Epidemics on Networks

Introduction to Network Science

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Content

- **Degree-based solution of SIS model on SF networks**
- **Real-world network epidemiology**

Modeling epidemics

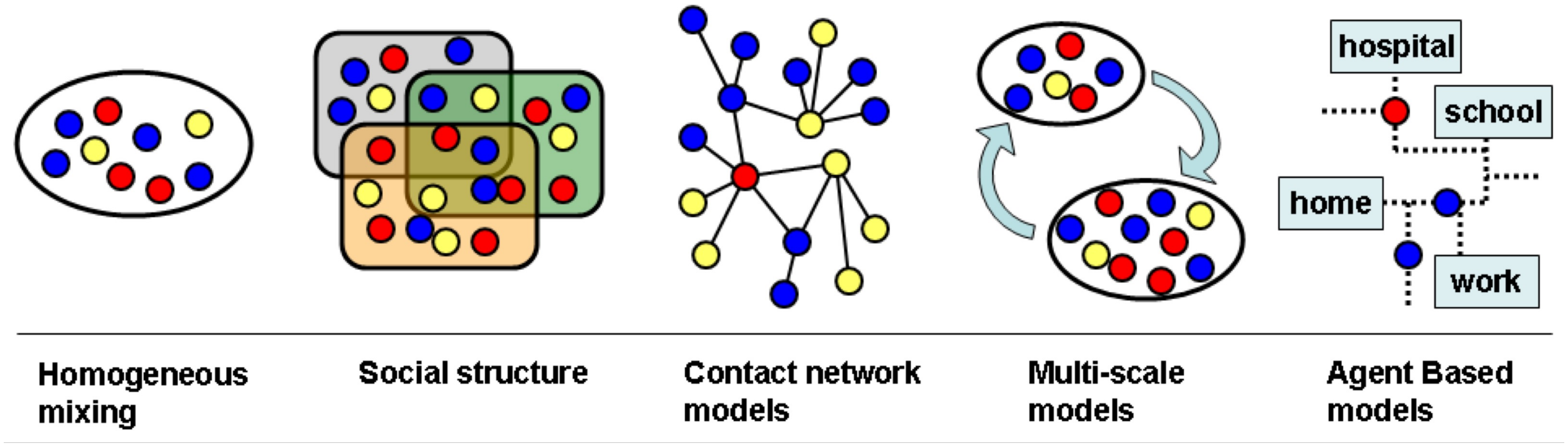
- **Modeling Epidemic process (dynamics):**
  - Branching process
  - SI model
  - SIR model
  - SIS model
- **Modeling underlying network substrate (static)**
  - Mean-field mixing (fully connected network)
  - Homogeneous networks (ER networks)
  - Heterogeneous networks (SF networks)

Modeling underlying network

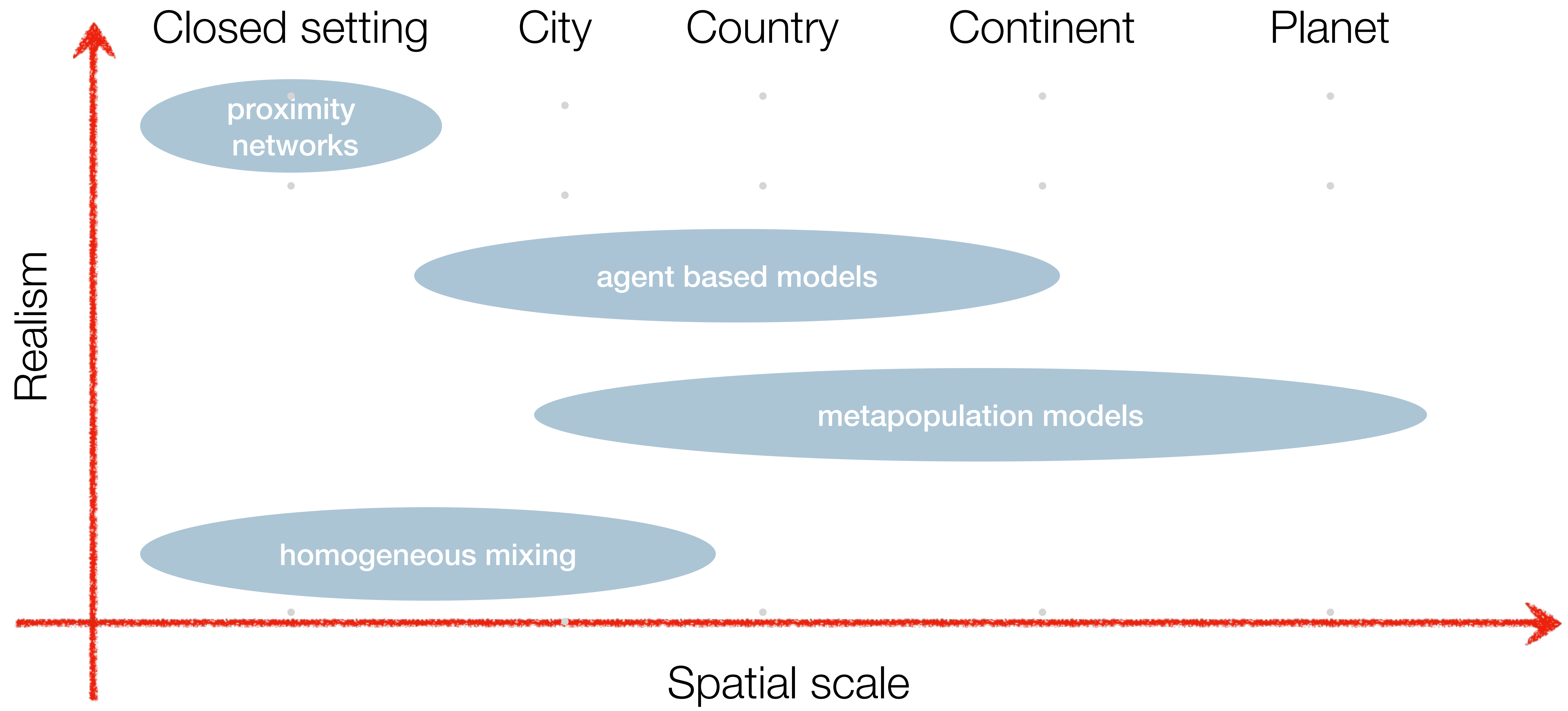
reality

abstraction,
conceptualization

Modeling underlying networks

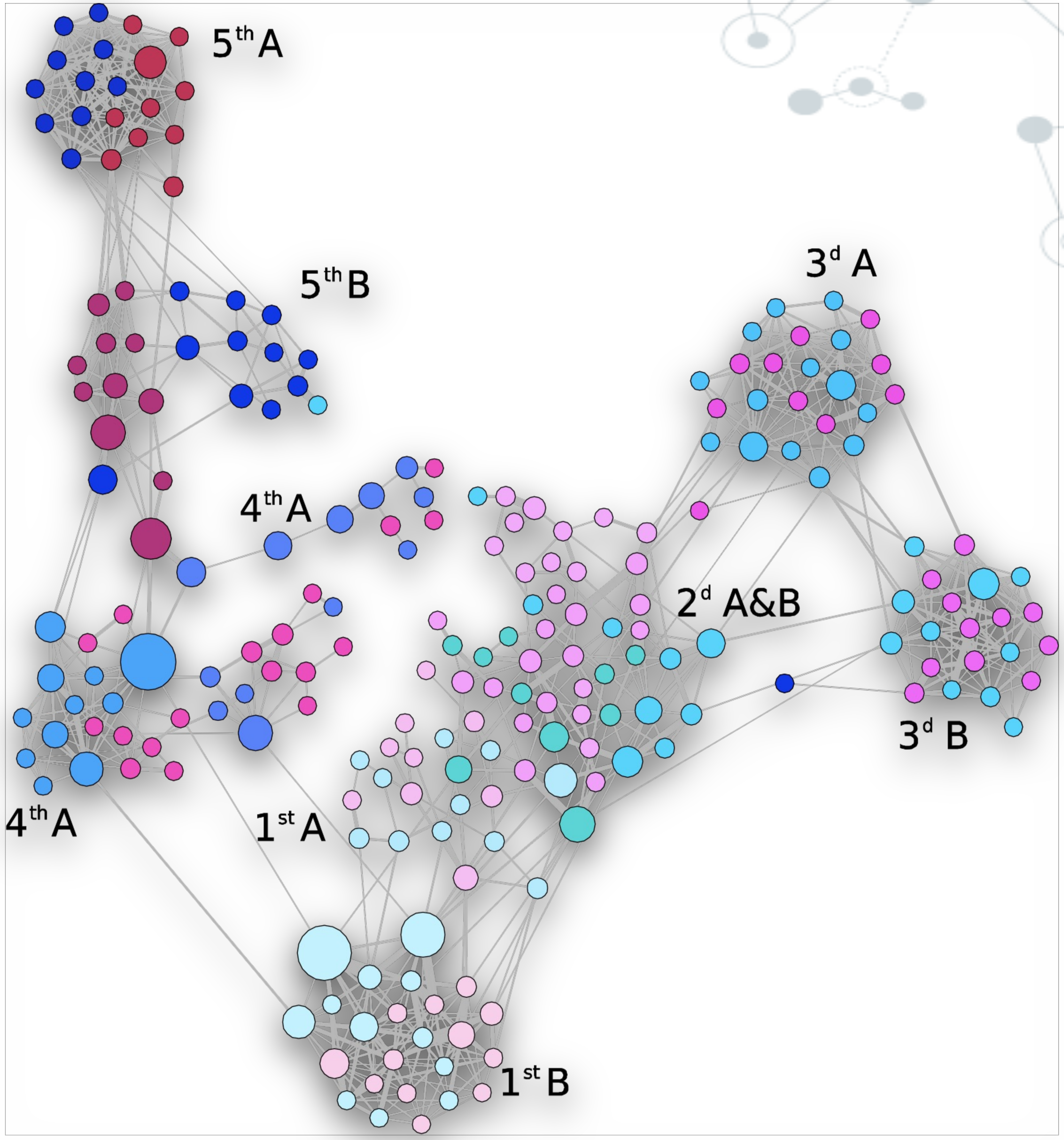


Spatial scales



Epidemics on networks

- Homogeneous mixing is not always realistic
- Contacts are not equal and not constant across groups.
- Real contact networks display high heterogeneities



Degree-based solution of the SIS model on scale-free networks

Epidemics on networks

- We consider a network of N nodes where each node can be in an epidemic state, S, I or R
- We define the density of nodes in a given state, as:

$$\rho^S(t) = \frac{S(t)}{N}, \rho^I(t) = \frac{I(t)}{N}, \rho^R(t) = \frac{R(t)}{N}$$

Degree-based mean field

- Nodes with the **same degree** k are considered as **statistically equivalent**
- Fraction of nodes in each compartment: $\rho_k^\alpha,\ \alpha = S, I, R$
- These variables are not independent: $\sum_\alpha \rho_k^\alpha = 1$
- Fraction of individuals in compartment α at time t to $\rho^\alpha(t) = \sum_k P(k)\rho_k^\alpha(t)$

Degree-based mean field

- The network is considered in a mean-field perspective (**annealed network** approximation).
- The adjacency matrix is completely “destroyed”. Only the degree and the two-vertex correlations of each node are preserved.
- The adjacency matrix is replaced by its ensemble average:

$$\overline{A}_{ij} = \frac{k_j P(k_i|k_j)}{N P(k_i)}$$

The DBMF SIS model

$$\frac{d\rho_k^I(t)}{dt} = \beta k \left[1 - \rho_k^I(t)\right] \sum_{k'} P(k'|k)\rho_{k'}^I(t) - \mu\rho_k^I(t)$$

Sum over all possible k'

Number of nodes recovering

Transmission happens over k links

Prob of finding a node with degree k, susceptible

Probability that a node of degree k is connected to an infected node of degree k'

The DBMF SIS model

$$\frac{d\rho_k^I(t)}{dt} = \beta k[1 - \rho_k^I(t)]\sum_{k'} P(k'|k)\rho_{k'}^I(t) - \mu\rho_k^I(t)$$

If we assume the network to be **uncorrelated:** $P(k'|k) = \frac{k'P(k')}{\langle k \rangle}$

then $\frac{d\rho_k^I(t)}{dt} = \boldsymbol{\beta} k[1 - \rho_k^I(t)]\Theta - \mu\rho_k^I(t)$

where $\Theta = \sum_{k'} \frac{k'P(k')}{\langle k \rangle} \rho_{k'}^I(t)$ **prob. of finding an infected node following a randomly chosen edge**

Solution

Early stage approximation: $\rho_k^I(t) \ll 1$

then $$\frac{d\Theta}{dt} = \left(\frac{\beta}{\mu}\frac{\langle k^2\rangle}{\langle k\rangle} - 1\right)\Theta$$

which implies that Θ will grow only if:

$$\frac{\beta}{\mu} > \frac{\langle k\rangle}{\langle k^2\rangle}$$

Epidemic threshold

The DBMF threshold

$$\frac{\beta}{\mu} > \frac{\langle k \rangle}{\langle k^2 \rangle}$$

- In an infinite scale-free network, with $P(k) \sim k^{-\gamma}$, and $2 \leq \gamma \leq 3$, $\langle k^2 \rangle \to \infty$ which implies that **the epidemic threshold vanishes** .
- There is a finite prevalence for any value of the spreading parameters.

Homogeneous networks

In the case of a **homogeneous network** with a regular (Poisson) degree distribution:

$$\langle k^2 \rangle = \langle k \rangle^2 + \langle k \rangle$$

$$\langle k^2 \rangle / \langle k \rangle \simeq \langle k \rangle$$

The epidemic threshold then becomes:

$$\frac{\beta}{\mu} \gtrsim \frac{1}{\langle k \rangle}$$

which is finite and it does only depend on the average connectivity of the network.

Immunization

In the case of complex networks, we can consider three different immunization strategies:

- uniform immunization
- proportional immunization
- targeted immunization

Uniform immunization

In the case of uniform immunization, **individuals are randomly chosen to be vaccinated** with a density of immune nodes g.

This corresponds to an effective rescaling of the spreading rate:

$$\beta \rightarrow \beta(1-g)$$

The threshold is affected in a uniform way:

$$\frac{\beta}{\mu}(1-g) > \frac{\langle k \rangle}{\langle k^2 \rangle}$$

Uniform immunization

$$\frac{\beta}{\mu}(1-g) > \frac{\langle k \rangle}{\langle k^2 \rangle}$$

In infinite scale-free network, with $P(k) \sim k^{-\gamma}$, and $2 \leq \gamma \leq 3$, $\langle k^2 \rangle \rightarrow \infty$

which implies that the **uniform immunization is not effective** unless we

immunize all the network: $g = 1$

Proportional immunization

We can find a better solution through a **proportional immunization**.

Let us define the fraction of immune individuals with connectivity k: g_k

If we impose the condition:

$$\tilde{\beta} \equiv \beta k(1 - g_k) = const.$$

The system equation becomes:

$$\frac{d\rho_k^I(t)}{dt} = \tilde{\beta}[1 - \rho_k^I(t)]\Theta - \mu\rho_k^I(t)$$

Proportional immunization

In the case of early stage approximation and low density of infectious individuals, we recover an epidemic threshold:

$$\beta k(1 - g_k) - \mu > 0$$

which defines a threshold on density of immunized individuals:

$$g_k > 1 - \frac{\mu}{\beta k}$$

for every class of degree k, to stop the epidemic.

Targeted immunization

Optimum approach: immunize a fraction of all nodes with the largest degree.

This way we introduce a cut-off in the degree distribution.

We need to immunize a fraction of nodes g such that:

$$\frac{\beta}{\mu} < \frac{\langle k \rangle_g}{\langle k^2 \rangle_g}$$

In the case of the BA network, it is possible to show that: $g_c \simeq e^{-\frac{2\mu}{m\beta}}$

The fraction of nodes to immunize is exponentially small with. β

How do we find the hubs?

- Targeted immunisation is very hard to achieve in practice, the full network structure is not known
- We need a strategy to find hubs based on a **local knowledge** of the network
- In scale-free networks, this can be done efficiently with the **acquaintance immunisation** (Cohen et al. Phys. Rev. Lett. 2003)
- Instead of immunizing nodes at random, we pick random nodes and for each we immunise one of their neighbours at random.

How do we find the hubs?

- Instead of immunizing nodes at random, we pick random nodes and for each we immunise one of their neighbours at random.

$$k_{nn}^{\mathbf{unc}} = \frac{\langle k^2 \rangle}{\langle k \rangle}$$

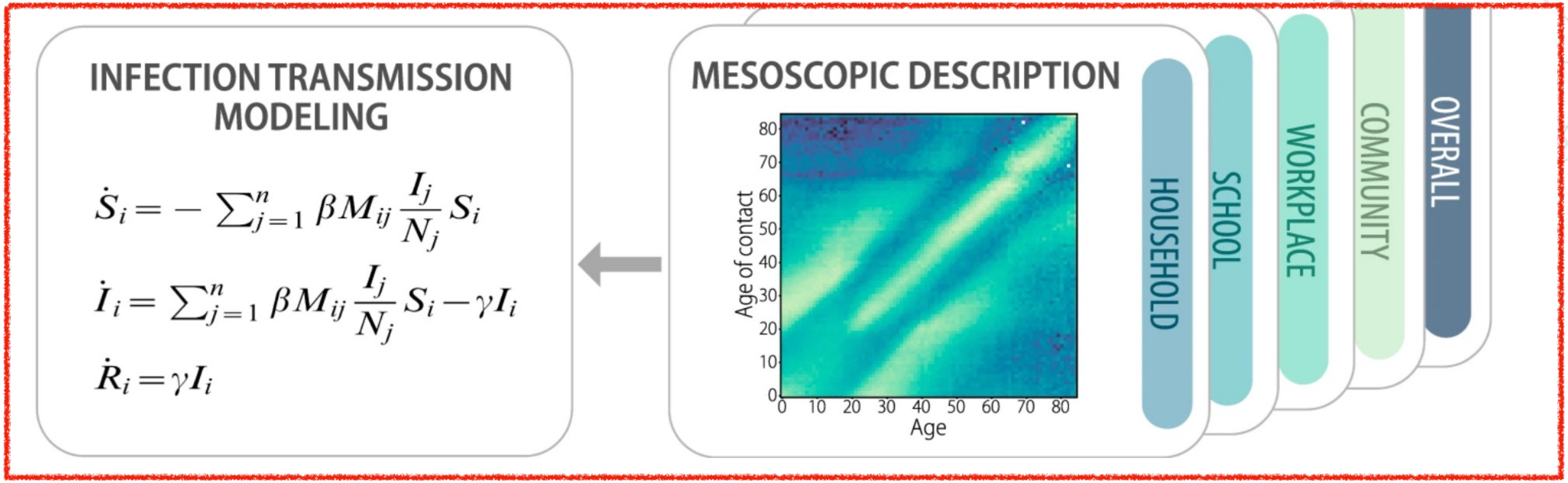
- My neighbours are more probably hubs than myself! This is also known as the **friendship paradox**

Real network epidemiology

Real network epidemiology

- More sophisticate compartmental models (incubation period, hospitalization)
- Age-structured population
- Estimation of real contact matrices
- Mobility
- Lots of numerical simulations (no nice analytical solutions!)

Age-structured models



- Compartments are structured into n age classes
- M_{ij} represents the average contact rate between individuals of age i and j

Contact matrices

- Contact matrices can be estimated in different ways

- Through **empirical surveys,** which are more accurate but require significant resources (Mossong et al. 2008).

- By the creation of **synthetic populations** (Fumanelli et al. 2012).

PLOS COMPUTATIONAL BIOLOGY

OPEN ACCESS PEER-REVIEWED

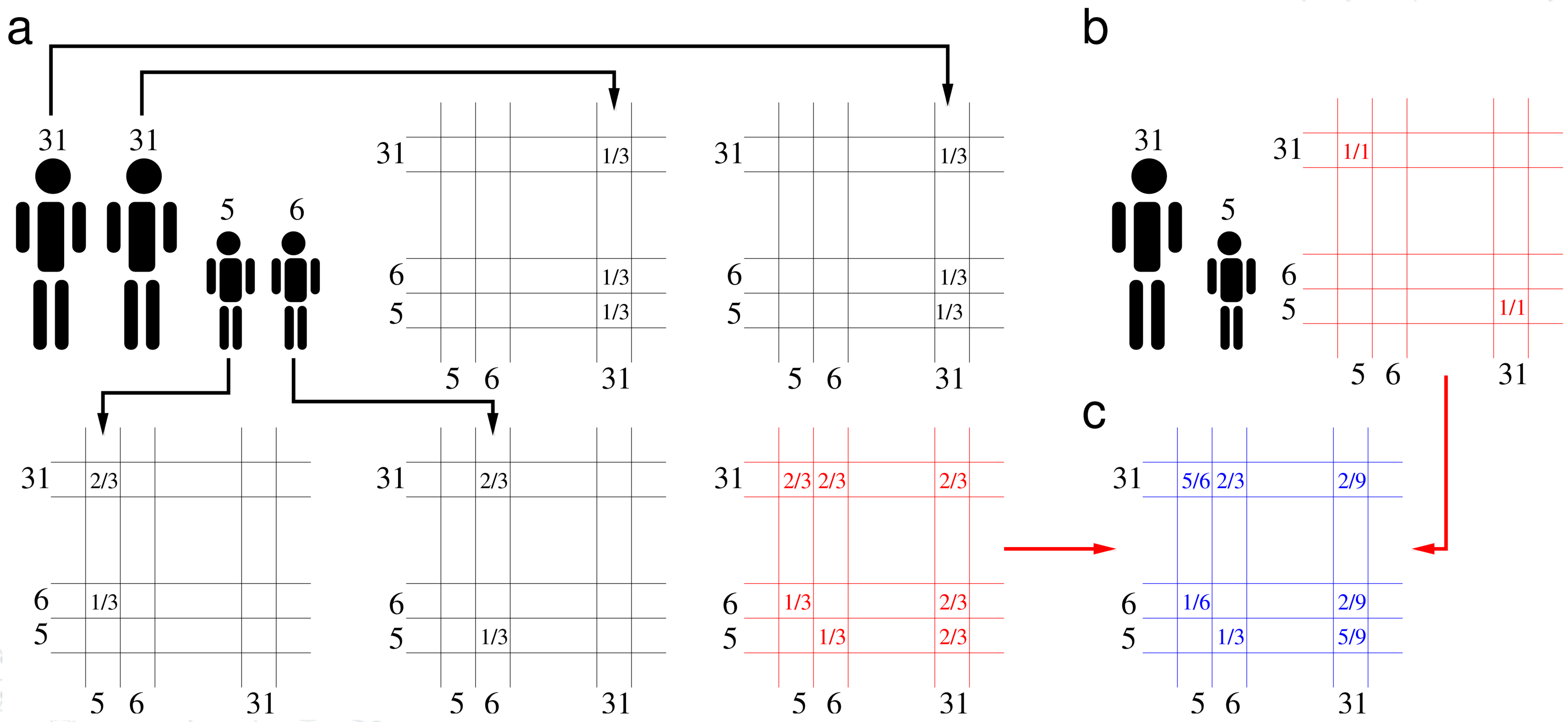
RESEARCH ARTICLE

Inferring the Structure of Social Contacts from Demographic Data in the Analysis of Infectious Diseases Spread

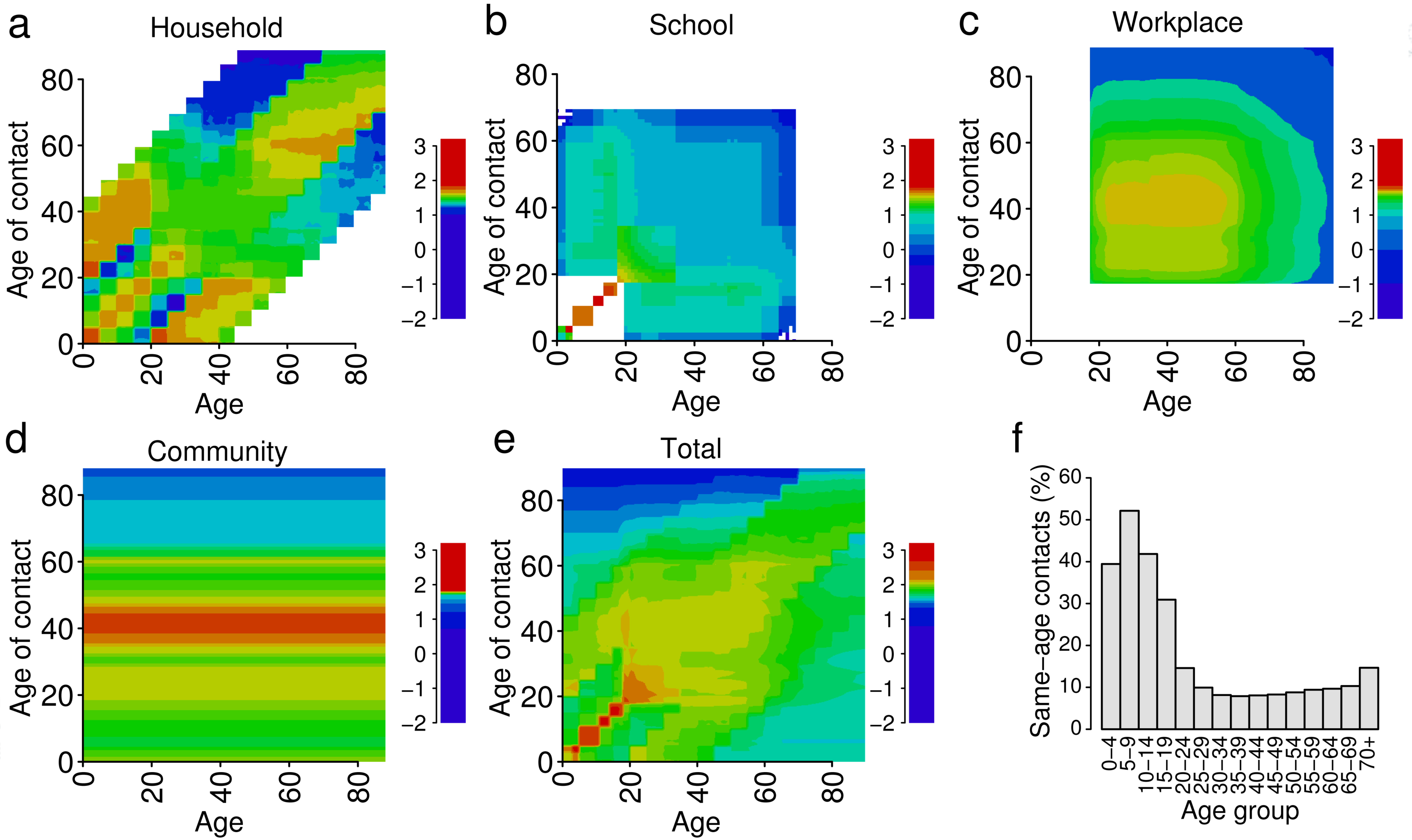
Laura Fumanelli, Marco Ajelli, Piero Manfredi, Alessandro Vespignani, Stefano Merler

Published: September 13, 2012 • https://doi.org/10.1371/journal.pcbi.1002673

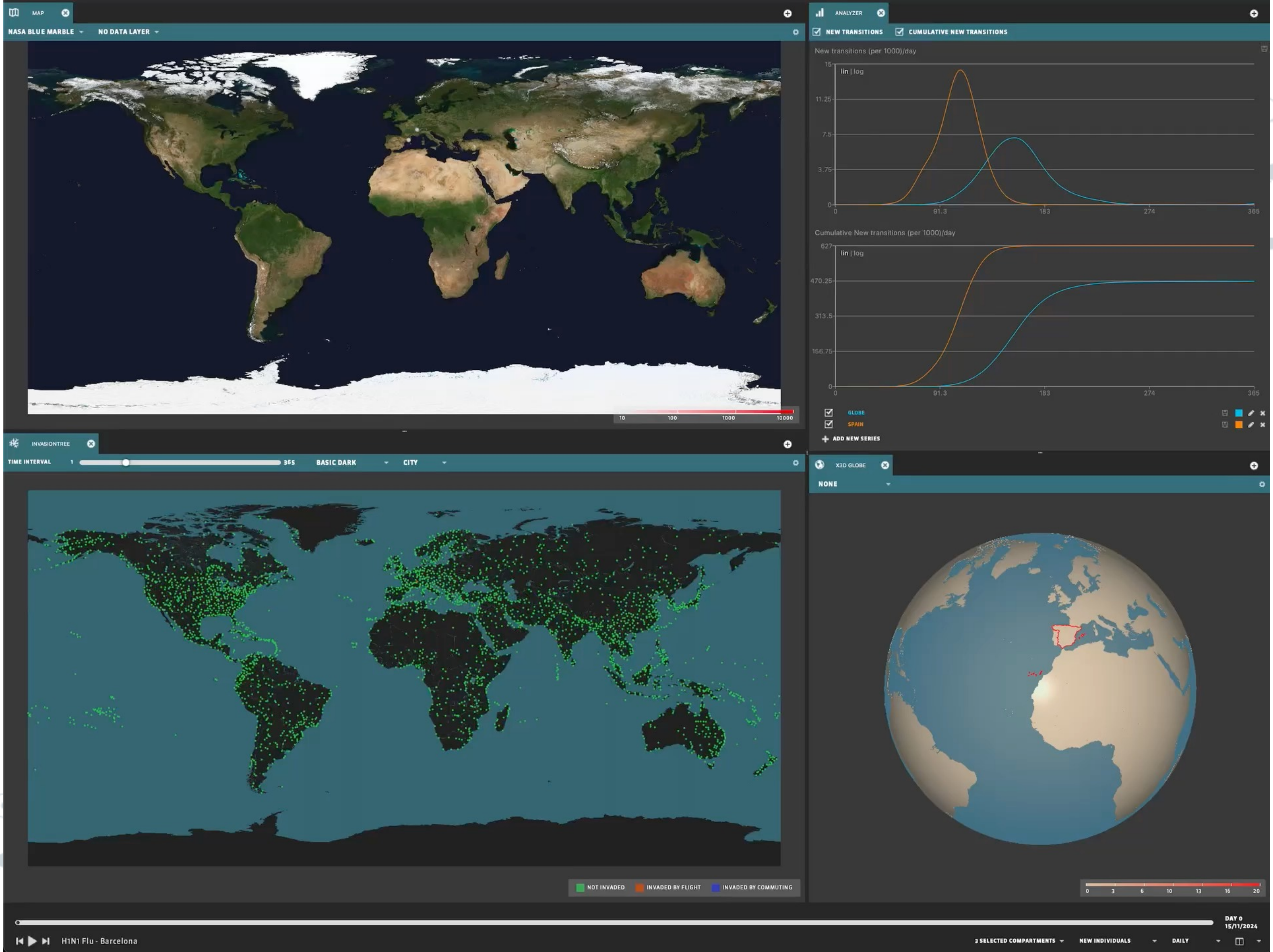
Synthetic populations



Synthetic populations

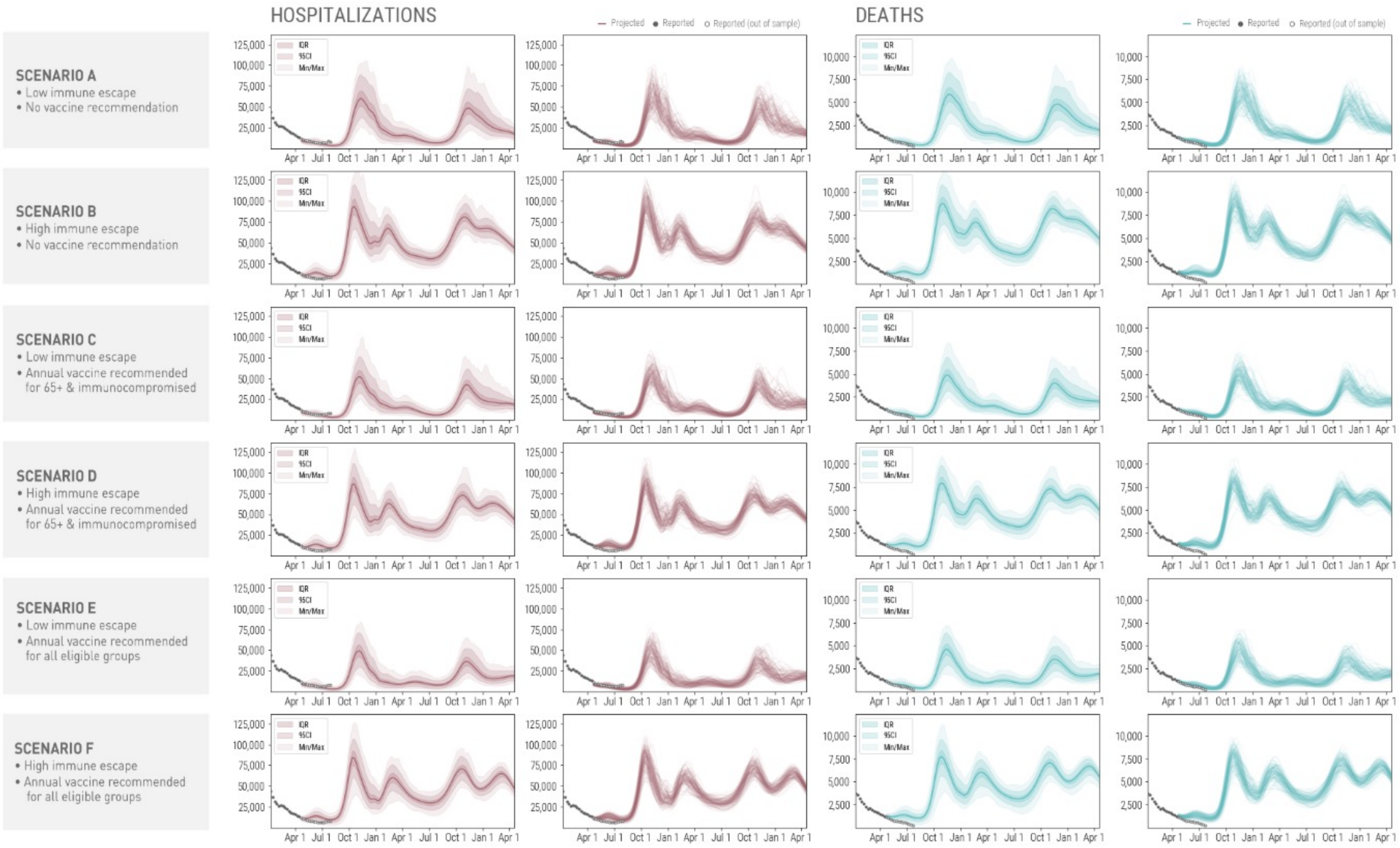


Global Epidemic and Mobility project
https://www.youtube.com/watch?v=YstB9VWDUqE


MAP
NASA BLUE MARBLE
NO DATA LAYER
ANALYZER
NEW TRANSITIONS
CUMULATIVE NEW TRANSITIONS
New transitions (per 1000)/day
lin | log
Cumulative New transitions (per 1000)/day
GLOBE
SPAIN
ADD NEW SERIES
INVASIONTREE
TIME INTERVAL
BASIC DARK
CITY
X3D GLOBE
NONE
NOT INVADED
INVADED BY FLIGHT
INVADED BY COMMUTING
H1N1 Flu - Barcelona
DAY 0
15/11/2024
3 SELECTED COMPARTMENTS
NEW INDIVIDUALS
DAILY

UNITED STATES SCENARIO PROJECTIONS

https://www.gleamproject.org/covid19-scenario-projections



Sources

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- Pastor-Satorras, and Vespignani. Epidemic spreading in scale-free networks. Phys. Rev. Lett. 86, 14 (2000)
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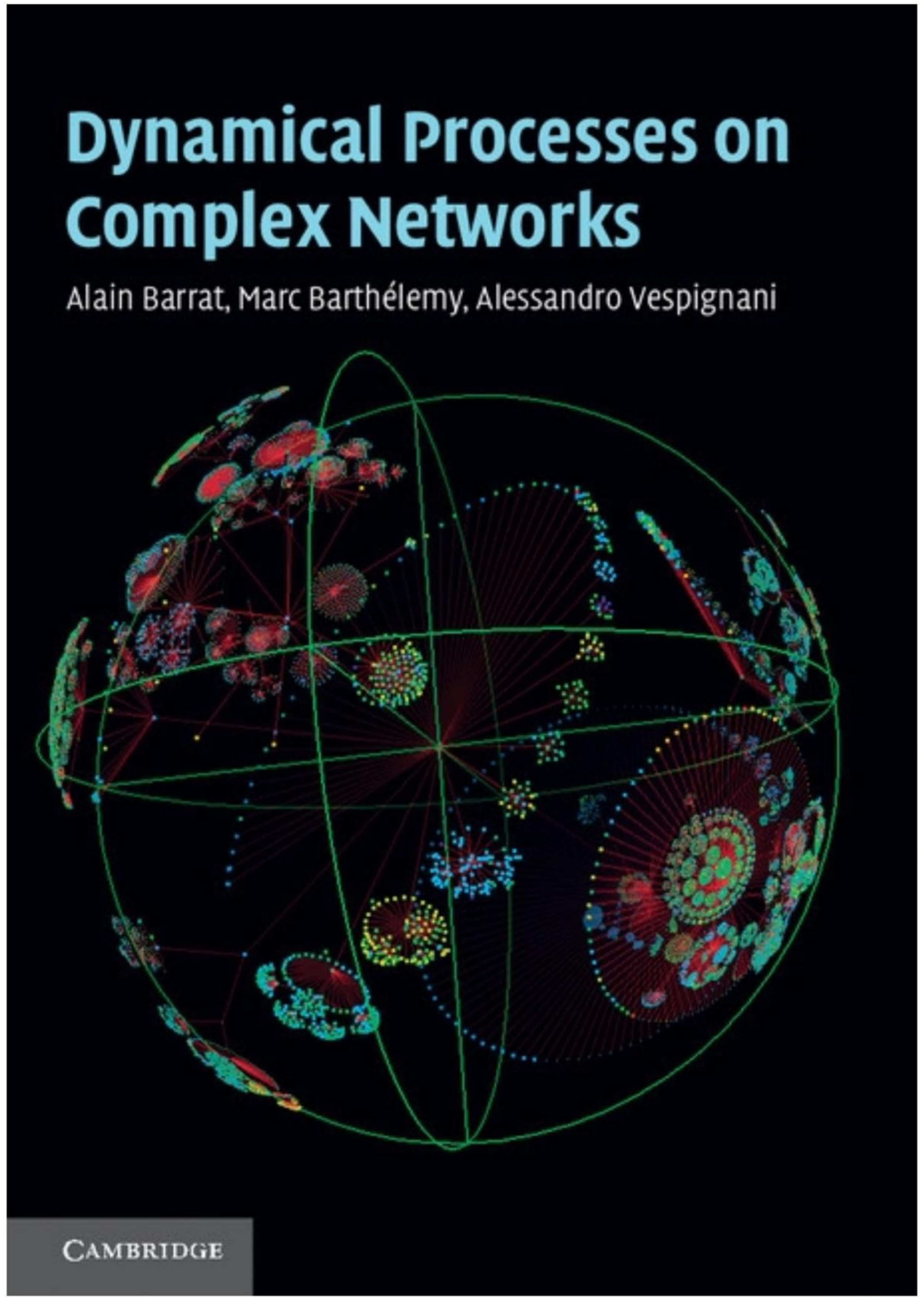

Thank you!

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