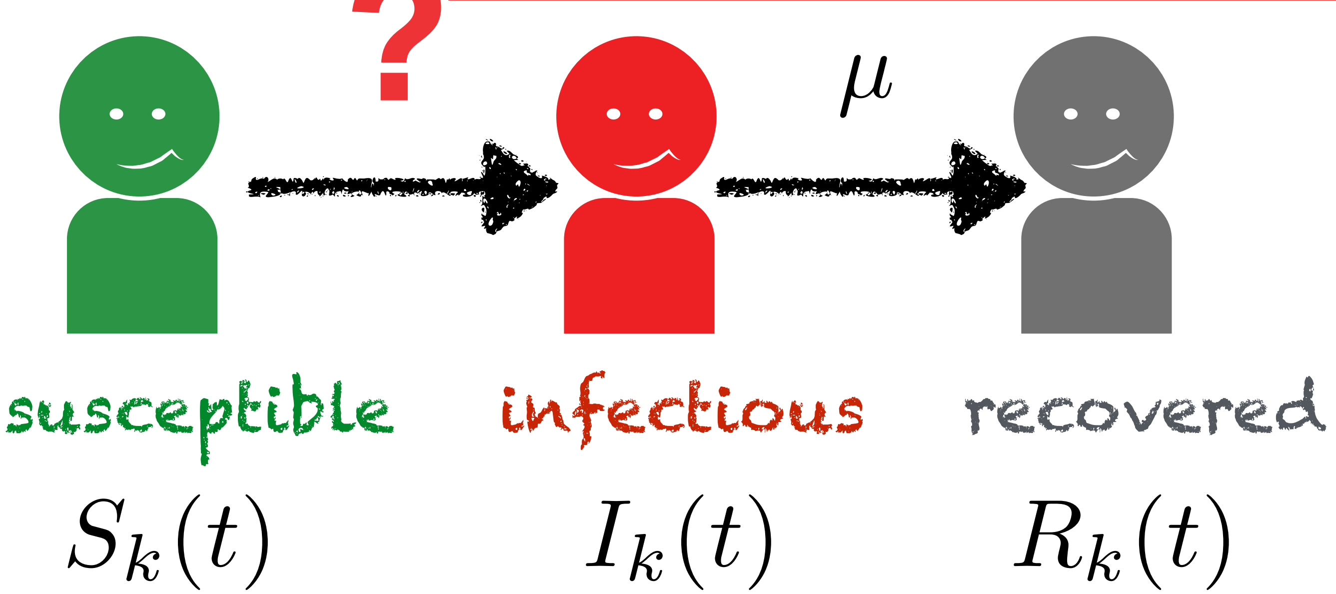
Degree distribution

[Pastor-Satorras & Vespignani PRL 2001, review :Pastor Satorras et al. Rev Mod Phys 2015]

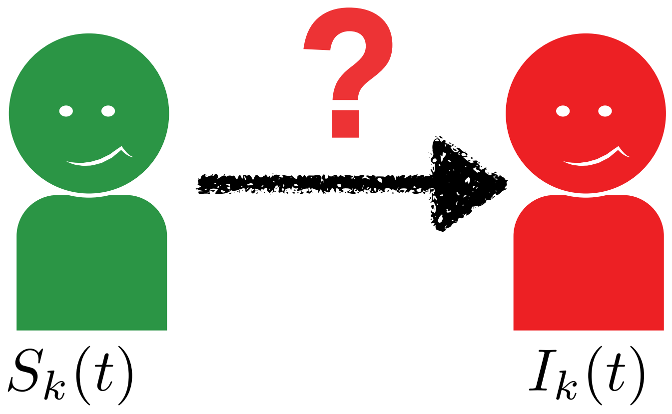
heterogeneous mean field approach

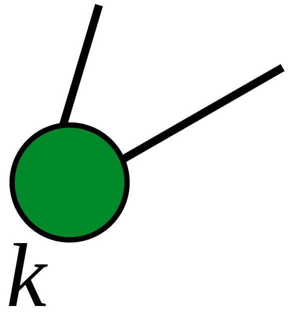


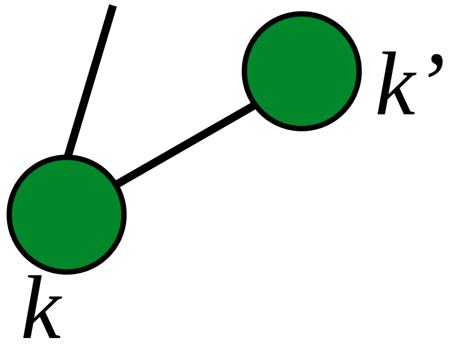
what is the probability that a node with degree *k* is linked to an infected node of whatever degree *k'* ?

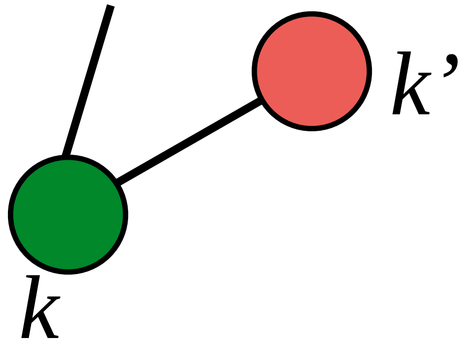


heterogeneous mean field approach









β **X** number of possible contacts: **X** probability of contact with k': **X** number of infectious within the k'-class:

k

$P(k'|k)$

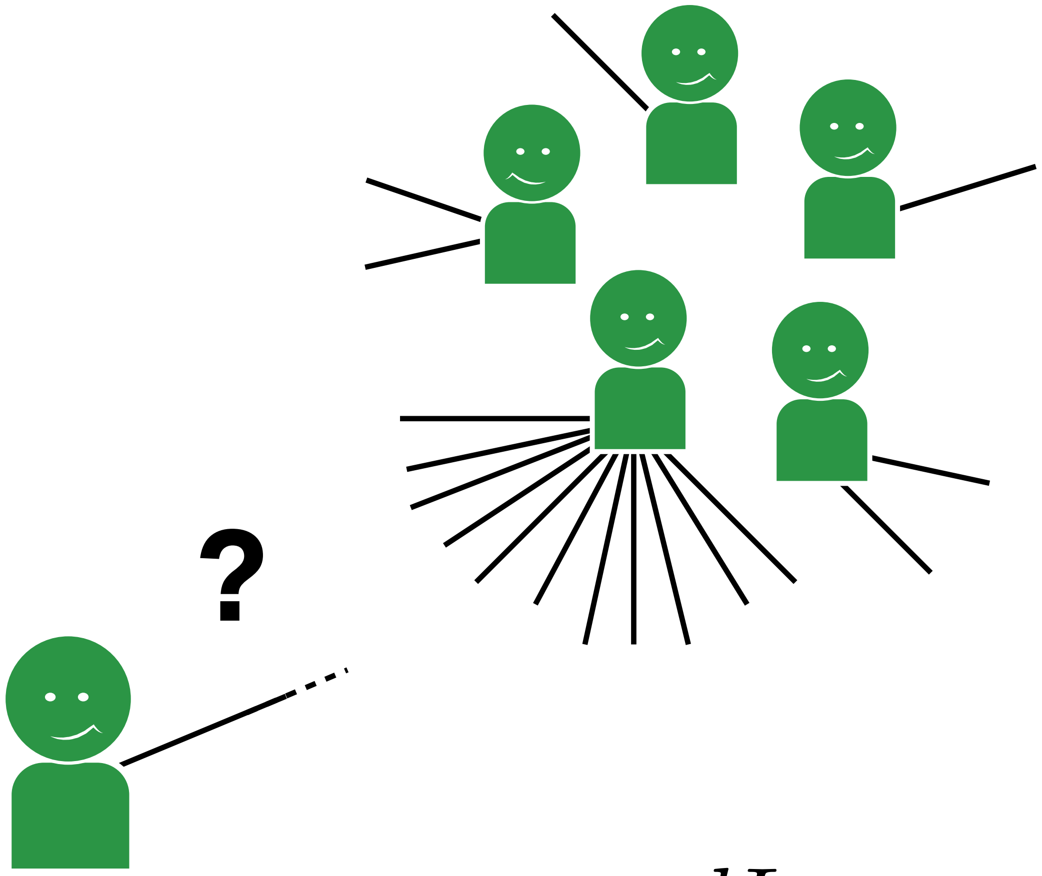
I_k

force of infection= $\beta k \sum_{k'} P(k'|k) I_{k'}$

heterogeneous mean field approach

$$P(k'|k) = k'\frac{P(k')}{\langle k \rangle}$$

If I make a connection at random I will do it more likely with someone that is very social (more stubs)



force of infection=

$$\beta k \sum_{k'} k' \frac{p(k')}{\langle k \rangle} I_{k'}$$

$$\frac{dI_k}{dt} = -\mu I_k(t) + S_k(t)\beta k \sum_{k'} k' \frac{p(k')}{\langle k \rangle} I_{k'}$$

heterogeneous mean field approach

$$\frac{dI_k}{dt} = -\mu I_k(t) + S_k(t)\beta k \sum_{k'} k' \frac{p(k')}{\langle k \rangle} I_{k'}$$

…

Exponential growth $$\beta \frac{\langle k^2 \rangle}{\langle k \rangle} - (\mu + \beta)\langle k \rangle$$

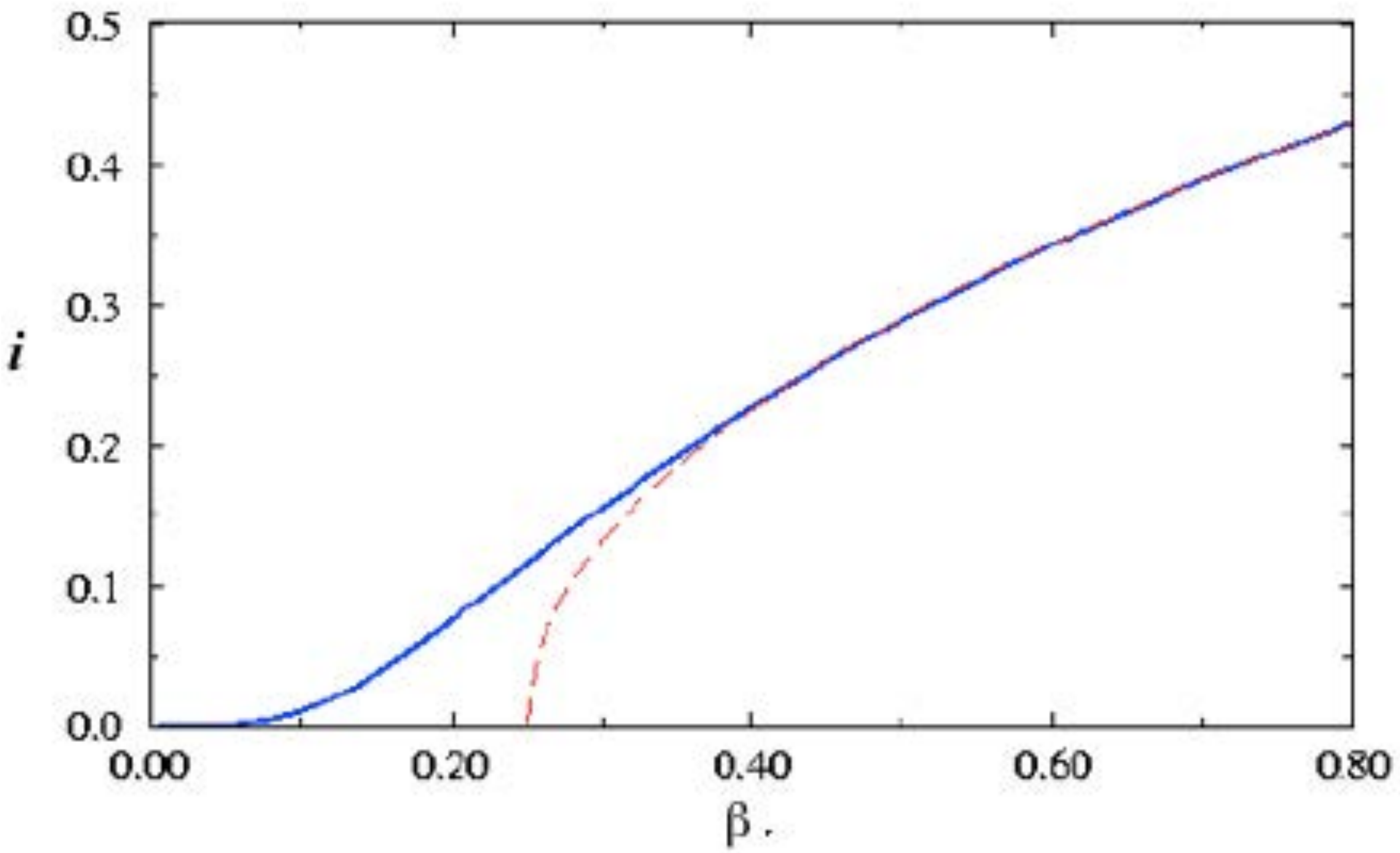
$$\boxed{\beta_c = \frac{\langle k \rangle}{\langle k^2 \rangle}}$$

vanishing epidemic threshold in the infinite size limit!

[Pastor-Satorras & Vespignani PRL 2001, review :Pastor Satorras et al. Rev Mod Phys 2015]

heterogeneous mean field approach

heterogeneity favours epidemic spreading



[Pastor-Satorras & Vespignani PRL 2001, review :Pastor Satorras et al. Rev Mod Phys 2015]

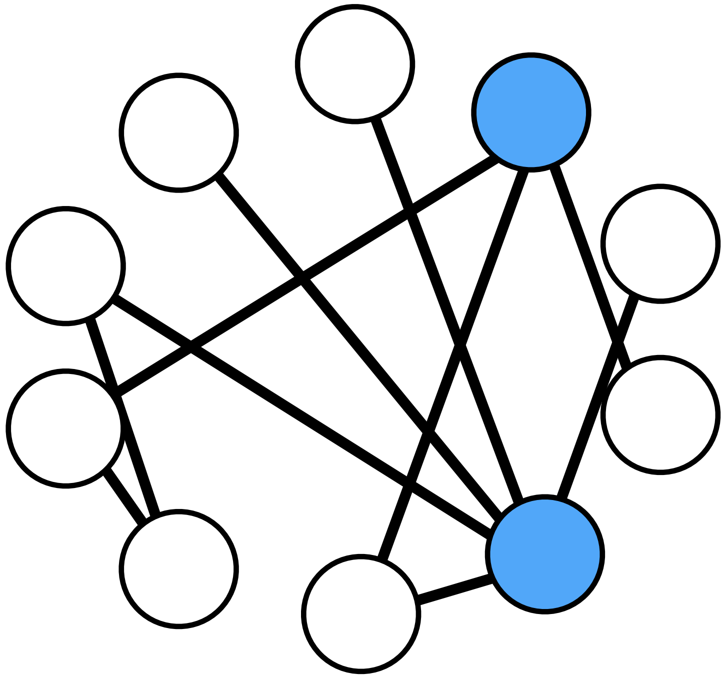
immunisation in heterogeneous networks

imagining of immunising a fraction g of individuals

$$\beta\,(1-\mathbf{g}) \leq \beta_c$$

immunisation threshold $g_c = 1$

random immunisation is totally ineffective



targeted immunisation is extremely effective

[Pastor-Satorras & Vespignani, PRE 65, 036104 (2002)]
[Dezso & Barabasi cond-mat/0107420; Havlin et al. preprint (2002)]

immunisation in heterogeneous networks

my friend has more friends than me …

$$\kappa_{\mathrm{nn},i} = \frac{1}{k_i} \sum_{j \in \mathcal{V}(i)} k_j$$

average nearest neighbour degree

$$\kappa_{\mathrm{nn},i} = \sum_{k'} k' P(k'|k_i) = \sum_{k'} \frac{k'^2 P(k')}{\langle k \rangle}$$

$$P(k'|k) = k' \frac{P(k')}{\langle k \rangle}$$

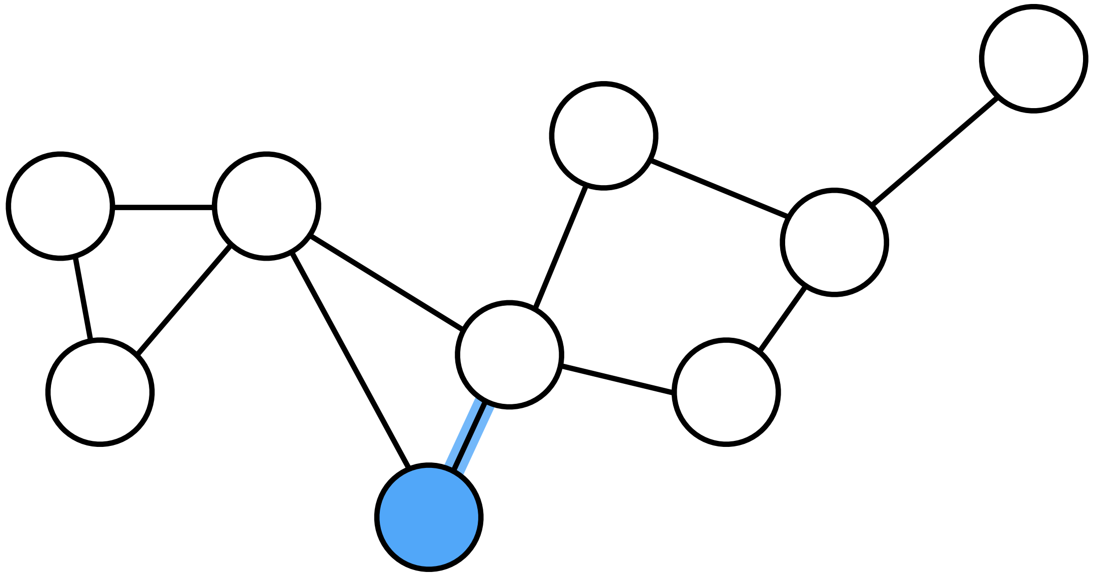
$$\kappa_{\mathrm{nn},i} = \frac{\langle k^2 \rangle}{\langle k \rangle}$$

[Cohen et la PRL 2003; Christakis & Fowler PLoS ONE 2010]

immunisation in heterogeneous networks

my friend has more friends than me …

$$\kappa_{\mathrm{nn},i} = \frac{\langle k^2 \rangle}{\langle k \rangle}$$



choose a person at random,
immunise one of his friends

friends also as sensor to monitor an outbreak

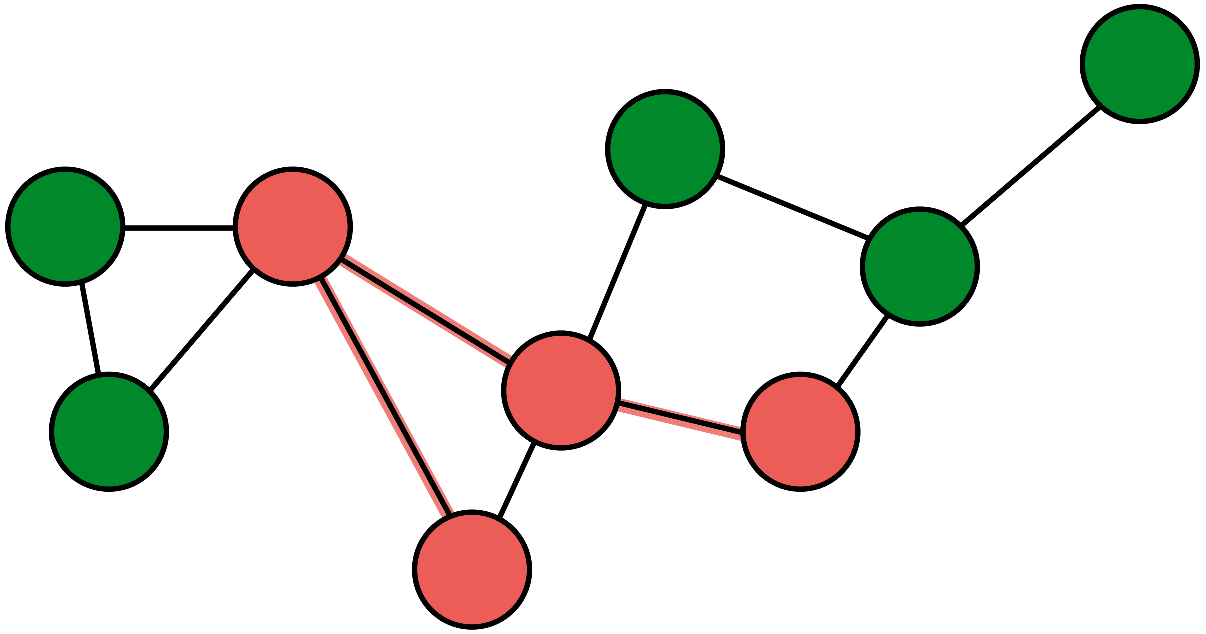
[Cohen et la PRL 2003; Christakis & Fowler PLoS ONE 2010]

network properties

- small world
- high clustering
- heterogeneous contact behaviours
- presence of communities
- degree-degree correlations

quenched mean field approach

$$S \xrightarrow{\beta} I \xrightarrow{\mu} S$$



$$A_{ij}$$

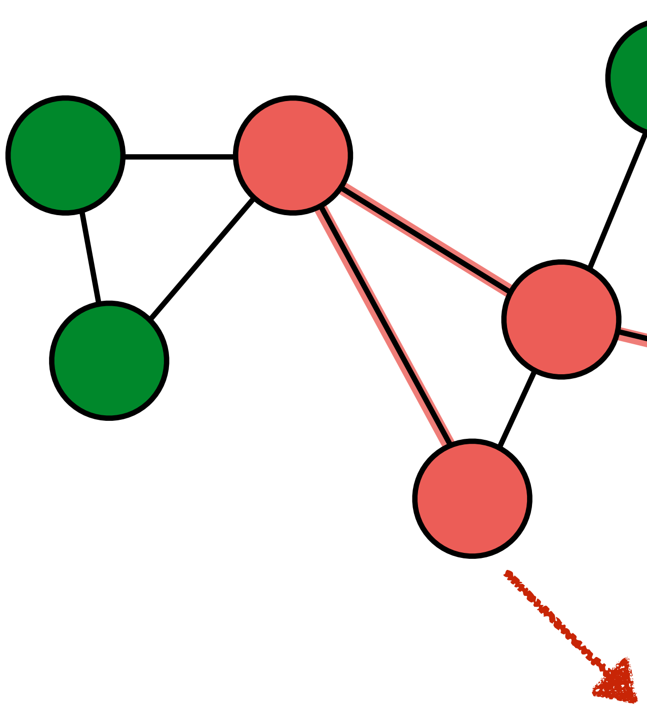
Adjacency matrix

accounting for the whole network knowledge

[Wang et al. SRDS 2003, Gómez et al. EPL 2010]

quenched mean field approach

$$S \xrightarrow{\beta} I \xrightarrow{\mu} S$$



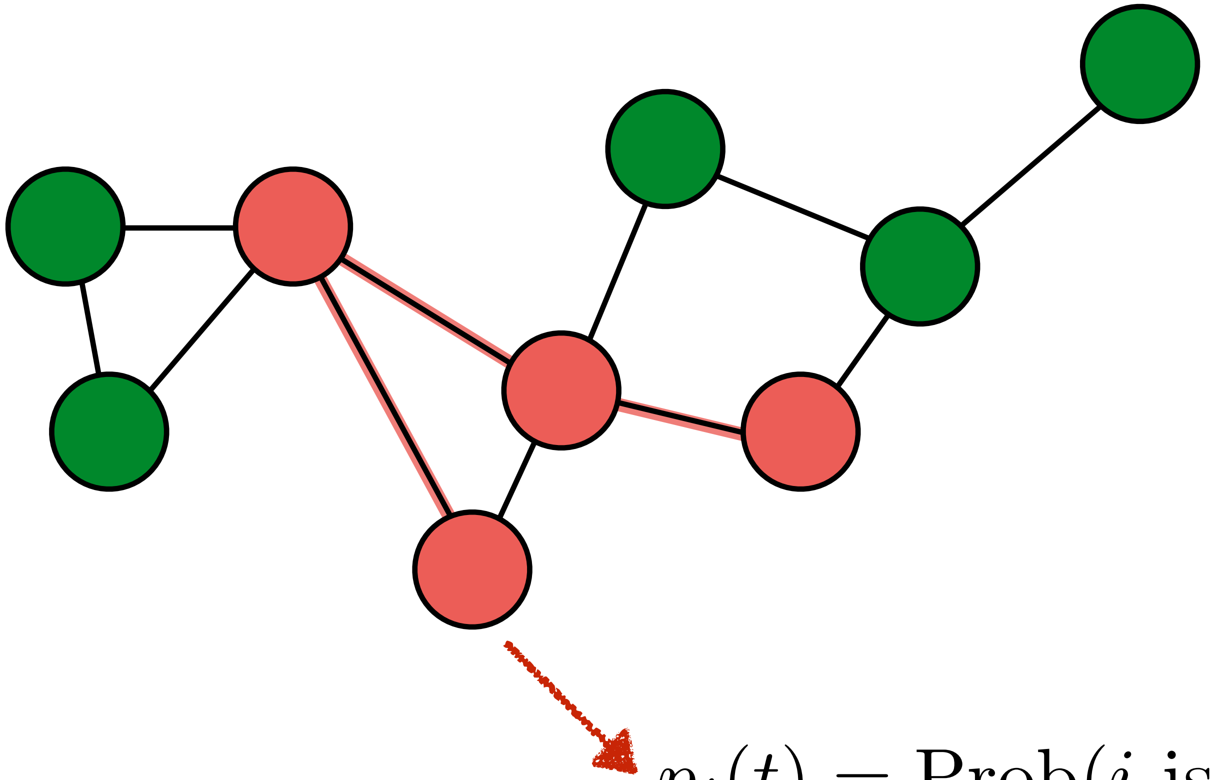
$$A_{ij}$$

Adjacency matrix

$$p_i(t) = \text{Prob}(i \text{ is infectious})$$

[Wang et al. SRDS 2003, Gómez et al. EPL 2010]

quenched mean field approach



$$A_{ij}$$

Adjacency matrix

$$p_i(t) = \mathrm{Prob}(i \text{ is infectious})$$

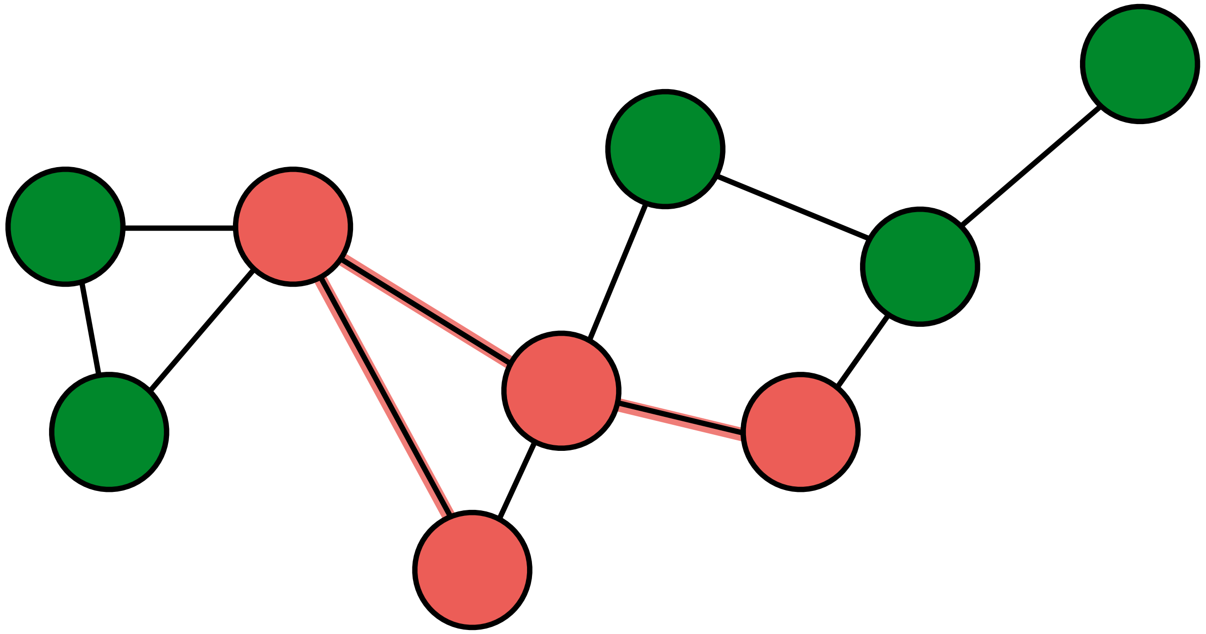
Markov chain

$$\mathrm{Prob}(i \text{ is infectious}, j \text{ is infectious}) = p_i p_j$$

$$p_i(t+1) = 1 - [1-(1-\mu)p_i(t)]\,\Pi_j\,[1-\beta A_{ji} p_j(t)]$$

[Wang et al. SRDS 2003, Gómez et al. EPL 2010]

quenched mean field approach



A_{ij}

Adjacency matrix

$p_i(t) = \text{Prob}(i \text{ is infectious})$

Markov chain

$\text{Prob}(i \text{ is infectious}, j \text{ is infectious}) = p_i p_j$

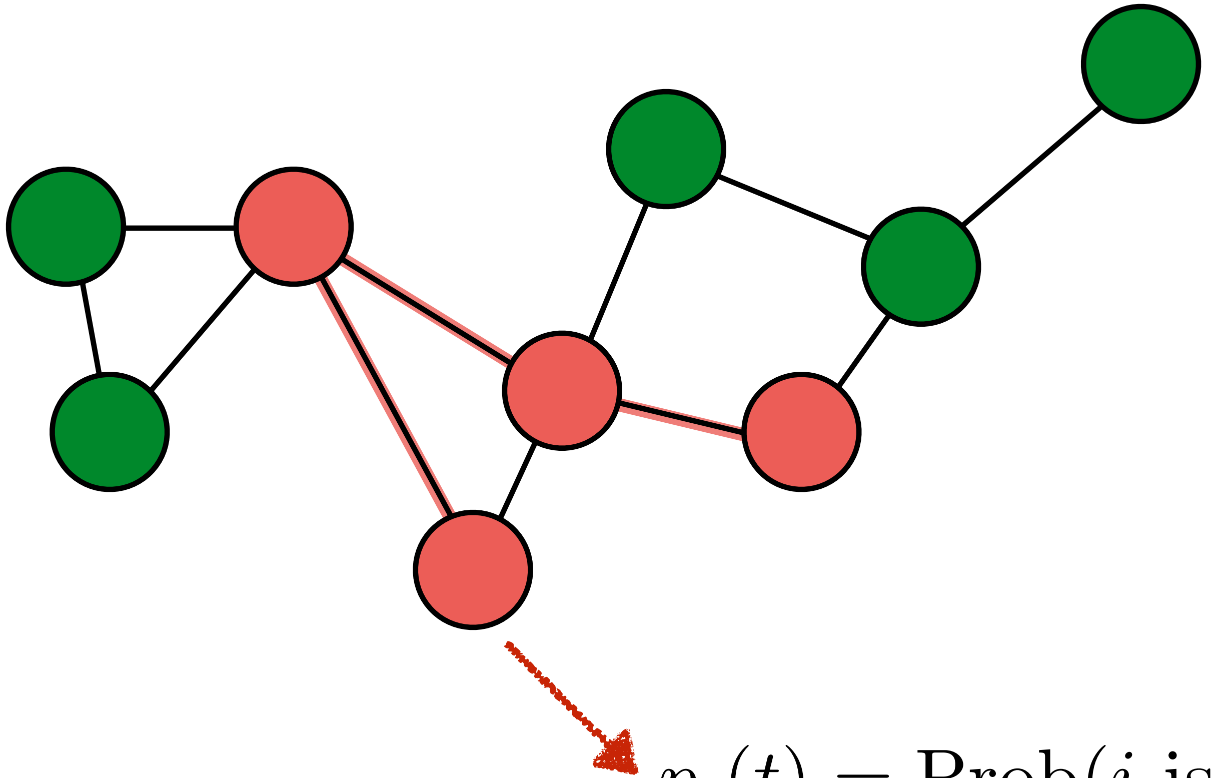
$$p_i(t+1) = 1 - \underbrace{[1-(1-\mu)p_i(t)]}_{\text{prob } i \text{ is not infectious from before}} \underbrace{\Pi_j\,[1-\beta A_{ji} p_j(t)]}_{\text{prob } i \text{ does not get infected}}$$

prob *i* is not infectious from before

prob *i* does not get infected

[Wang et al. SRDS 2003, Gómez et al. EPL 2010]

quenched mean field approach



$$A_{ij}$$

Adjacency matrix

$$p_i(t) = \text{Prob}(i \text{ is infectious})$$

Markov chain

$$\text{Prob}(i \text{ is infectious}, j \text{ is infectious}) = p_i p_j$$

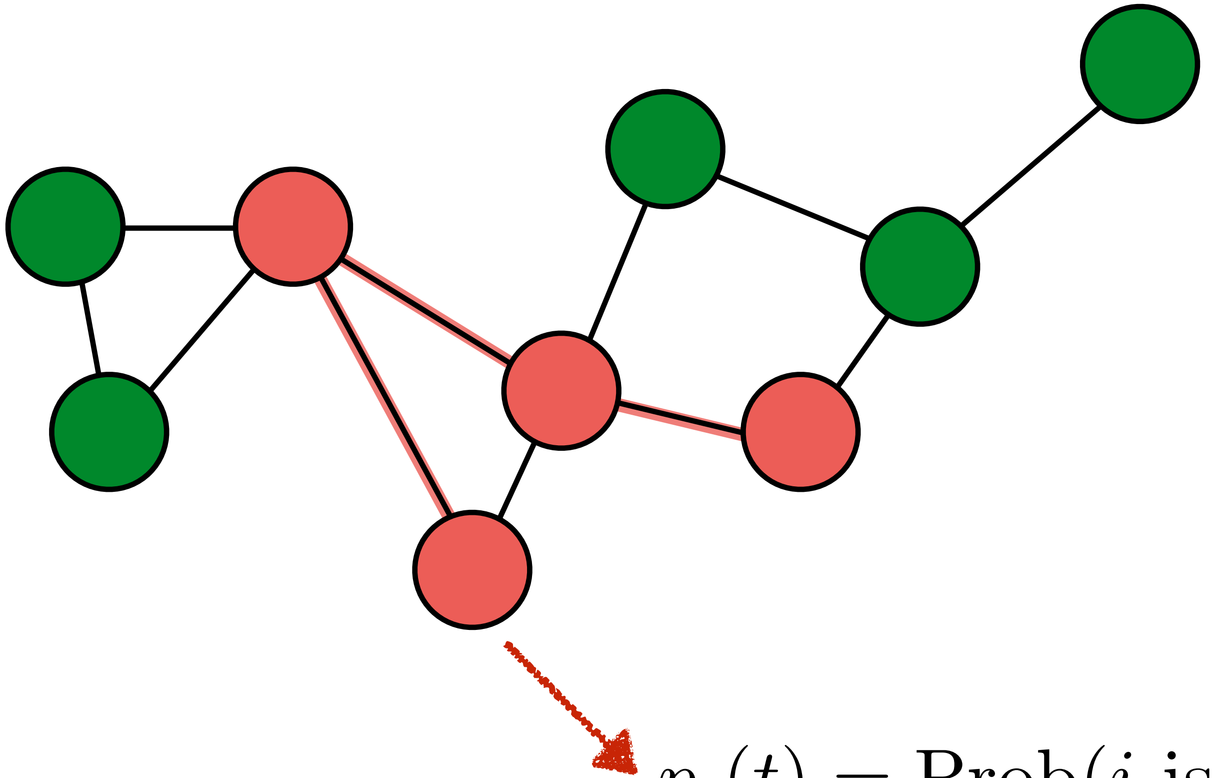
$$p_i(t+1) = 1 - [1 - (1-\mu) p_i(t)]\,\Pi_j\,[1 - \beta A_{ji} p_j(t)]$$

linearize

$$p(t+1) = (1 - \mu + \beta A^{\dagger}) p(t) + \mathcal{O}(||p(t)||^2)$$

[Wang et al. SRDS 2003, Gómez et al. EPL 2010]

quenched mean field approach



$$A_{ij}$$

Adjacency matrix

$$p_i(t) = \mathrm{Prob}(i \text{ is infectious})$$

$$p(t+1) = (1 - \mu + \beta A^{\dagger})p(t) + \mathcal{O}(||p(t)||^2)$$

$$\left(\frac{\beta}{\mu}\right)_{\text{critical}} = \frac{1}{\rho[A]}$$

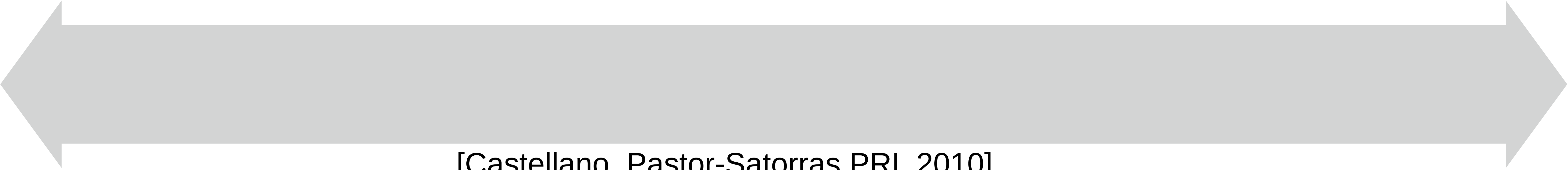
spectral radius
(largest eigenvalue)

[Wang et al. SRDS 2003, Gómez et al. EPL 2010]

quenched vs. heterogeneous

quenched mean field approximation

heterogeneous mean field approximation



[Castellano, Pastor-Satorras PRL 2010]

exact structure of the network

-fully account for network information

-comparison with null models for assessing relevant properties

-test possible interventions

[Wang et al. SRDS 2003; Gómez et al. 2010]

coarse graining - statistical properties

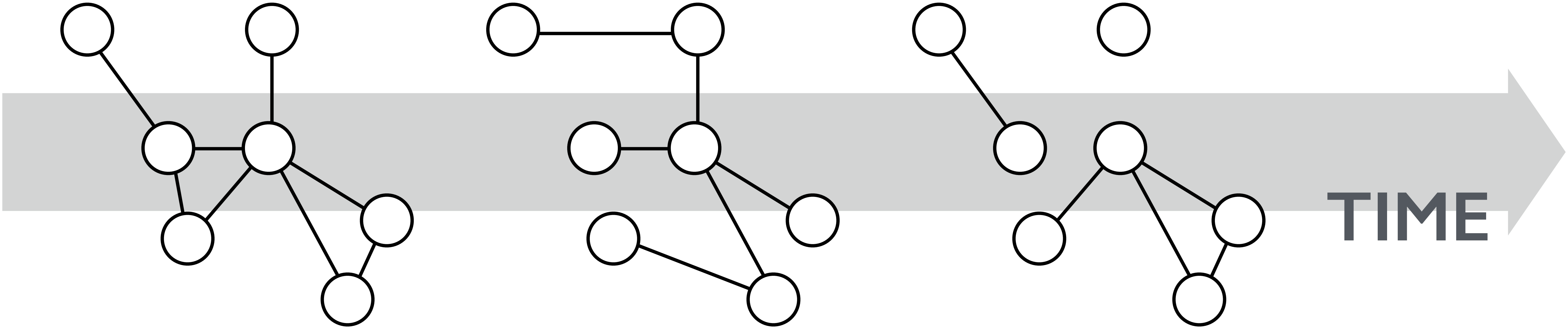
-simple transparent formula

-analytical understanding of immunisation processes

-full network information not available in many cases

[Pastor-Satorras & Vespignani PRL 2001,
Pastor Satorras et al. Rev Mod Phys 2015]

temporal dimension of networks



recent network data

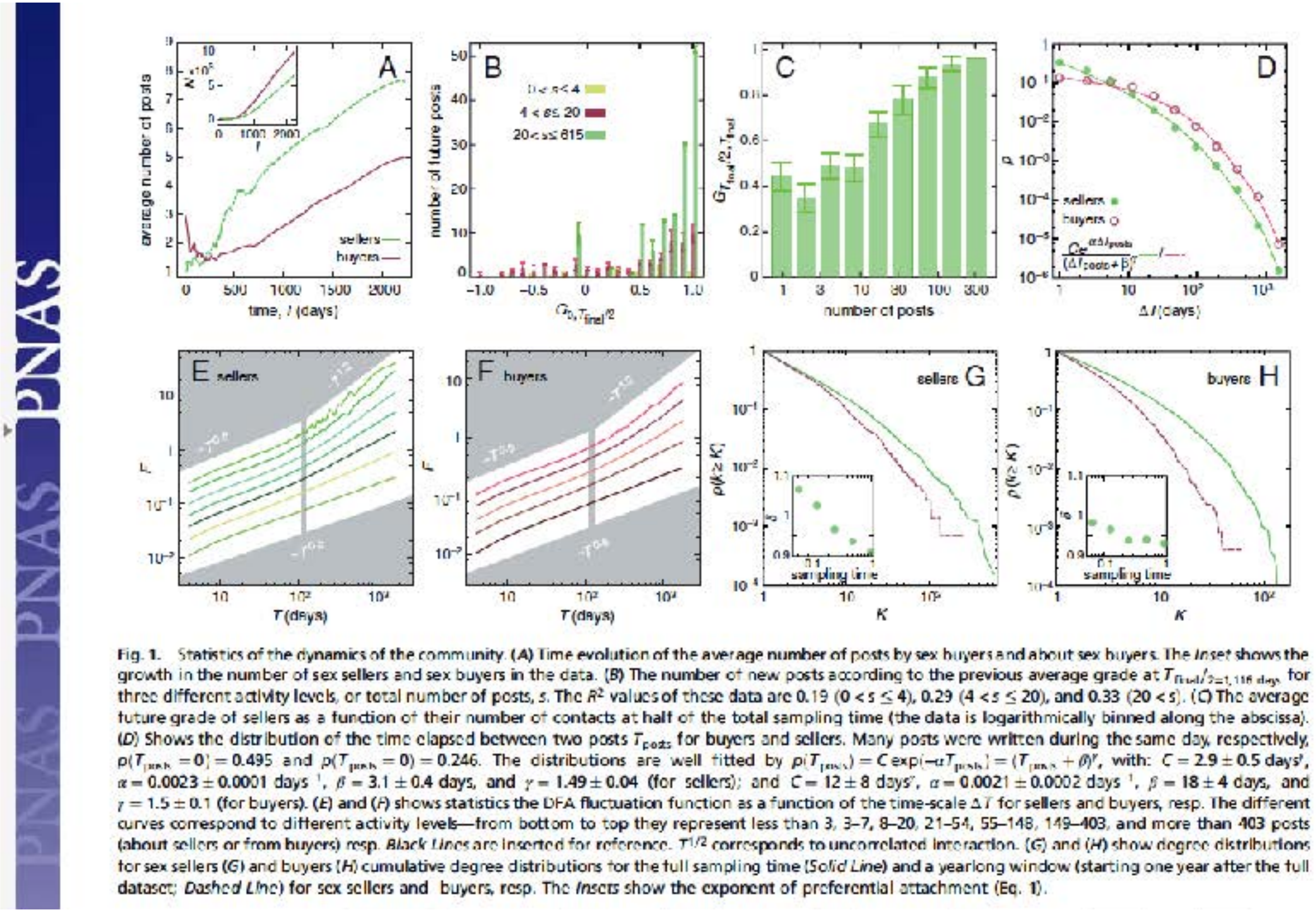


Fig. 1. Statistics of the dynamics of the community. (*A*) Time evolution of the average number of posts by sex buyers and about sex buyers. The *Inset* shows the growth in the number of sex sellers and sex buyers in the data. (*B*) The number of new posts according to the previous average grade at $T_{\rm final}/2 = 1{,}116$ days for three different activity levels, or total number of posts, *s*. The R^2 values of these data are 0.19 ($0 < s \leq 4$), 0.29 ($4 < s \leq 20$), and 0.33 ($20 < s$). (*C*) The average future grade of sellers as a function of their number of contacts at half of the total sampling time (the data is logarithmically binned along the abscissa). (*D*) Shows the distribution of the time elapsed between two posts $T_{\rm posts}$ for buyers and sellers. Many posts were written during the same day, respectively, $p(T_{\rm posts} = 0) = 0.495$ and $p(T_{\rm posts} = 0) = 0.246$. The distributions are well fitted by $p(T_{\rm posts}) = C\exp(-\alpha T_{\rm posts}) = (T_{\rm posts} + \beta)^{\gamma}$, with: $C = 2.9 \pm 0.5$ days$^{\gamma}$, $\alpha = 0.0023 \pm 0.0001$ days^{-1}, $\beta = 3.1 \pm 0.4$ days, and $\gamma = 1.49 \pm 0.04$ (for sellers); and $C = 12 \pm 8$ days$^{\gamma}$, $\alpha = 0.0021 \pm 0.0002$ days^{-1}, $\beta = 18 \pm 4$ days, and $\gamma = 1.5 \pm 0.1$ (for buyers). (*E*) and (*F*) shows statistics the DFA fluctuation function as a function of the time-scale ΔT for sellers and buyers, resp. The different curves correspond to different activity levels—from bottom to top they represent less than 3, 3–7, 8–20, 21–54, 55–148, 149–403, and more than 403 posts (about sellers or from buyers) resp. *Black Lines* are inserted for reference. $T^{1/2}$ corresponds to uncorrelated interaction. (*G*) and (*H*) show degree distributions for sex sellers (*G*) and buyers (*H*) cumulative degree distributions for the full sampling time (*Solid Line*) and a yearlong window (starting one year after the full dataset; *Dashed Line*) for sex sellers and buyers, resp. The *Insets* show the exponent of preferential attachment (Eq. 1).

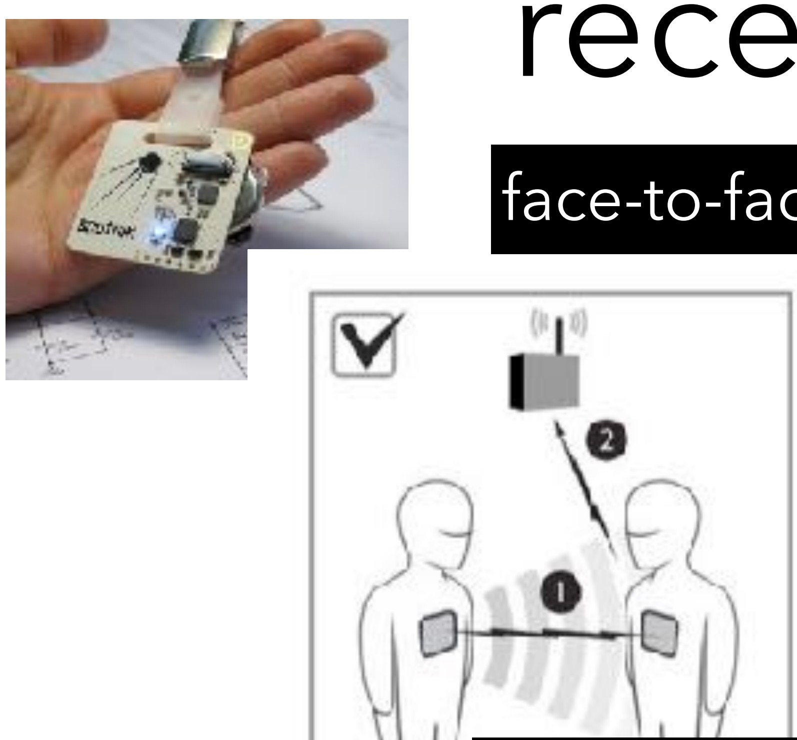
internet mediated prostitution

sexual contacts between 6,624 escorts and 10,106 sex buyers extracted from an online community

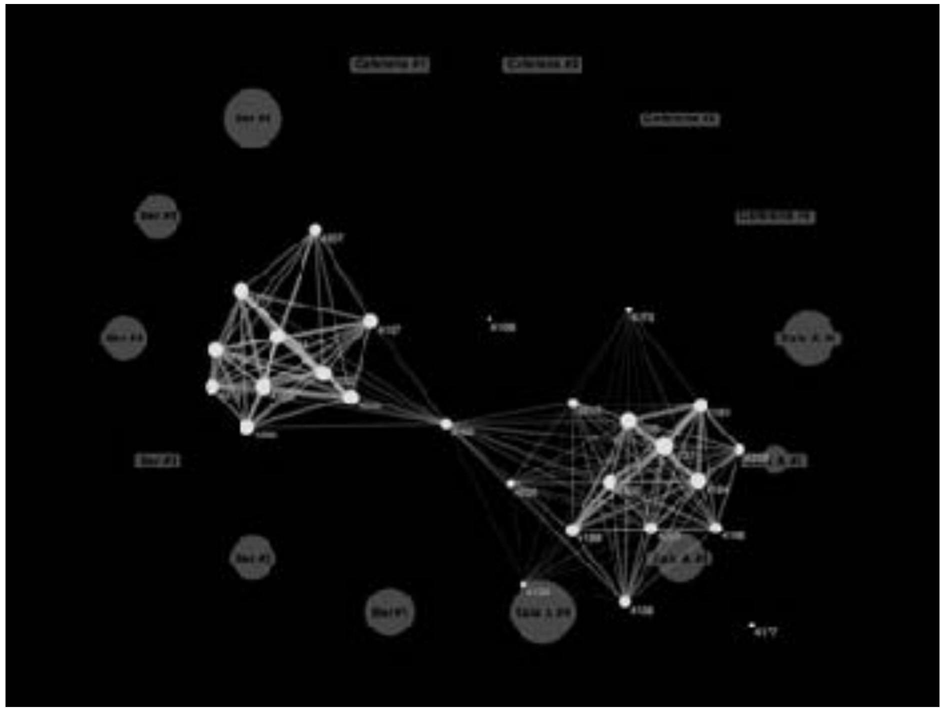
[LEC. Rocha, et al, PNAS 2009]

recent network data

face-to-face contacts



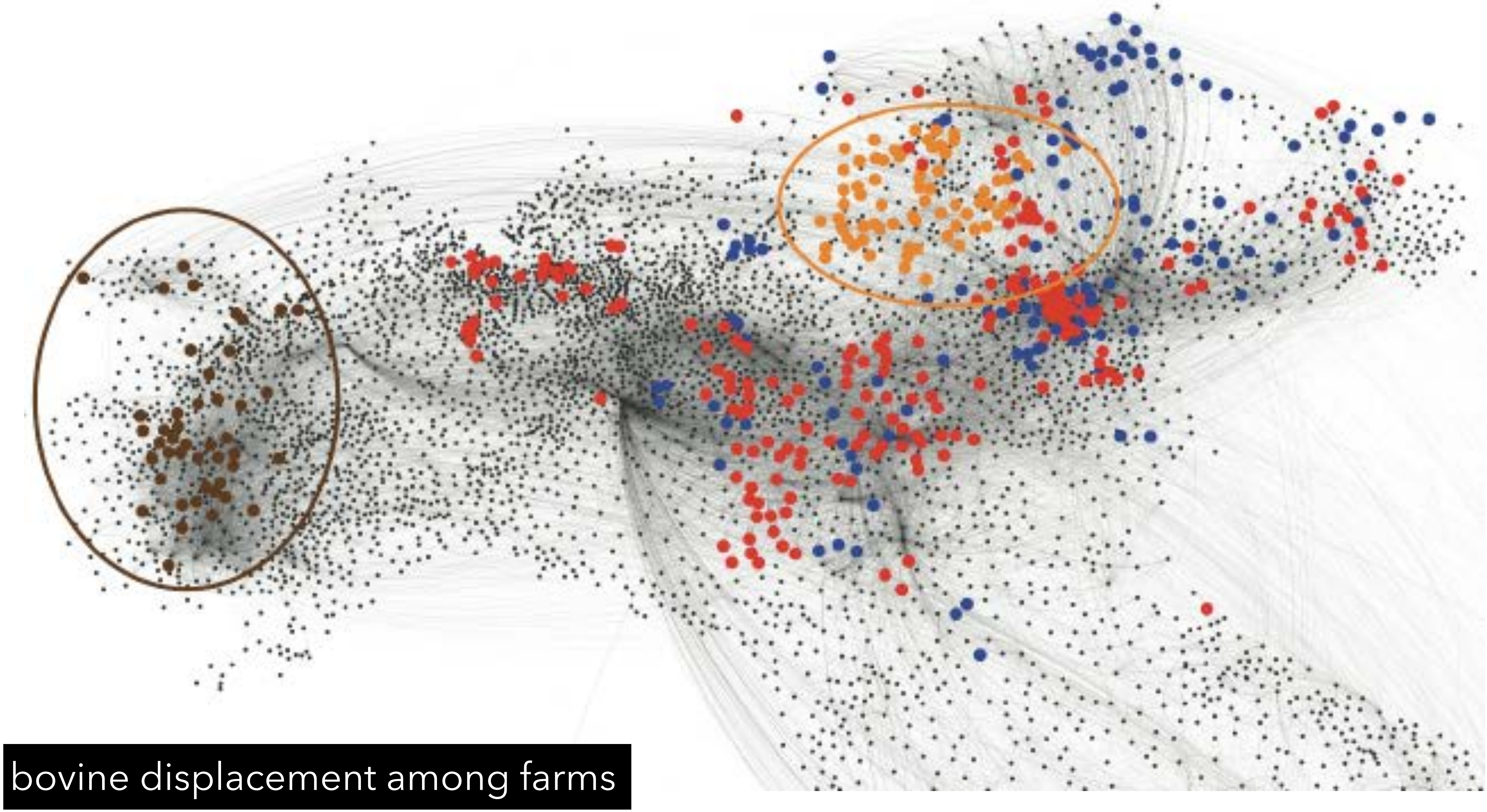
RFID technology



schools - workplaces - hospitals - museums - conferences - households - rural Africa

[Salathé et al. Proc Natl Acad Sci 2010; **Sociopatterns.org** - Stehlé et al. BMC Medicine 2011; Kiti et al. EPJ Data Science 2016; Ozella et al. PLoS ONE 2018; **iBird** - Obadia et al. PLoS Comp Bio 2015]

recent network data



bovine displacement among farms

[Bajardi, PLoS ONE (2011)]

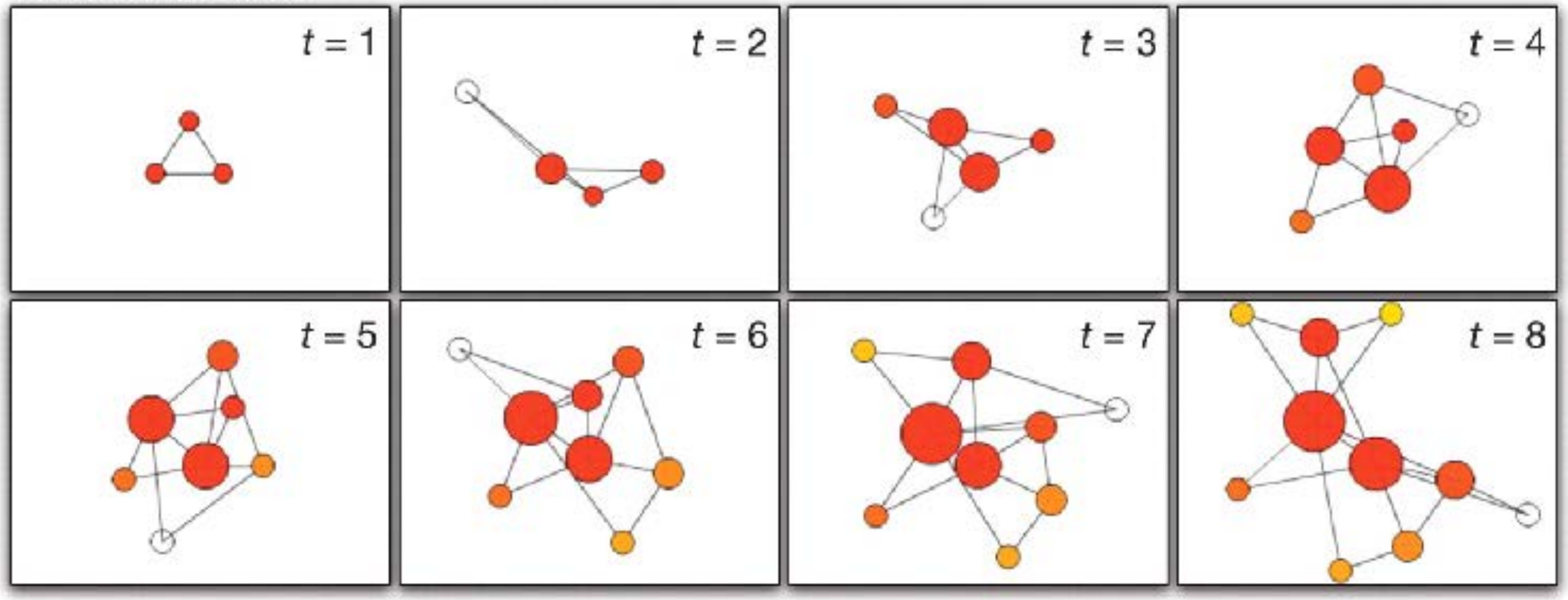
temporal dimension of networks

in the 90’s **generative network models**

generative network models

in the 90's **generative network models**

preferential attachment model: rich gets richer



- m_0 initial nodes
- each time step: a new node enters with m stubs
- probability it connects with a node with degree k_i: $\Pi(k_i) = \dfrac{k_i}{\sum_j k_j}$

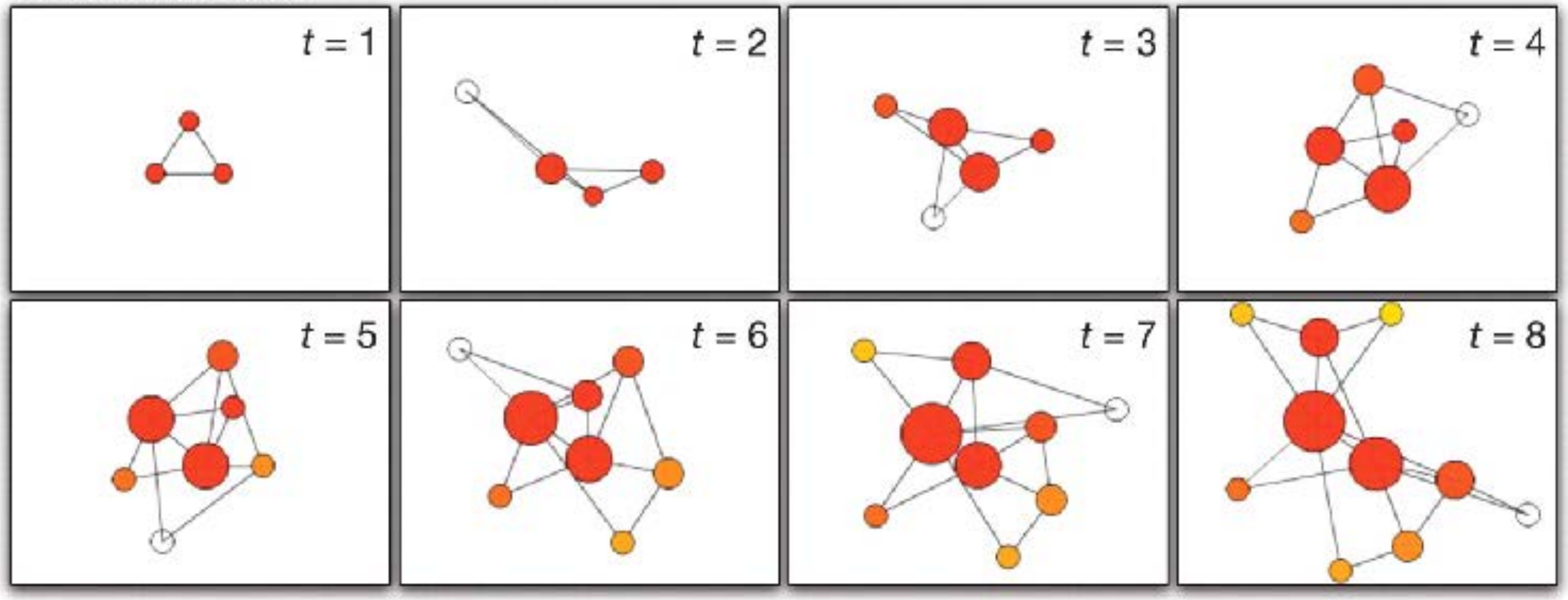
degree distribution in the stationary limit: $P(k) = \dfrac{2m^2}{k^3}$

[Barabasi, Albert, Science, 1999]

generative network models

in the 90's **generative network models**

preferential attachment model: rich gets richer



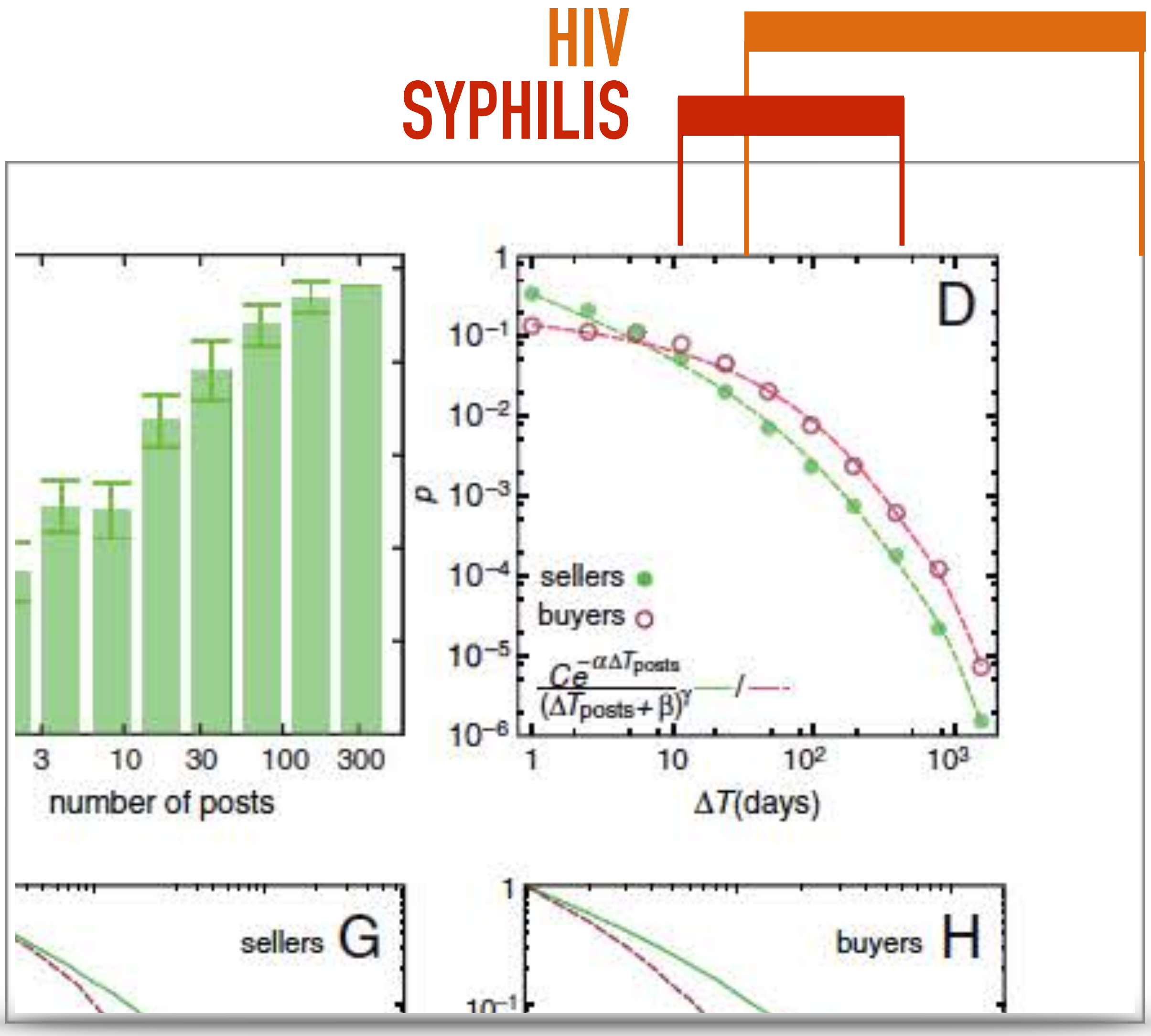
the model explains the topology of the network but

the network dynamics is decoupled from the dynamical process unfolding on the top of the network

[Barabasi, Albert, Science, 1999]

temporal dimension of networks

time scale separation not applicable in many cases



internet mediated prostitution

[LEC. Rocha, et al, PNAS 2009]

temporal dimension of networks

Nowadays **temporal network models**

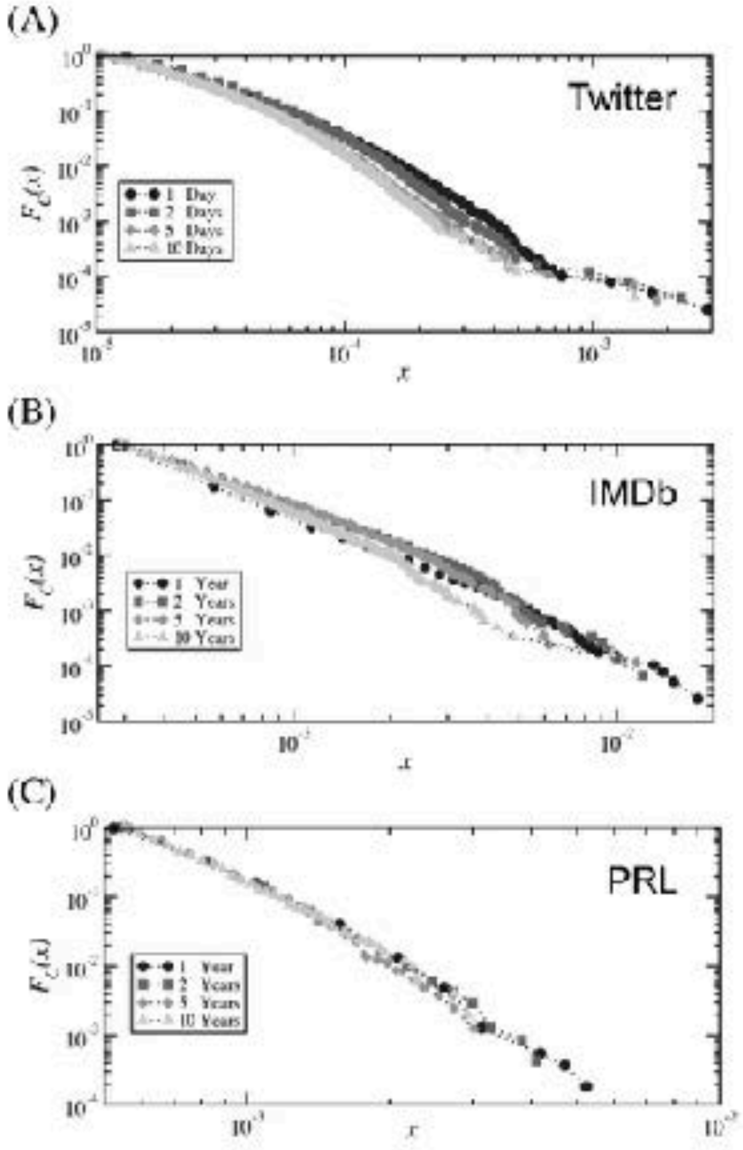
temporal dimension of networks

Nowadays **temporal network models**

activity driven model

[Perra et al, Sci Rep 2012]

- activity potential x_i : number of activation in a Δt
- $F(x)$: distribution of the activity potential
- a node activates with rata $a_i = \eta x_i$ and forms *m* connections



activity driven model

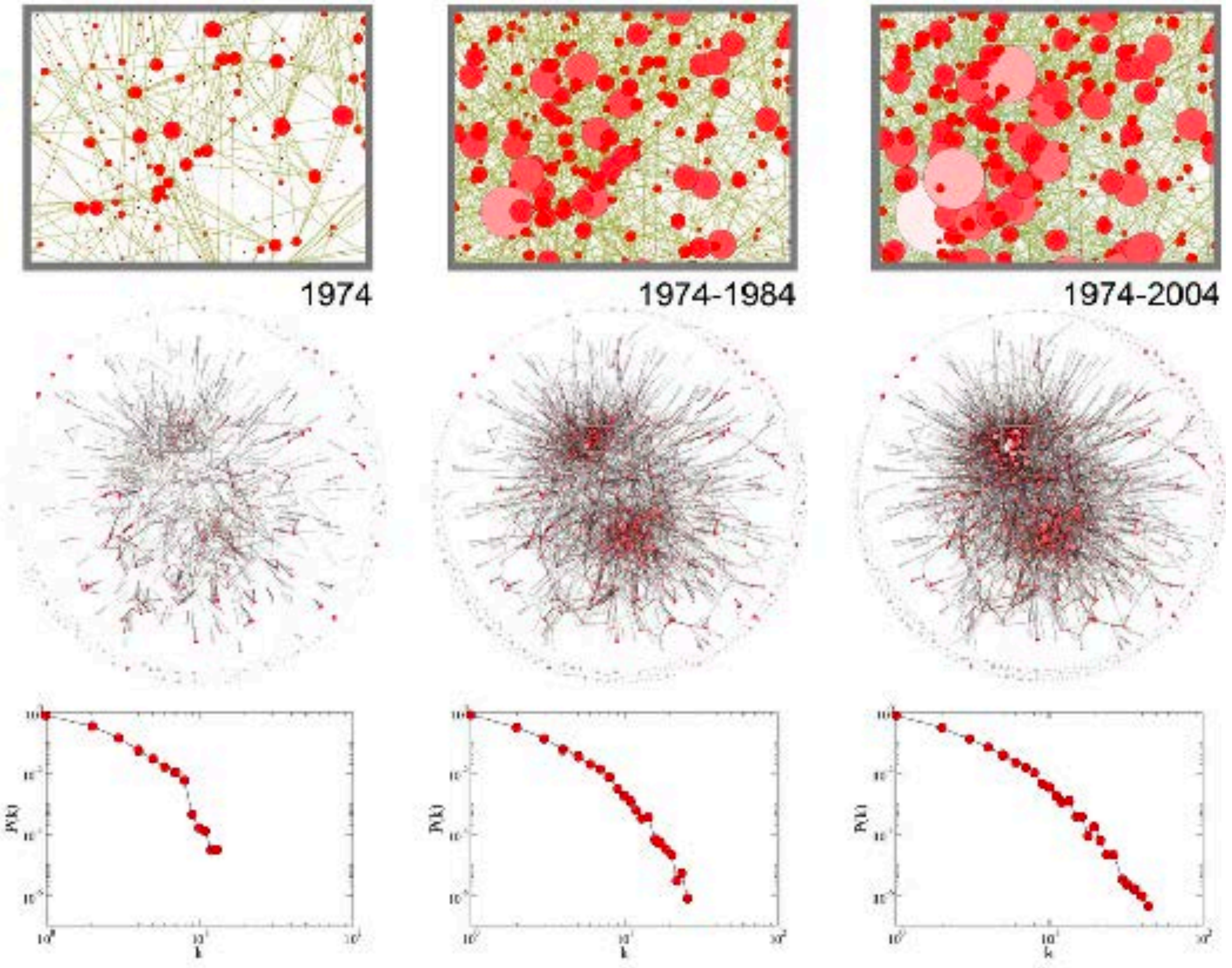
Nowadays **temporal network models**

activity driven model

[Perra et al, Sci Rep 2012]

heterogenous topology in the aggregated network, over a window T, result from a heterogeneous activity potential

$$P_T(k) \sim F\left[\frac{k}{Tm\eta}\right]$$



activity driven model

Nowadays **temporal network models**

activity driven model

[Perra et al, Sci Rep 2012]

activity potential affects spreading and the epidemic threshold

spreading dynamics

$$I_a^{t+\Delta t} = -\mu \Delta t I_a^t + I_a^t +$$

$$\lambda m (N_a^t - I_a^t) a \Delta t \int da' \frac{I_{a'}^t}{N} + \lambda m (N_a^t - I_a^t) \int da' \frac{I_{a'}^t a' \Delta t}{N}$$

epidemic threshold

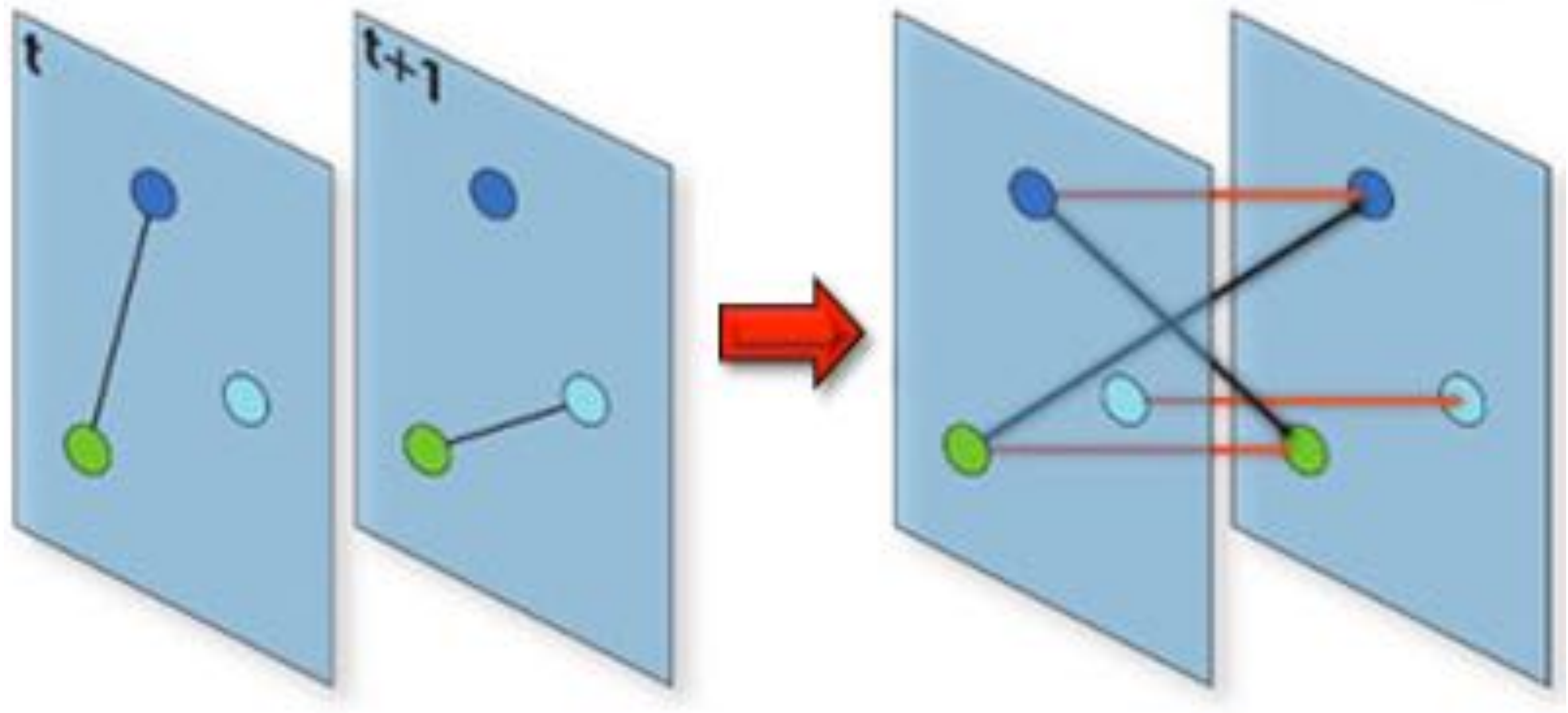
$$\frac{\beta}{\mu} > \frac{2\langle a \rangle}{\langle a \rangle + \sqrt{\langle a^2 \rangle}}$$

temporal network properties

Nowadays **temporal network models**

- activation rate
- turn over
- inter-contact time
- memory

account for the full temporal dimension



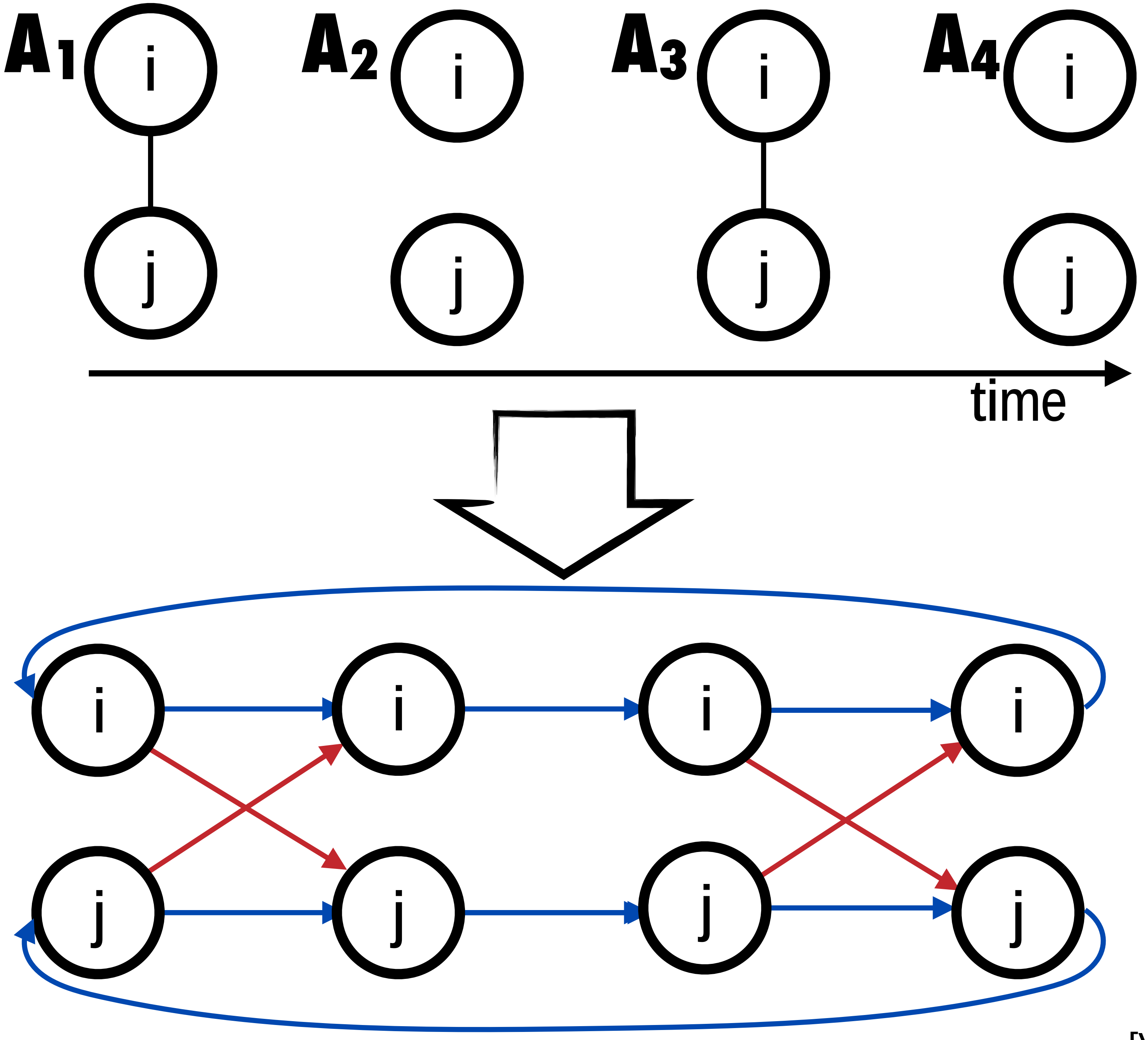
multilayer formalism ⟶ quenched mean field approach

[De Domenico et al PRX 2013, Kivelä et al Comp Networks 2014]

[Granell et al PRL 2013, Cozzo et al PRE 2013, Sanz et al PRX 2014]

[Valdano et al PRX 2015]

infection propagator approach

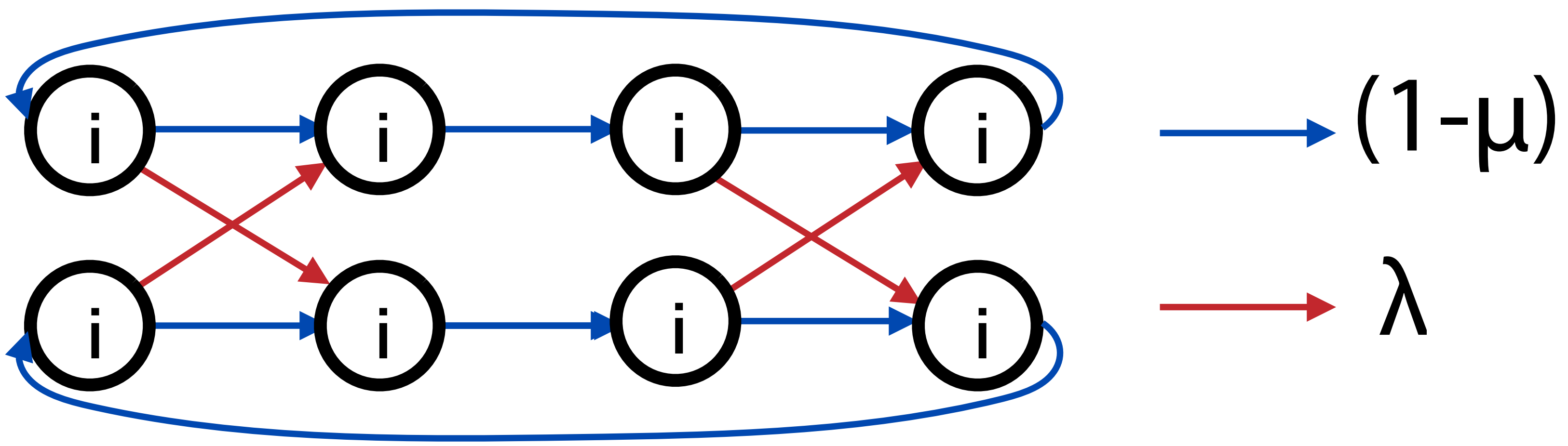


[Scholtes et al
Nature Com 2015]

[Valdano et al PRX 2015]

infection propagator approach

$$S \xrightarrow{\lambda} I \xrightarrow{\mu} S$$



NT x NT supra-adjacency matrix

$$M = \begin{pmatrix} 0 & 1-\mu+\lambda A_1 & 0 & \cdots & 0 \\ 0 & 0 & 1-\mu+\lambda A_2 & \cdots & 0 \\ \vdots & \vdots & \vdots & \cdots & \vdots \\ 0 & 0 & 0 & \cdots & 1-\mu+\lambda A_{T-1} \\ 1-\mu+\lambda A_T & 0 & 0 & \cdots & 0 \end{pmatrix}$$

N x N blocks

[Valdano et al PRX 2015]

infection propagator approach

threshold on temporal network ⟷ threshold on STATIC network

epi threshold

$$\rho[\mathbf{M}(\lambda_{thr},\mu)] = 1$$

dim = NT

↓ [Powell, arXiv, 2011]

dim = N

$$\rho[\mathbf{P}(\lambda_{thr},\mu)] = 1$$

$$\mathbf{P} = (1-\mu + \lambda \mathbf{A}_1)\,(1-\mu + \lambda \mathbf{A}_2) \cdots (1-\mu + \lambda \mathbf{A}_T)$$

[Lentz et al, PRL 2013]

infection propagator

[Valdano et al PRX 2015]

conclusion

- Network topology affect spreading
- Degree heterogeneity lower the epidemic threshold
- heterogenous mean field approach vs. quenched mean field approach
- network temporal dimension and interplay with spreading process
- activity driven vs. infectious propagator approach

Outline

-modeling an epidemic

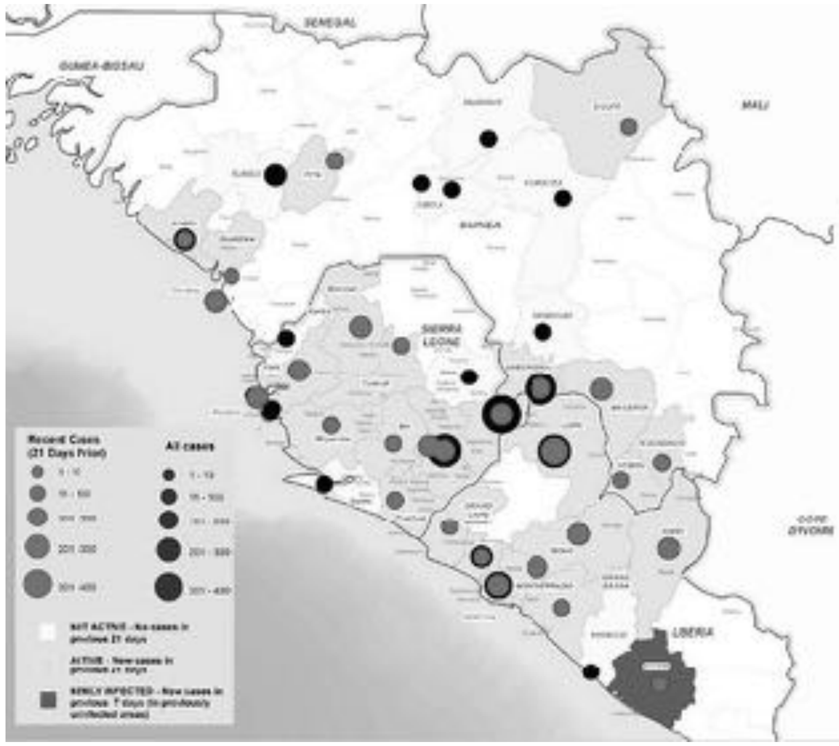
-epidemics on networks

-epidemics in space

-interacting epidemics

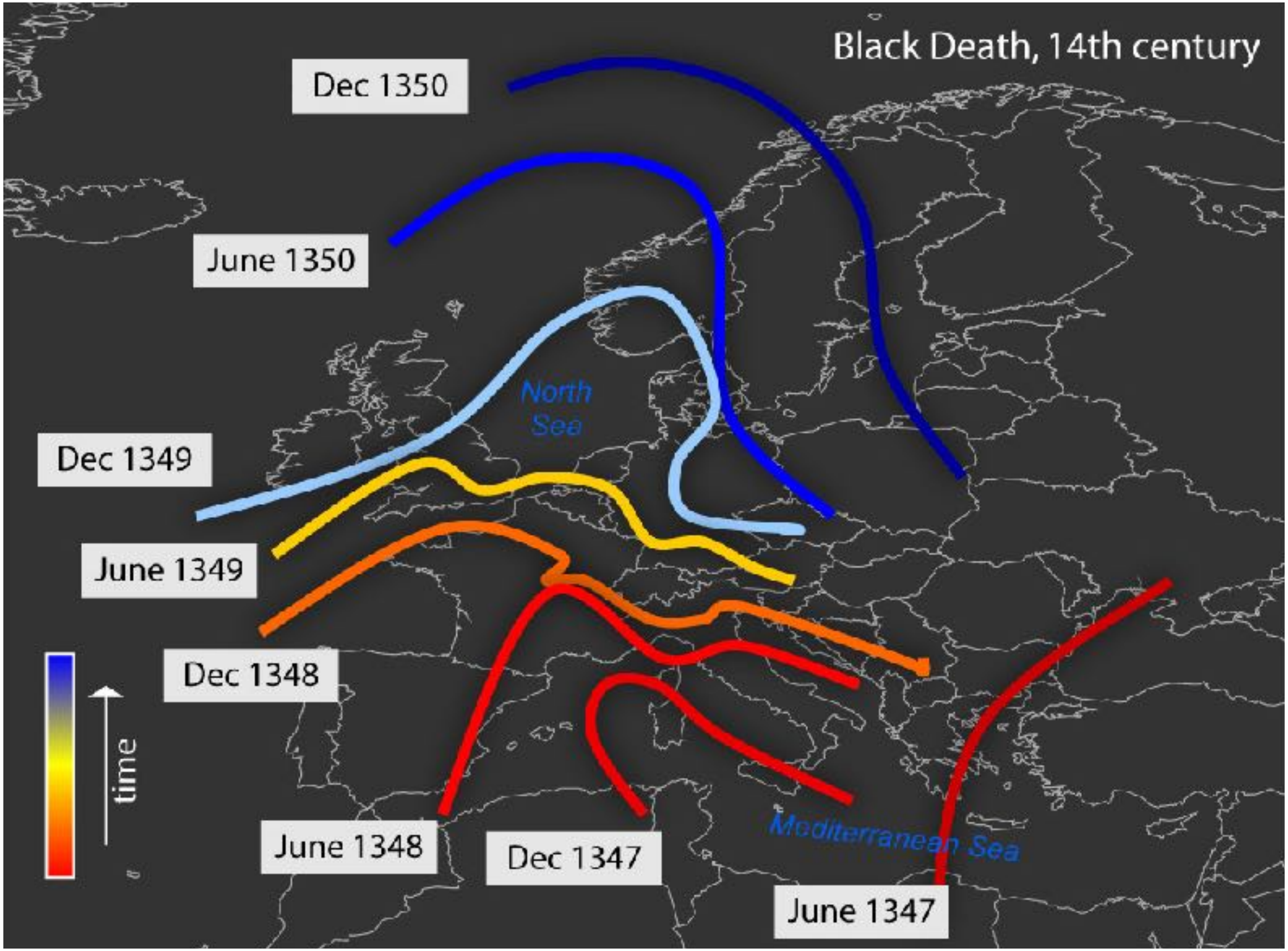
-computer simulations

Western Africa ebola outbreak, 2014

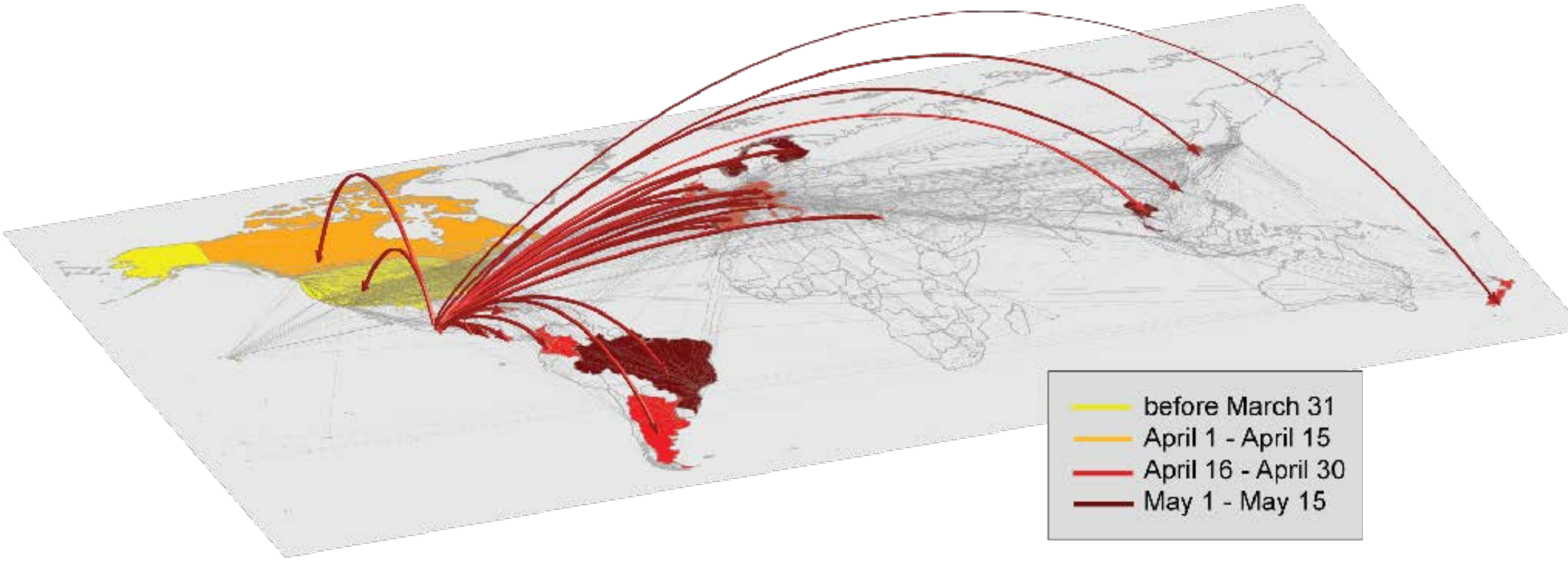


Western Africa ebola outbreak, 2014

black death, 14th century



H1N1 influenza pandemic, 2009



H1N1 influenza pandemic, 2009

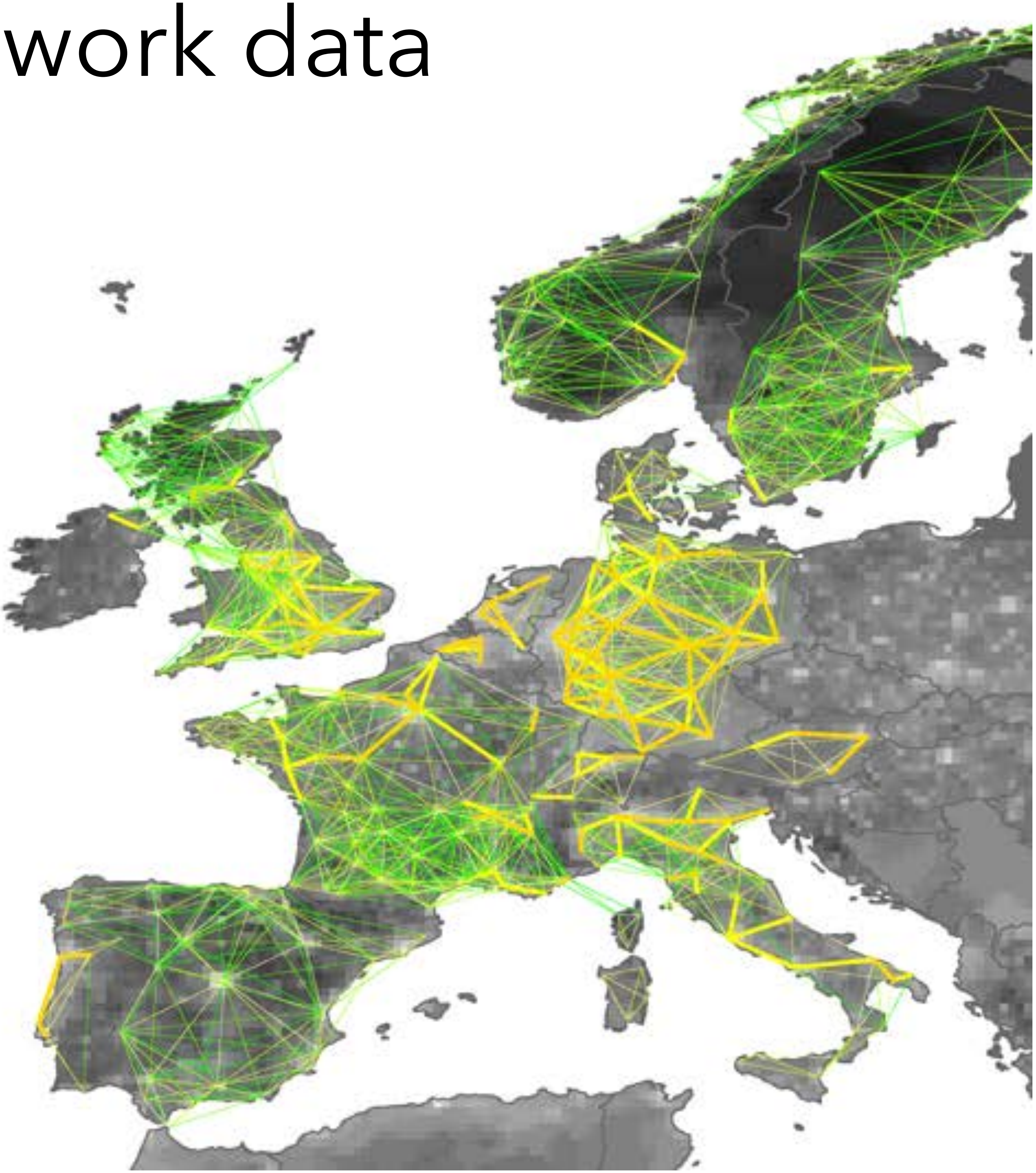
mobility network data

air traveling

data collected by the
International Air Trasport
Association

[Hufnagel et al. PNAS 2004; Colizza et al.
PLoS Med 2007; Balcan et al. PNAS 2009]

mobility network data

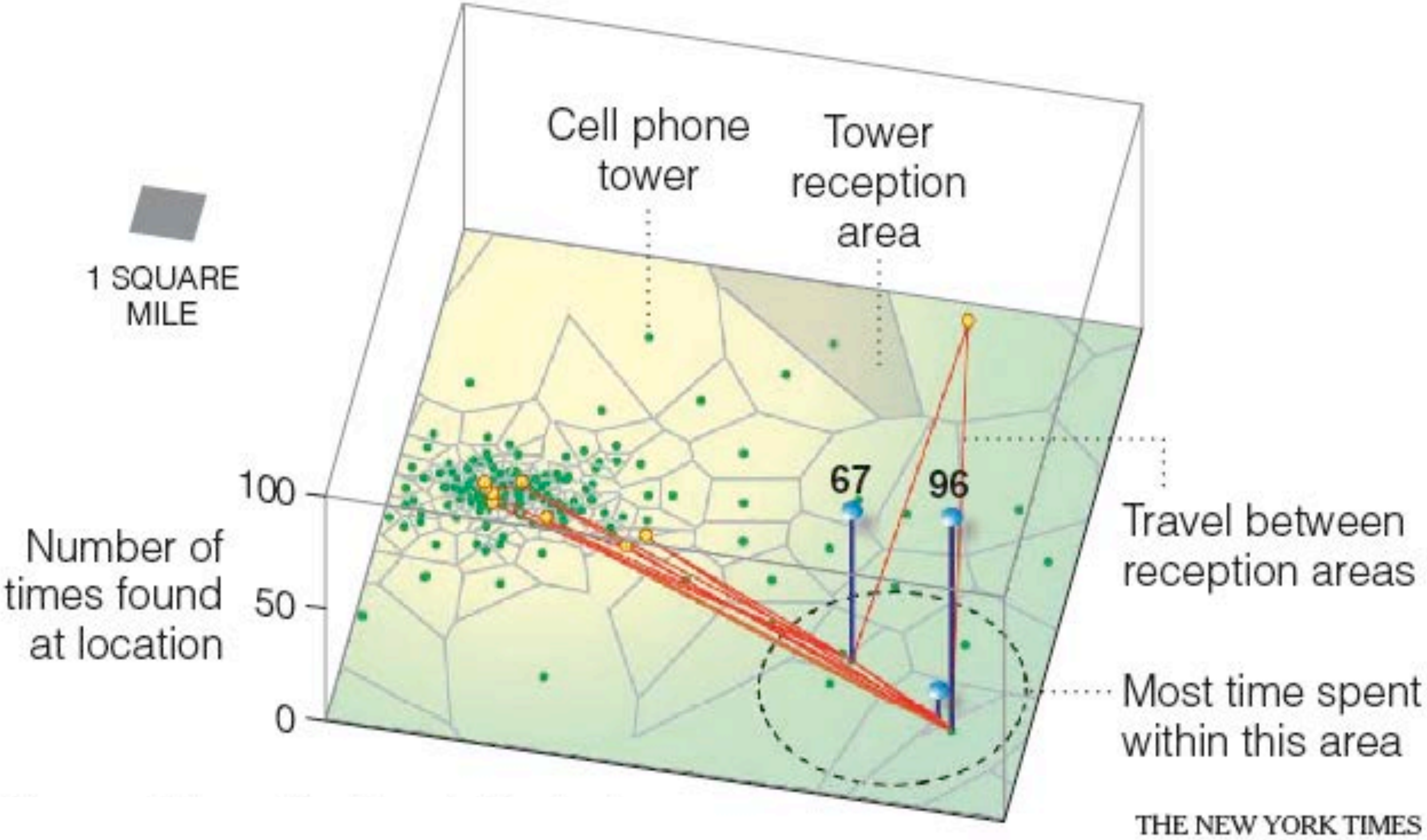


commuting data

census data of different countries

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

mobility network data



local mobility

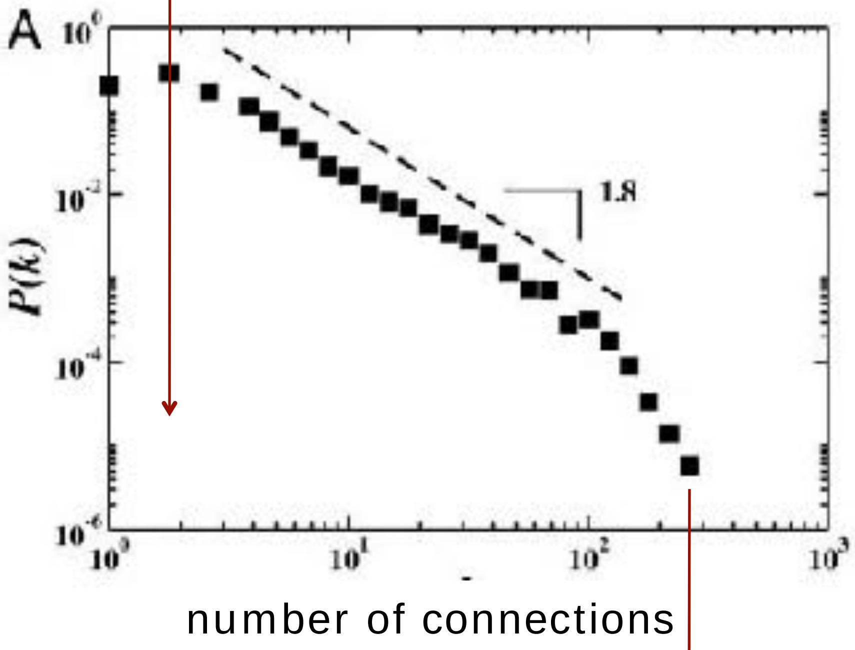
mobile phone data

[Gonzalez et al, Nature (2008)]

mobility network properties

... heterogeneous!

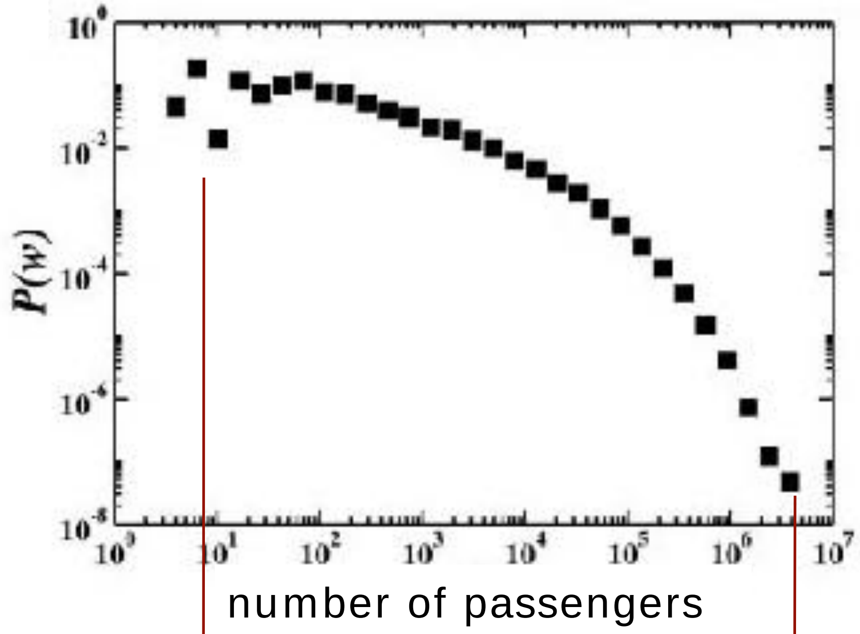
topological heterogeneity



peripheral
airports

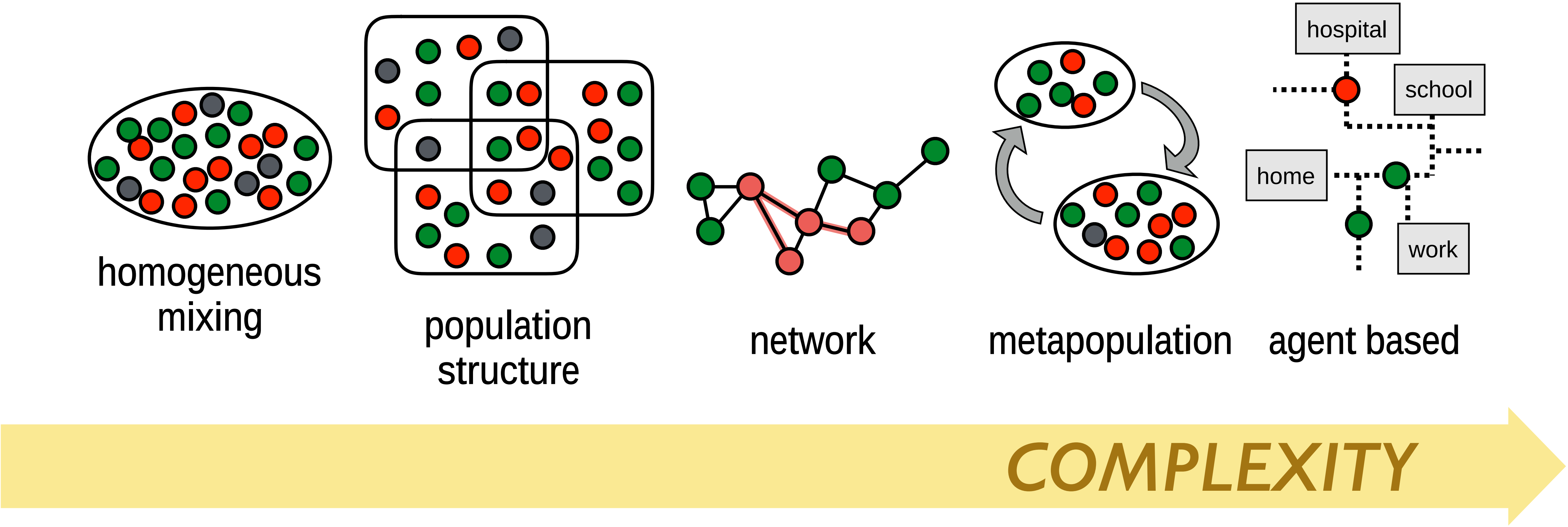
Frankfurt,
318 connections

traffic heterogeneity



low traffic
airports

Tokyo-Sapporo
17000 p/day



homogeneous mixing

population structure

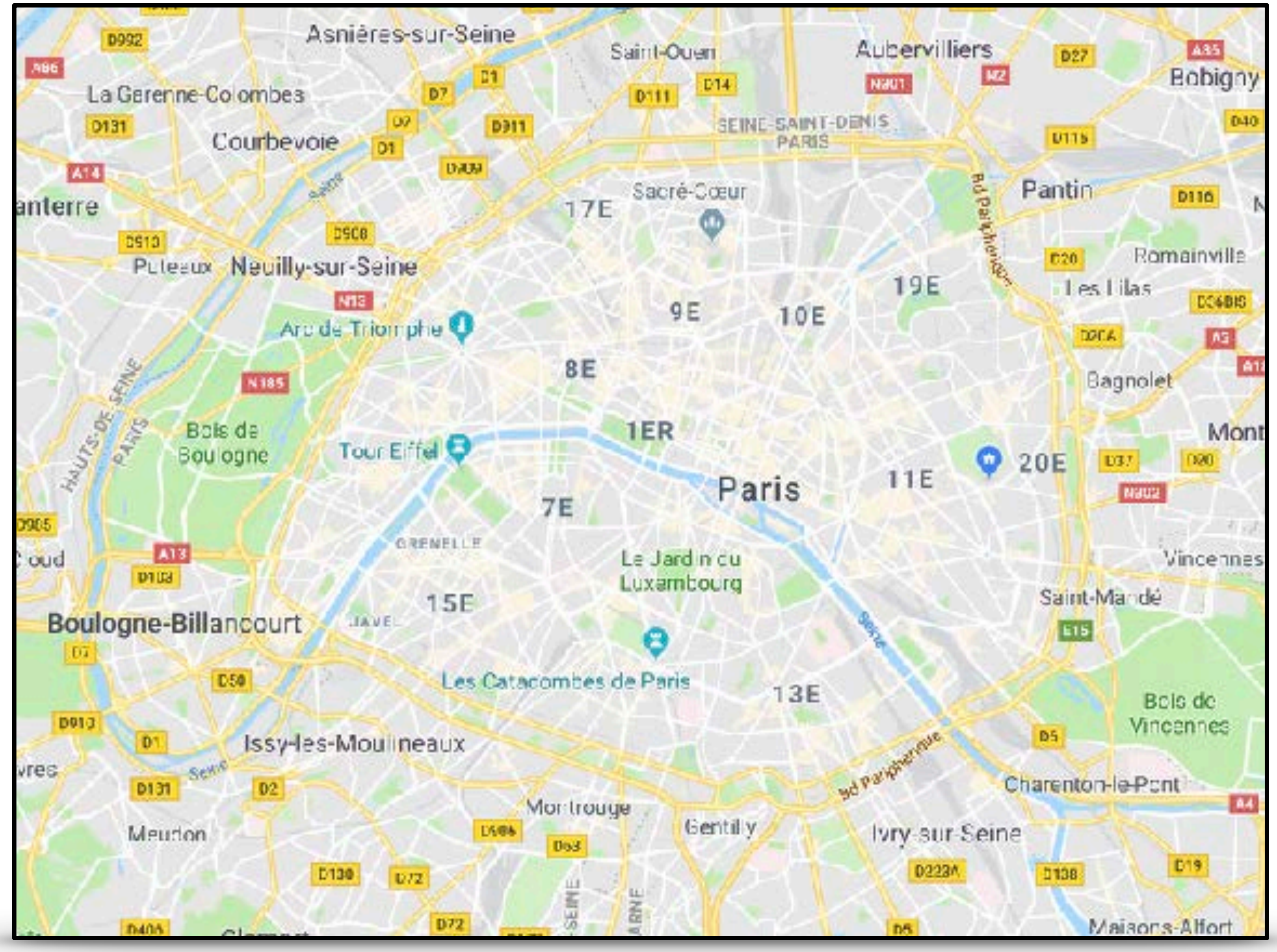
network

metapopulation

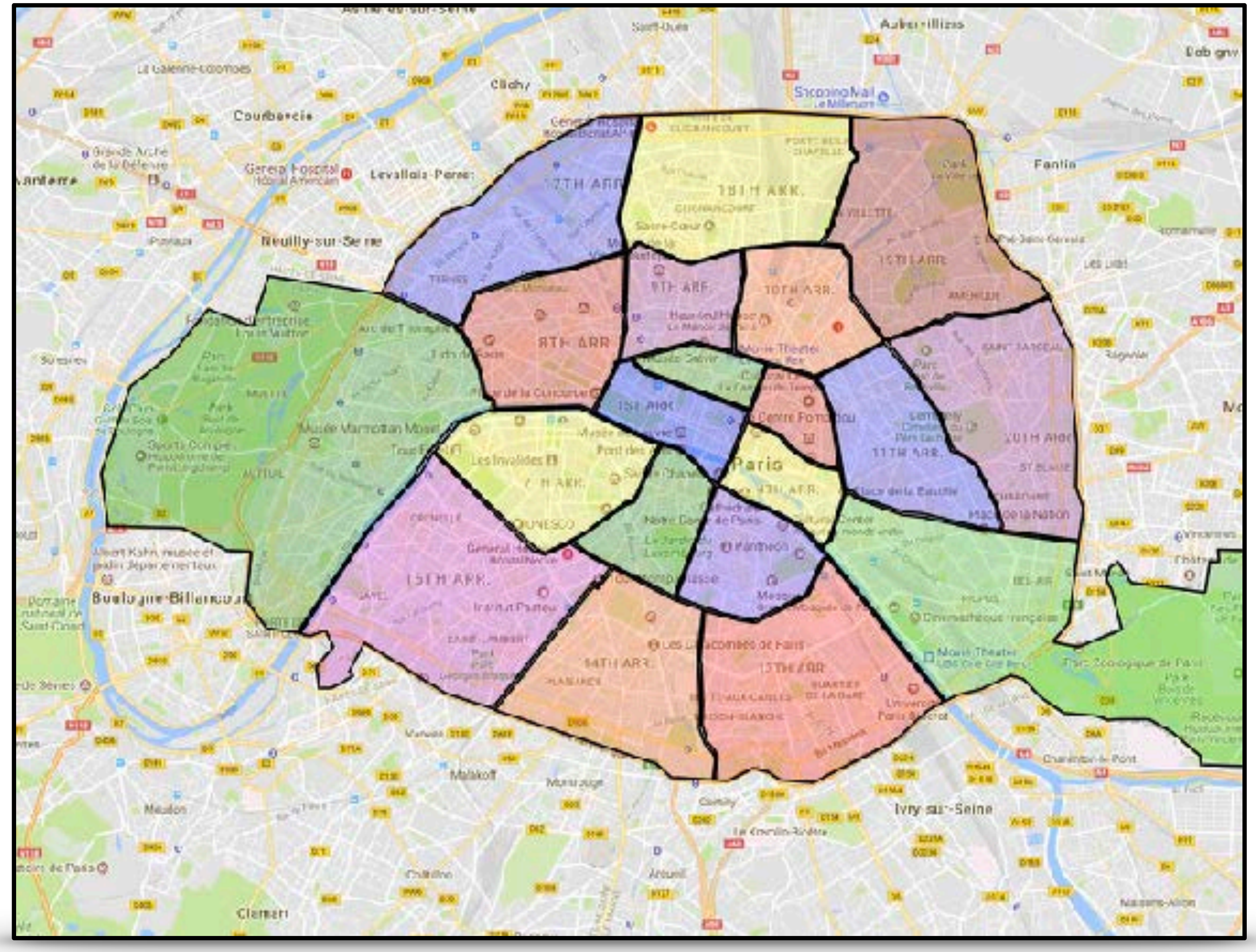
agent based

COMPLEXITY

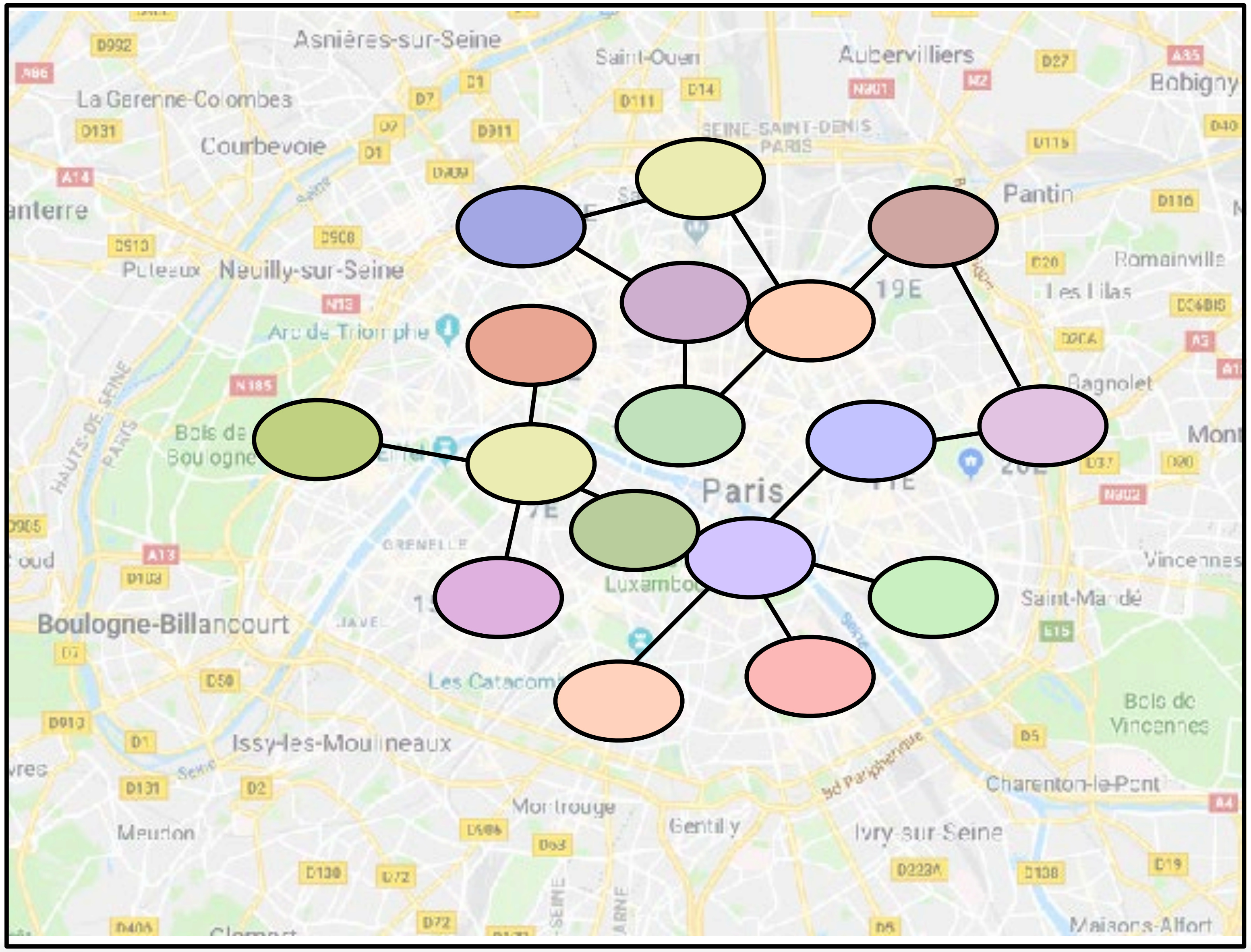
metapopulation models: a compromise



metapopulation models: a compromise



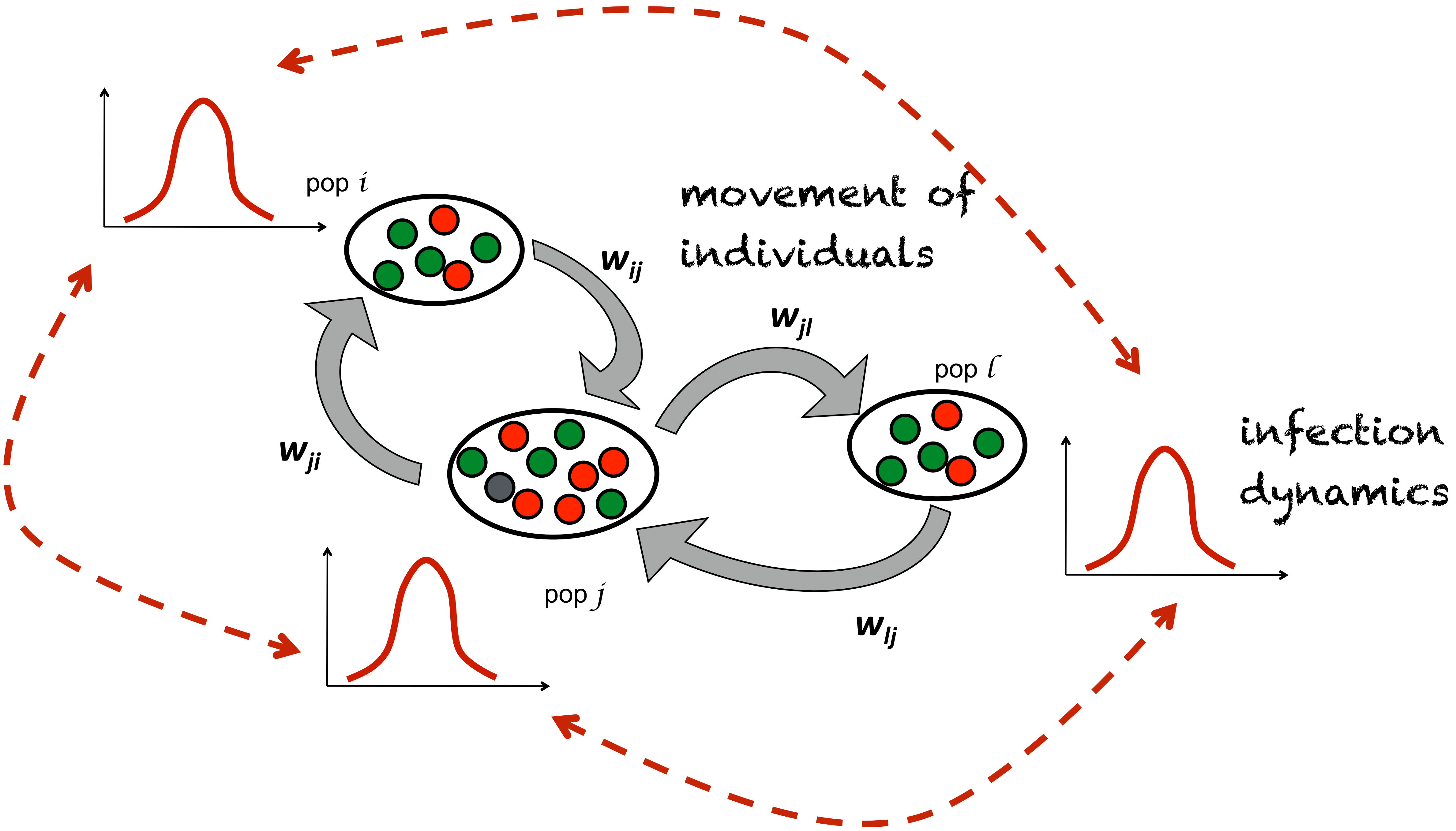
metapopulation models: a compromise



local populations:

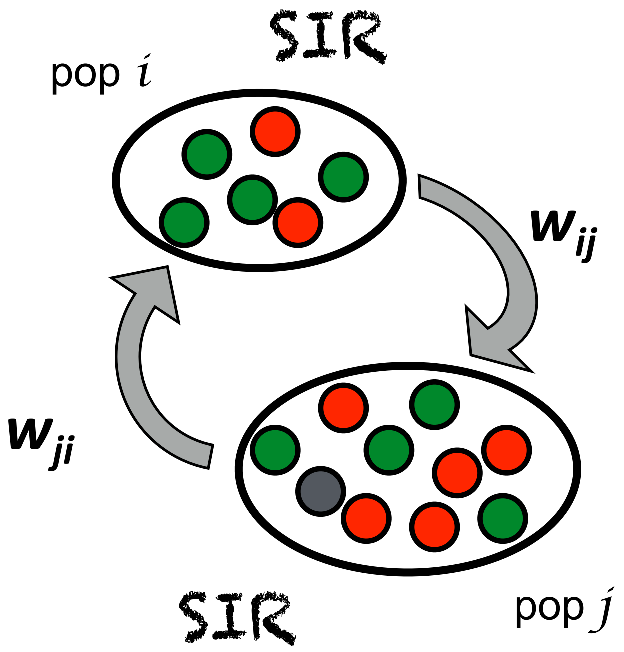
- discrete entities in space: *patches*
- interaction between populations : *coupling, flows*

metapopulation models



[Hanski, I. & Gaggiotti, Elsevier, Academic Press, 2004]

SIR metapopulation models



$S(t)$

$I(t)$

$R(t)$

$N(t)$

⇨

V: # populations

$S_i(t)$

$I_i(t)$

$R_i(t)$

$N_i(t) = S_i(t) + I_i(t) + R_i(t)$

global variables

$$S(t) = S_1(t) + S_2(t) + S_3(t) + \ldots + S_V(t) = \sum_i S_i(t)$$

$$I(t) = I_1(t) + I_2(t) + I_3(t) + \ldots + I_V(t) = \sum_i I_i(t)$$

$$R(t) = R_1(t) + R_2(t) + R_3(t) + \ldots + R_V(t) = \sum_i R_i(t)$$

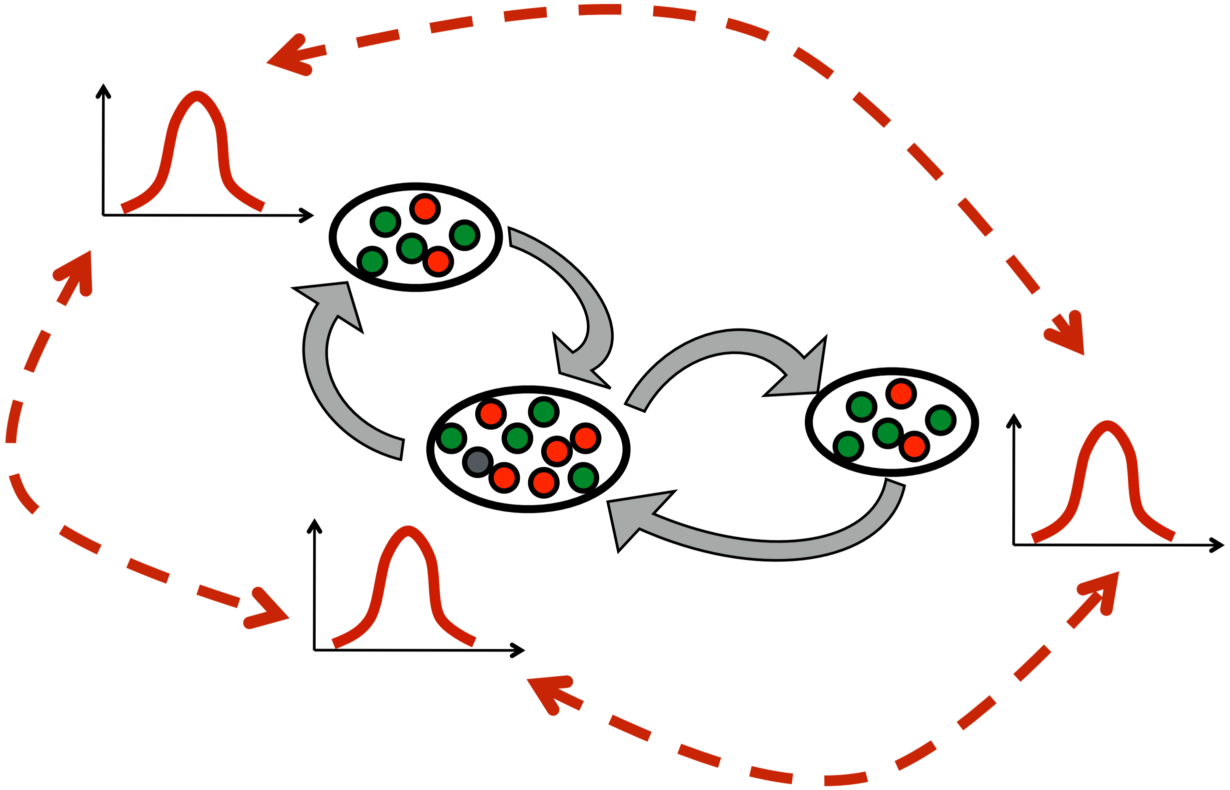
$$N(t) = N_1(t) + N_2(t) + N_3(t) + \ldots + N_V(t) = \sum_i N_i(t)$$

SIR metapopulation models

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

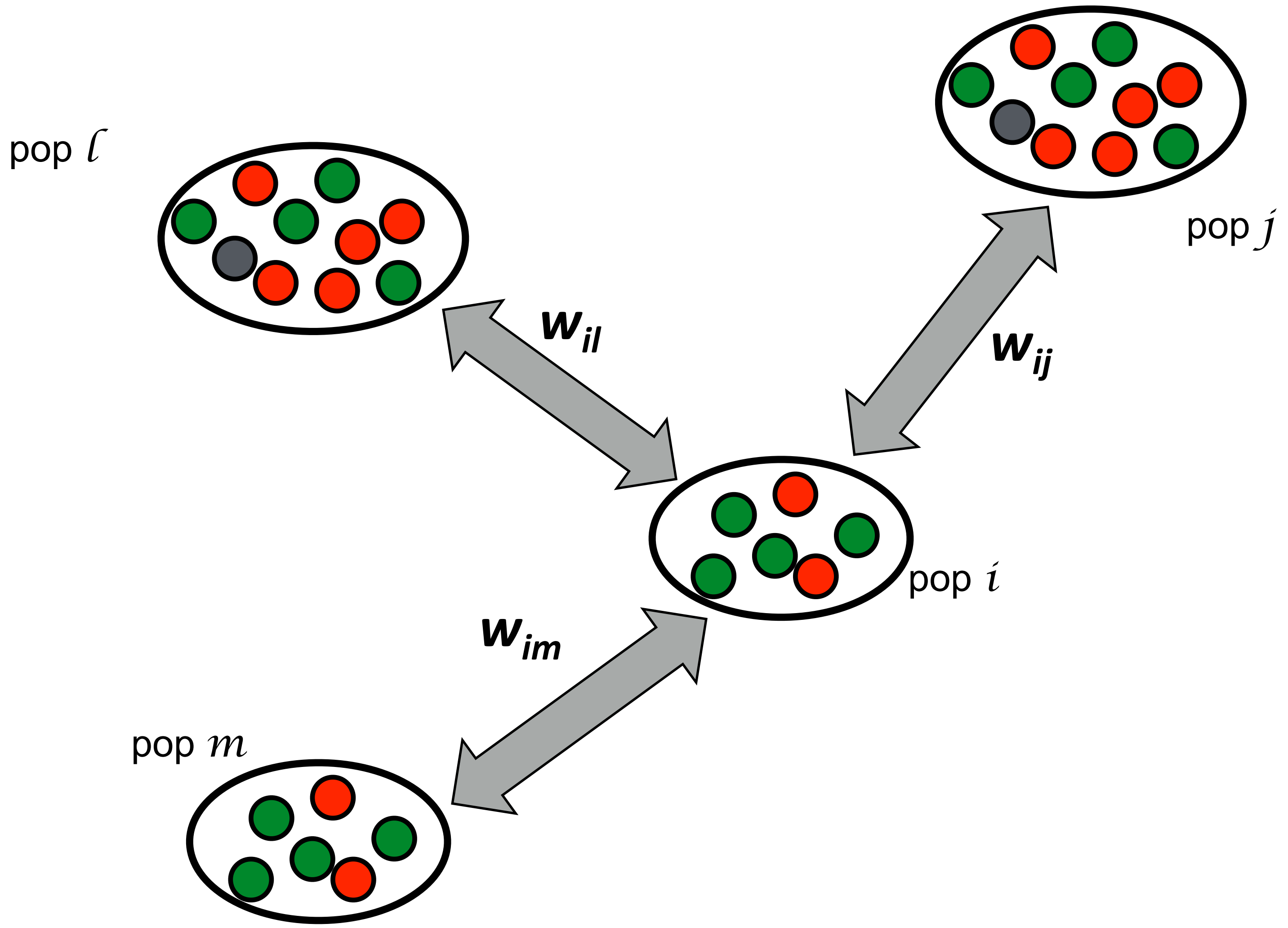
$$\frac{dI_i}{dt} = \beta \frac{I_i(t)S_i(t)}{N_i} - \mu I_i(t) + \Omega_i^I$$

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



Ω_i^X Measure of *in-flow* and *out-flow* of people in compartment *X*

coupling



N_i live in *i*

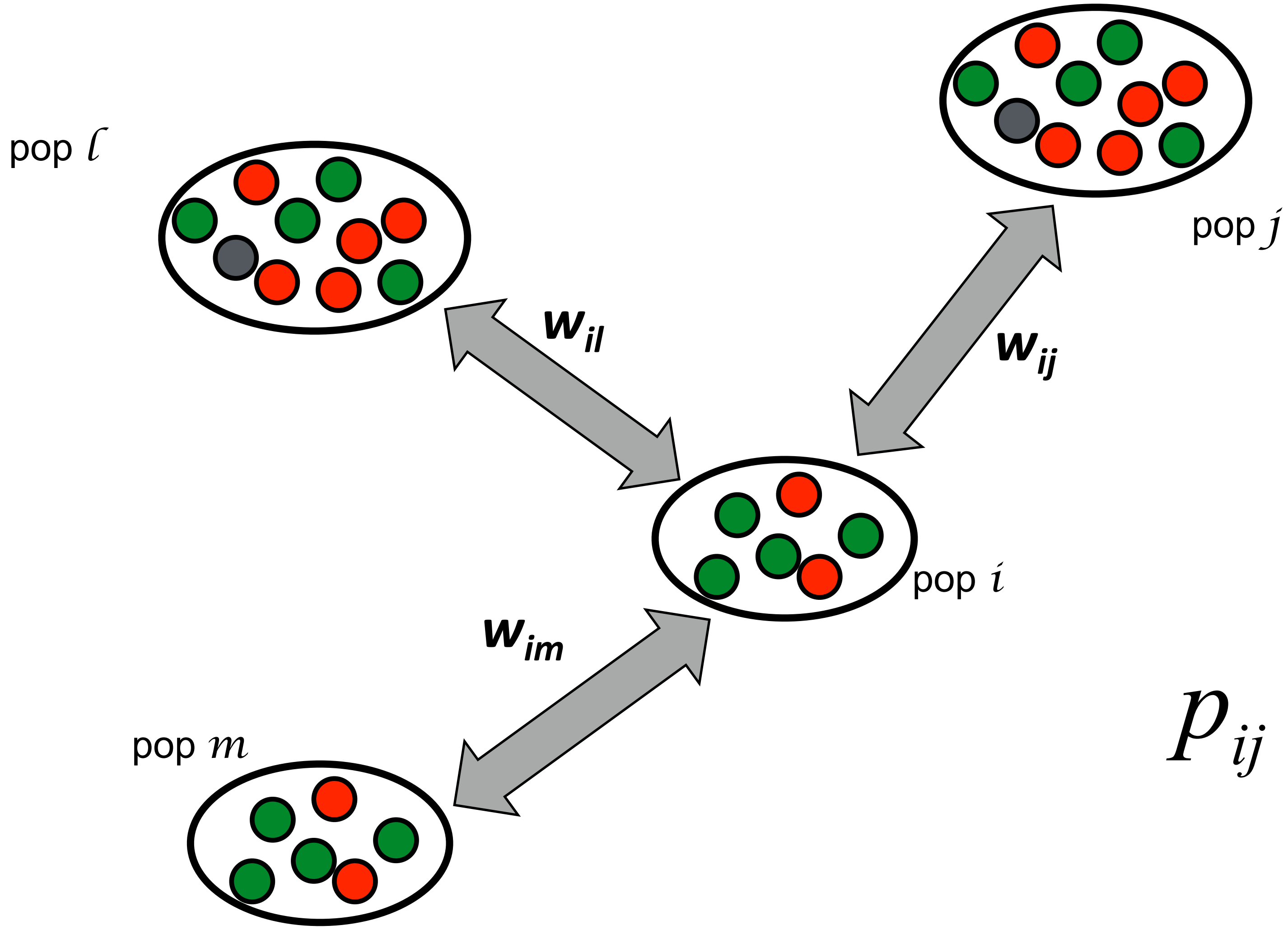
w_{ij} travel from *i* to *j*

probability for an individual in *i*
to travel from *i* to *j* ?

$$p_{ij} = \frac{w_{ij}}{N_i}$$

for all compartments

coupling



N_i live in *i*

w_{ij} travel from *i* to *j*

$$p_{ij} = \frac{w_{ij}}{N_i}$$ probability travel from *i* to *j*

average number of individuals in compartment *X* in *i* traveling from *i* to *j* ?

$$\left\langle T_{ij}^{X} \right\rangle = p_{ij} X_i(t) = \frac{w_{ij}}{N_i} X_i(t)$$

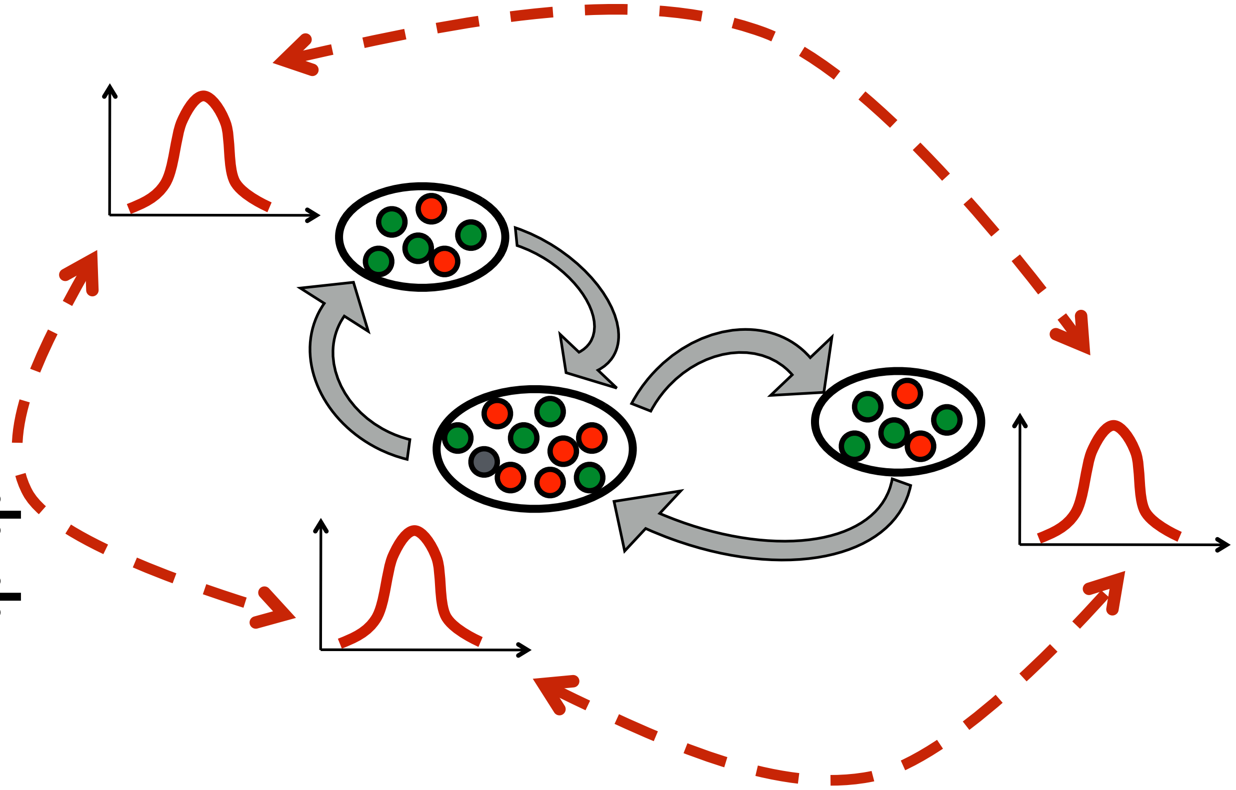
SIR metapopulation models

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

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

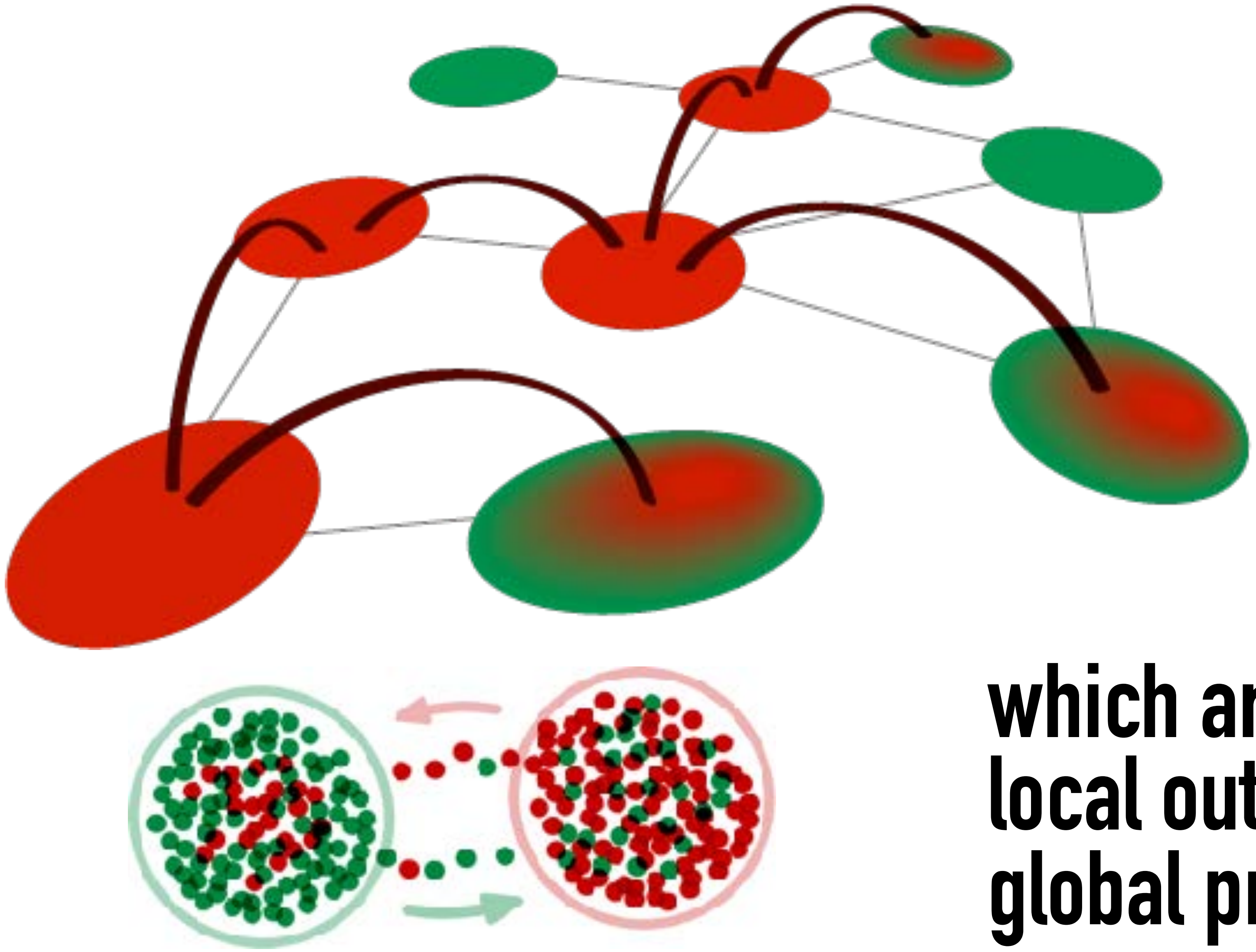
$$\frac{dR_i}{dt} = \mu I_i(t) + \Omega_i^R$$

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



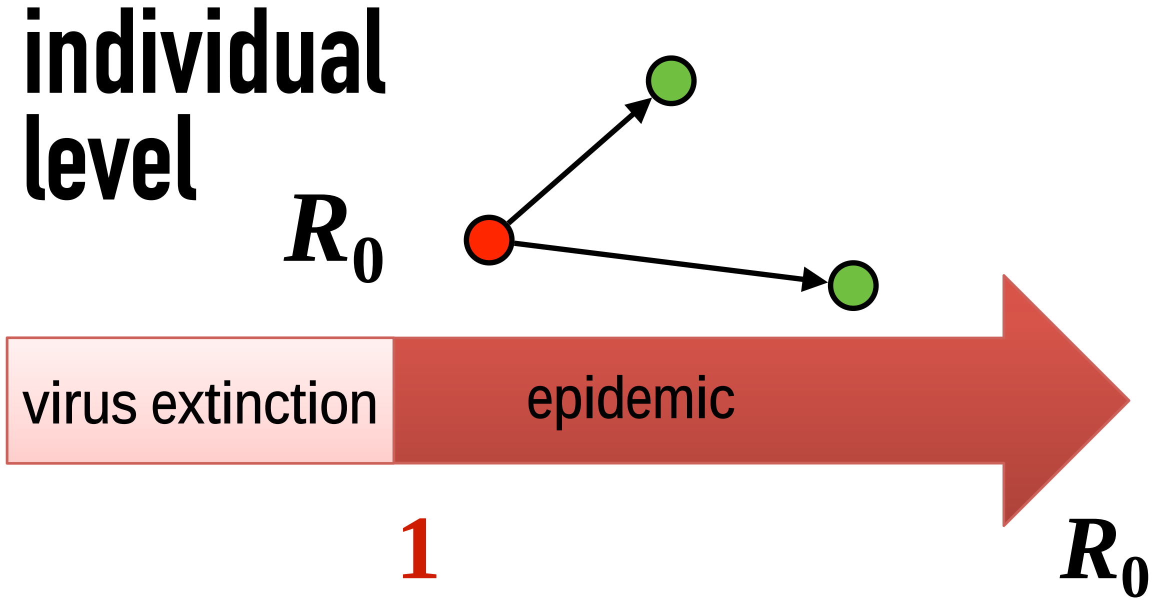
- *global invasion threshold*
- *spatial propagation & predictability*

global invasion threshold



which are the condition for a local outbreak to spread at global proportion?

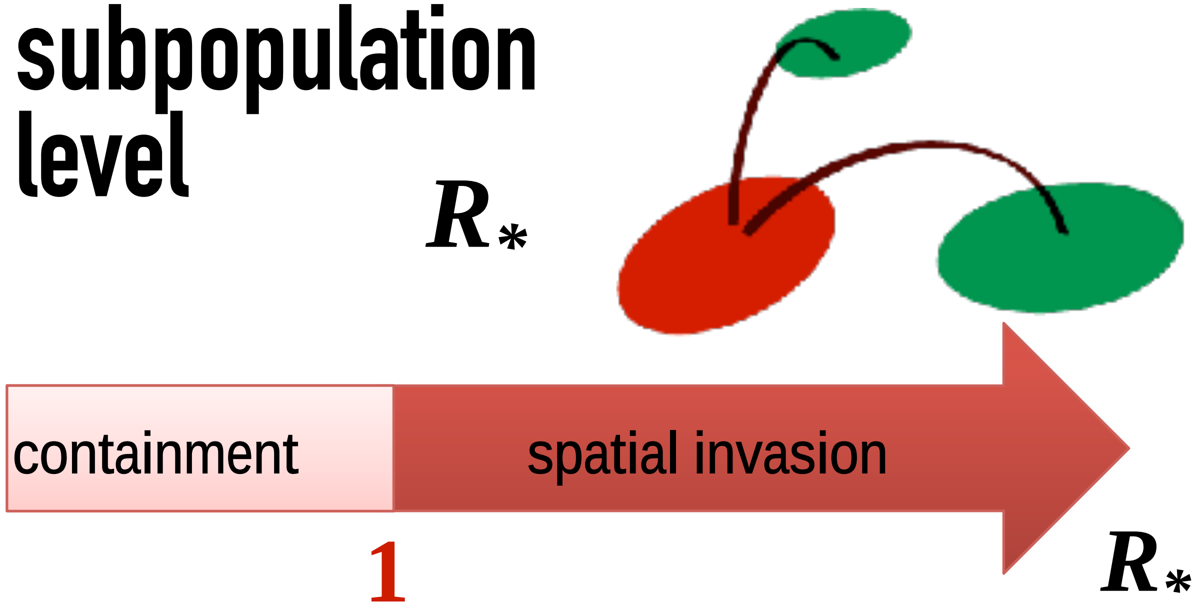
global invasion threshold



coarse graining

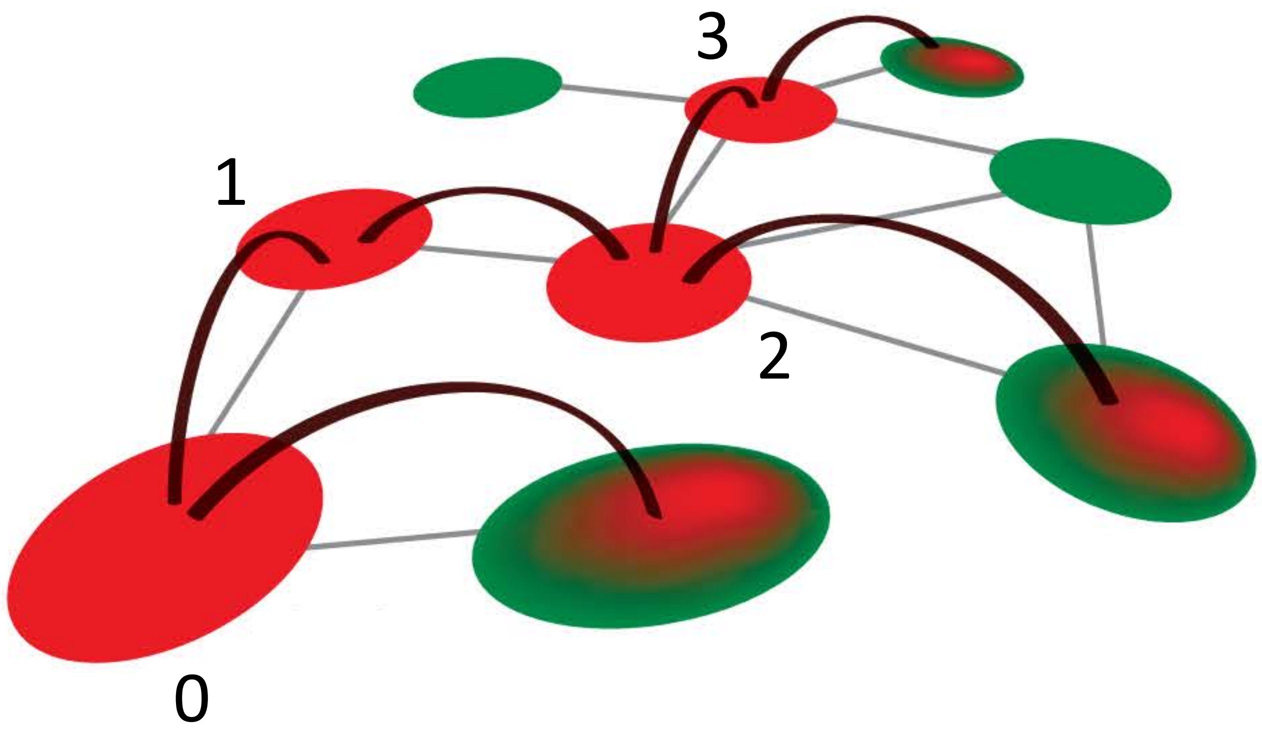
following the spread from one subpopulation to another

mapping the spreading dynamics among subpopulation into the spreading on a network



[Colizza & Vespignani, PRL 2007, JTB 2008;
Cross, et al. JRSoc Interface 2007]

global invasion threshold

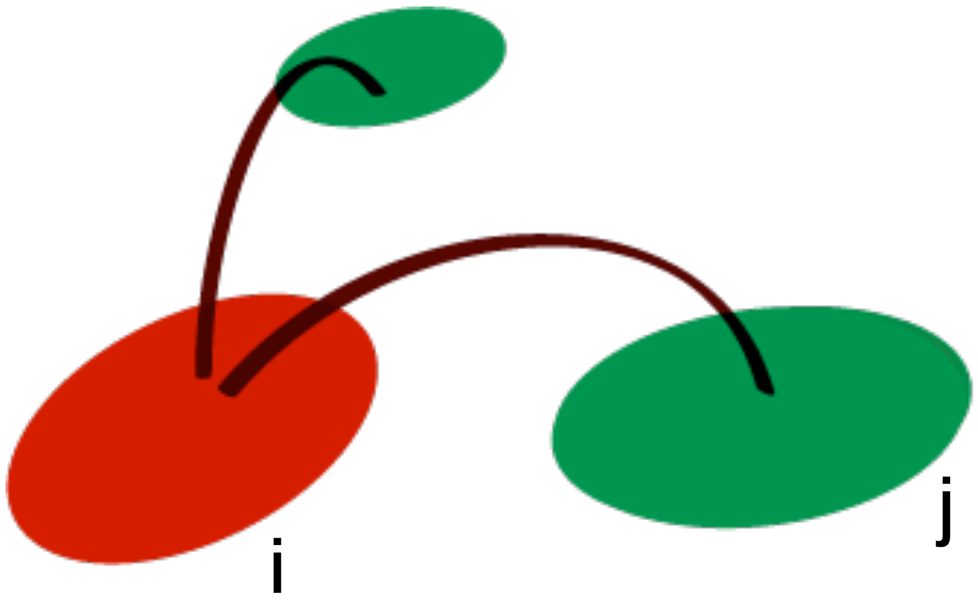


- Invasion dynamics at the subpopulation level
- branching process approximation

D^n: diseased subpopulations at generation n

[Colizza & Vespignani, PRL 2007, JTB 2008]

invasion threshold: homogeneous system



p traveling probability along each link

$\langle k \rangle$ # connection of each subpopulation

total # infectious individuals sent from i to j during the local outbreak $\lambda_{ij} = \frac{pR_\infty}{\mu}$

probability of early extinction $P_{\text{ext}} = \left(\frac{1}{R_0}\right)^{\lambda_{ij}}$

$$D^n = (\langle k \rangle - 1)\,(1 - P_{\text{ext}}) \left(1 - \sum_{m=0}^{n-1} \frac{D^n}{V}\right) D^{n-1}$$

[Colizza & Vespignani, PRL 2007, JTB 2008]

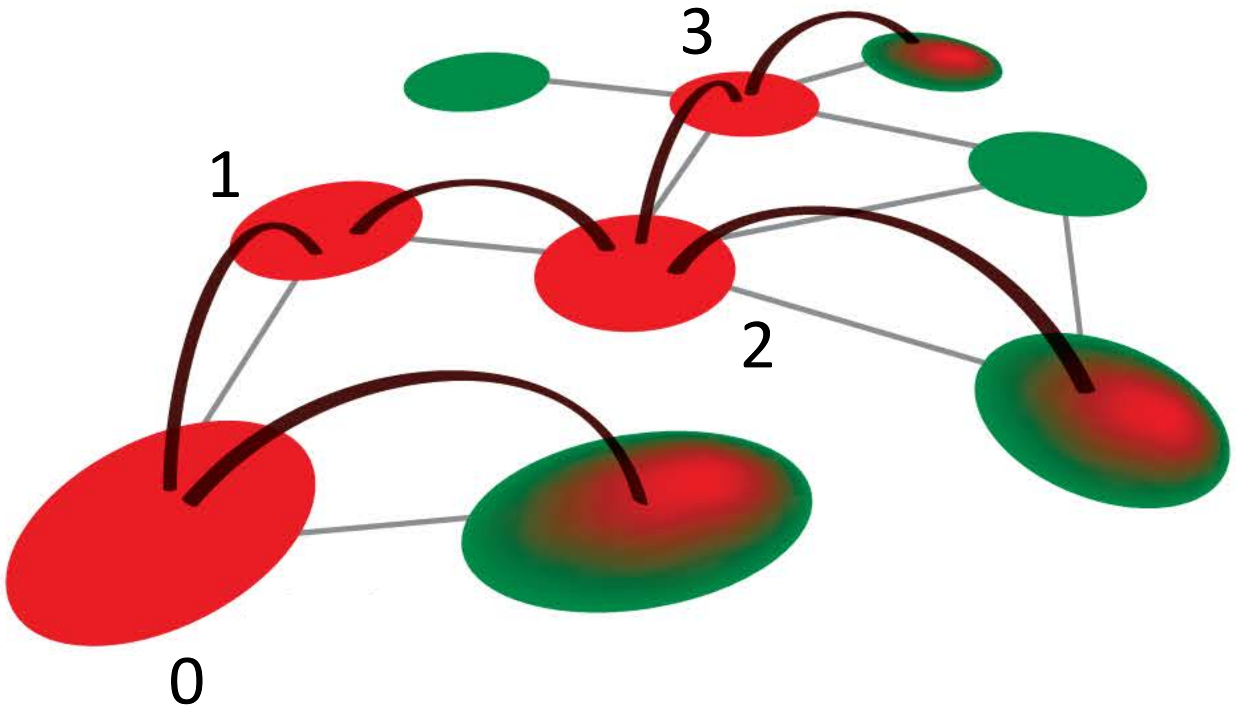
invasion threshold: homogeneous system

$$D^n = (\langle k \rangle - 1)\,(1 - P_{\mathrm{ext}})\left(1 - \xcancel{\sum_{m=0}^{n-1} \frac{D^n}{V}}\right) D^{n-1}$$

$$R_* = (\langle k \rangle - 1)\,(1 - P_{\mathrm{ext}})$$

[Colizza & Vespignani, PRL 2007, JTB 2008]

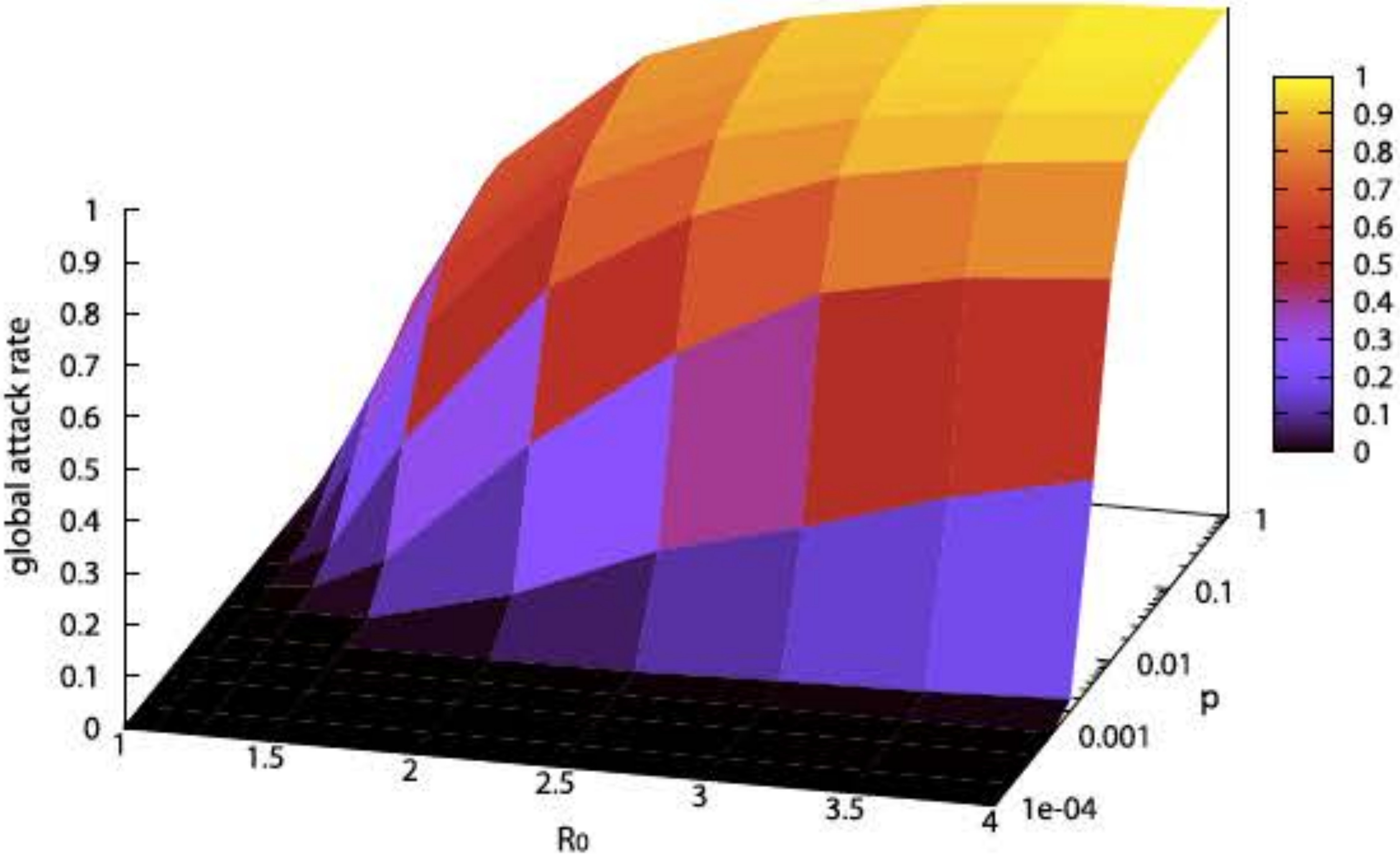
invasion threshold: heterogeneous system



$$D_k^n = \sum_{k'} D_{k'}^{n-1} \boxed{(k'-1)P(k\,|\,k')} \boxed{\left(1-\sum_{m=0}^{n-1}\frac{D_k^m}{V_k}\right)} \boxed{(1-\mathrm{P}_{\mathrm{ext}}(\lambda_{k'k}))}$$

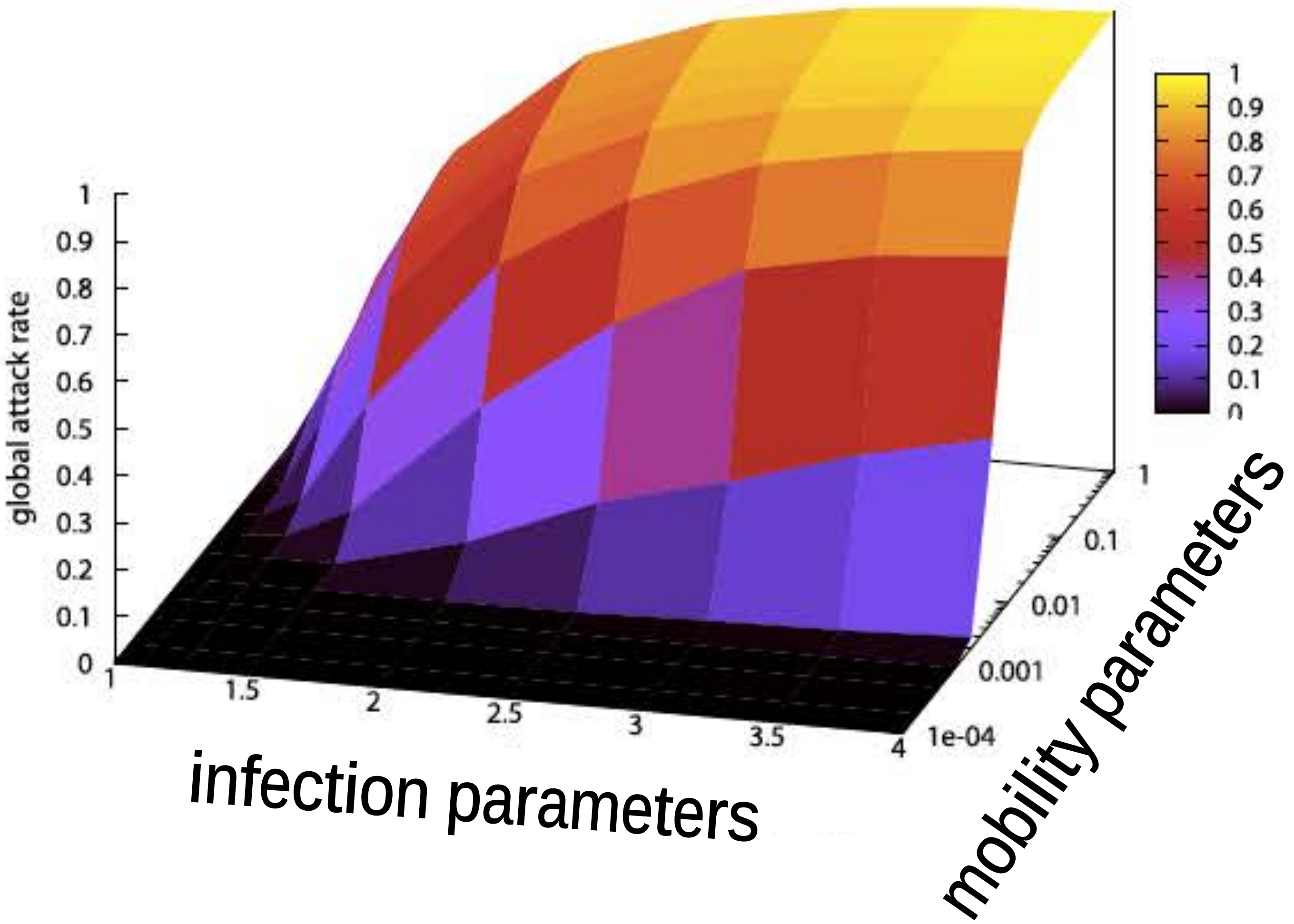
[Colizza & Vespignani, PRL 2007, JTB 2008]

invasion threshold: heterogeneous system



[Colizza & Vespignani, PRL 2007, JTB 2008]

invasion threshold: increasingly realistic models



commuting and recurrent mobility patterns: beyond the markovian assumption
[Balcan & Vespignani Nat Phys 2011, Belik et al PRX 2011]

heterogeneous travel duration
[Poletto et al Sci Rep 2012]

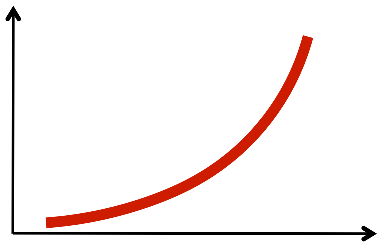
heterogeneity in travel frequency: children are more social but travel less
[Apolloni et al BMC Inf Dis 2013]

behavioural response to the presence of a disease
[Meloni et al Sci Rep 2011]

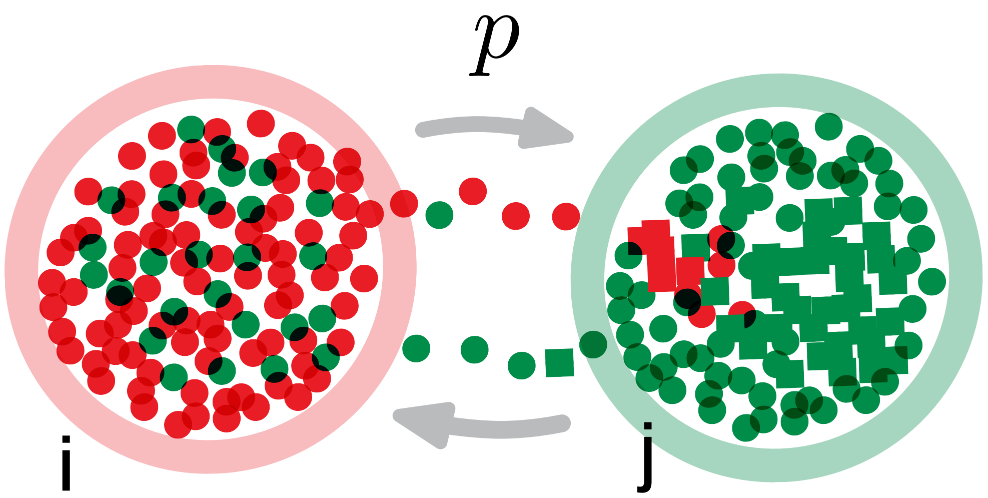
* *global invasion threshold*

* *spatial propagation & predictability*

spatial propagation



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



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

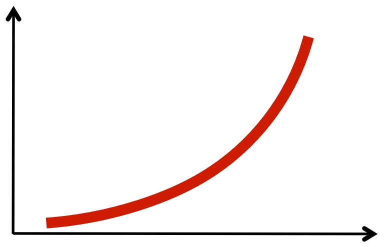
probability that the **first** infectious arrives in *j* at time *t*:

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

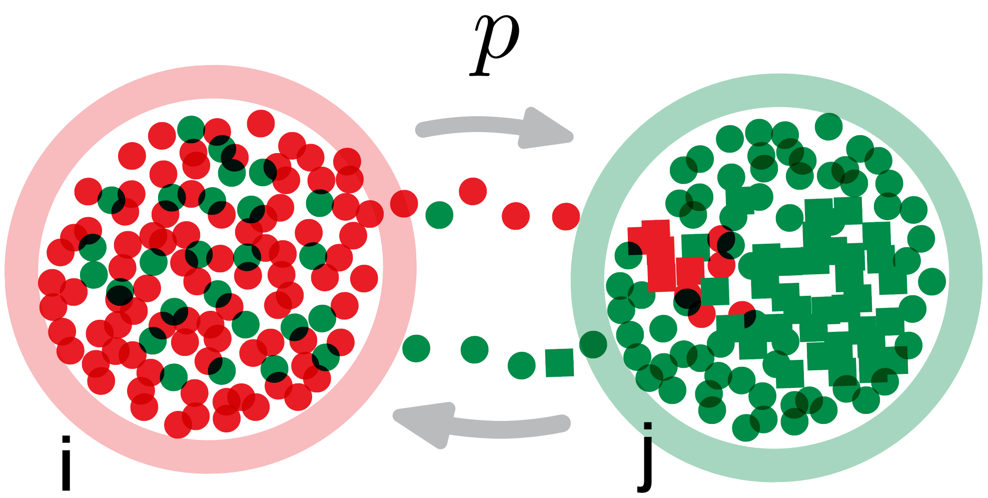
$$\Big\downarrow \; p \to 0$$

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

spatial propagation



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



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

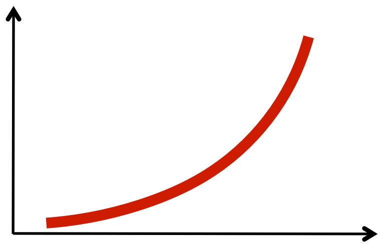
$$a = \mu(R_0 - 1)$$

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

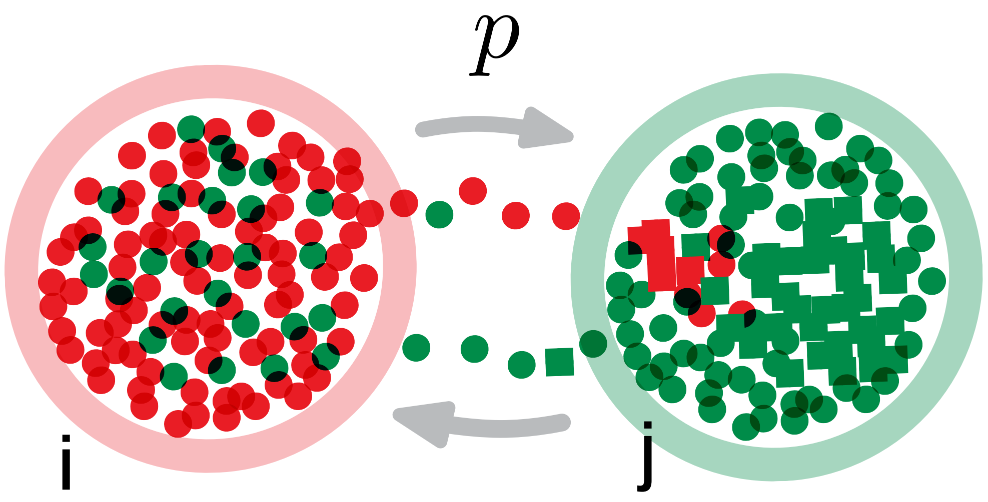
Gumbel distribution

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

spatial propagation: travel restrictions



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

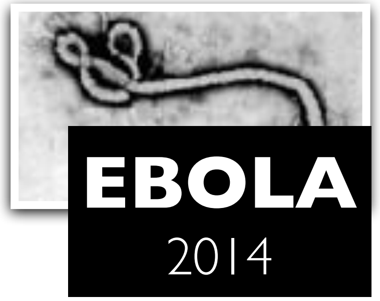


I reduce the traffic with the epidemic origin: is it effecting in containing or delaying the propagation?

p rescaled of a factor α

$$\boxed{\Delta \langle t_{\text{seeding}} \rangle = -\frac{1}{a} \ln(\alpha)}$$

[Gautreau et al JTB 2008; Bajardi et al PLoS ONE 2011; Hollingsworth et al Nature Med 2006; Scalia Tomba et al Math Biosci 2008]



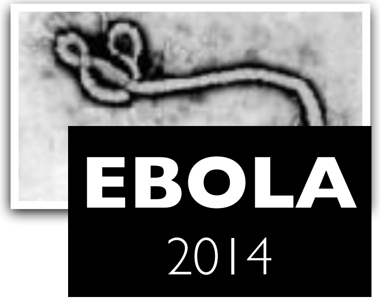
how did restriction in mobility affect spreading?

FLIGHT SUPPRESSION

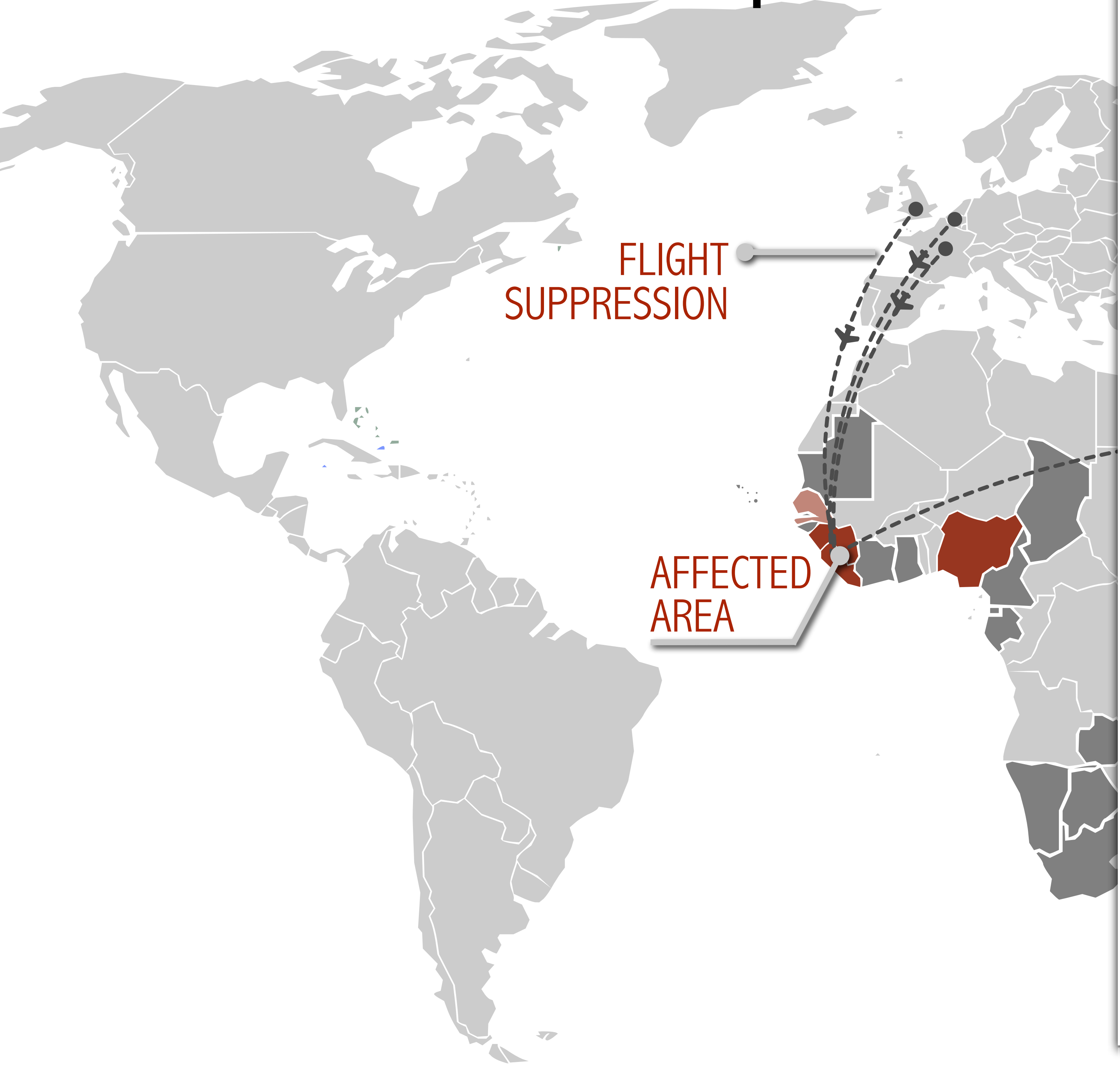
AFFECTED AREA

TRAVEL BAN & BORDER CLOSURE

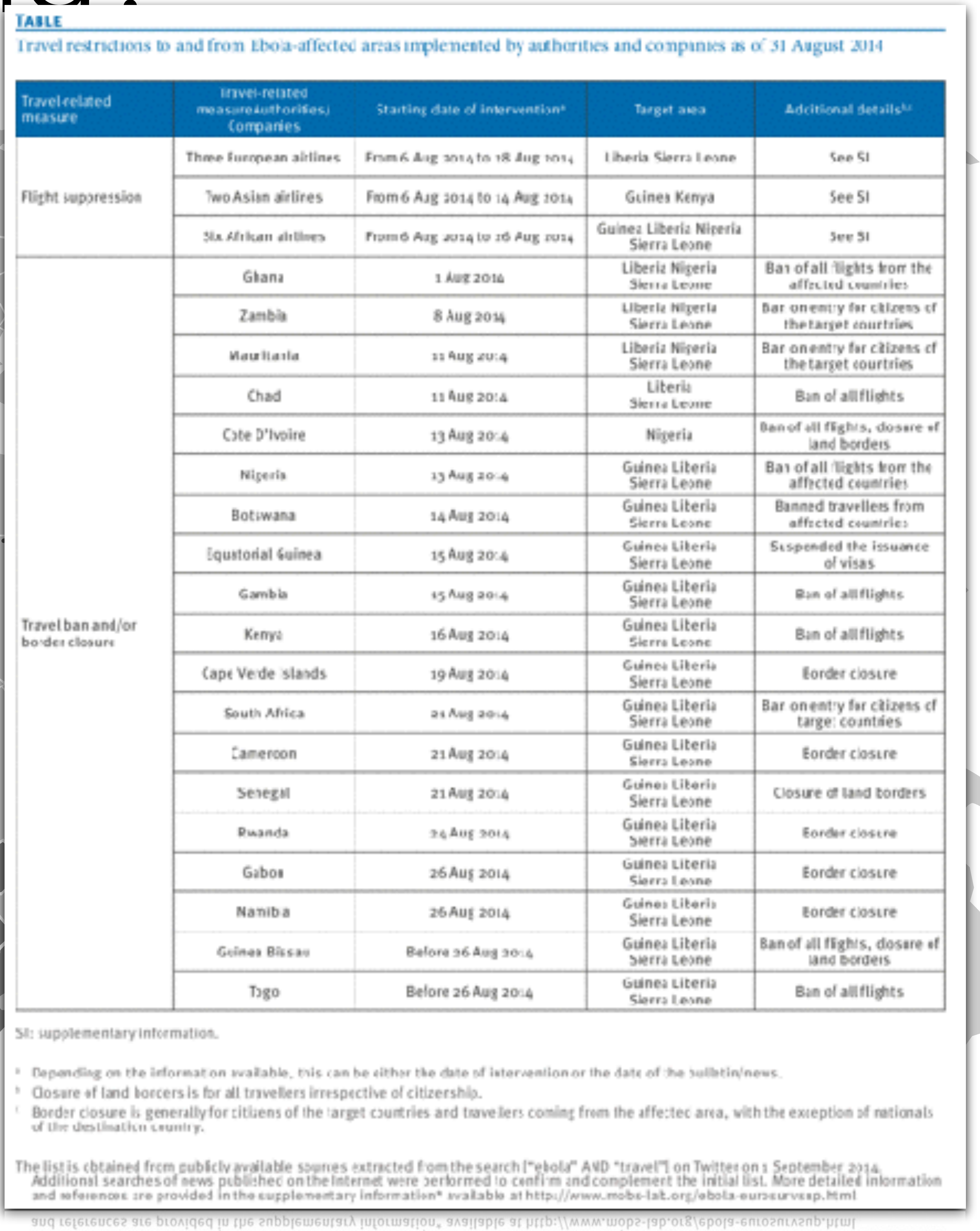
[Poletto, Eurosurveillance 2014]



how did restriction in mobility affect spreading?


FLIGHT SUPPRESSION

AFFECTED AREA



TABLE

Travel restrictions to and from Ebola-affected areas implemented by authorities and companies as of 31 August 2014

Travel-related measure	Travel-related measure/authorities/ Companies	Starting date of intervention[a]	Target area	Additional details[b,c]
Flight suppression	Three European airlines	From 6 Aug 2014 to 18 Aug 2014	Liberia Sierra Leone	See SI
	Two Asian airlines	From 6 Aug 2014 to 14 Aug 2014	Guinea Kenya	See SI
	Six African airlines	From 6 Aug 2014 to 26 Aug 2014	Guinea Liberia Nigeria Sierra Leone	See SI
Travel ban and/or border closure	Ghana	1 Aug 2014	Liberia Nigeria Sierra Leone	Ban of all flights from the affected countries
	Zambia	8 Aug 2014	Liberia Nigeria Sierra Leone	Bar on entry for citizens of the target countries
	Mauritania	11 Aug 2014	Liberia Nigeria Sierra Leone	Bar on entry for citizens of the target countries
	Chad	11 Aug 2014	Liberia Sierra Leone	Ban of all flights
	Cote D'Ivoire	13 Aug 2014	Nigeria	Ban of all flights, closure of land borders
	Nigeria	13 Aug 2014	Guinea Liberia Sierra Leone	Ban of all flights from the affected countries
	Botswana	14 Aug 2014	Guinea Liberia Sierra Leone	Banned travellers from affected countries
	Equatorial Guinea	15 Aug 2014	Guinea Liberia Sierra Leone	Suspended the issuance of visas
	Gambia	15 Aug 2014	Guinea Liberia Sierra Leone	Ban of all flights
	Kenya	16 Aug 2014	Guinea Liberia Sierra Leone	Ban of all flights
	Cape Verde Islands	19 Aug 2014	Guinea Liberia Sierra Leone	Border closure
	South Africa	21 Aug 2014	Guinea Liberia Sierra Leone	Bar on entry for citizens of target countries
	Cameroon	21 Aug 2014	Guinea Liberia Sierra Leone	Border closure
	Senegal	21 Aug 2014	Guinea Liberia Sierra Leone	Closure of land borders
	Rwanda	24 Aug 2014	Guinea Liberia Sierra Leone	Border closure
	Gabon	26 Aug 2014	Guinea Liberia Sierra Leone	Border closure
	Namibia	26 Aug 2014	Guinea Liberia Sierra Leone	Border closure
	Guinea Bissau	Before 26 Aug 2014	Guinea Liberia Sierra Leone	Ban of all flights, closure of land borders
	Togo	Before 26 Aug 2014	Guinea Liberia Sierra Leone	Ban of all flights

SI: supplementary information.

[a] Depending on the information available, this can be either the date of intervention or the date of the bulletin/news.

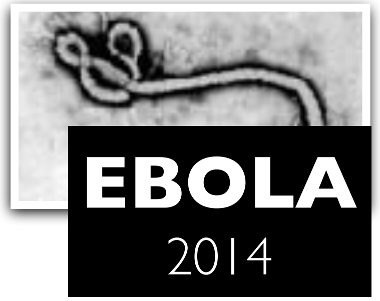
[b] Closure of land borders is for all travellers irrespective of citizenship.

[c] Border closure is generally for citizens of the target countries and travellers coming from the affected area, with the exception of nationals of the destination country.

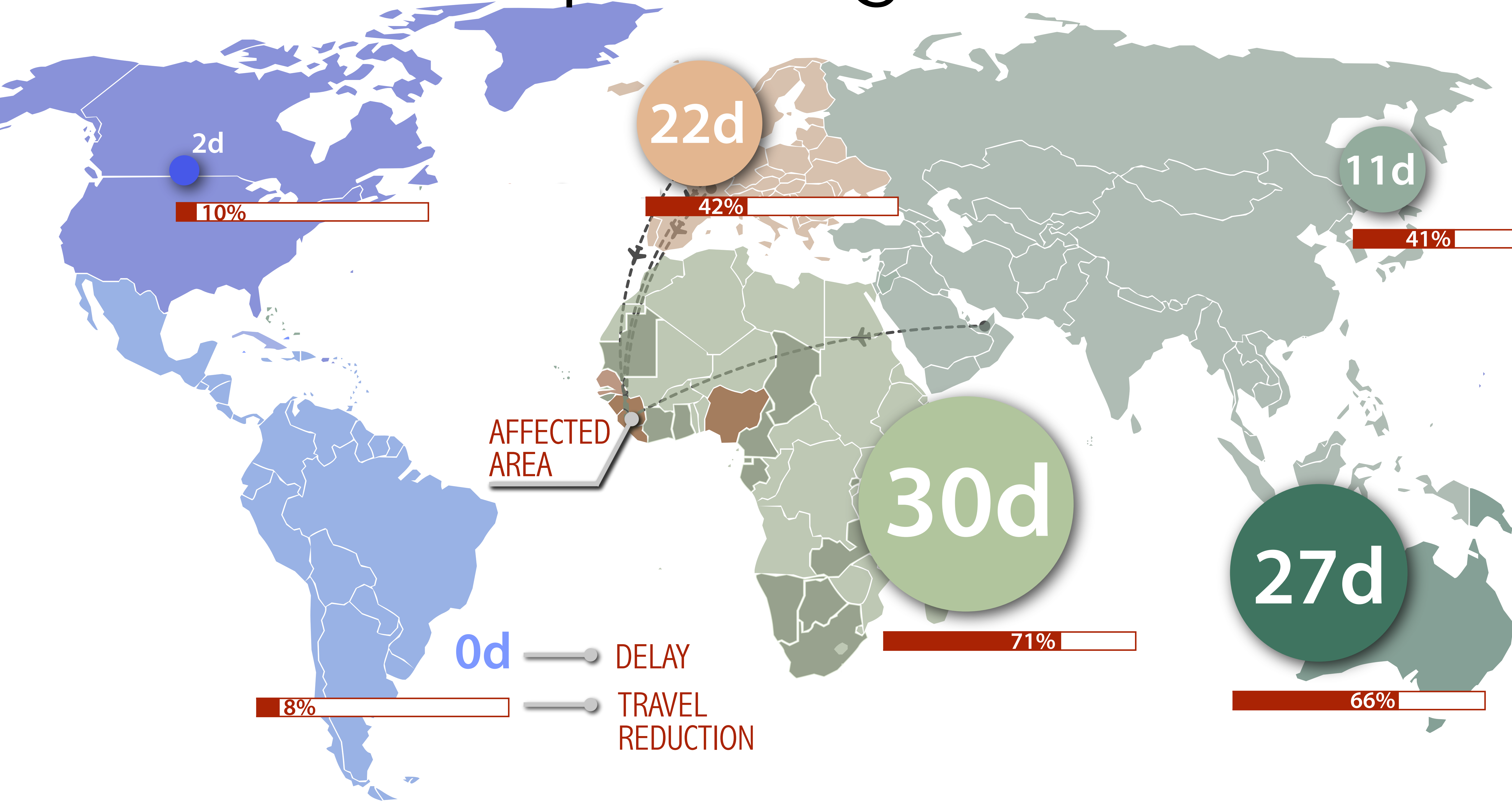
The list is obtained from publicly available sources extracted from the search ["ebola" AND "travel"] on Twitter on 1 September 2014. Additional searches of news published on the Internet were performed to confirm and complement the initial list. More detailed information and references are provided in the supplementary information* available at http://www.mobs-lab.org/ebola-eurosurvesp.html

overall reduction with Western Africa = ~60%

[Poletto et al, Eurosurveillance 2014]

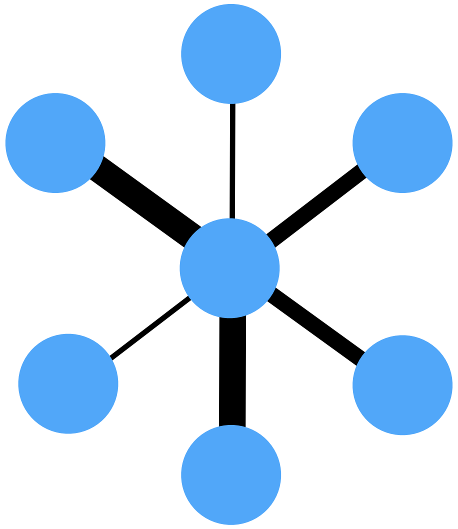


how did restriction in mobility affect spreading?



[Poletto et al, Eurosurveillance 2014]

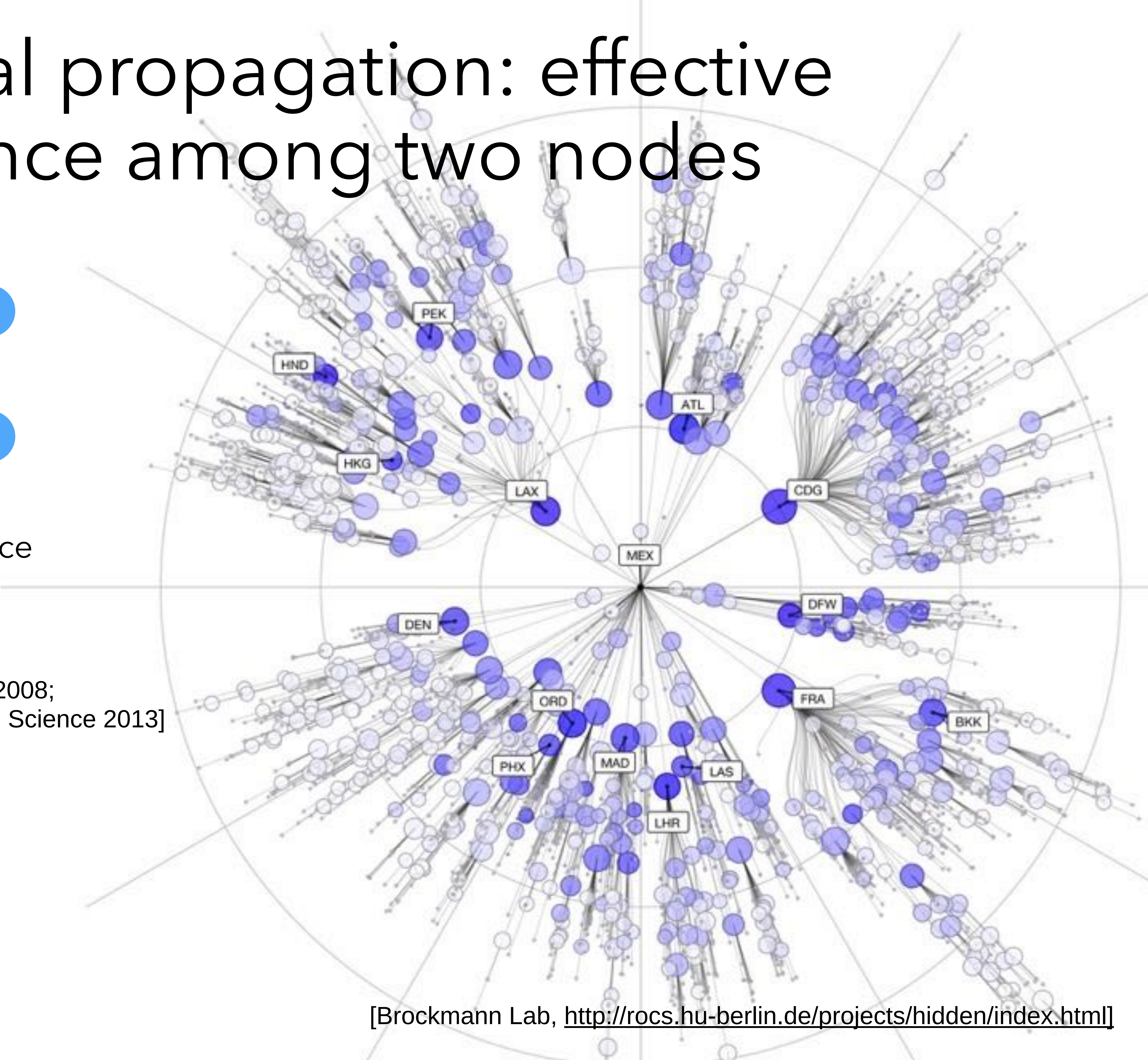
spatial propagation: effective distance among two nodes



effective distance along the link

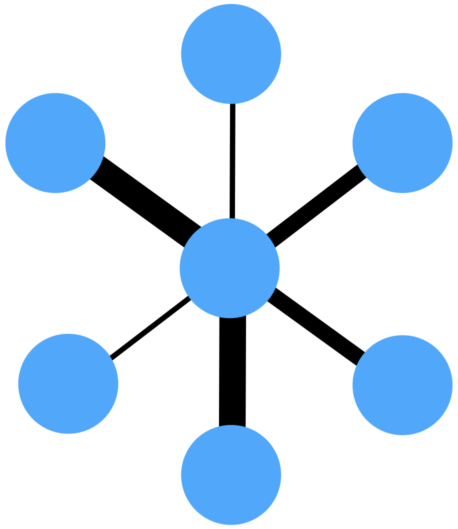
$\ln(p_{ij})$

[Gautreau et al JTB 2008;
Brockmann, Helbing, Science 2013]



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

spatial propagation: effective distance among two nodes



effective distance along the link

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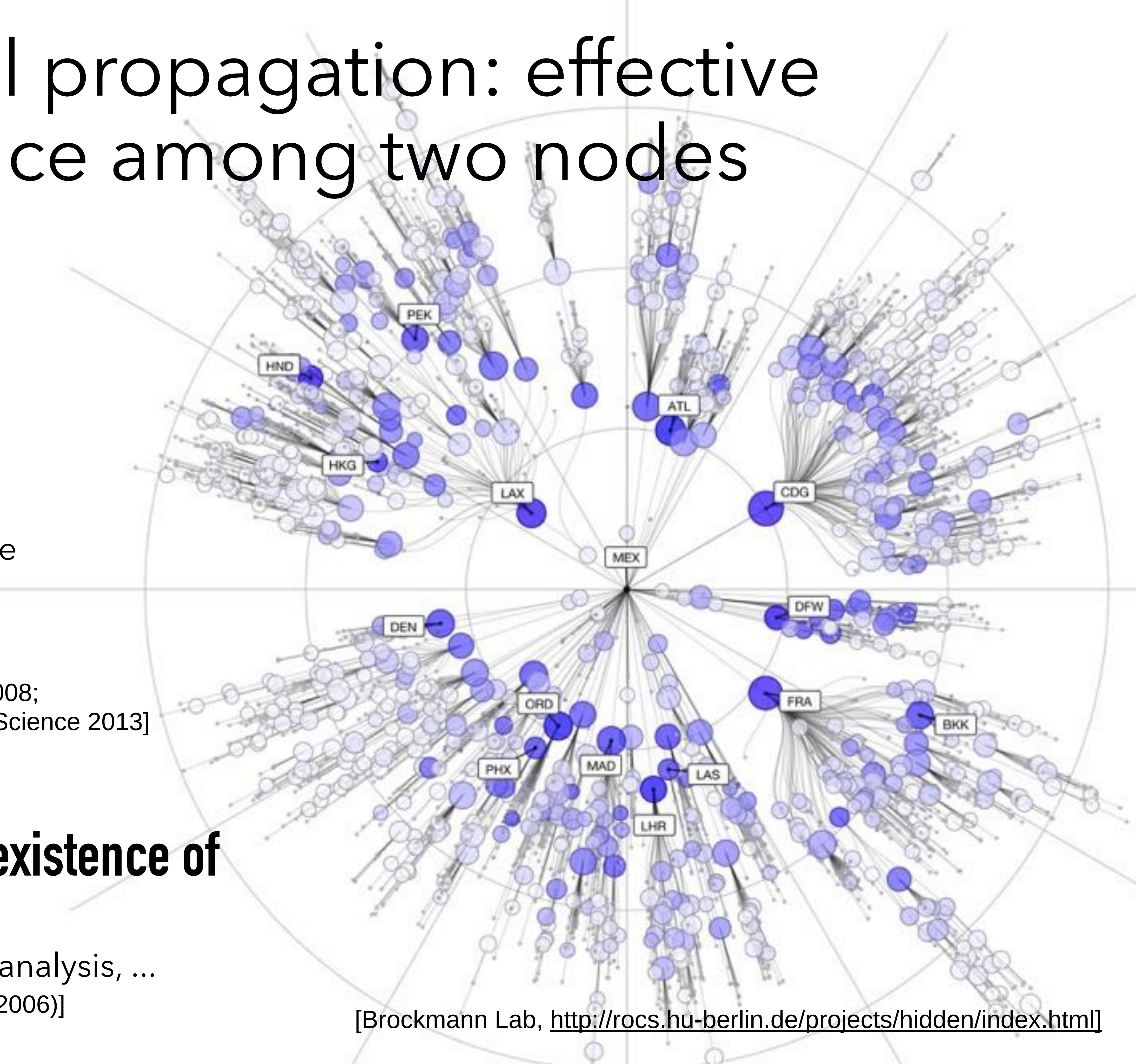


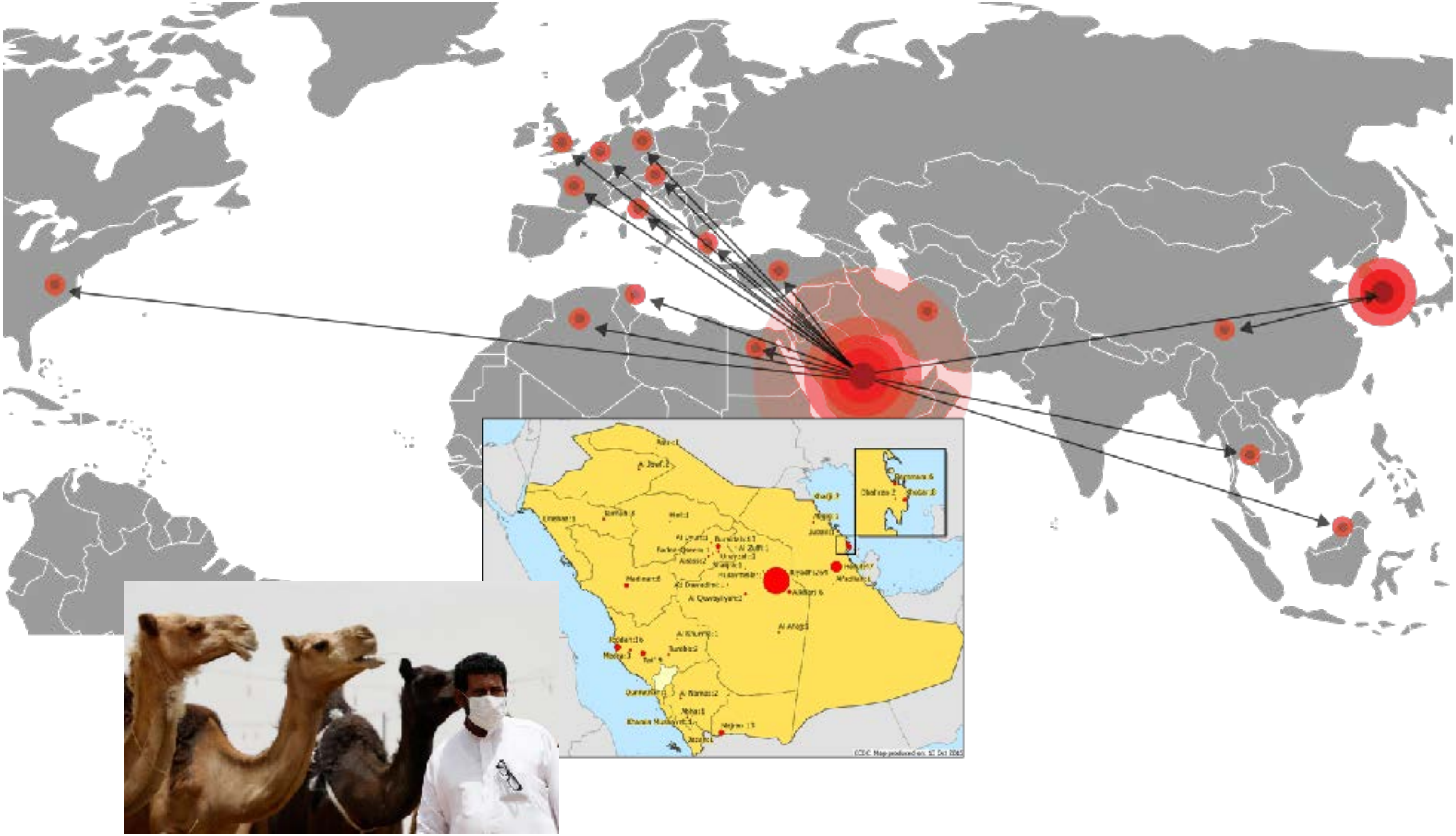
[Brockmann Lab, http://rocs.hu-berlin.de/projects/hidden/index.html]

good news: existence of pathways !

risk assessment analysis, …

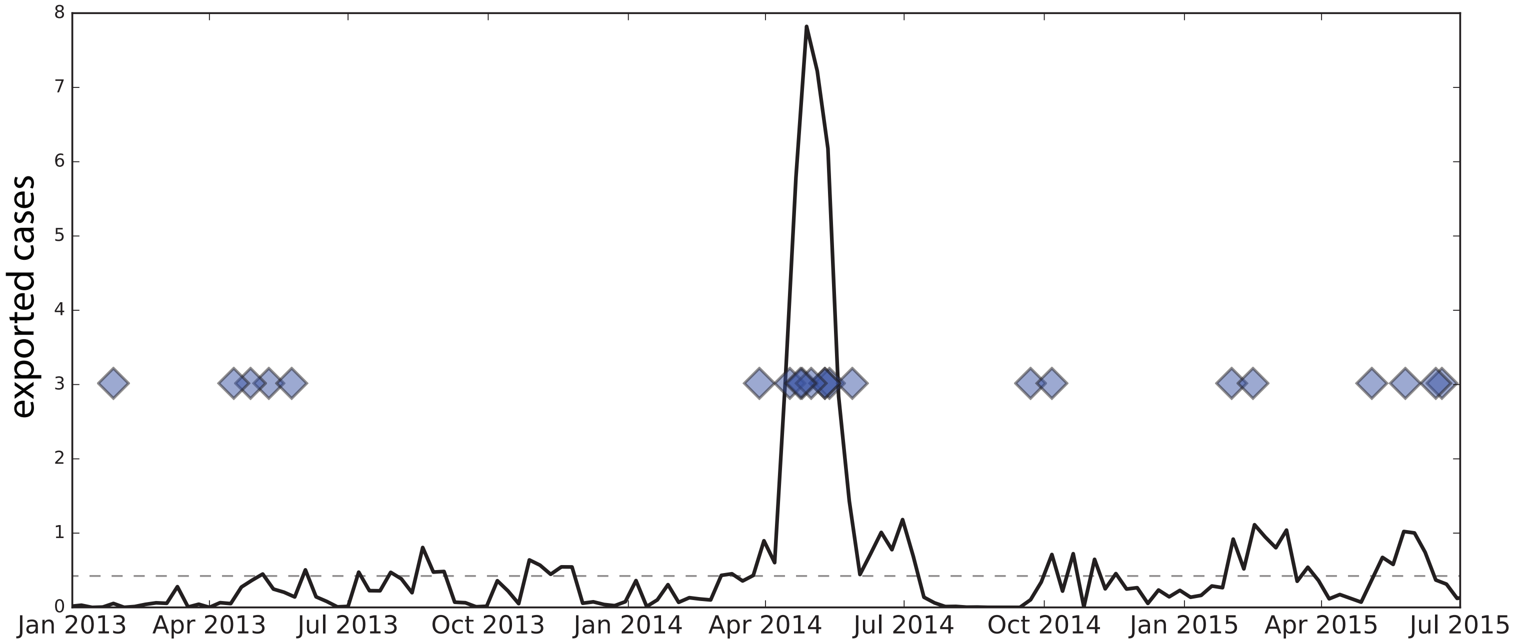
[Colizza, et al PNAS (2006)]

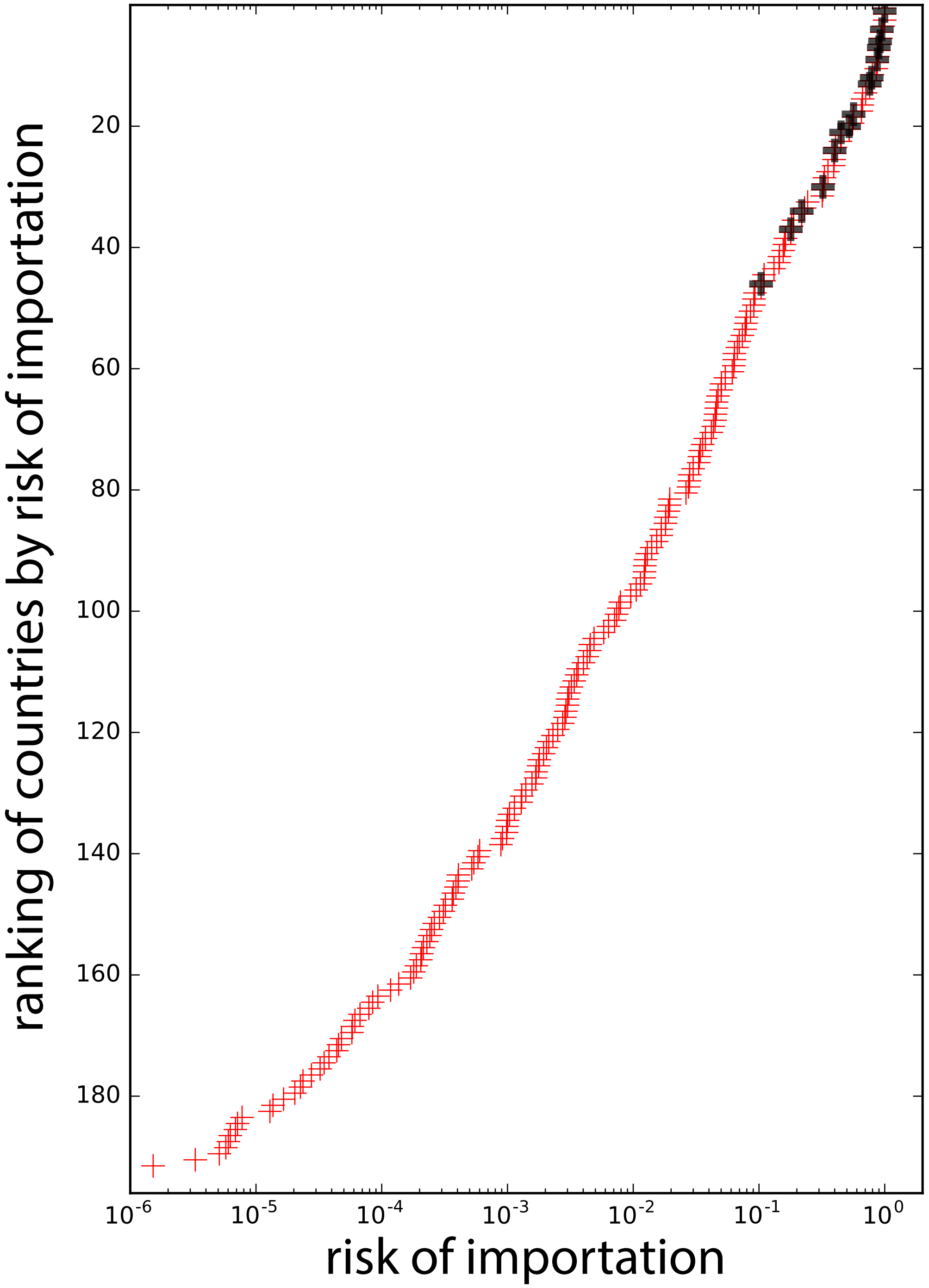
middle east respiratory syndrome 2012-2015



International spread follows simple rules

computed risk of exportation from
incidence in Middle East + monthly air-traffic



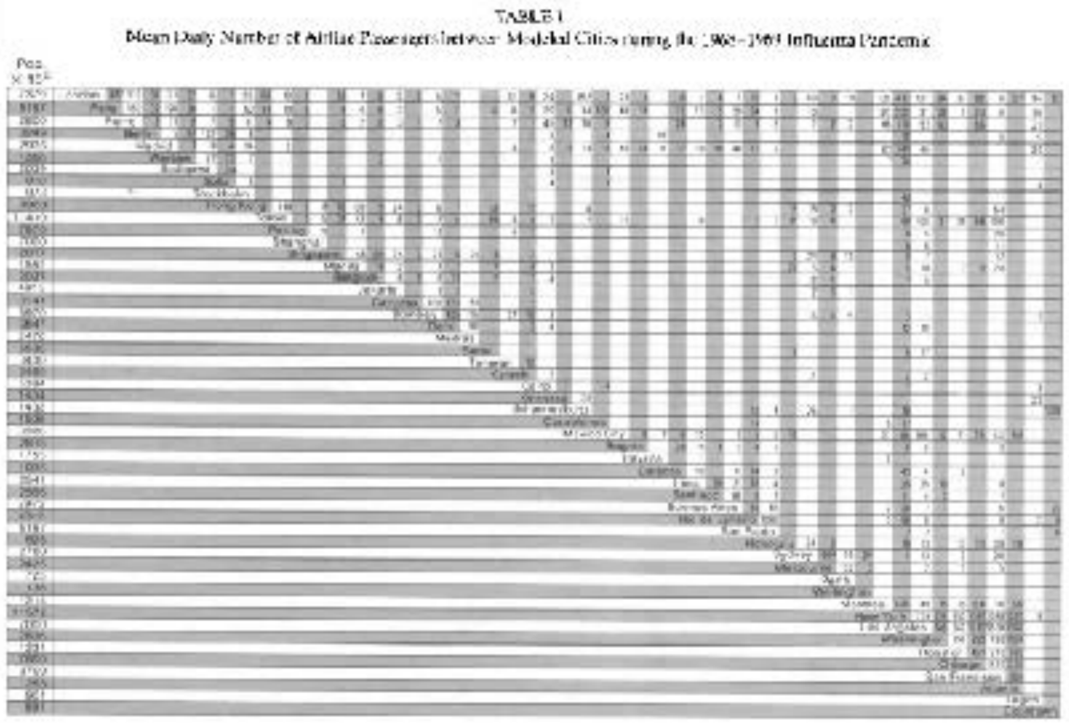


[Poletto et al. BMC Inf Dis 2016]

modelling worldwide spread of epidemics

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

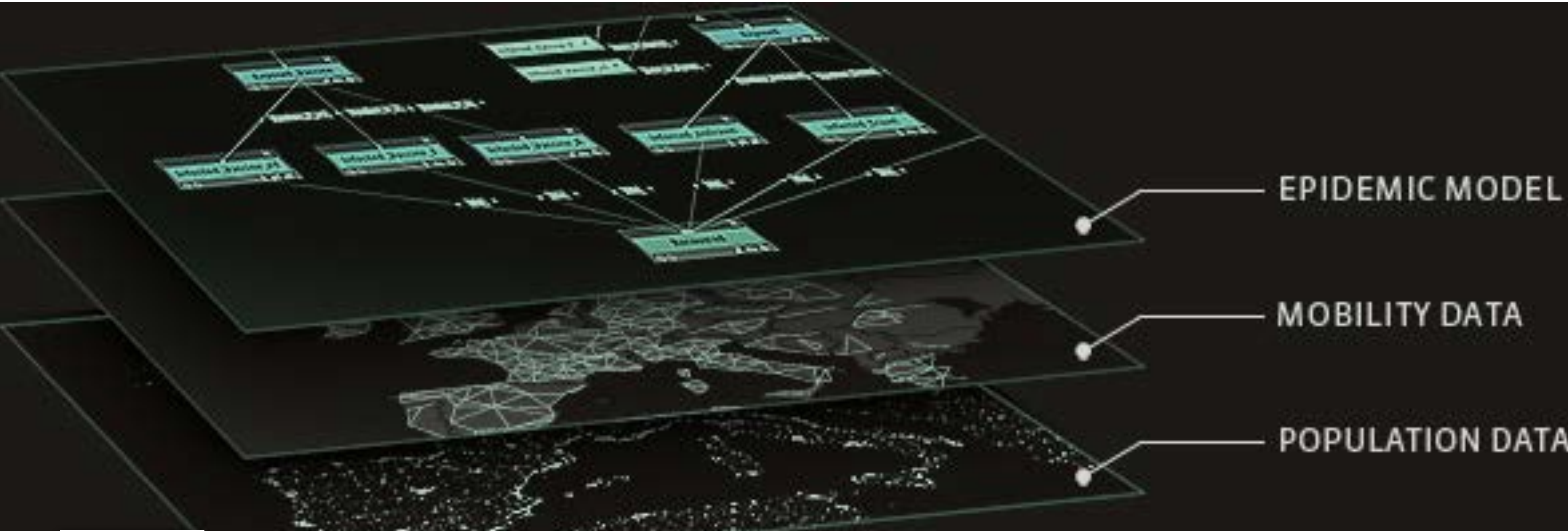
[Rvachev, Longini, Math. Biosci. 1985]

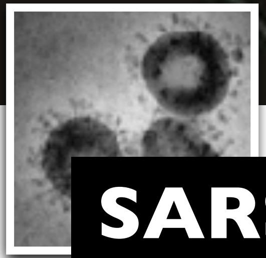


~ 3000 - 4000 cities:
spread of SARS, 2009 H1N1
pandemic, MERS, Ebola,
hypothetical pandemic scenarios

[Hufnagel et al. PNAS 2004; Colizza et al. PLoS Med 2007; Balcan et al. PNAS 2009; Poletto et al. Eurosurveillance 2014; Gomes et al. PLoS Curr 2014]

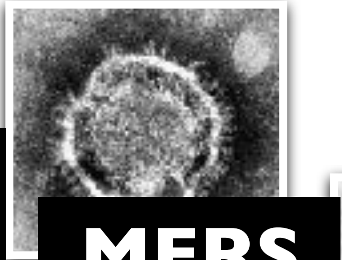
GLEaM: GLobal Epidemic and Mobility model





SARS
2003

HINI
2009

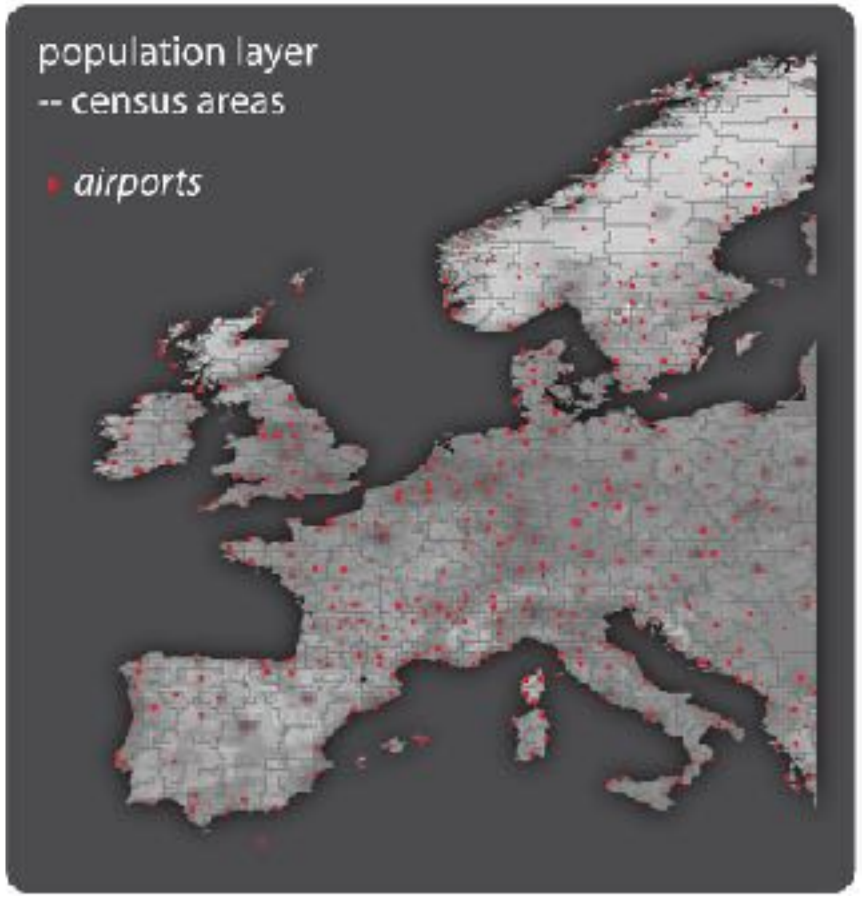


MERS
2012

EBOLA
2014

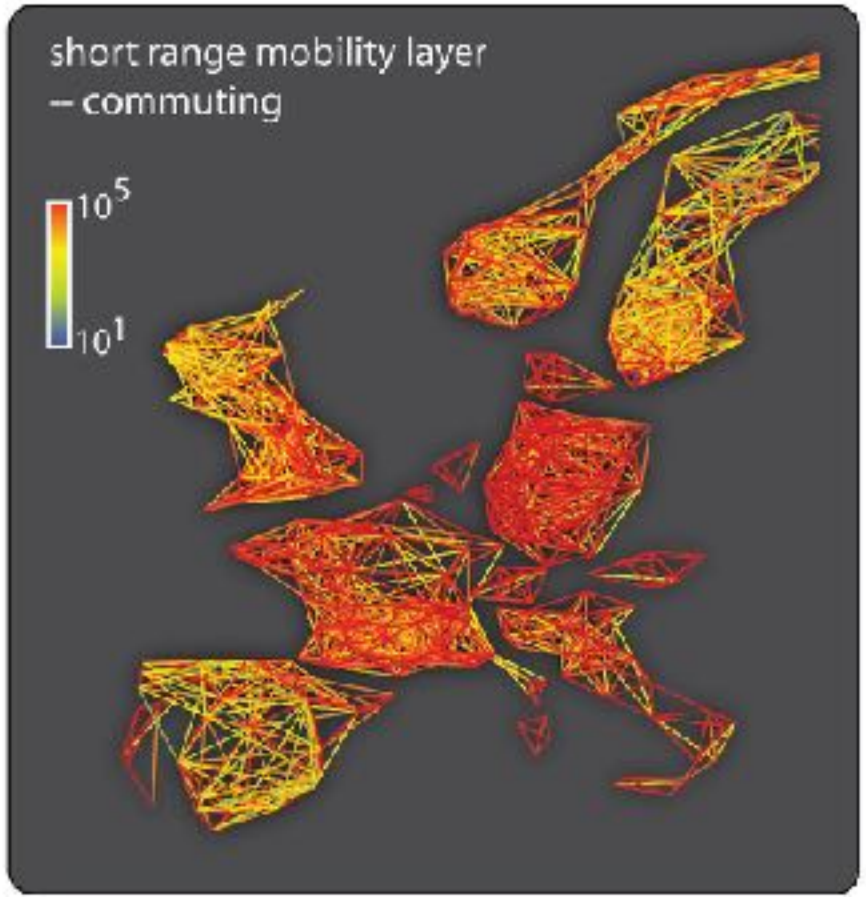
[www.gleamviz.org Balcan et al. PNAS 2009]

GLEaM: demography and mobility



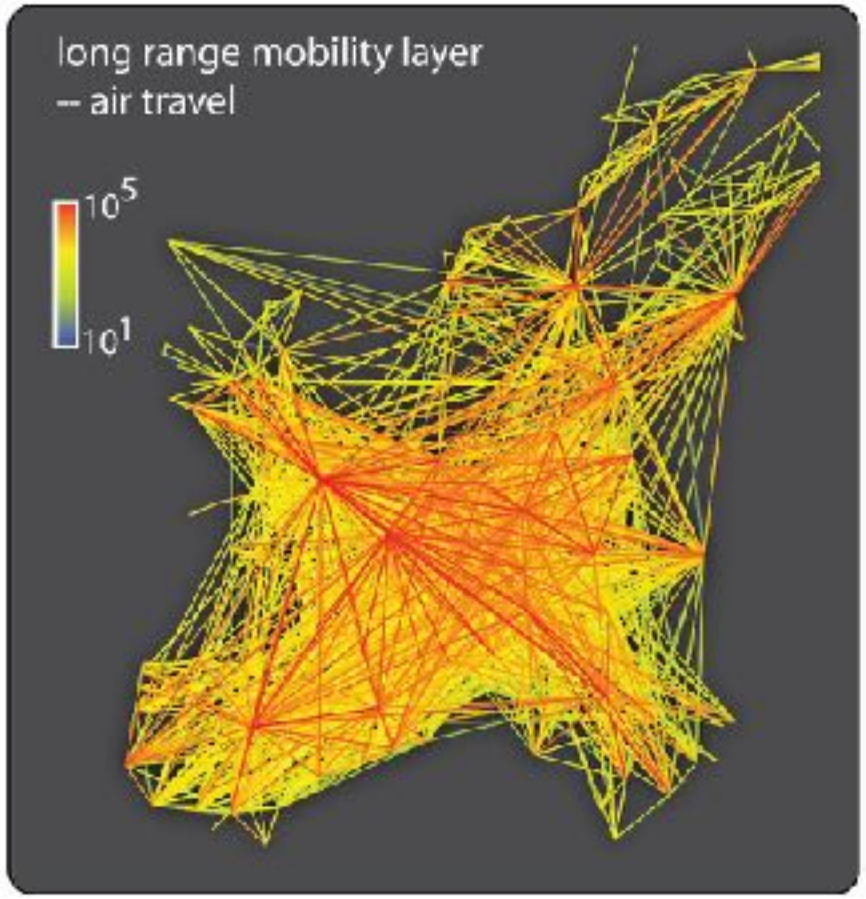
Population Distribution

- 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



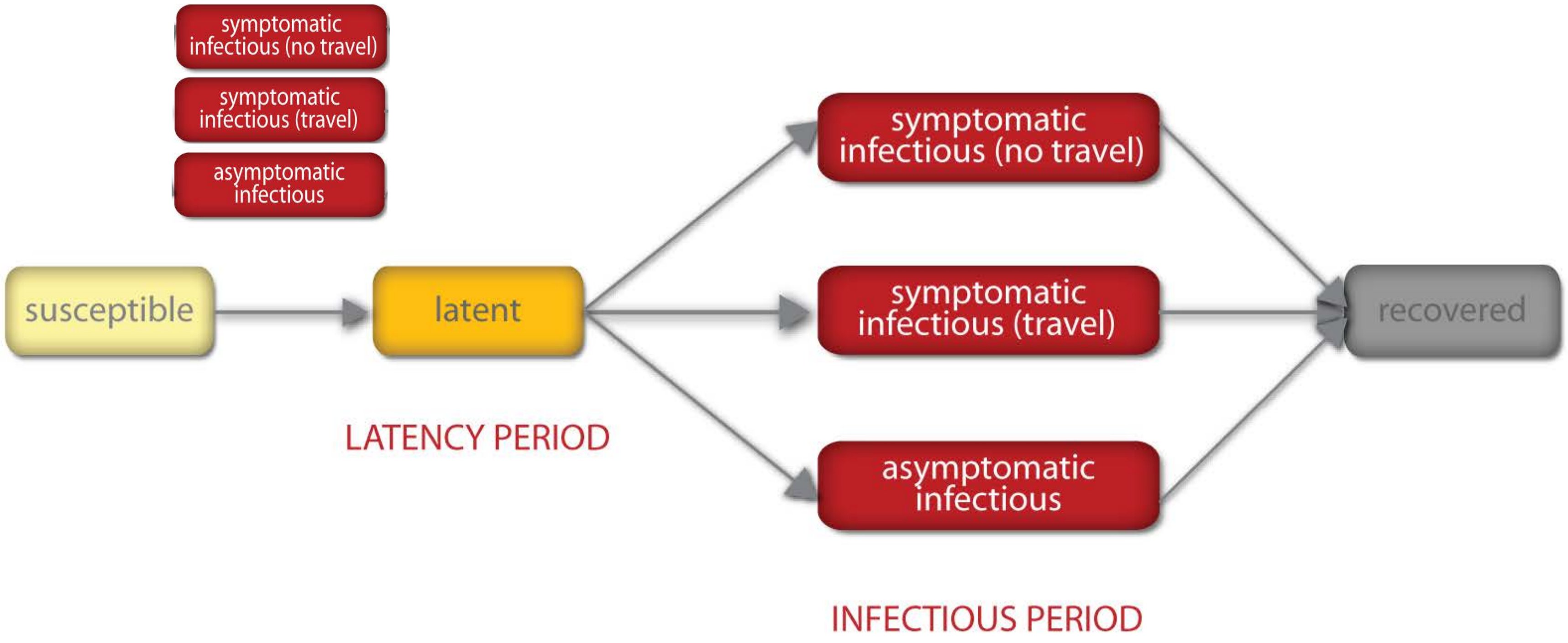
World Airport Network

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

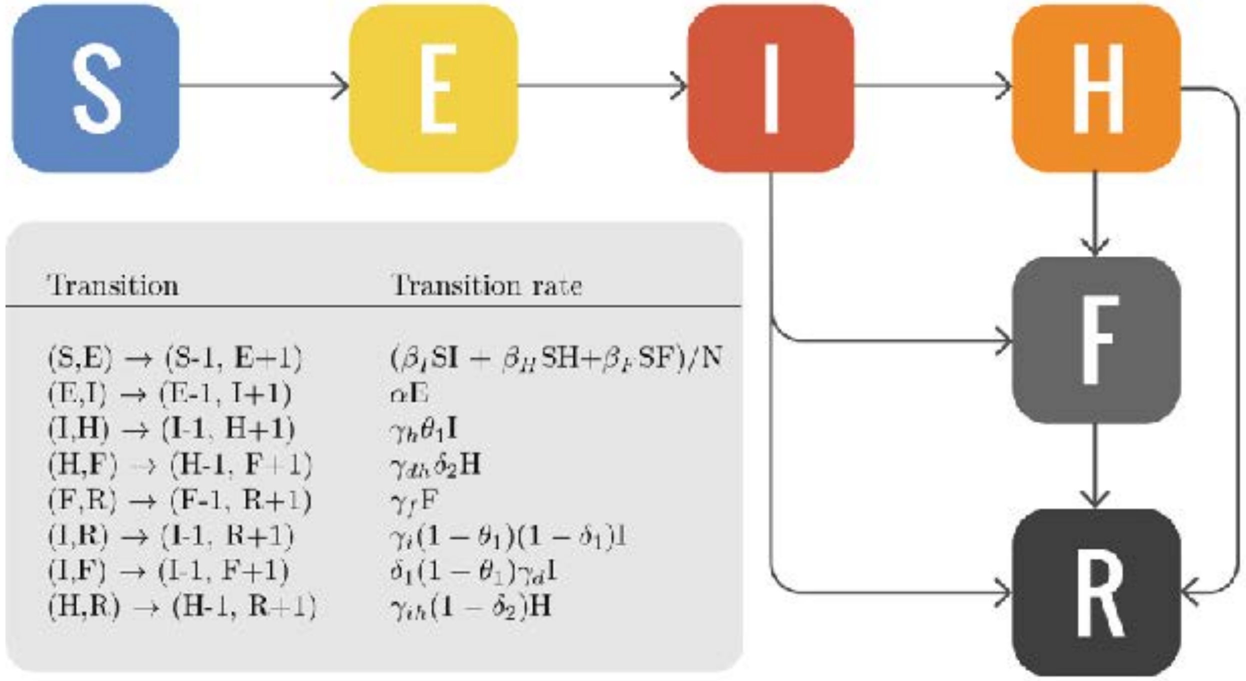
[www.gleamviz.org Balcan et al. PNAS 2009]

GLEaM: epidemic model

H1N1 pandemic:



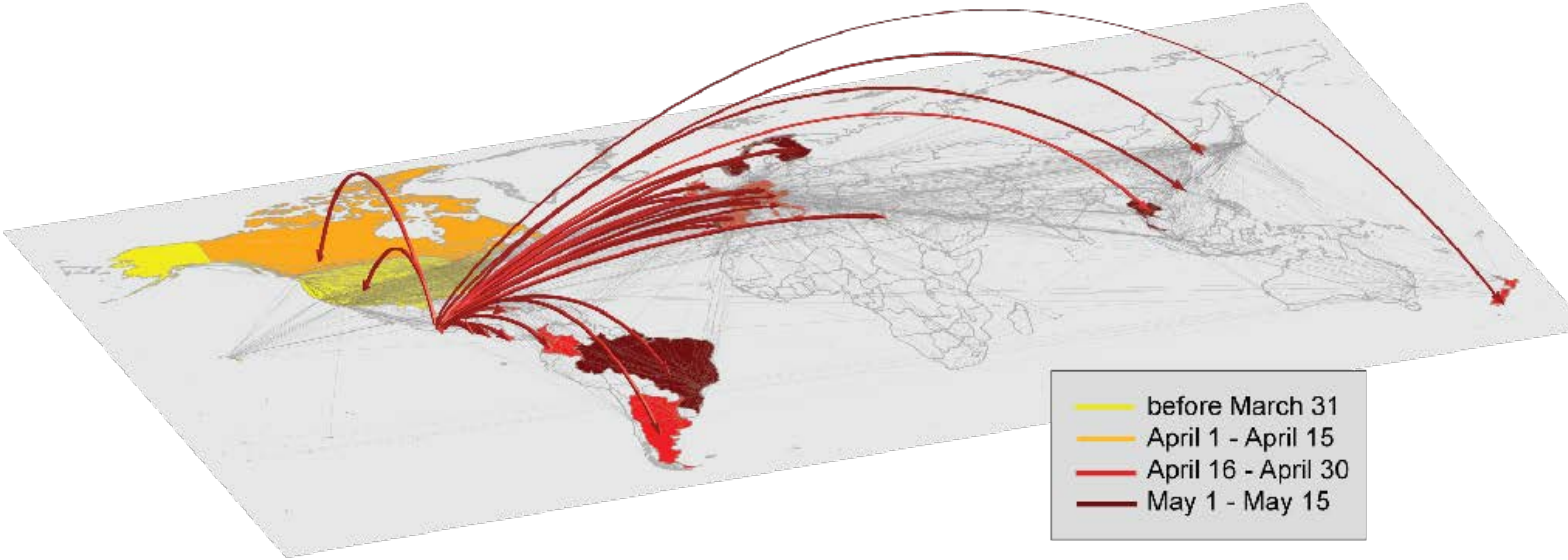
Ebola:



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

[www.gleamviz.org Balcan et al. PNAS 2009]

H1N1 influenza pandemic 2009



[www.gleamviz.org
Balcan et al. BMC Med 2009]

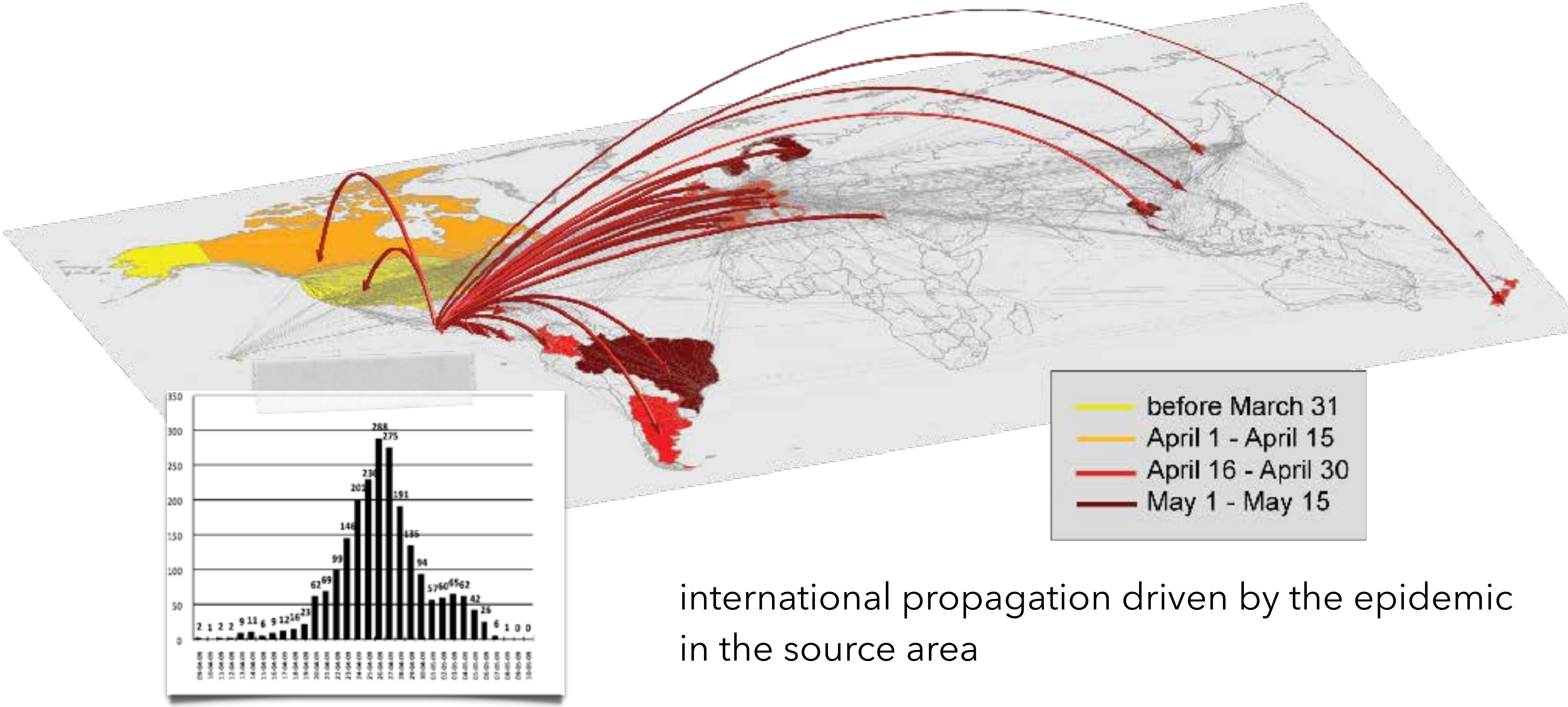
H1N1 influenza pandemic, 2009

... ... ???

end of April **mid May** **mid June** **.... ....** **Oct/Nov/Dec**

[www.gleamviz.org Balcan et al. BMC Med 2009]

H1N1 influenza pandemic, 2009

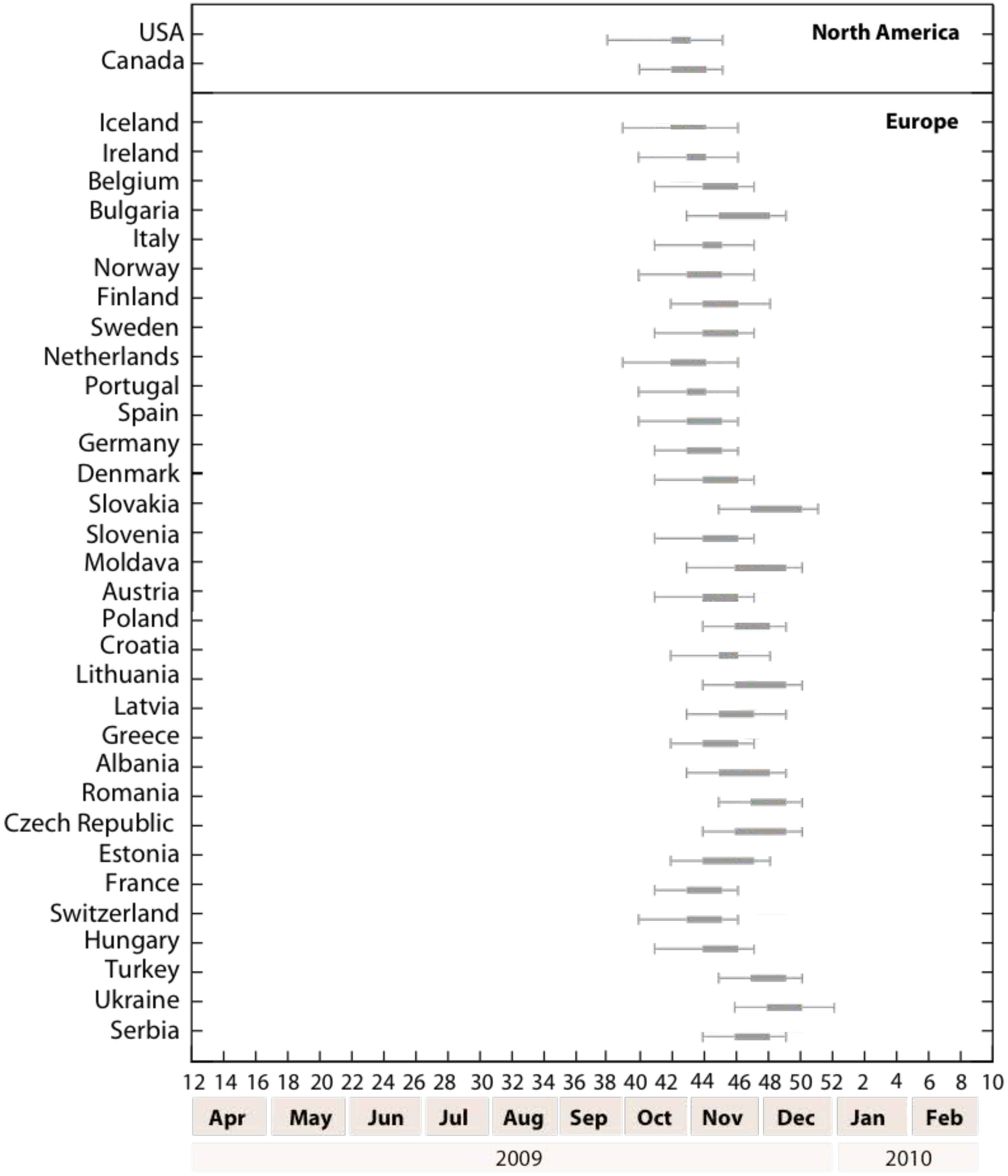


international propagation driven by the epidemic in the source area

exploit knowledge of the international propagation to ***infer*** the spread in the source area

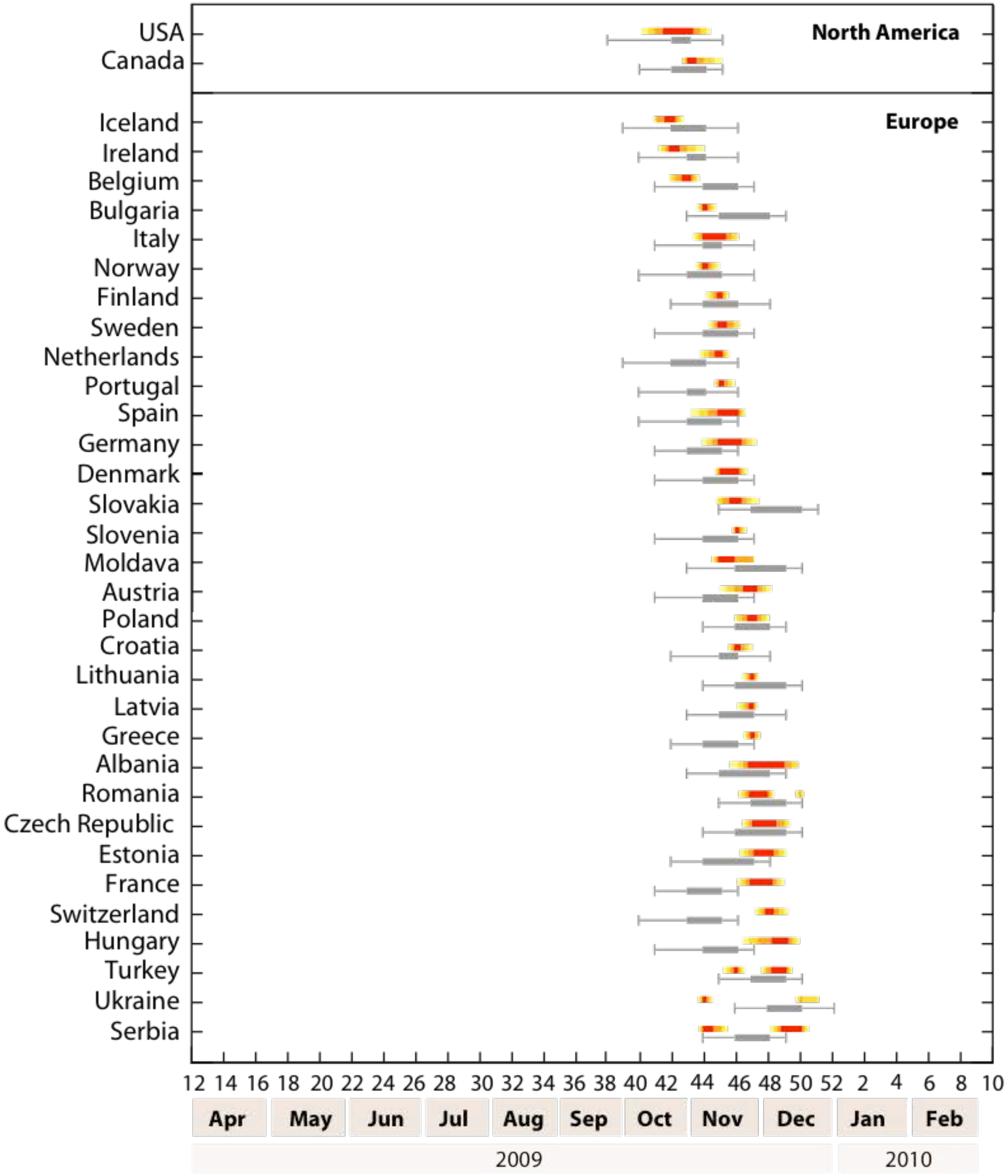
[Poletto et al. Eurosurveillance 2014; Poletto et al. Epidemics 2016; also: Cauchemez, et al. Lancet Infect Dis 2014; Balcan et al. BMC Med 2009, Fraser et al. Nature 2009]

H1N1 influenza pandemic, 2009



[www.gleamviz.org
Balcan et al. BMC Med 2009]

H1N1 influenza pandemic, 2009



[www.gleamviz.org
Balcan et al. BMC Med 2009]

conclusion

- metapopulation model simple enough to allow for mathematical understanding
- yet enough accurate to allow for realistic description of outbreaks
- international travel: highly populated patched connected by relatively small mobility fluxes
- out from this regime modelling spatial spread more complicated & lack of data

Outline

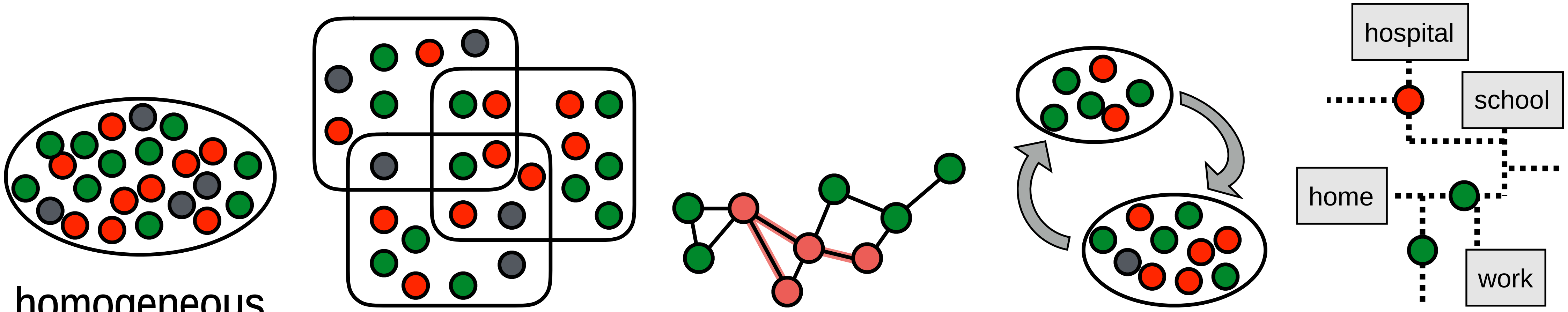
-modeling an epidemic

-epidemics on networks

-epidemics in space

-interacting epidemics

-computer simulations



homogeneous mixing

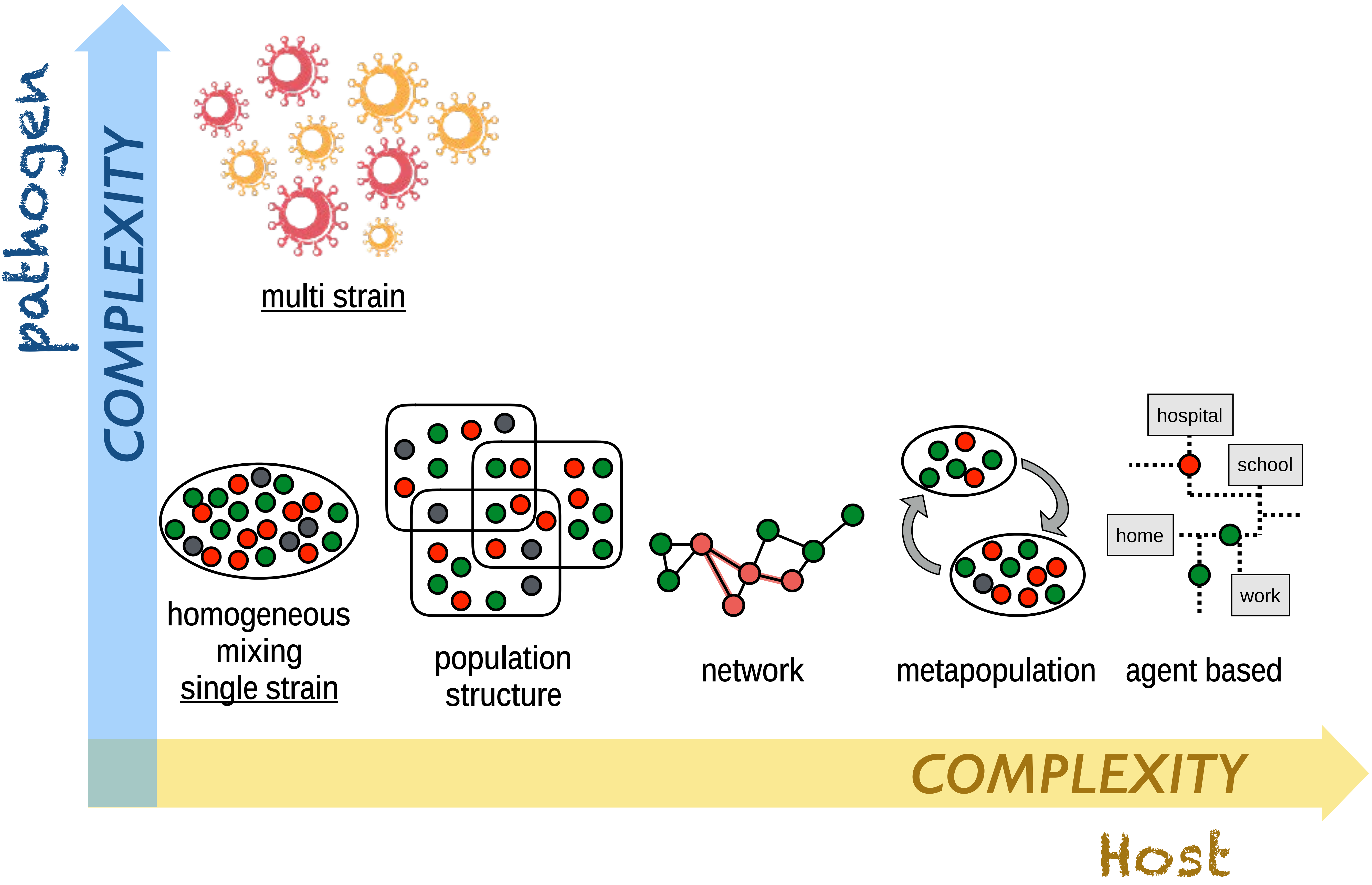
population structure

network

metapopulation

agent based

COMPLEXITY



pathogen COMPLEXITY

multi strain

homogeneous mixing
single strain

population structure

network

metapopulation

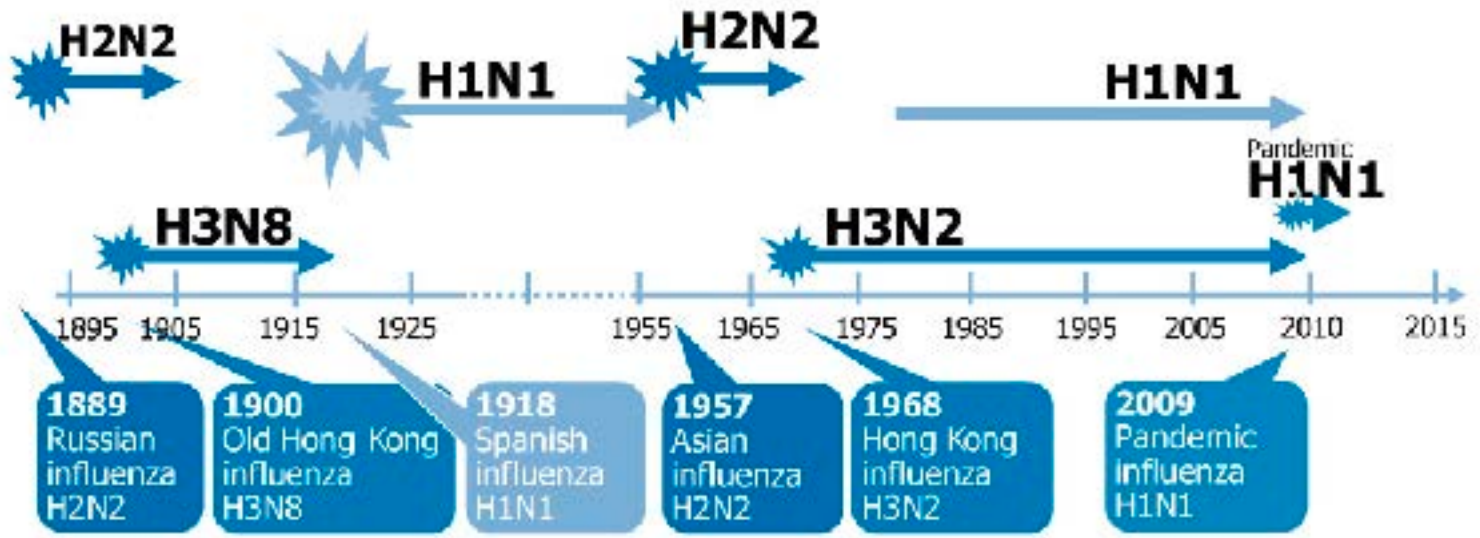
agent based

COMPLEXITY
Host

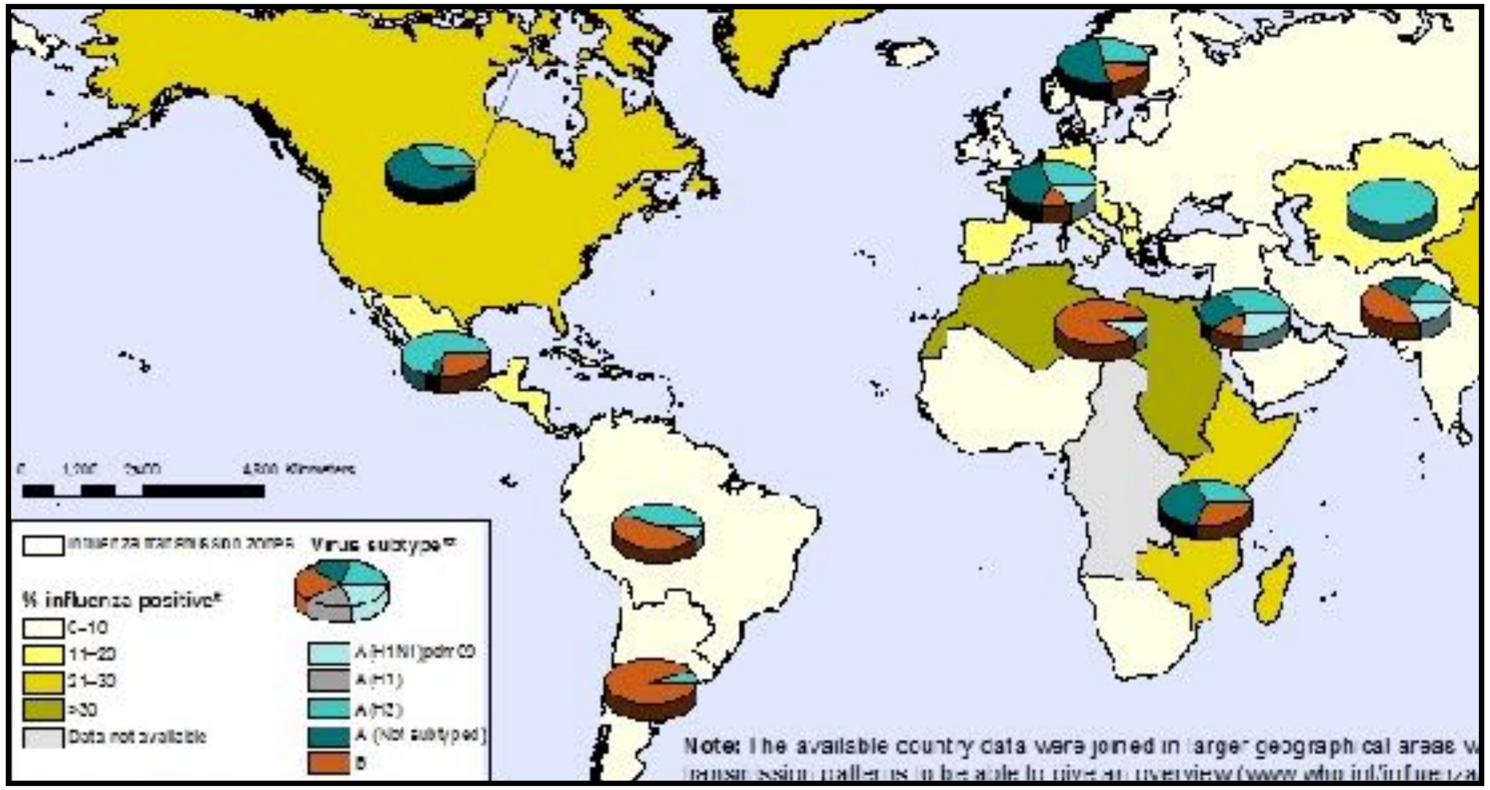
multistrain & influenza

FIGURE

Recorded human pandemic influenzas since 1855 (early sub types inferred)



Source: European Centre for Disease Prevention and Control (ECDC) 2009
Reproduced and adapted (2009) with permission of Dr Masato Tashiro, Director, Center for Influenza Virus Research, National Institute of Infectious Diseases (NIID), Japan.



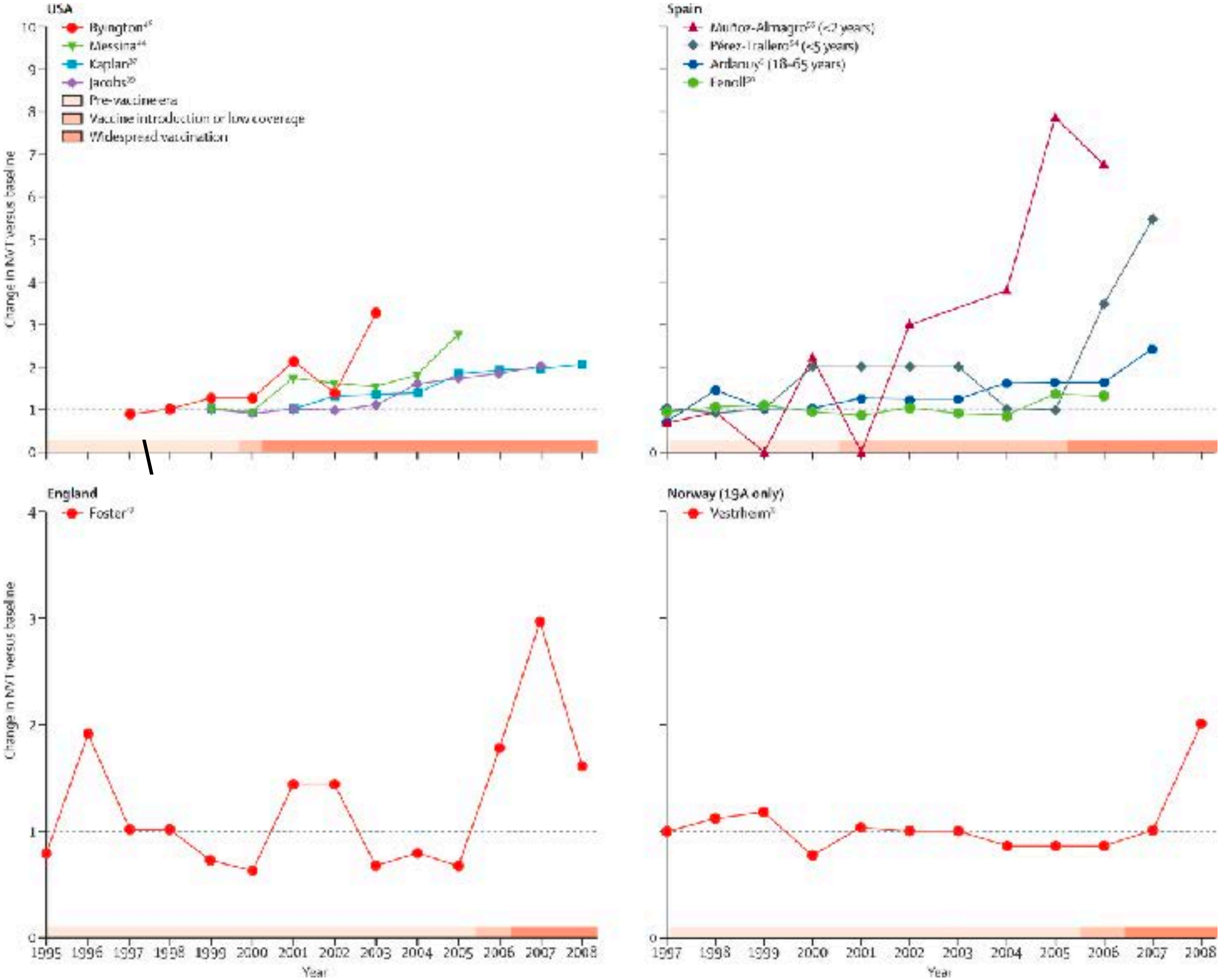
[http://www.cdc.gov/flu/professionals/vaccination/effectiveness-studies.htm]

- 3 circulating subtypes + continuous mutation
- ~ billion cases annually (~3–5 million severe illness)
- ~300,000–500,000 deaths
- vaccine effectiveness:

23% (in 2014-15)
47% (in 2015-16)

can we increase the impact of vaccination?

multistrain & pneumococcal disease

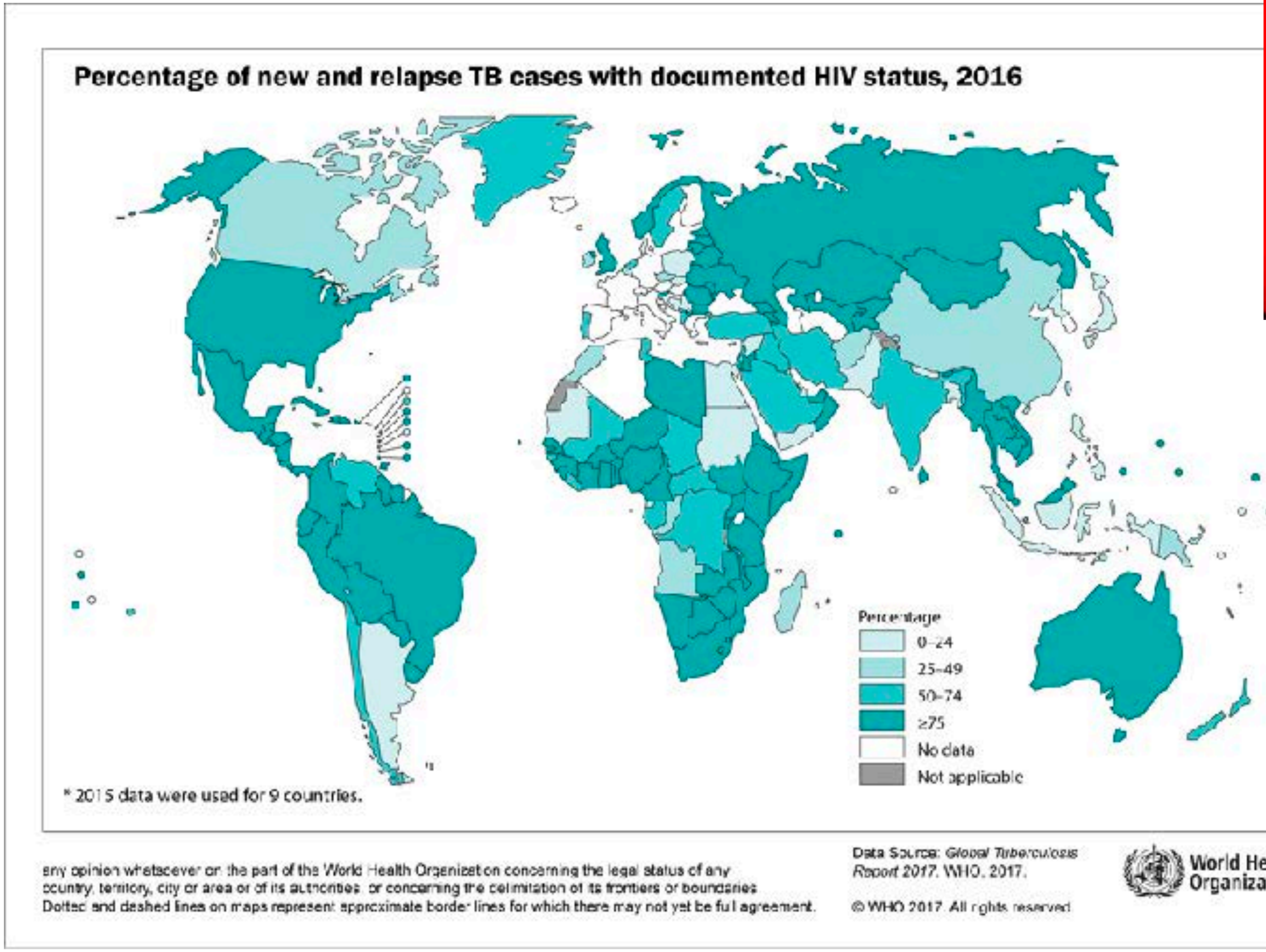


- *S. pneumoniae* major cause of meningitis, sepsis, pneumonia
- ~90 serotypes
- vaccine target few of them

strain replacement?

[Weinberger et al. the Lancet 2011]

HIV & TB



Percentage of new and relapse TB cases with documented HIV status, 2016

* 2015 data were used for 9 countries.

any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

Data Source: *Global Tuberculosis Report 2017*. WHO, 2017.

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World Health Organization

- risk of TB ~16-27 times greater in people living with HIV
- 10.4 million cases of TB disease globally, 1.2 million [11%] among HIV patient

multi strain: fundamental questions

cooperation

EPIDEMIOLOGICAL IMPACT

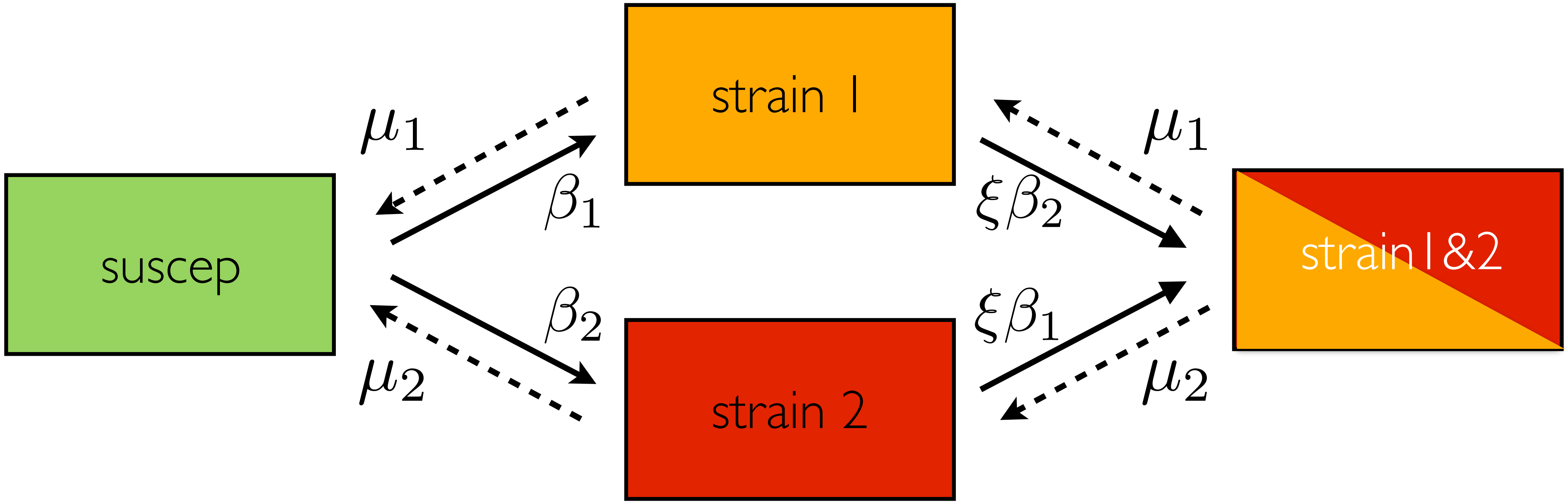
?

competition

dominance/co-dominance

COEXISTENCE

a simple model with 2 strains

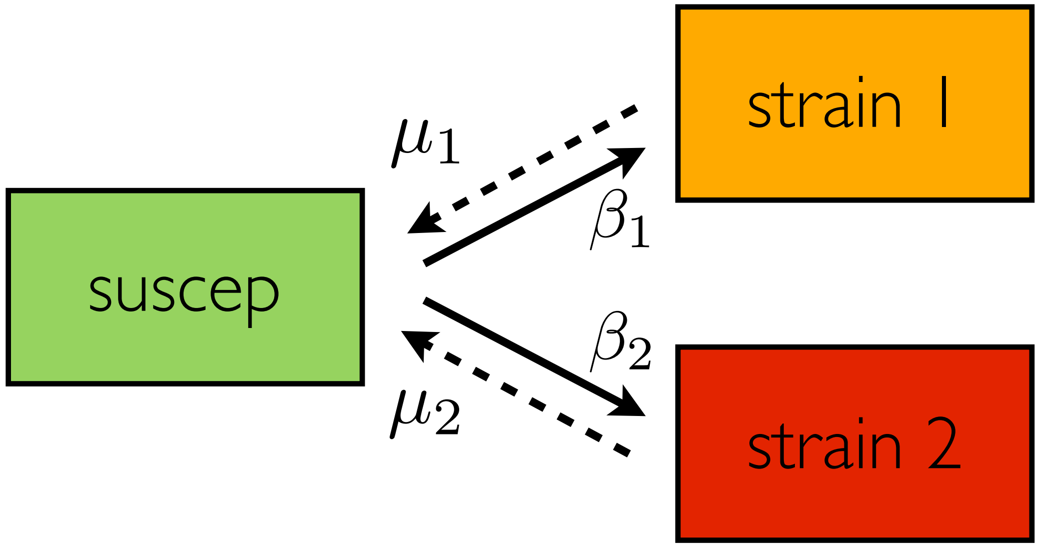


$\xi > 1$ cooperative

$\xi < 1$ competitive

competitive diseases: winner takes it all!

$\xi = 0$ mutual exclusion



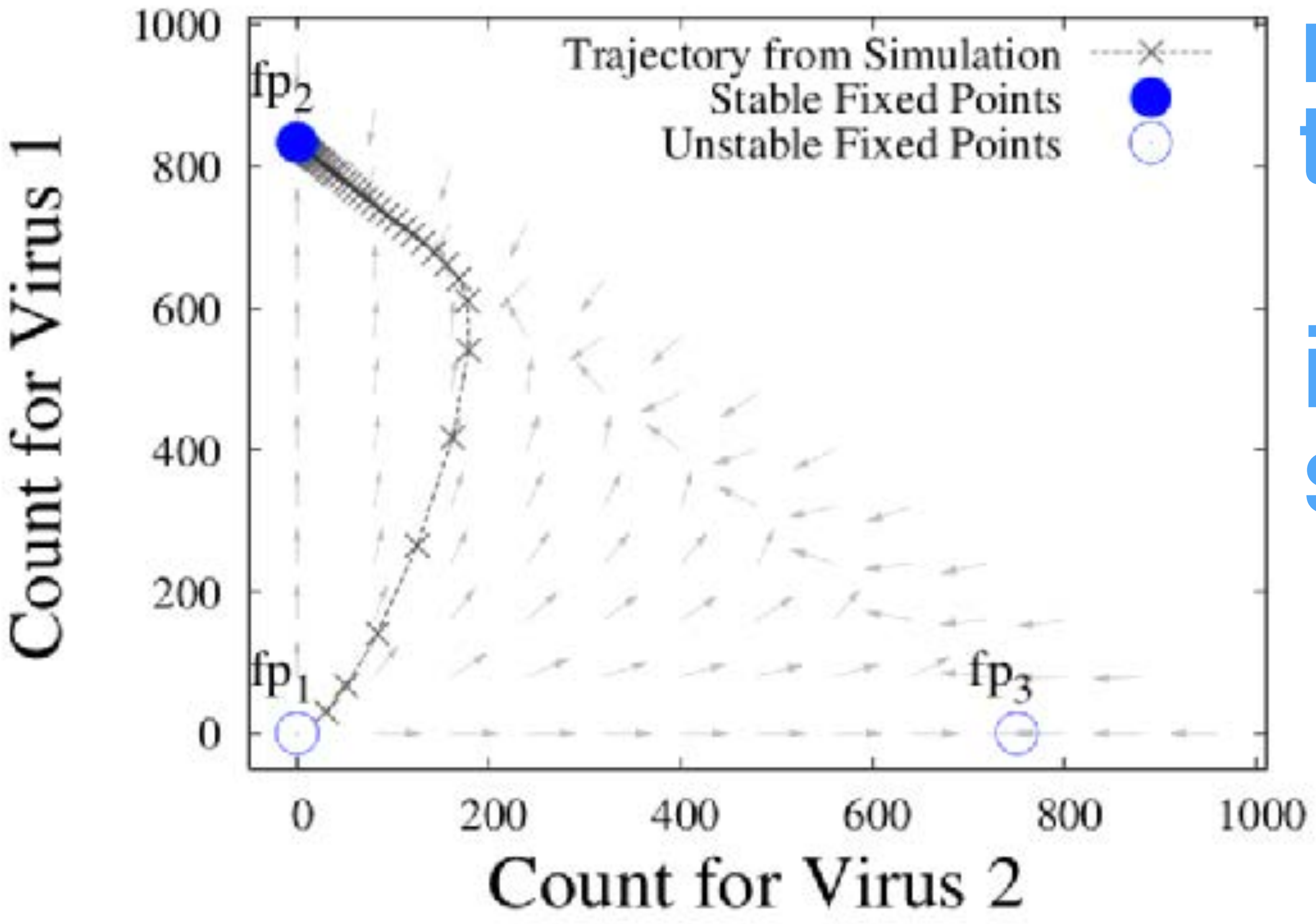
A_{ij} adjacency matrix

$\rho\left[A\right]$ spectral radius

$\rho\left[A\right]\beta/\mu$ strength of the strain

[Prakash et al, Proceedings of the 21 WWW 2012]

competitive diseases: winner takes it all!

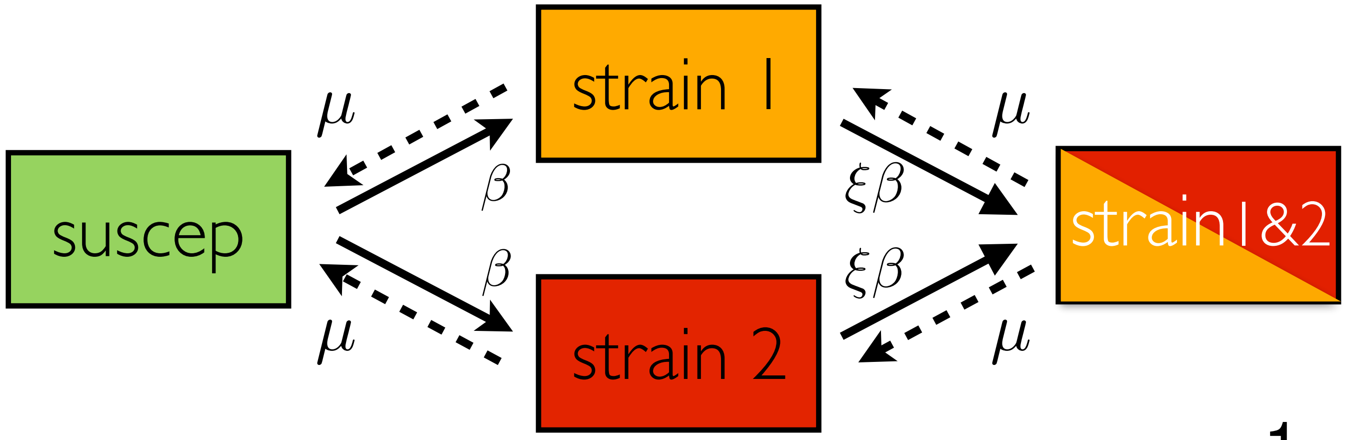


no co-existence
the stronger strain always wins

if the 2 are equal
still only 1 strain survives

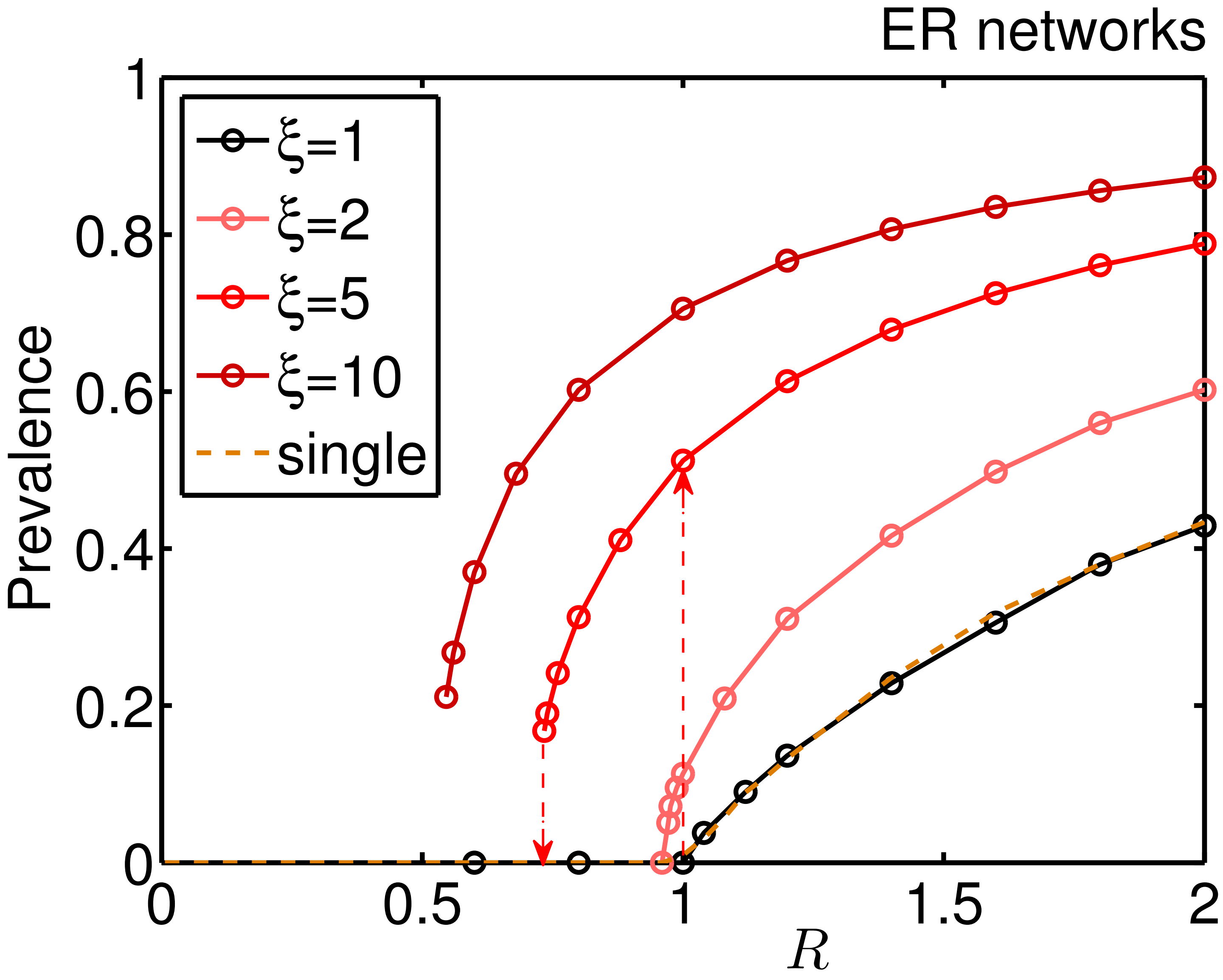
[Prakash et al, Proceedings of the 21 WWW 2012]

cooperative diseases



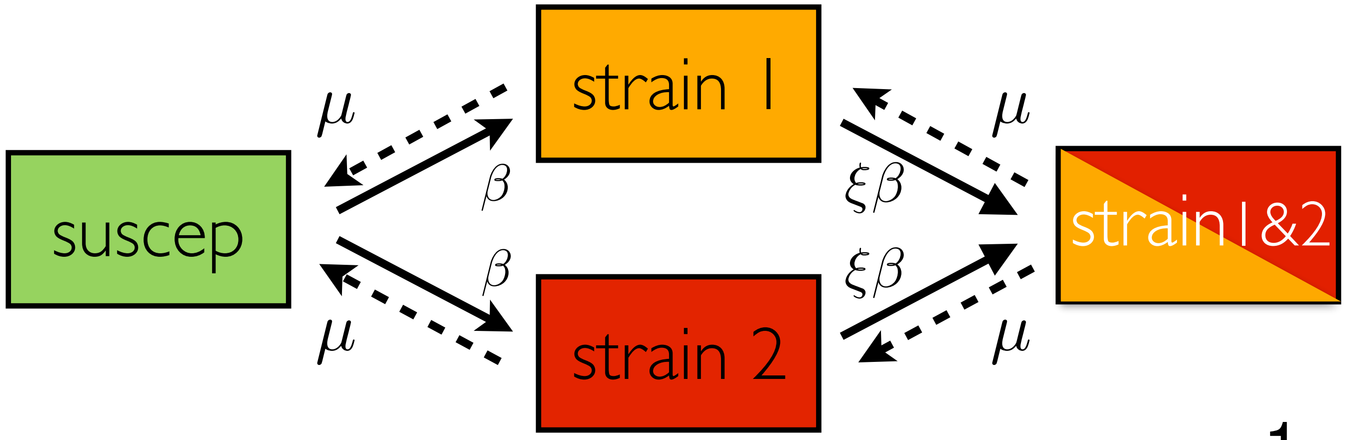
$\xi > 1$

- abrupt phase transitions



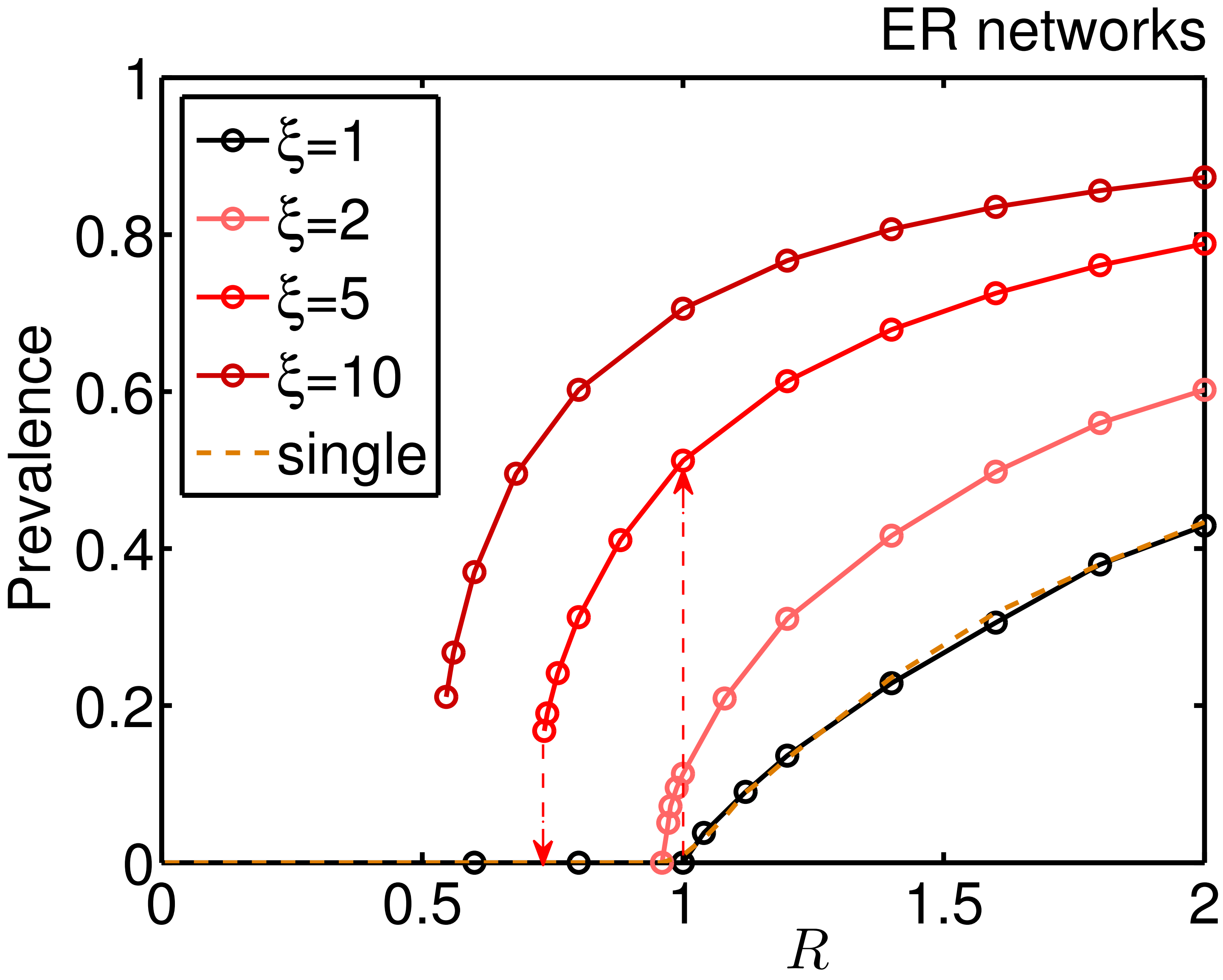
[Cai et al Nature Phys 11 936 2015; Chen et al New J Phys 19 103041 2017]

cooperative diseases



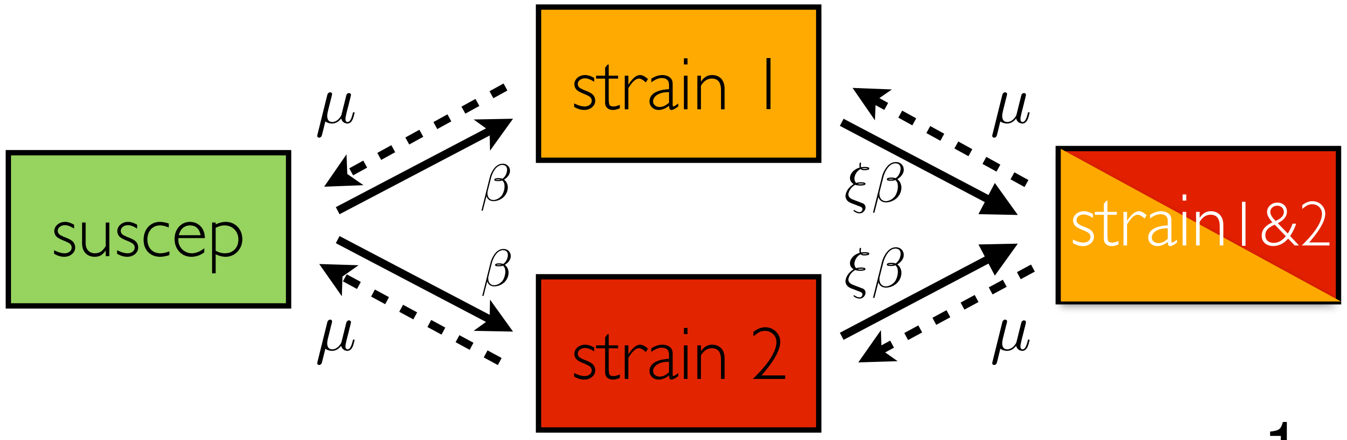
$\xi > 1$

- abrupt phase transitions
- hysteresis: epidemic threshold is different from the eradication threshold



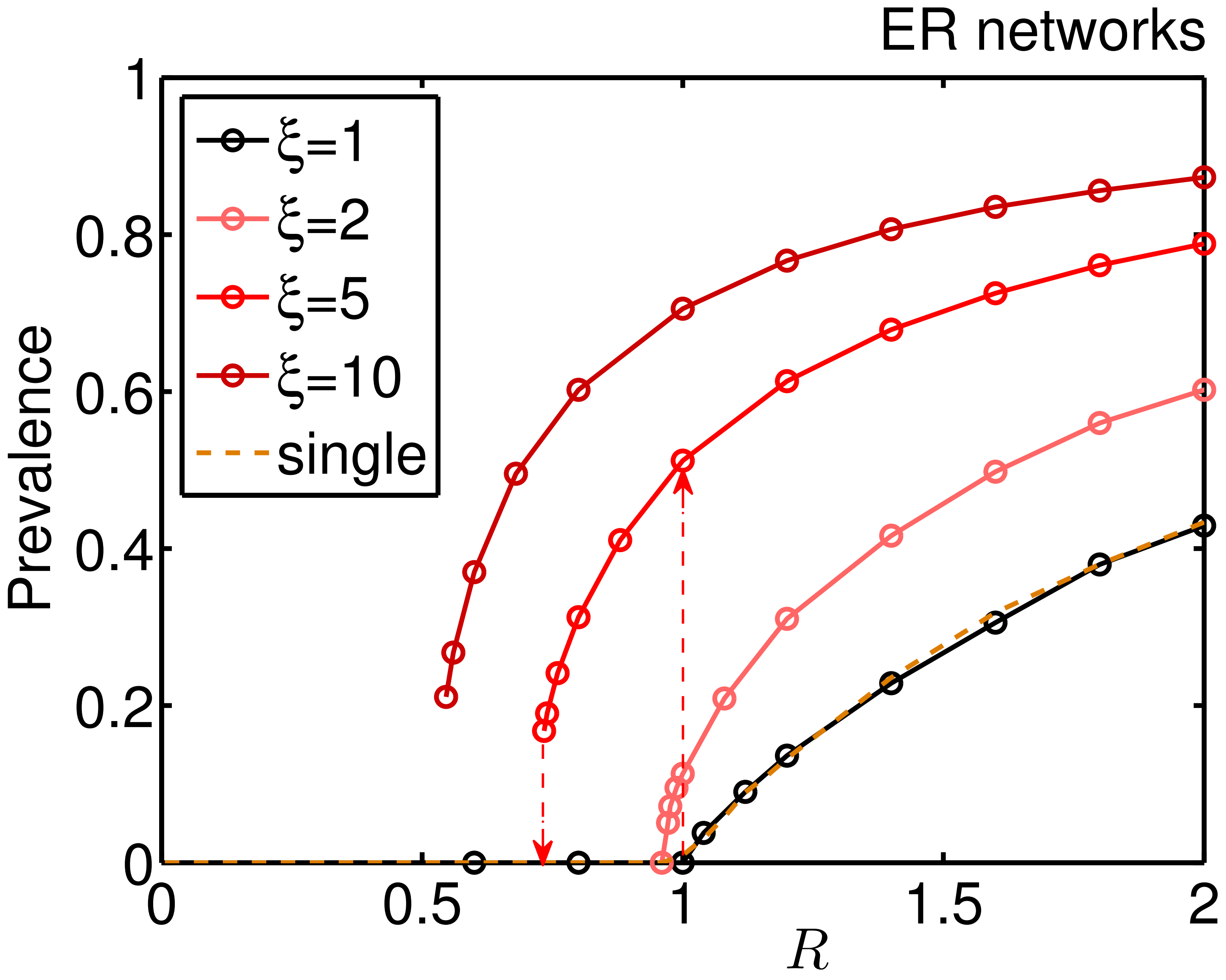
[Cai et al Nature Phys 11 936 2015; Chen et al New J Phys 19 103041 2017]

cooperative diseases



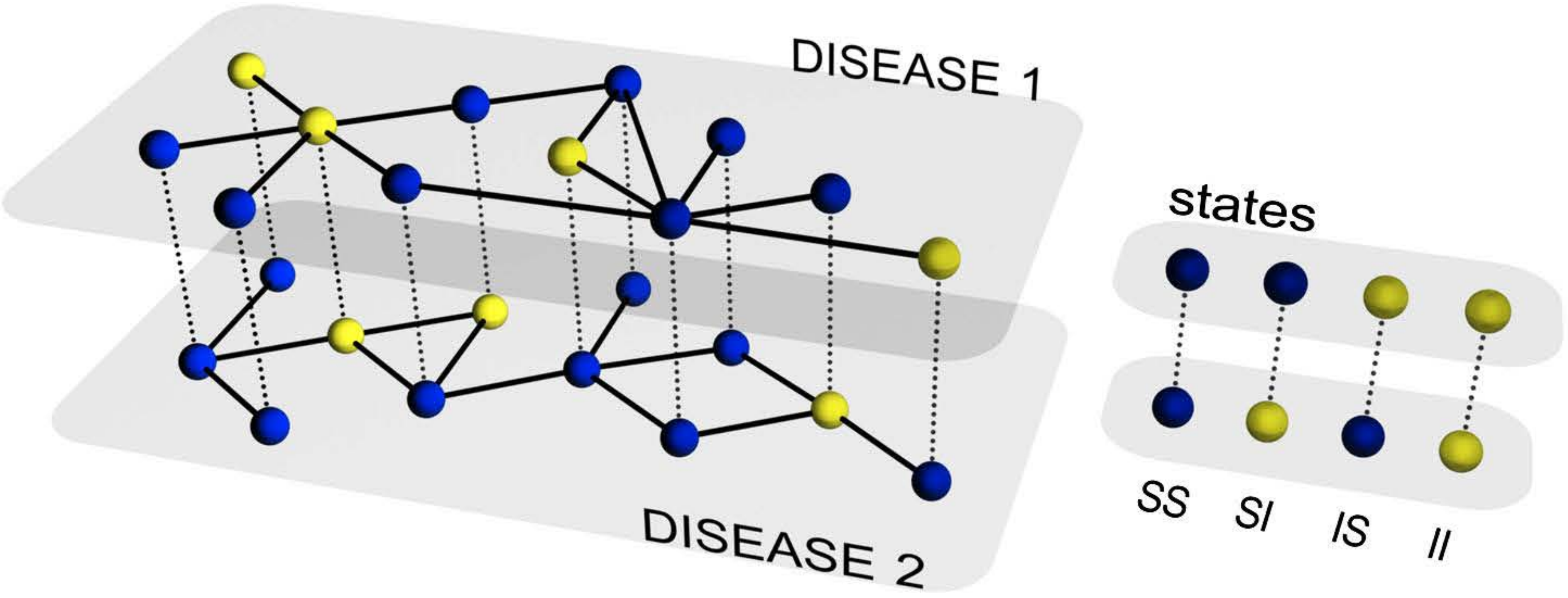
$\xi > 1$

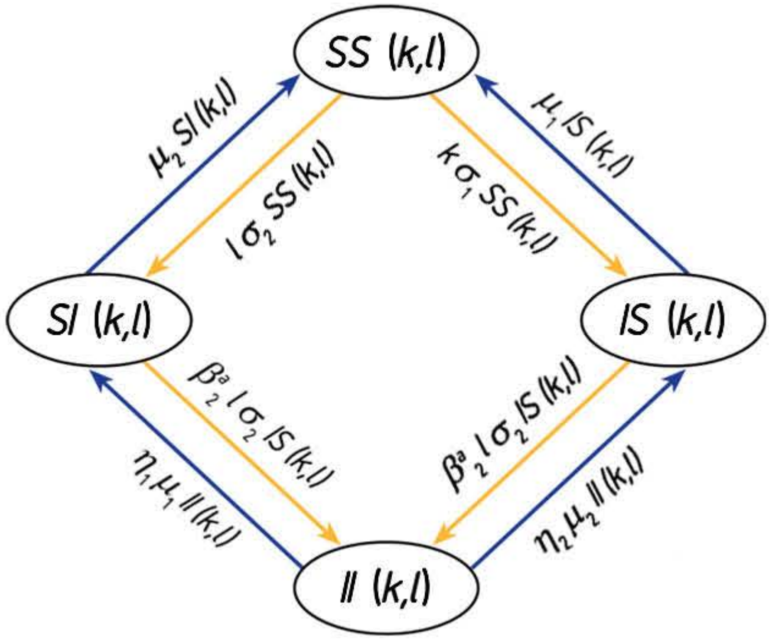
- abrupt phase transitions
- hysteresis: epidemic threshold is different from the eradication threshold
- the behaviour depends on the network topology



[Cai et al Nature Phys 11 936 2015; Chen et al New J Phys 19 103041 2017]

interacting diseases: general framework





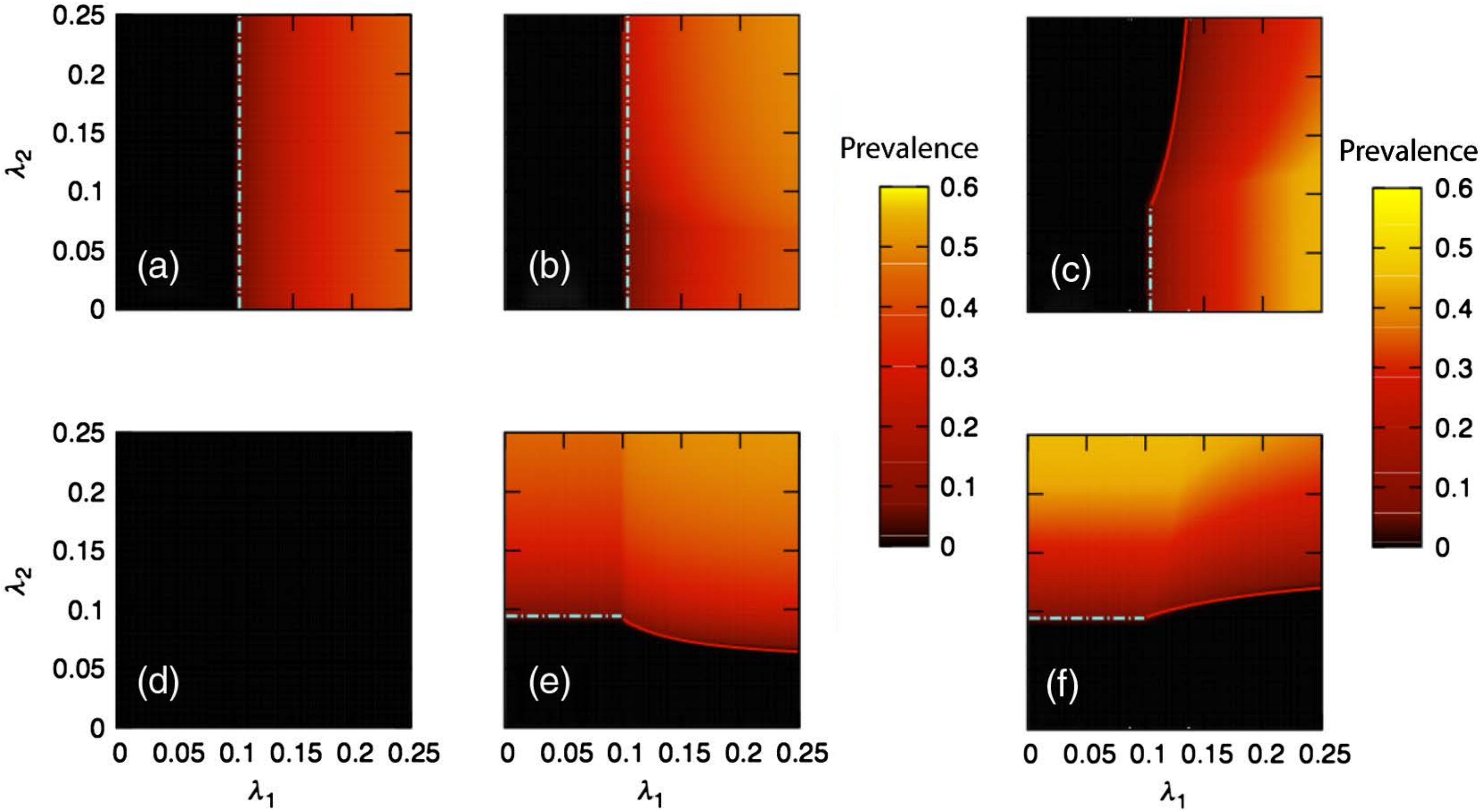
- heterogeneous mean-field approximation
- network underlying spreading is disease-specific
- accounting for a wide array of possible interaction
- second disease introduced at a certain time
- both SIS & SIS and SIR & SIR

TABLE I. Definition of model parameters.

Parameter	Dynamical meaning
λ_1	Baseline infectiousness of disease 1
λ_2	Baseline infectiousness of disease 2
μ_1	Baseline recovery rate of disease 1
μ_2	Baseline recovery rate of disease 2
β^a_1	Variation of disease 1 infectiousness due to the fact that the susceptible individual exposed to disease 1 is infected with disease 2
β^a_2	Variation of disease 2 infectiousness due to the fact that the susceptible individual exposed to disease 2 is infected with disease 1
β^b_1	Variation of disease 1 infectiousness due to the fact that the spreader is also infected with disease 2
β^b_2	Variation of disease 2 infectiousness due to the fact that the spreader is also infected with disease 1
η_1	Variation of disease 1 recovery rate for individuals also infected with disease 2
η_2	Variation of disease 2 recovery rate for individuals also infected with disease 1

[Sanz et al PRX 4, 04100 2014]

interacting diseases: general framework



introduction
strain 1

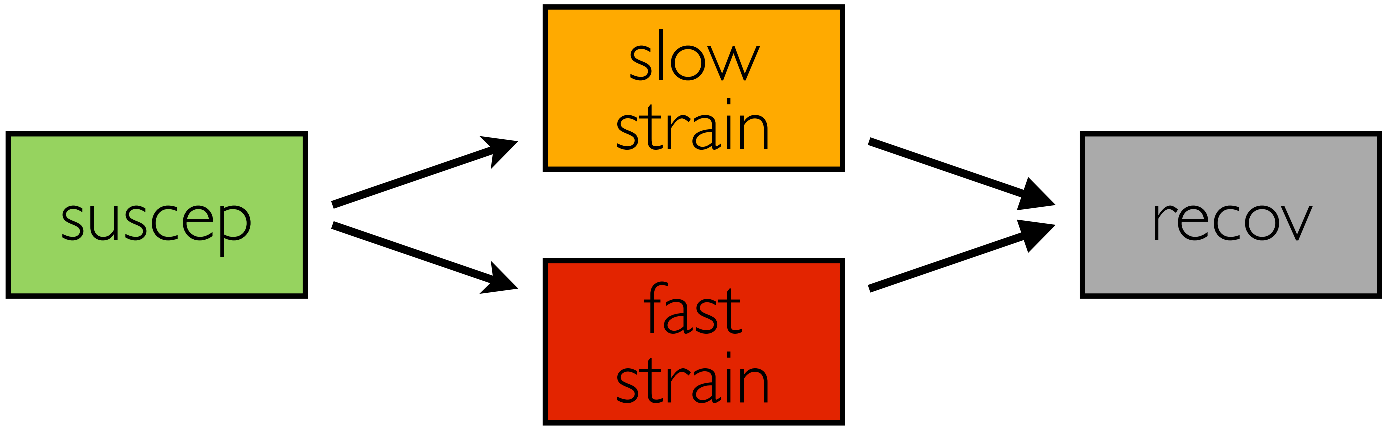
introduction
strain 2
cooperative

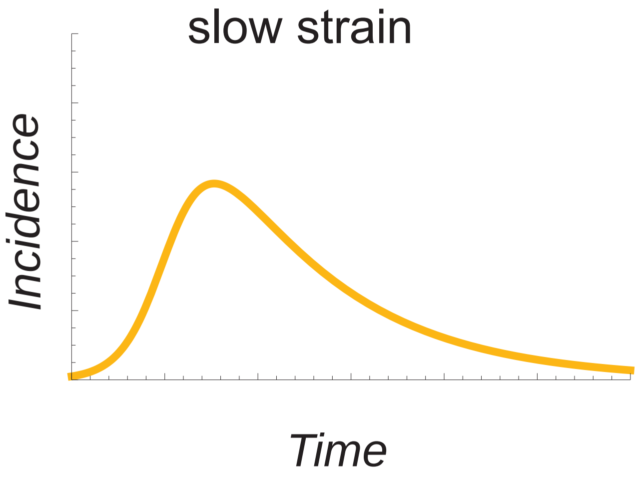
introduction
strain 2
competitive

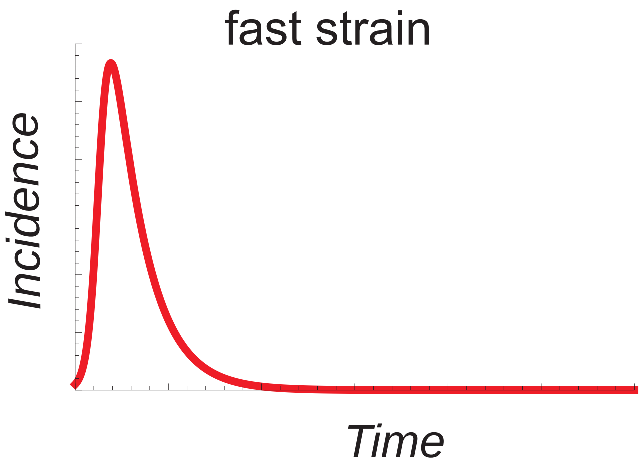
[Sanz et al PRX 4, 04100 2014]

competing diseases in space

- SIR
- same R_0
- different infectious period → $\tau_s > \tau_f$
- full cross-immunity







competing diseases in space

- SIR
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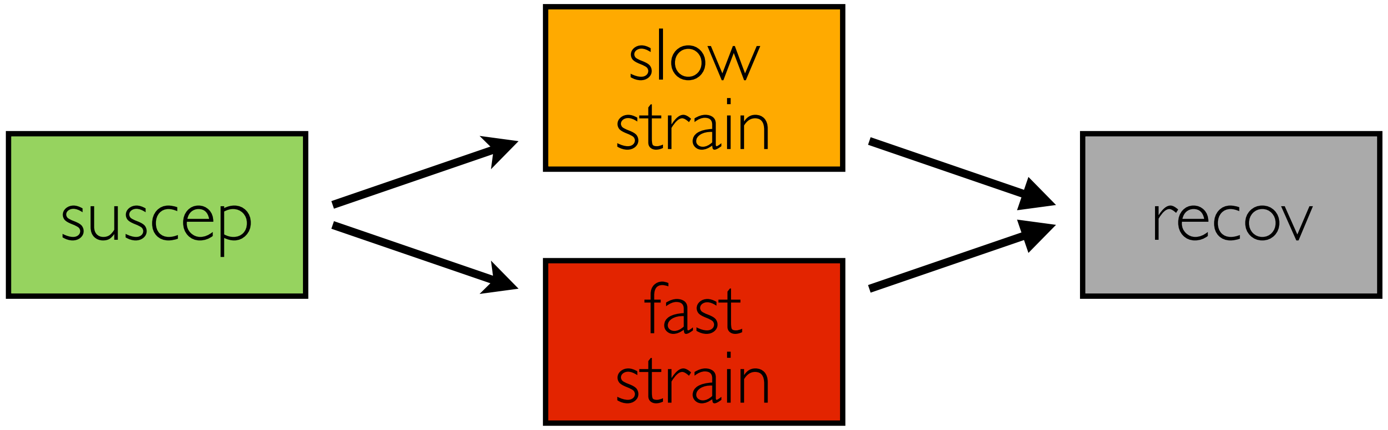
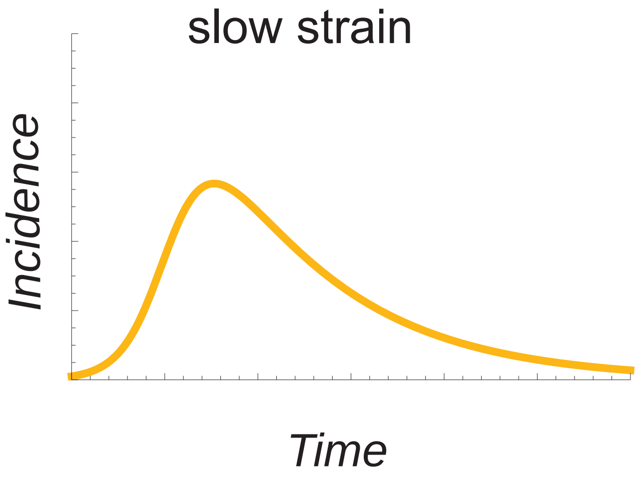
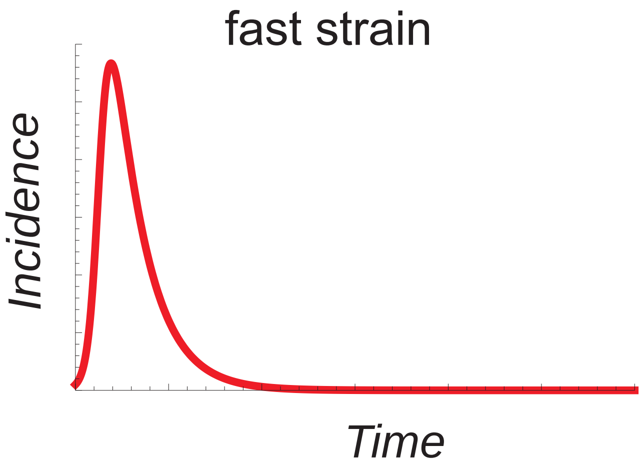
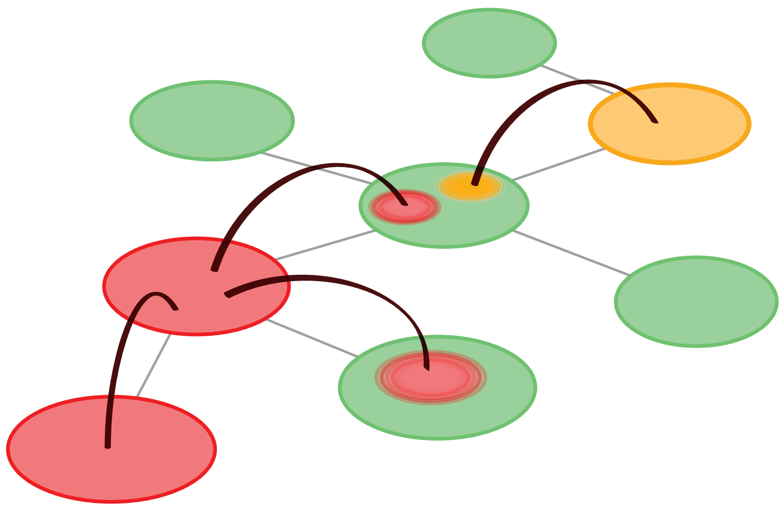




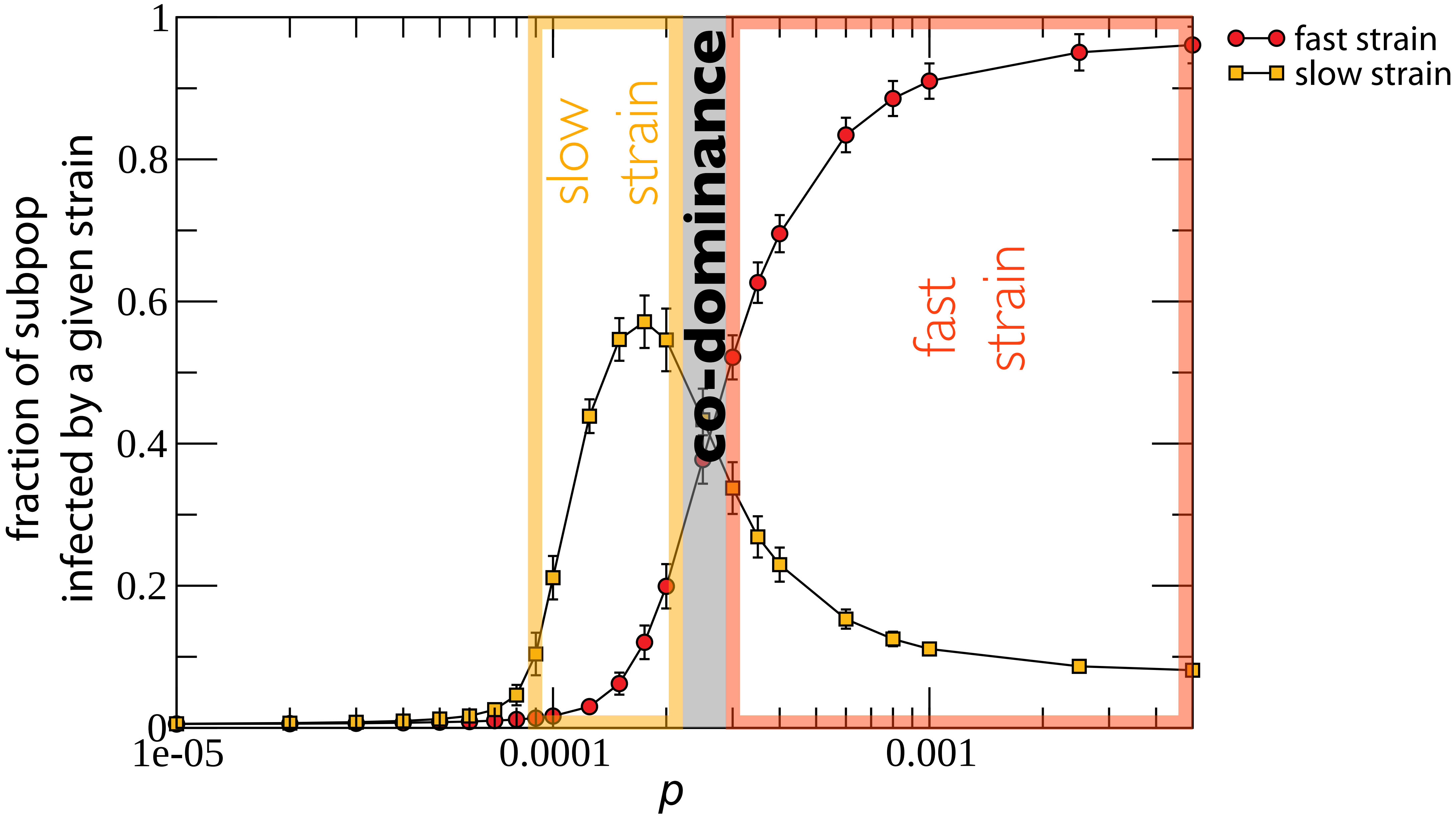




- the 2 strains originate from different patches
- stochastic simulations of the outbreak

role of p on dominance/co-dominance?

competing diseases in space

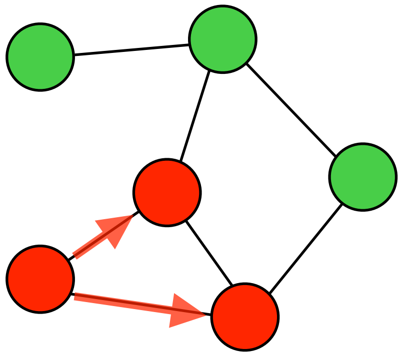


[Poletto et al. PLoS Comp Bio 2013]

competing diseases in space

scale of individuals

- μ^{-1} = infection duration
- R0

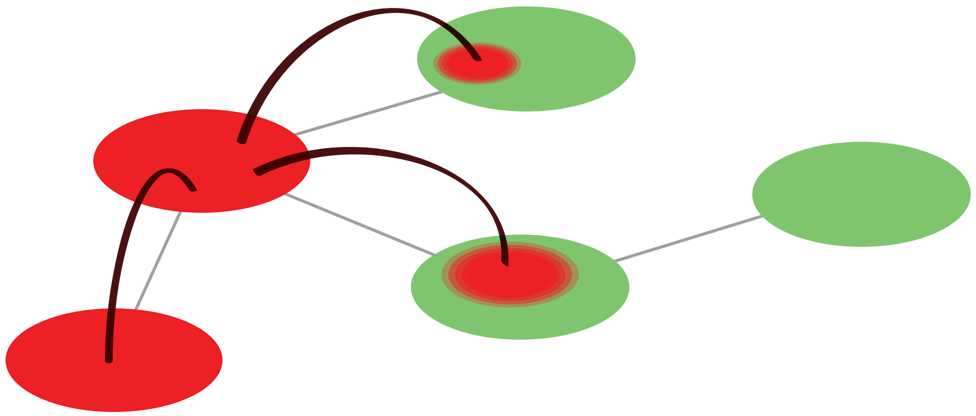


$$I(t) \sim e^{\mu(R_0-1)t}$$

scale of subpopulations

$D =$ # diseased subpop

$$D(t) \sim e^{\frac{1}{T}(R_*-1)t}$$



- $T =$ outbreak duration
- R*

[Poletto et al. PLoS Comp Bio 2013]

competing diseases in space

$$R_* = (\langle k \rangle - 1)\left[1 - \left(\frac{1}{R_0}\right)^{\frac{pR_\infty}{\mu}}\right]$$

R_* increasing function of μ^{-1} $\Rightarrow$ $R_*^s > R_*^f$

R_* increasing function of *p*

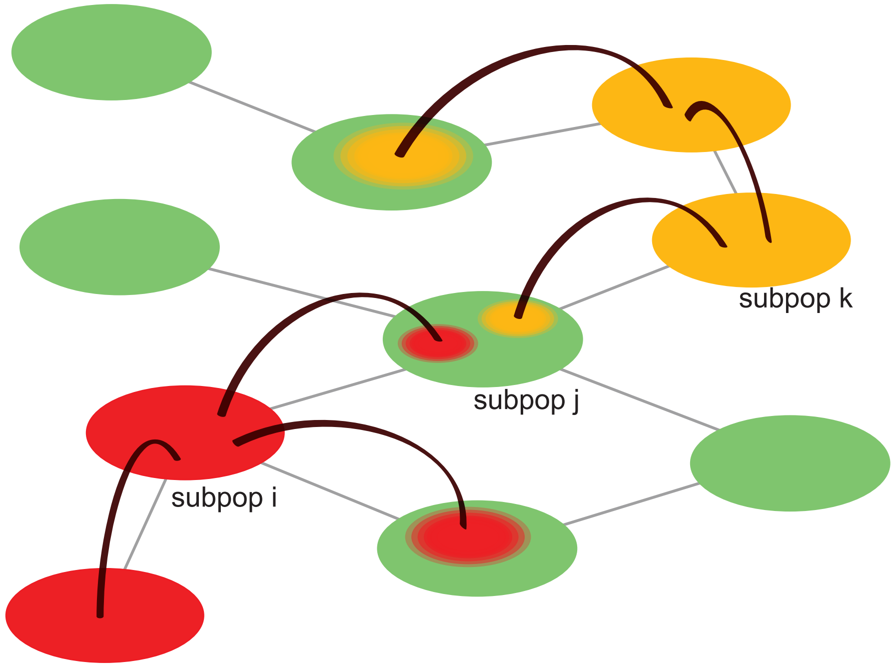
large *p*:

$$R_*^s \text{ and } R_*^f >> 1$$

fast strain reaches more rapidly new subpopulations

small *p*:

$R_*^s > R_*^f$ $\Rightarrow$ percolate more efficiently

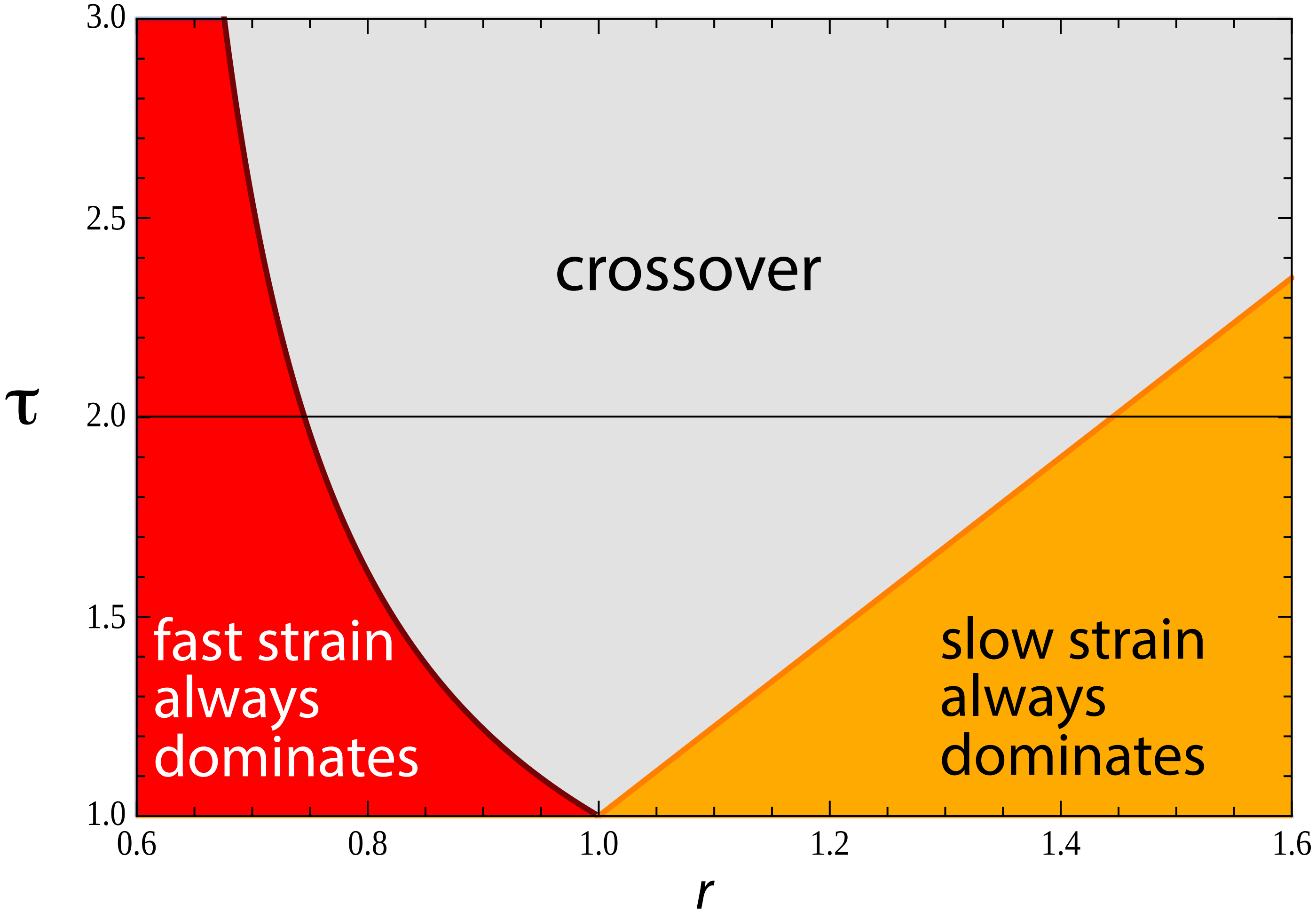


[Poletto et al. PLoS Comp Bio 2013]

competing diseases in space

allow for different R_0

→ when does mobility matters?



exponential growth in homogenous mixing

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

percolation capability

$$R_*$$

[Poletto et al. Sci Rep 2015]

conclusion

- interaction between pathogens critical for the epidemic outcome
- the interaction dynamics is critically affected by the structure of the host population, e.g. contact behaviour and mobility

Outline

-modeling an epidemic

-epidemics on networks

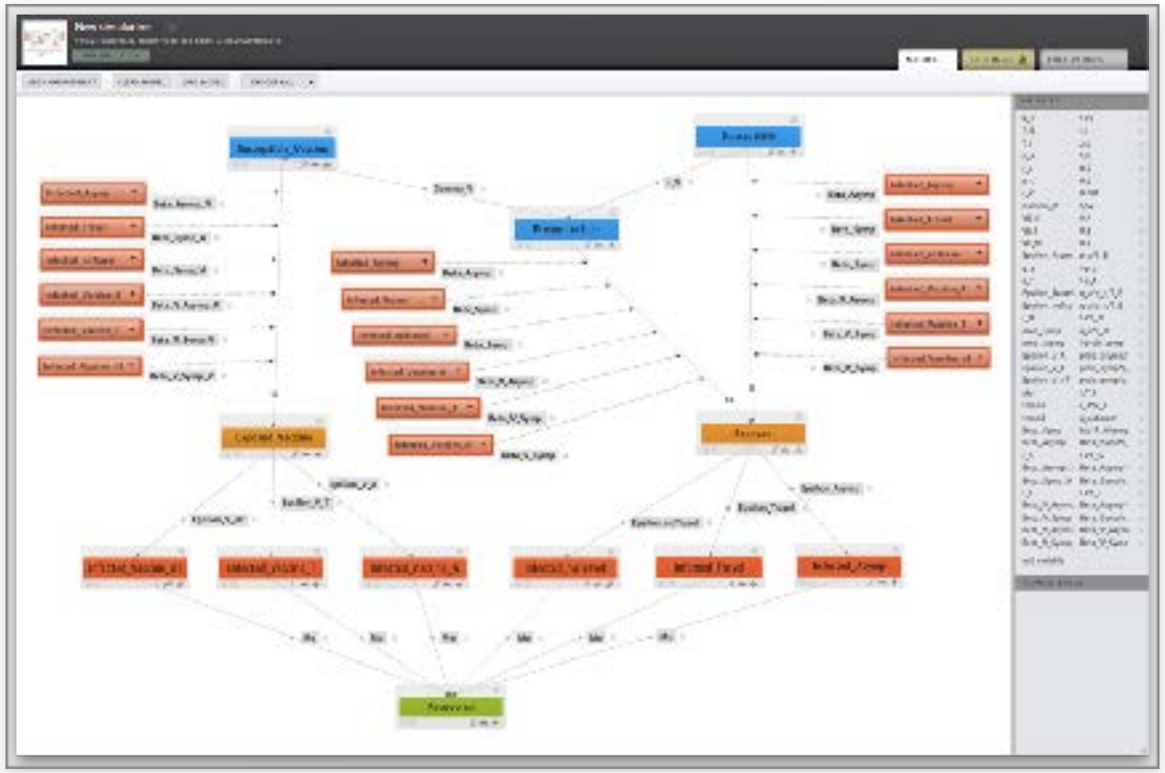
-epidemics in space

-interacting epidemics

-computer simulations

software: GLEaMviz.org

input

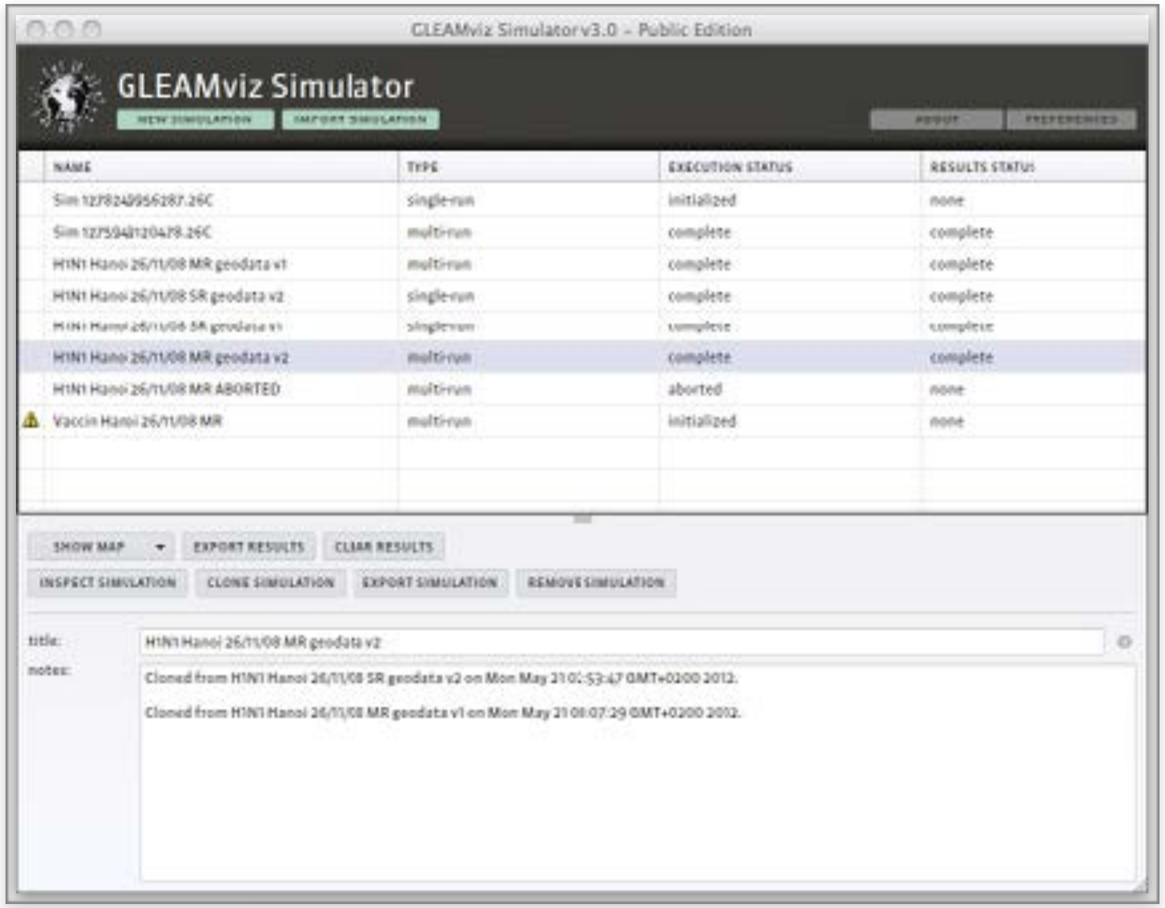


GLEaMviz.org

GLEAM Server + GLEAMviz Client

GLEAM Server: uses GLEAM as the engine to perform the simulations on high-performance computers

GLEAMviz Client: desktop application to interact with tGLEAM Server through a visual interface



NAME	TYPE	EXECUTION STATUS	RESULTS STATUS
Sim 1278240956287.26C	single-run	initialized	none
Sim 1275948120478.26C	multi-run	complete	complete
H1N1 Hanoi 26/11/08 MR geodata v1	multi-run	complete	complete
H1N1 Hanoi 26/11/08 SR geodata v2	single-run	complete	complete
H1N1 Hanoi 26/11/08 SR geodata v1	single-run	complete	complete
H1N1 Hanoi 26/11/08 MR geodata v2	multi-run	complete	complete
H1N1 Hanoi 26/11/08 MR ABORTED	multi-run	aborted	none
⚠ Vaccin Hanoi 26/11/08 MR	multi-run	initialized	none

title: H1N1 Hanoi 26/11/08 MR geodata v2

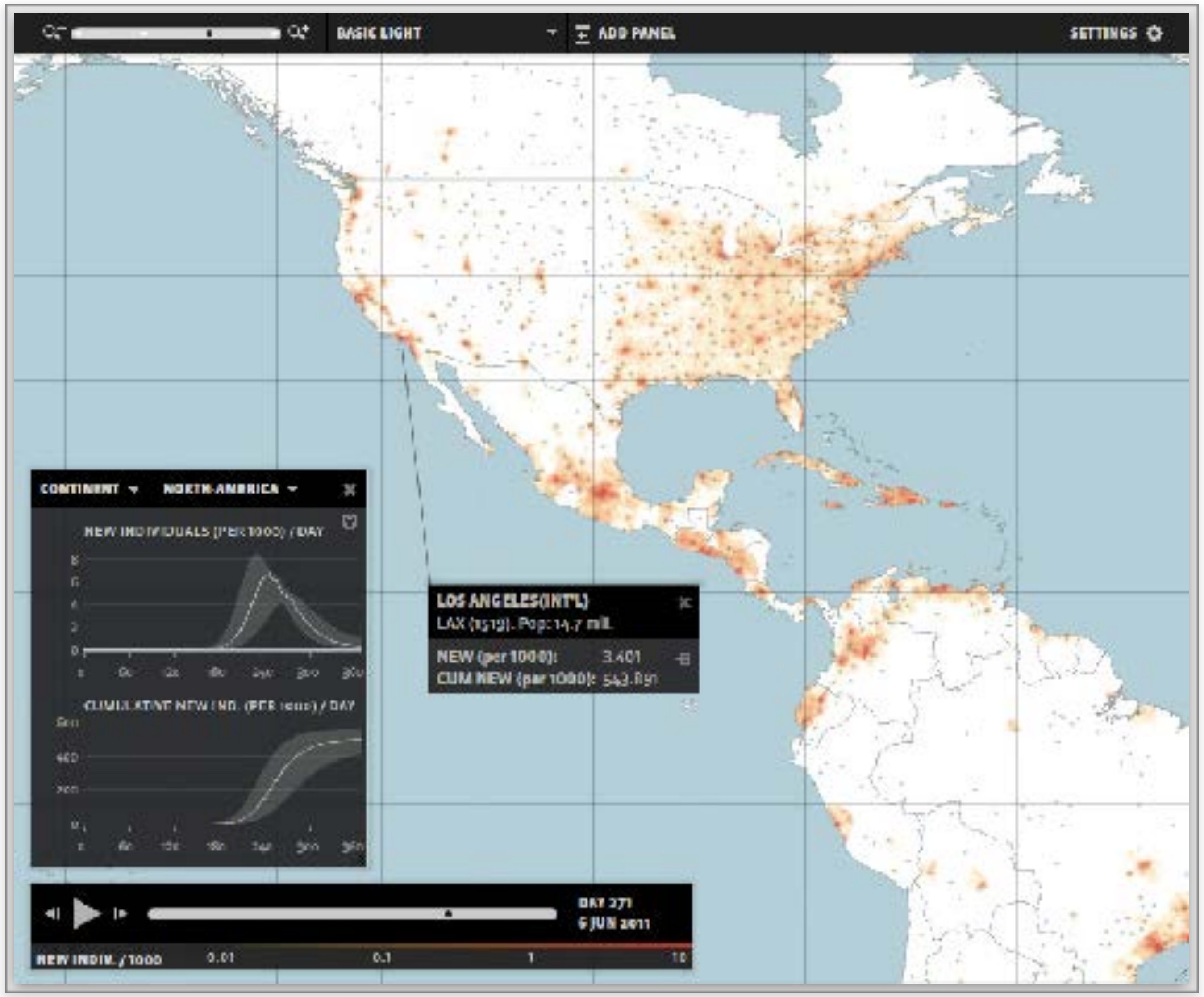
notes:

Cloned from H1N1 Hanoi 26/11/08 SR geodata v2 on Mon May 21 01:53:47 GMT+0200 2012.

Cloned from H1N1 Hanoi 26/11/08 MR geodata v1 on Mon May 21 01:07:29 GMT+0200 2012.

software: GLEaMviz.org

output



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GLEAM Server + GLEAMviz Client

GLEAM Server: uses GLEAM as the engine to perform the simulations on high-performance computers

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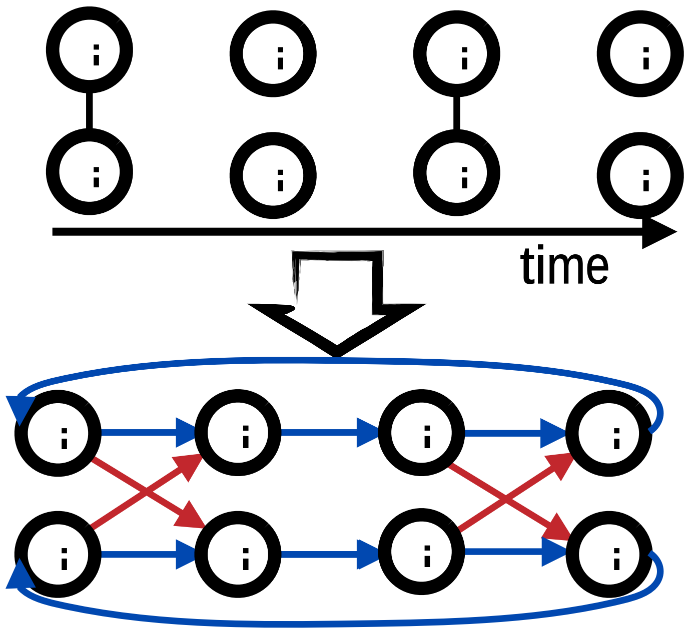
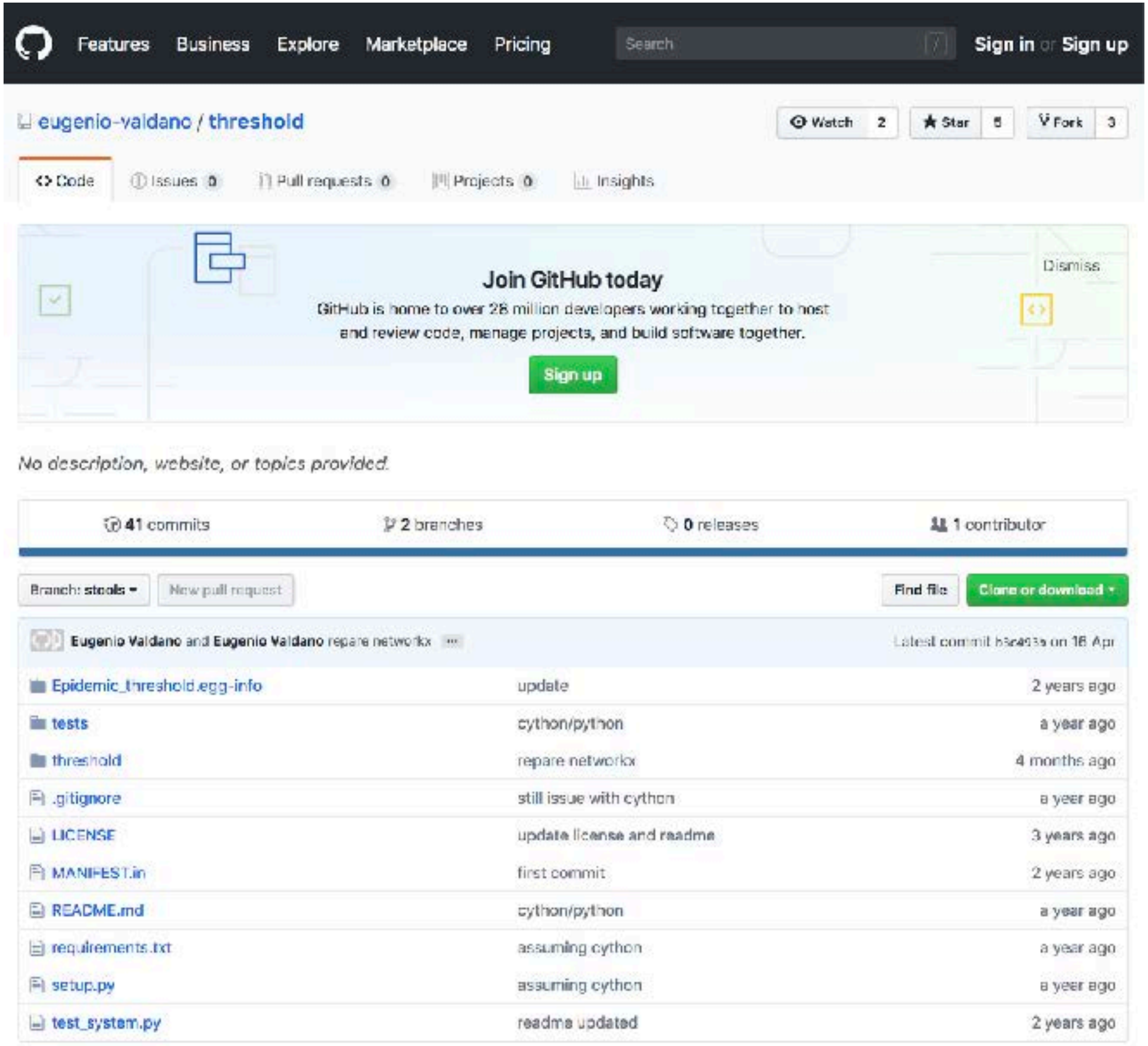
python package: epidemic threshold



infection propagator approach for temporal networks

[Valdano et al PRX 2015]



eugenio-valdano / threshold

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No description, website, or topics provided.

41 commits | 2 branches | 0 releases | 1 contributor

Eugenio Valdano and **Eugenio Valdano** repare networkx … Latest commit b5e493a on 16 Apr

Epidemic_threshold.egg-info	update	2 years ago
tests	cython/python	a year ago
threshold	repare networkx	4 months ago
.gitignore	still issue with cython	a year ago
LICENSE	update license and readme	3 years ago
MANIFEST.in	first commit	2 years ago
README.md	cython/python	a year ago
requirements.txt	assuming cython	a year ago
setup.py	assuming cython	a year ago
test_system.py	readme updated	2 years ago

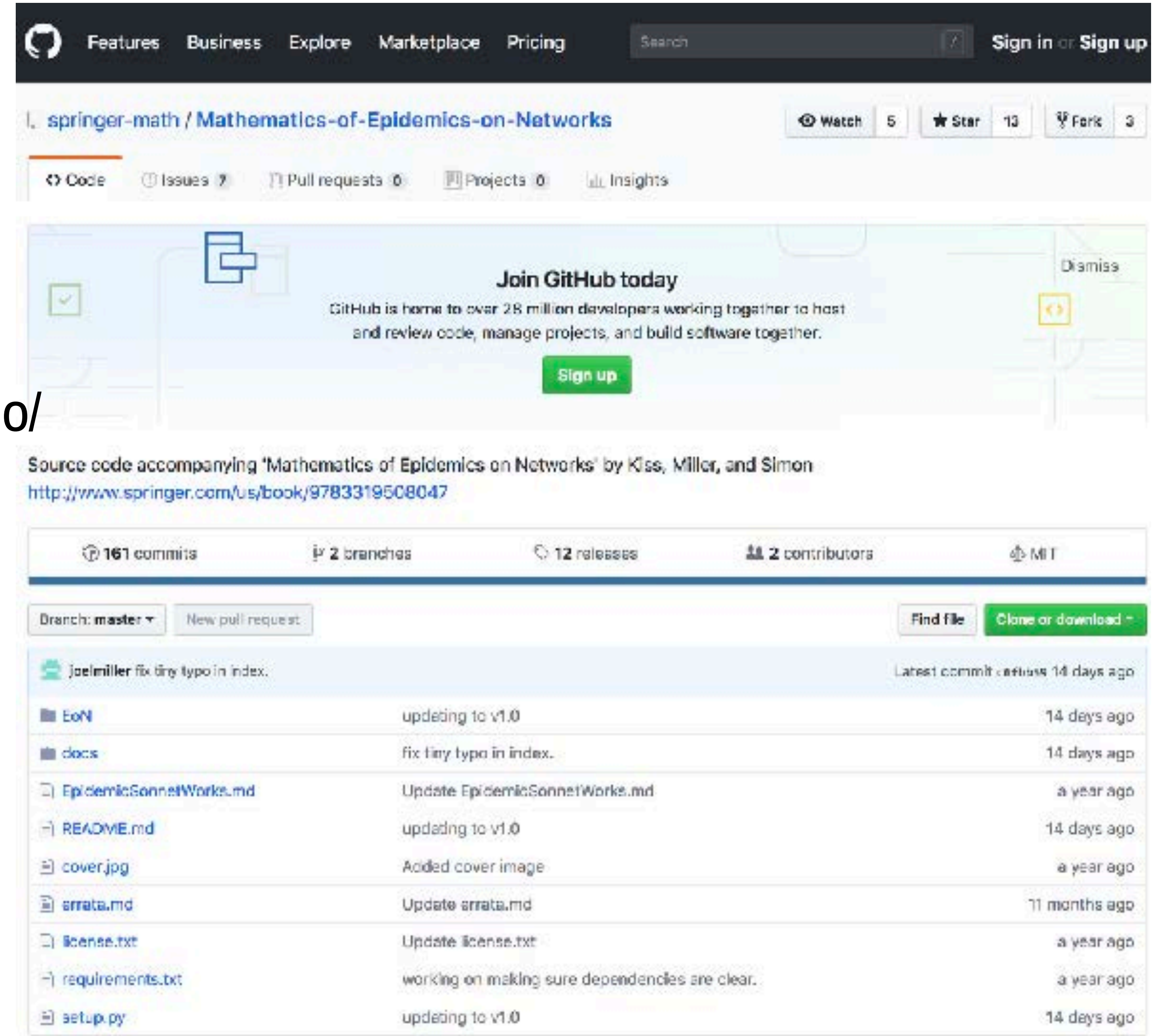
https://github.com/eugenio-valdano/threshold

python package: spreading dynamics on networks

github.com/springer-math/Mathematics-of-Epidemics-on-Networks

epidemicsonnetworks.readthedocs.io/en/latest/index.html

Mathematics of Epidemics on Networks' by Kiss, Miller, and Simon



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Source code accompanying 'Mathematics of Epidemics on Networks' by Kiss, Miller, and Simon
http://www.springer.com/us/book/9783319508047

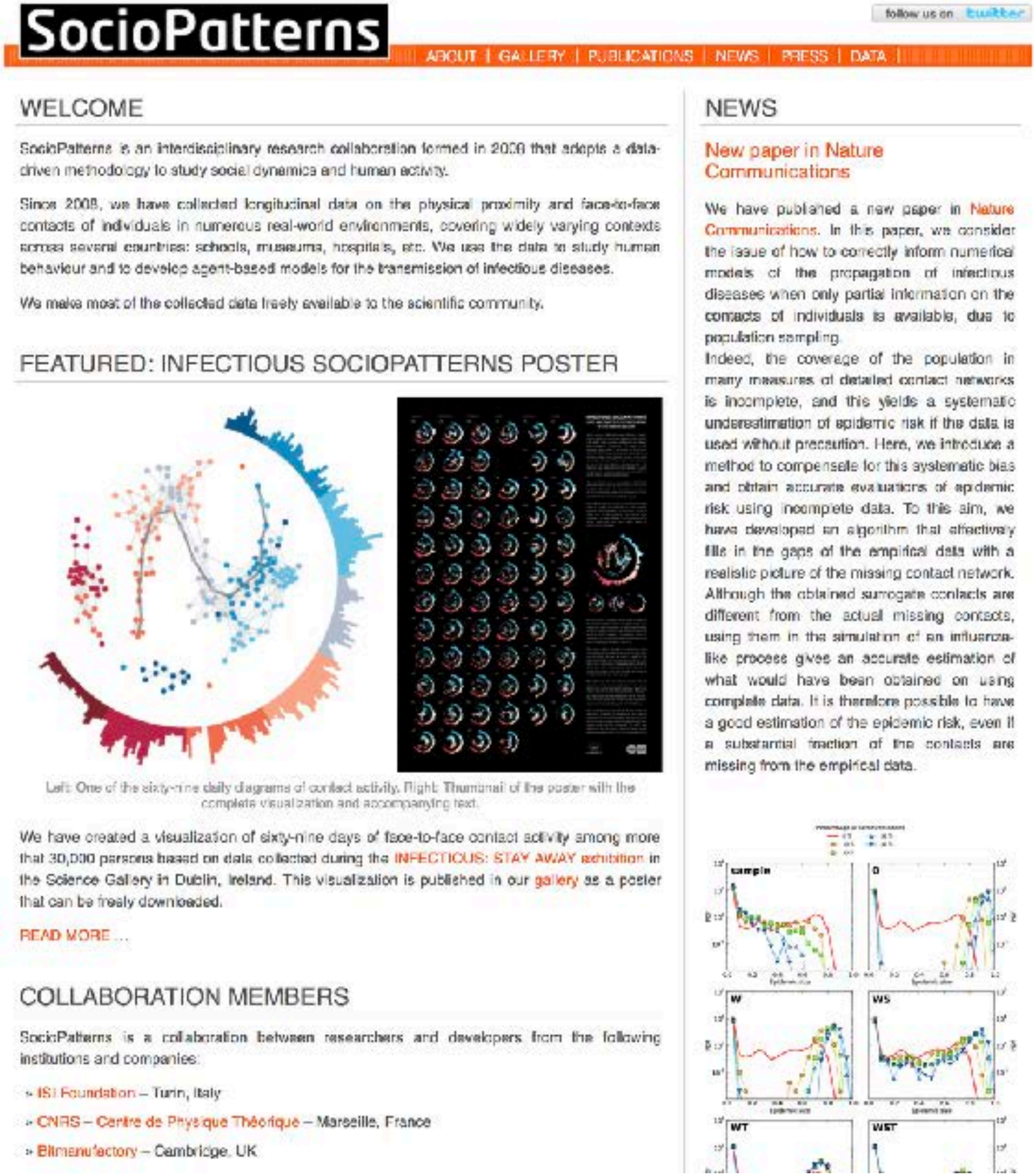
161 commits · 2 branches · 12 releases · 2 contributors · MIT

joelmiller fix tiny typo in index. Latest commit [illegible] 14 days ago

EoN	updating to v1.0	14 days ago
docs	fix tiny typo in index.	14 days ago
EpidemicSonnetWorks.md	Update EpidemicSonnetWorks.md	a year ago
README.md	updating to v1.0	14 days ago
cover.jpg	Added cover image	a year ago
errata.md	Update errata.md	11 months ago
license.txt	Update license.txt	a year ago
requirements.txt	working on making sure dependencies are clear.	a year ago
setup.py	updating to v1.0	14 days ago

data: sociopatterns.org

Close proximity interaction data collected with RFID tags in different settings



WELCOME

SocioPatterns is an interdisciplinary research collaboration formed in 2008 that adopts a data-driven methodology to study social dynamics and human activity.

Since 2008, we have collected longitudinal data on the physical proximity and face-to-face contacts of individuals in numerous real-world environments, covering widely varying contexts across several countries: schools, museums, hospitals, etc. We use the data to study human behaviour and to develop agent-based models for the transmission of infectious diseases.

We make most of the collected data freely available to the scientific community.

FEATURED: INFECTIOUS SOCIOPATTERNS POSTER

Left: One of the sixty-nine daily diagrams of contact activity. Right: Thumbnail of the poster with the complete visualization and accompanying text.

We have created a visualization of sixty-nine days of face-to-face contact activity among more that 30,000 persons based on data collected during the INFECTIOUS: STAY AWAY exhibition in the Science Gallery in Dublin, Ireland. This visualization is published in our gallery as a poster that can be freely downloaded.

READ MORE ...

COLLABORATION MEMBERS

SocioPatterns is a collaboration between researchers and developers from the following institutions and companies:

- ISI Foundation – Turin, Italy
- CNRS – Centre de Physique Théorique – Marseille, France
- Bitmanufactory – Cambridge, UK

NEWS

New paper in Nature Communications

We have published a new paper in Nature Communications. In this paper, we consider the issue of how to correctly inform numerical models of the propagation of infectious diseases when only partial information on the contacts of individuals is available, due to population sampling.

Indeed, the coverage of the population in many measures of detailed contact networks is incomplete, and this yields a systematic underestimation of epidemic risk if the data is used without precaution. Here, we introduce a method to compensate for this systematic bias and obtain accurate evaluations of epidemic risk using incomplete data. To this aim, we have developed an algorithm that effectively fills in the gaps of the empirical data with a realistic picture of the missing contact network. Although the obtained surrogate contacts are different from the actual missing contacts, using them in the simulation of an influenza-like process gives an accurate estimation of what would have been obtained on using complete data. It is therefore possible to have a good estimation of the epidemic risk, even if a substantial fraction of the contacts are missing from the empirical data.

SIR on network: pseudo-code

A_{ij} Adjacency matrix

n number of nodes

β transmission probability per link & per time step

- One variable=one individuals

Vector = (a_1,a_2,a_3,……………………….a_n)

For instance Tim= a_3

- We assign possible states to each value of each variable

a_i =0 => susceptible
a_i =1 => infected
a_i= 2 => removed

SIR on network: pseudo-code

A_{ij} Adjacency matrix

n number of nodes

β transmission probability per link & per time step

```
Do i=1, n
    If $a_i(t)=1$ with probability $\mu$ $\Longrightarrow$ $a_i(t+1)=2$
    If $a_i(t)=0$ then
    Do j=1, n
        If $A_{ij}=1$ and $a_j(t)=1$
        With proability $\beta$ $\Longrightarrow$ $a_i(t+1)=1$
    End do
End do
```

Repeat over time step until a_i is only 0 or 2

At each time step measure the quantities of infected etc.

thank you!

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