“Mathematical and data-driven models of infectious disease spreading”

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Cosnet

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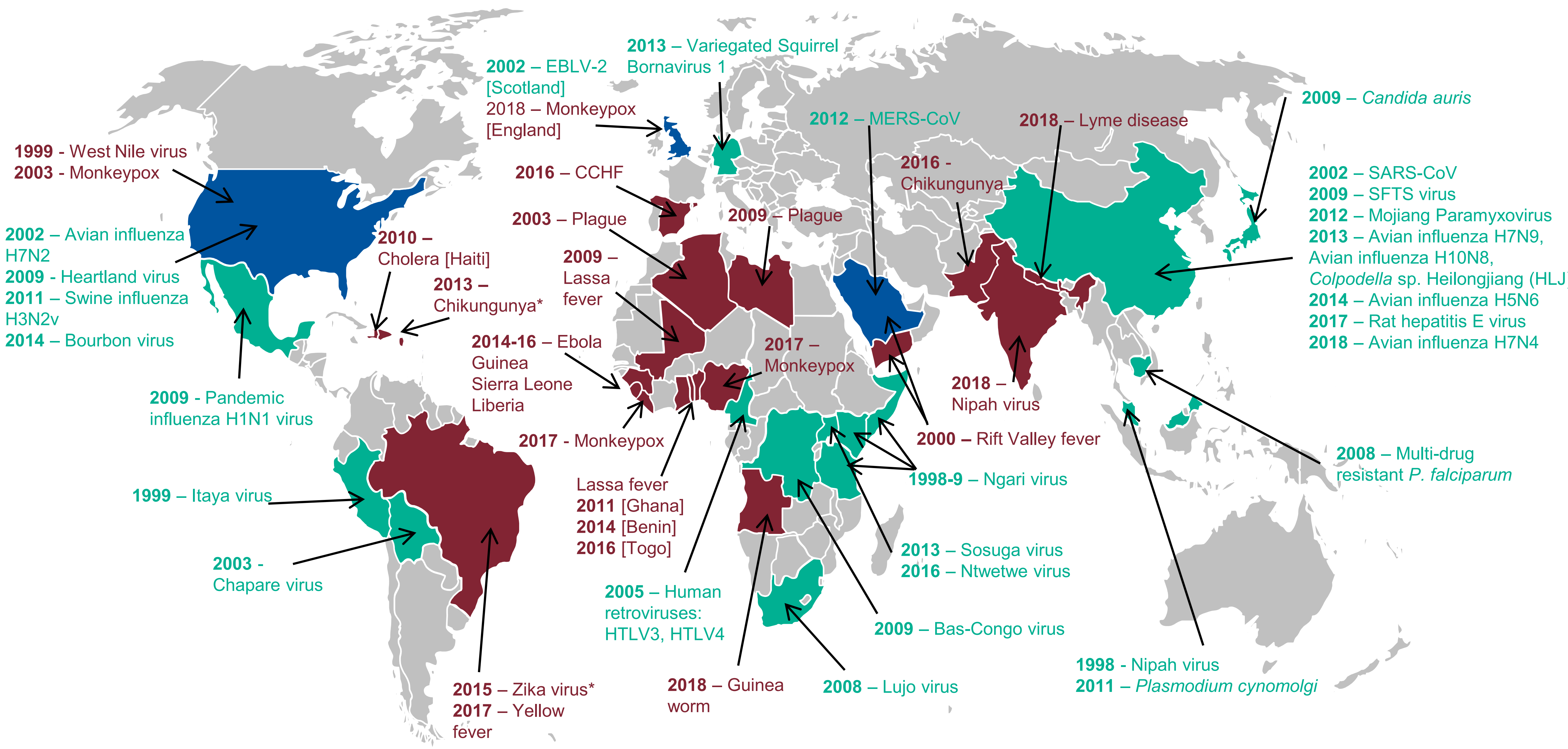
CENTAI

Global map of significant and new emerging infections in humans: spread to new areas since 1998

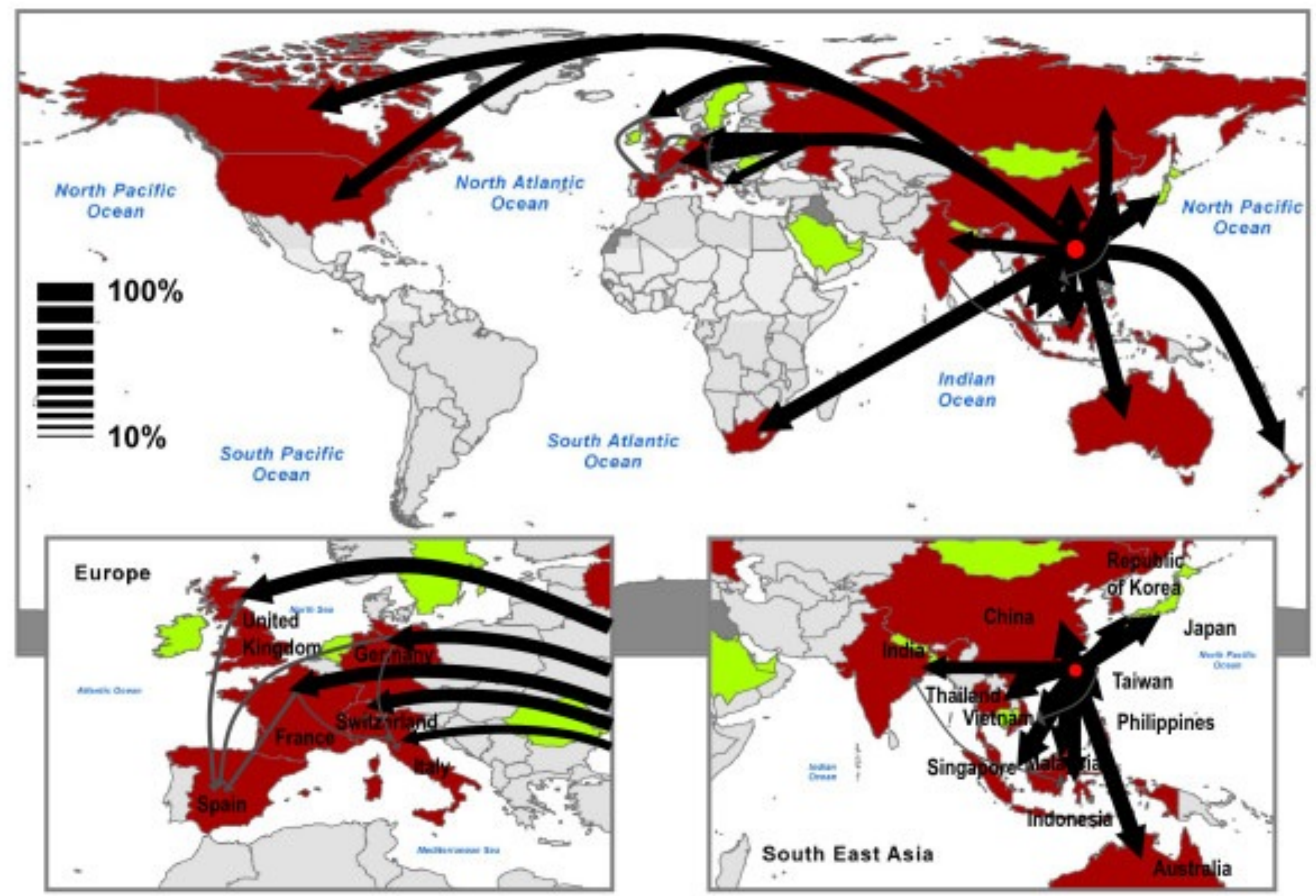


Newly identified emerging infection | Disease spread to new area | Emerging infection and disease spread

*Incursion followed by regional spread

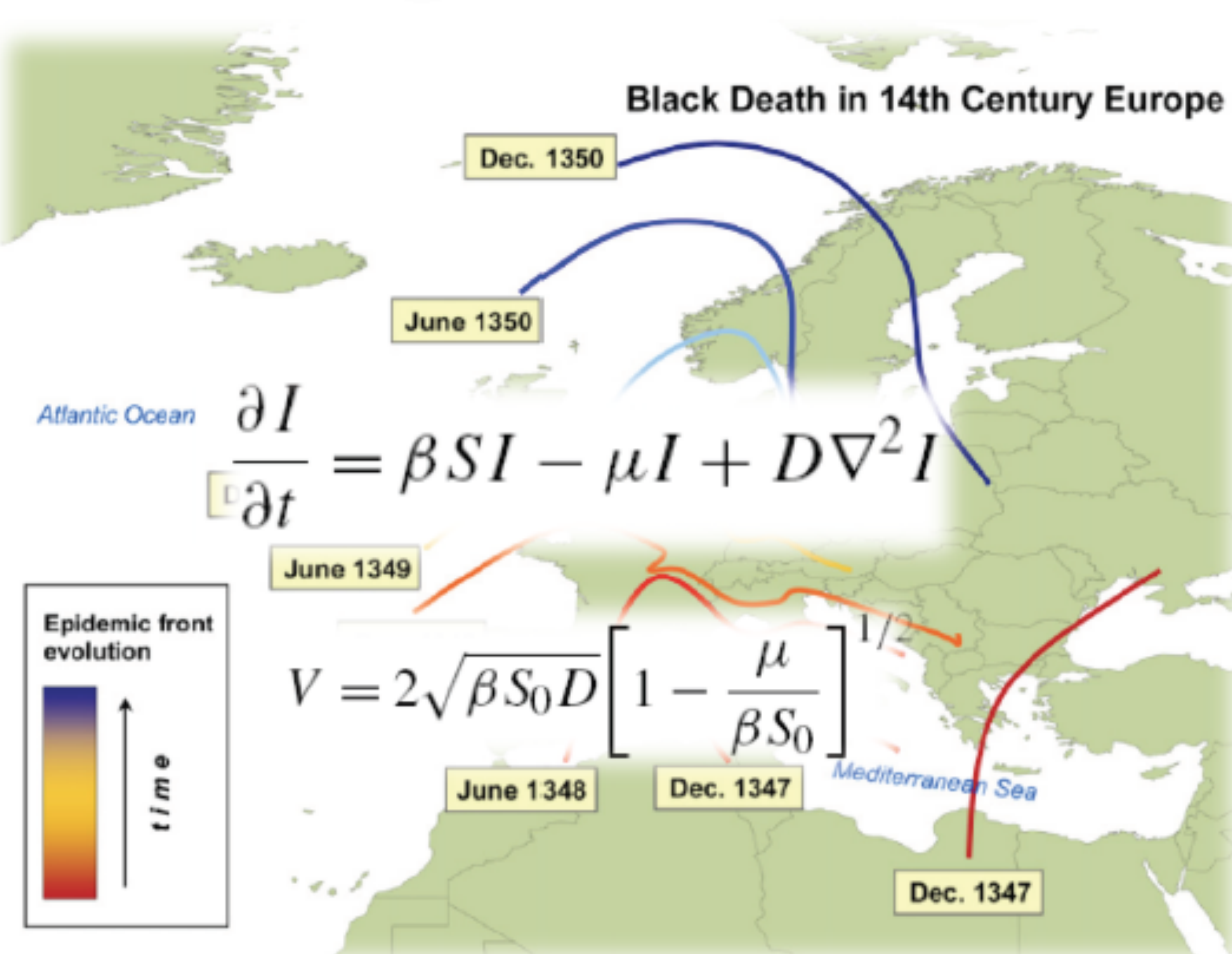
Despite all efforts, the prediction of the course and unfolding of a large-scale disease is a major challenge.

Why?



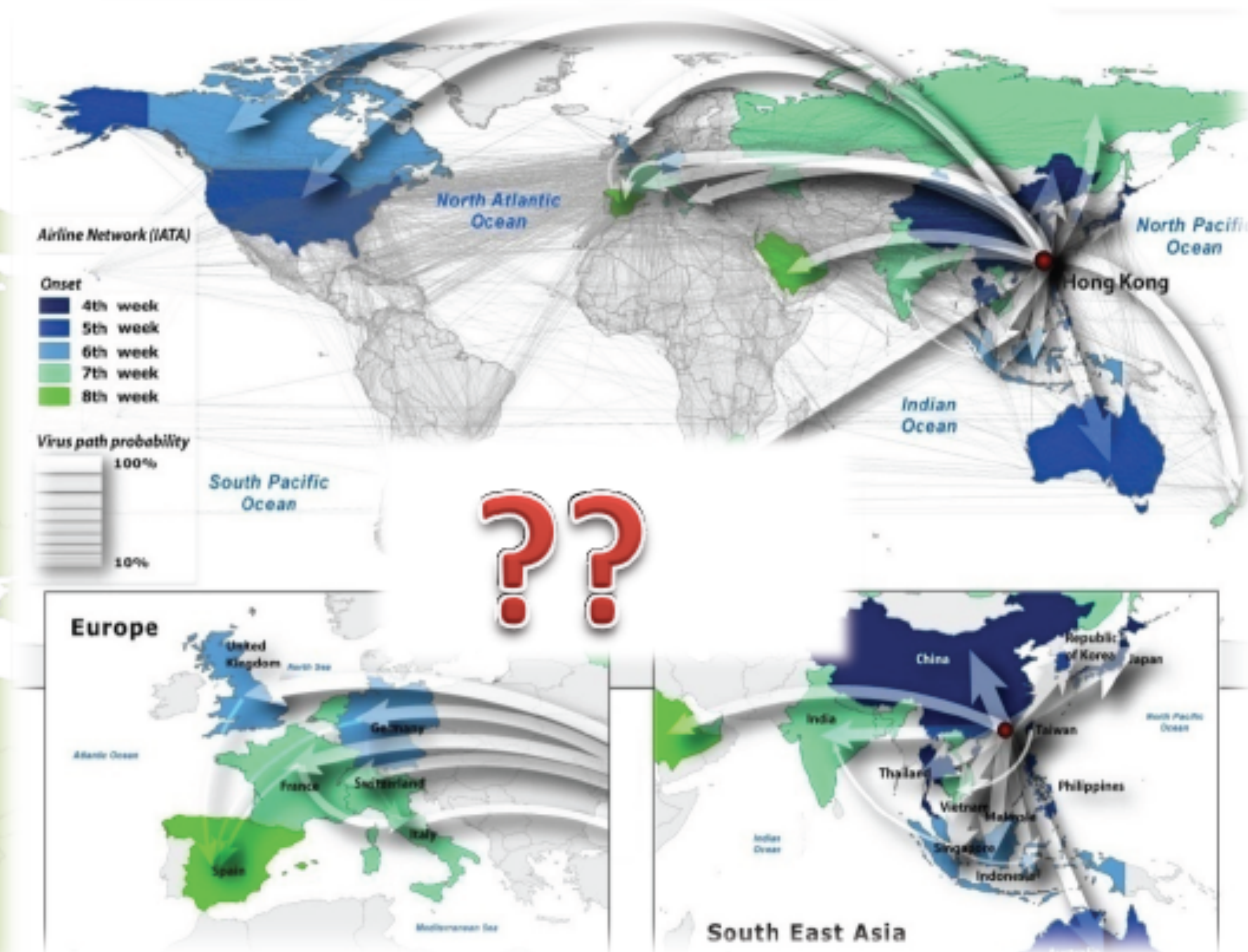
Black death in1347: a continuous diffusion process

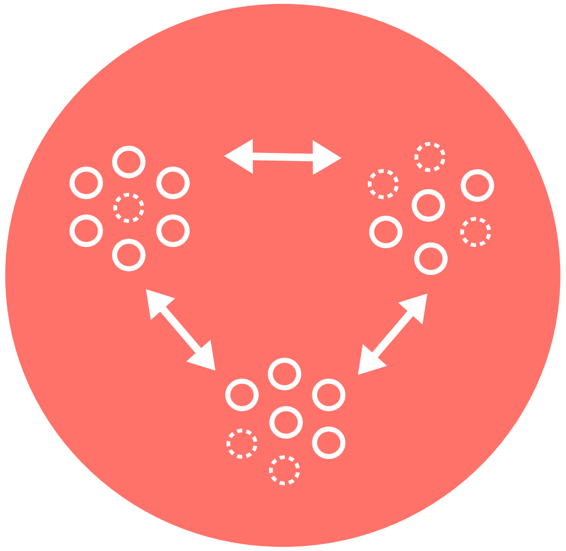
SARS epidemics: a discrete network driven process



$$\frac{\partial I}{\partial t} = \beta SI - \mu I + D\nabla^2 I$$

$$V = 2\sqrt{\beta S_0 D}\left[1 - \frac{\mu}{\beta S_0}\right]^{1/2}$$





What do we need to include?

- How the disease is transmitted
- What are the disease stages
- Human behavioural changes

What has changed?

What has changed?

The system is even more complex: humans adapt, which in principle makes predictions harder.

Interaction with the Environment

Experiment:

- Participants must pay for the milk consumed with coffee or tea.

- The amount due is fixed, but each one decides whether to pay or not.

- Each week the deposited money is collected.

*- **Biology letters,** 2(3): 412-414; 2006. "**Cues of being watched enhance cooperation in a real-world setting**" . M. Bateson, D. Nettle and G. Roberts.*

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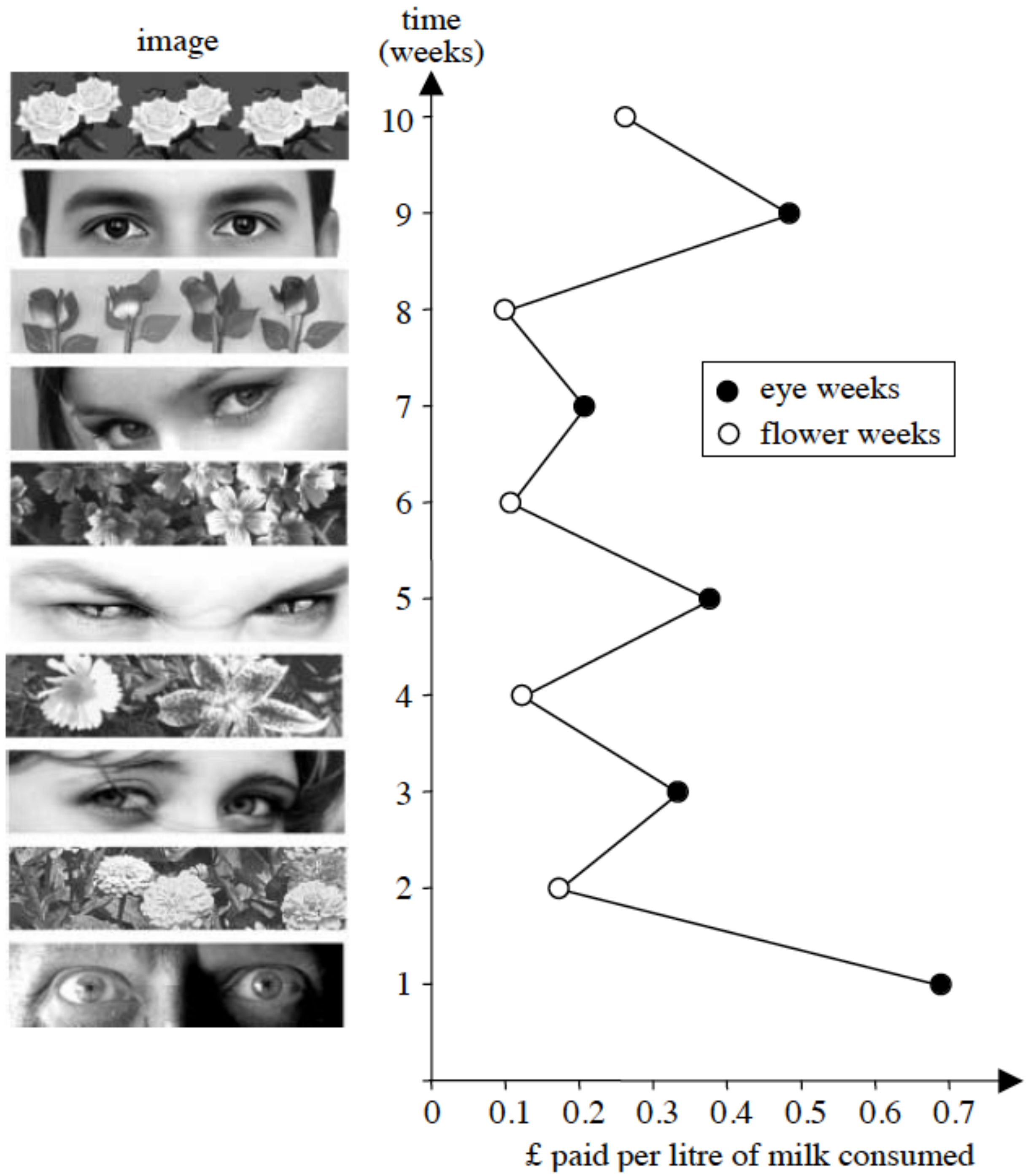
Interaction with the Environment



Experiment:

- Participants must pay for the milk consumed with coffee or tea.

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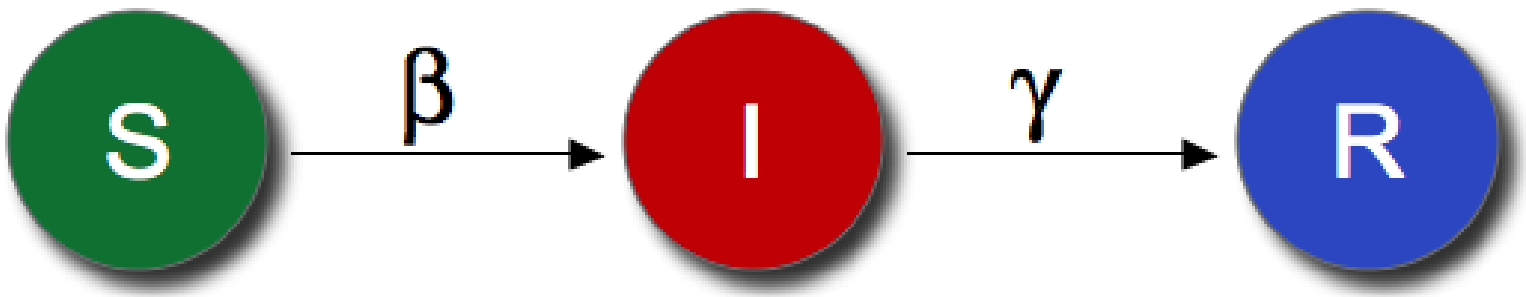
- Each week the deposited money is collected.

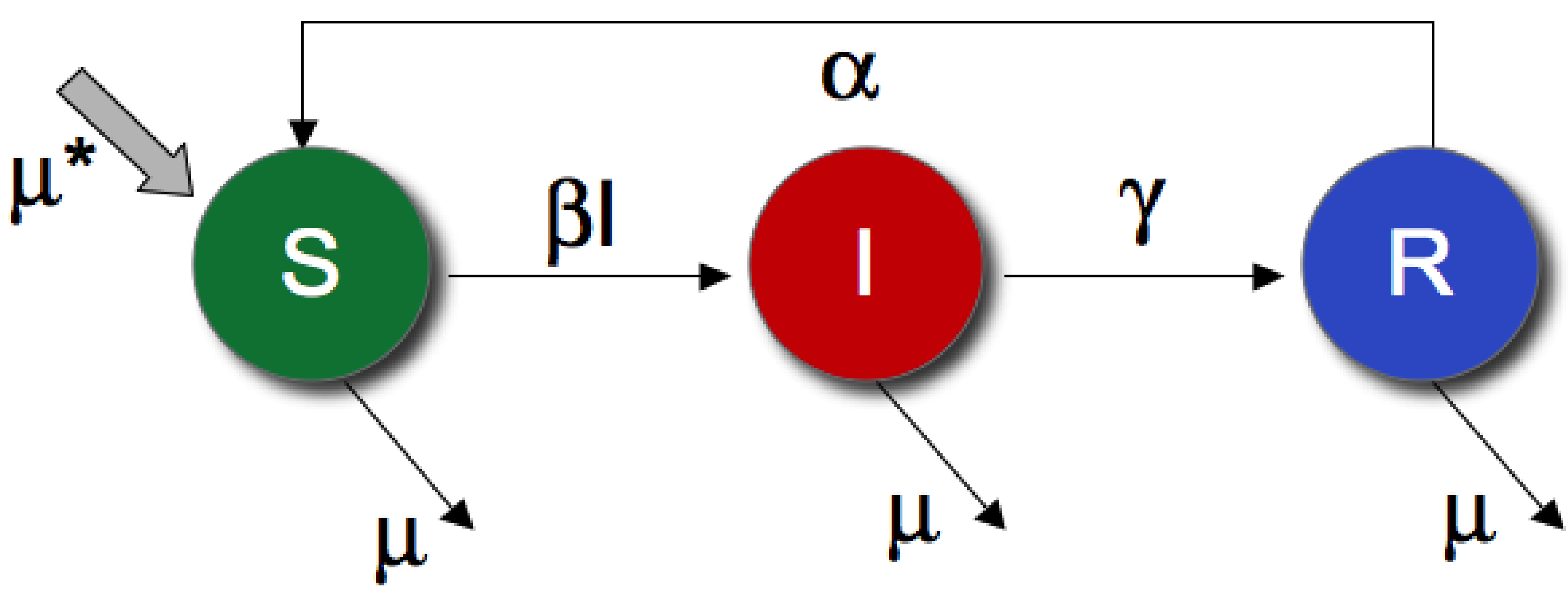
Humans can be fine-tuned!

- ***Biology letters,*** *2(3): 412-414; 2006. “**Cues of being watched enhance cooperation in a real-world setting**” . M. Bateson, D. Nettle and G. Roberts.*

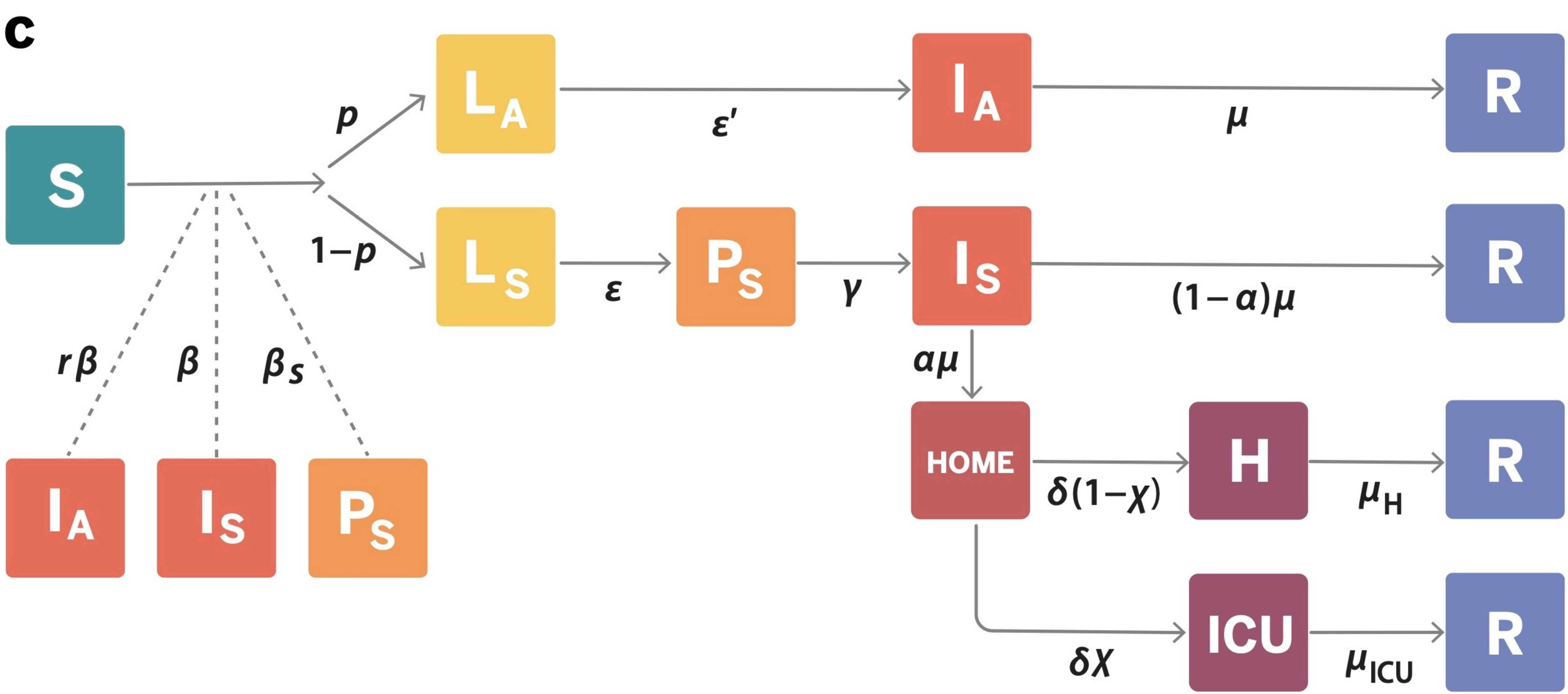
Mathematical Model

$$R_0 = \frac{\beta}{\gamma} k$$



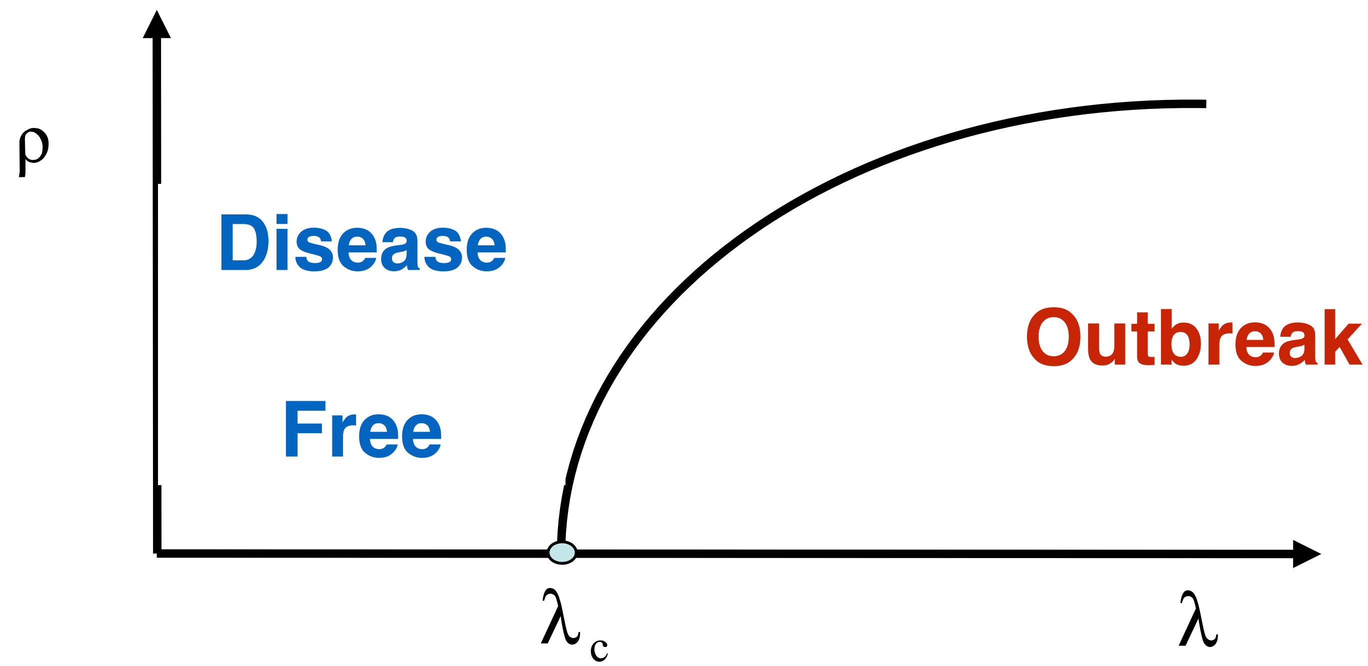


COVID-19 Natural history



SEIR-like model

Mathematical Model



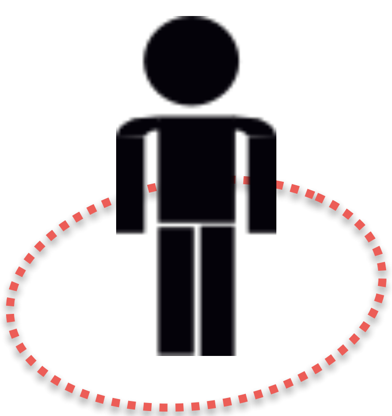
$$R_0 < 1$$ On average, less than 1 new infected

$$R_0 \geq 1$$ On average, more than 1 new infected

Disease propagation mechanisms:
Mobility and Networks of interaction

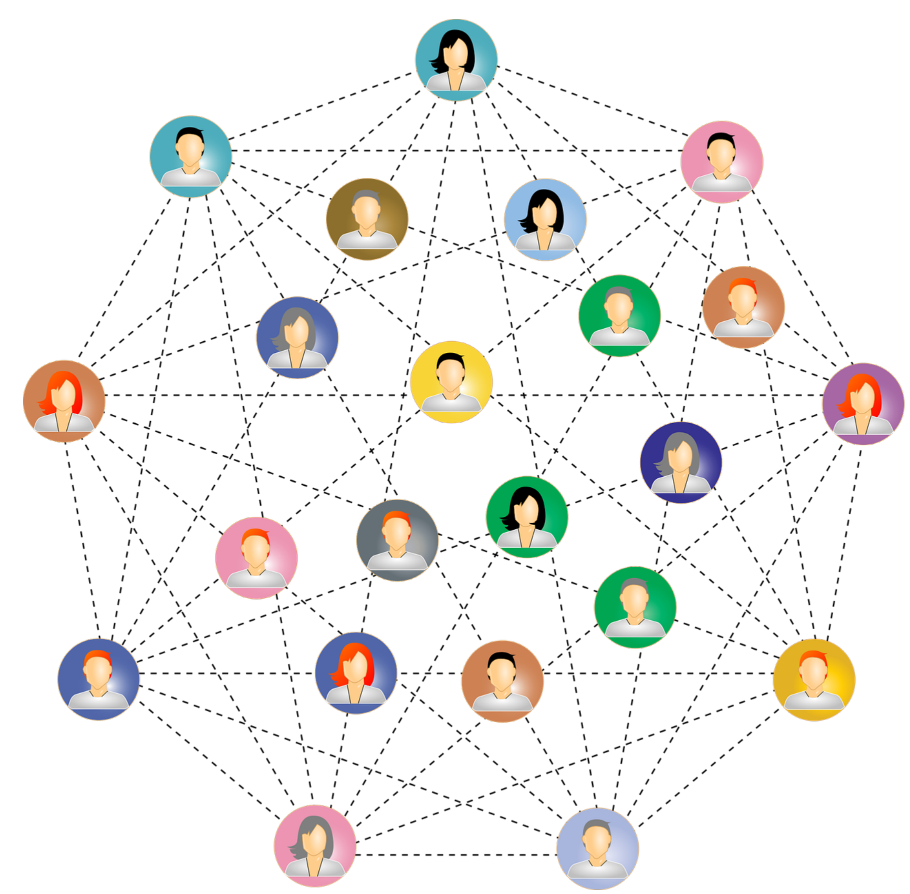
$$R_0 = \frac{\beta}{\gamma}k$$

Isolated Individual



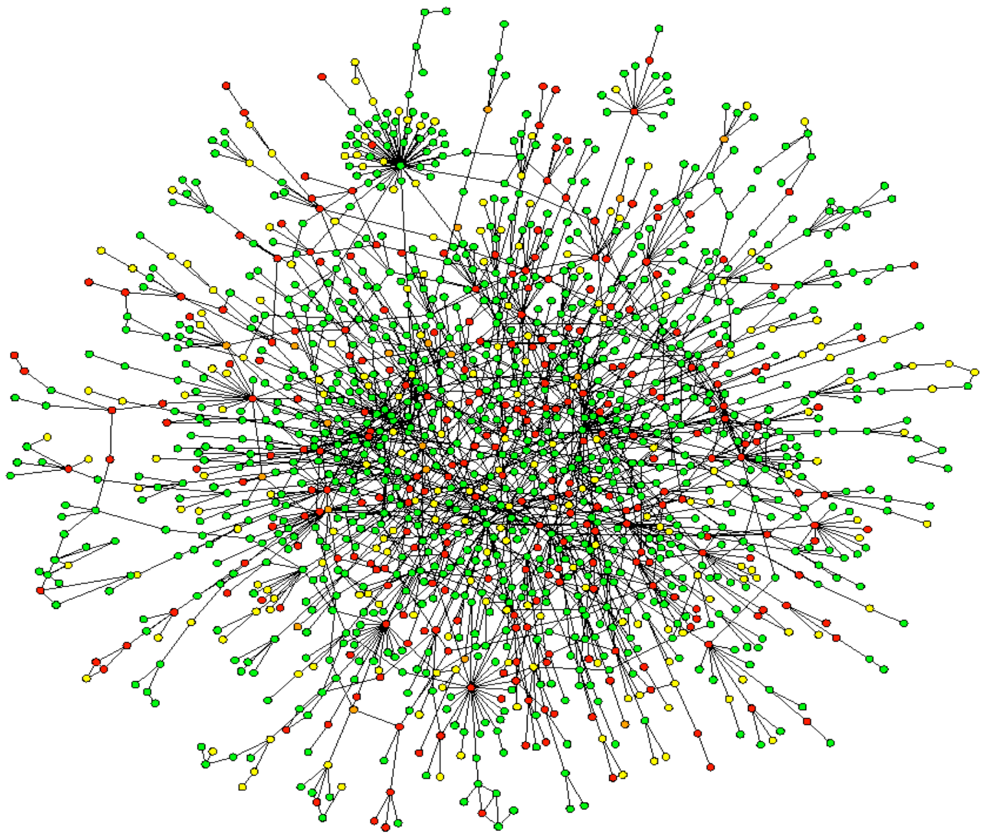
humans as social beings

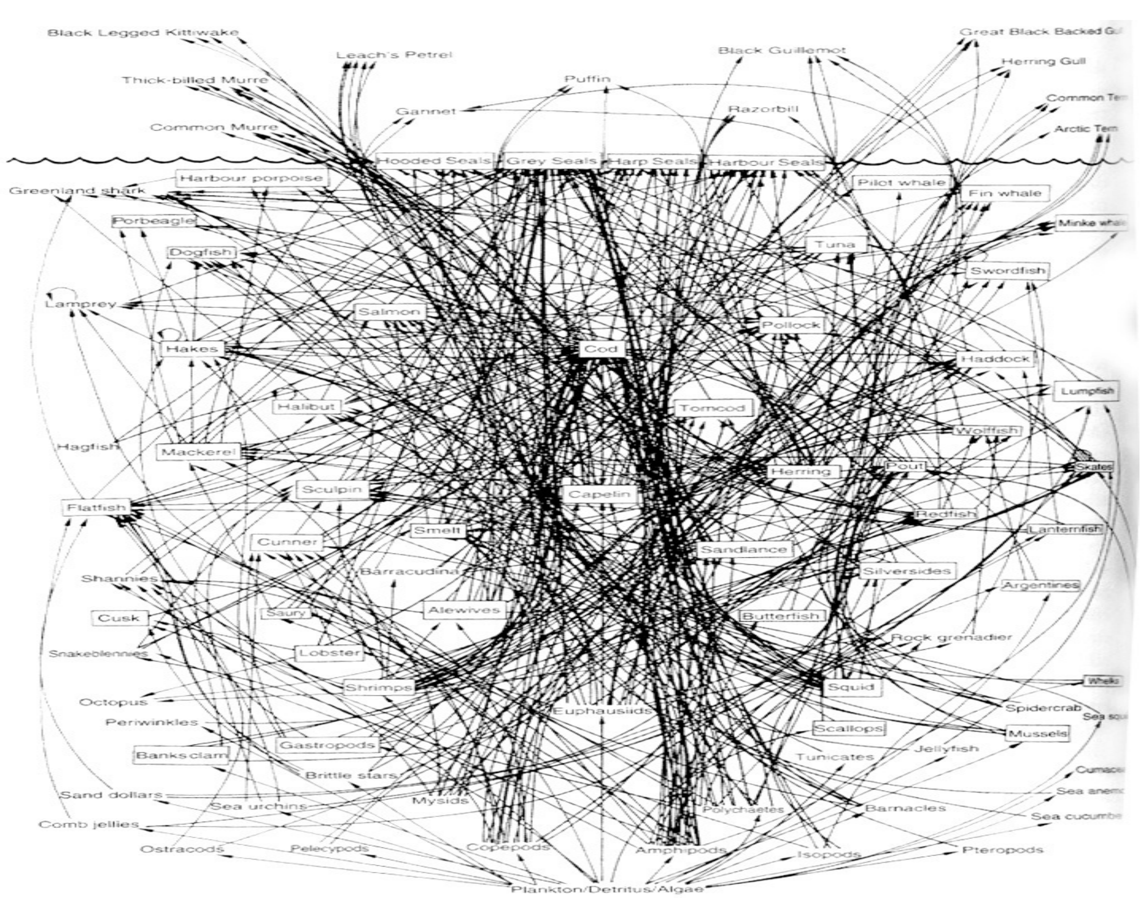
Human collective behavior



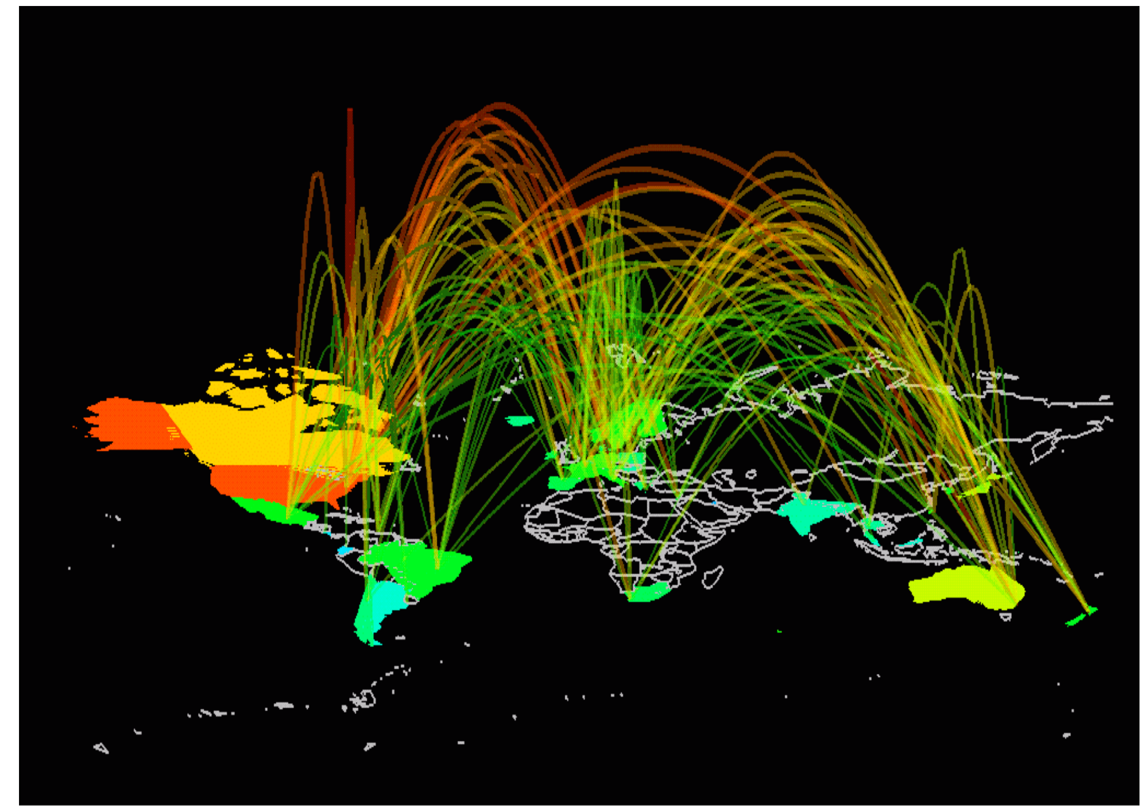
Networks of Interactions

Biology

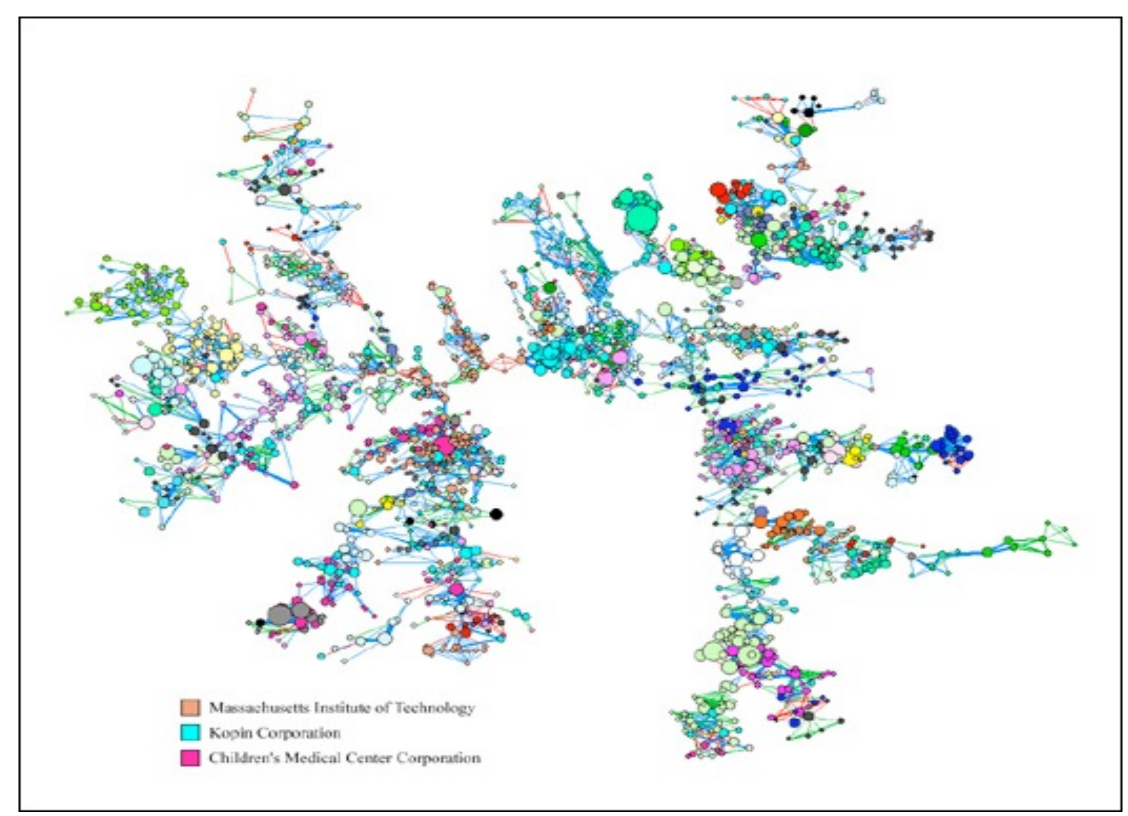




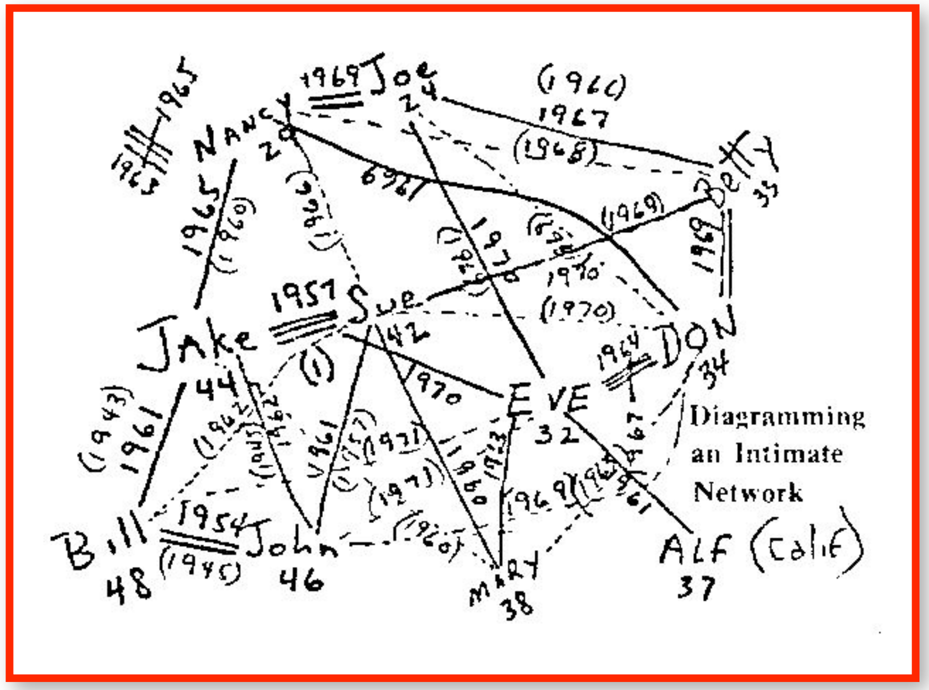
Communication



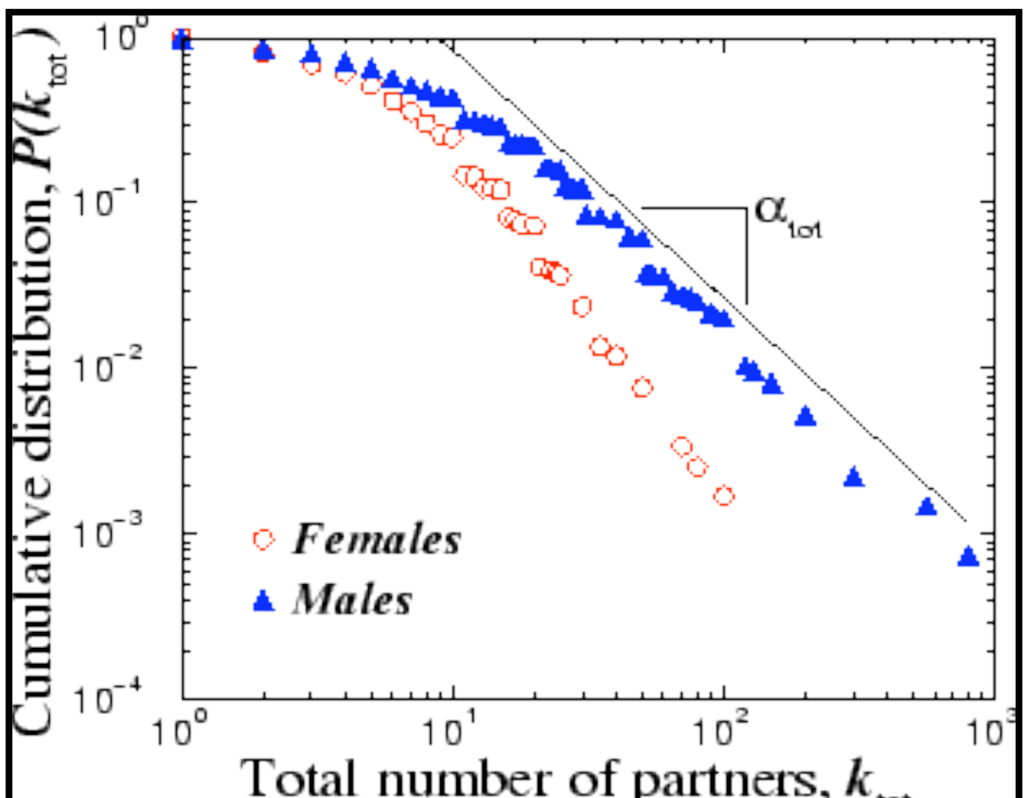
Social



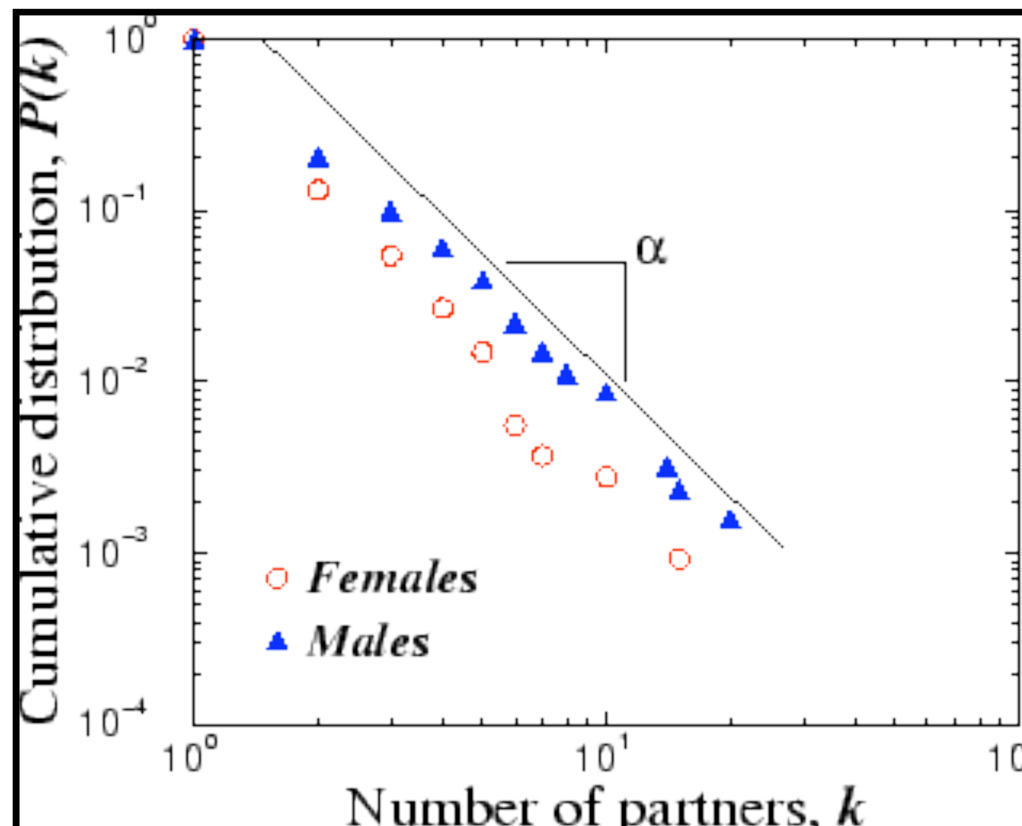
Networks



Diagramming an Intimate Network
NANCY 20
Joe 24
Betty 35
Jake 44
Sue 42
DON 34
EVE 32
Bill 48
John 46
MARY 38
ALF (Calif) 37

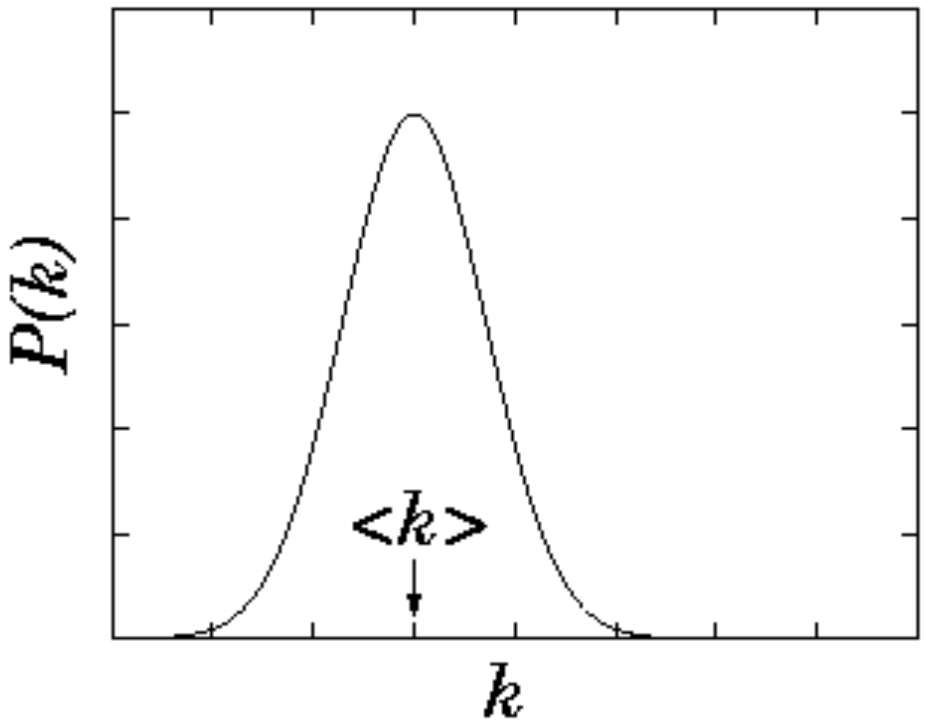


Cumulative distribution, $P(k_{tot})$
10^0
10^{-1}
10^{-2}
10^{-3}
10^{-4}
α_{tot}
Females
Males
10^0
10^1
10^2
10^3
Total number of partners, k_{tot}



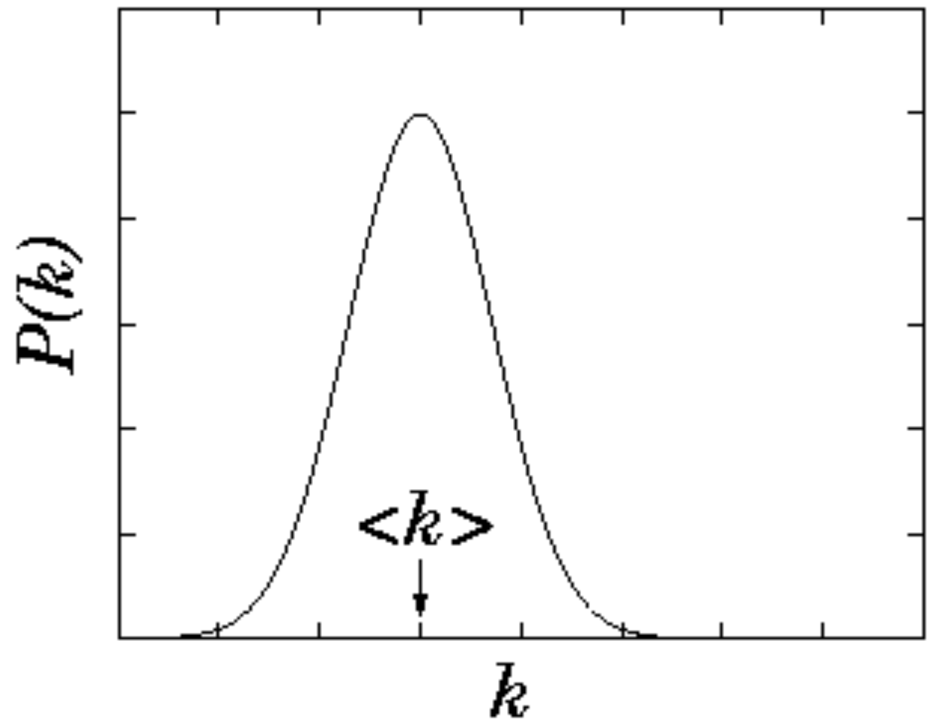
Cumulative distribution, $P(k)$
10^0
10^{-1}
10^{-2}
10^{-3}
10^{-4}
α
Females
Males
10^0
10^1
10^2
Number of partners, k

Poisson distribution

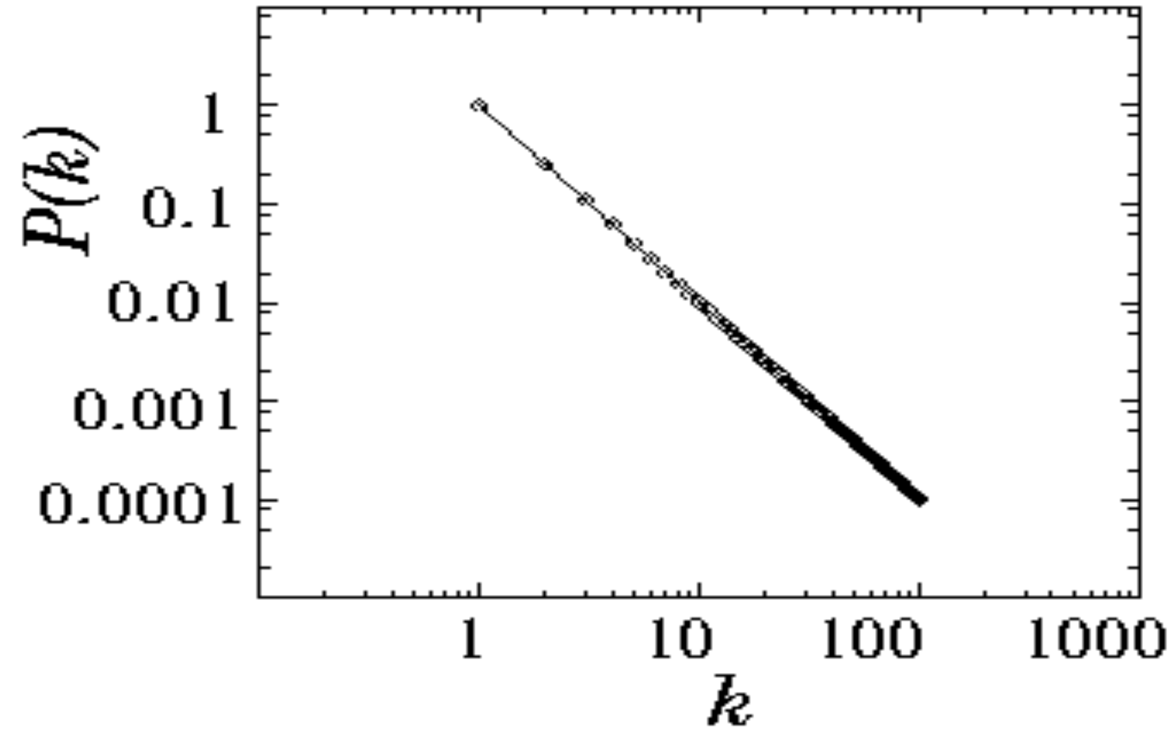


Exponential Network

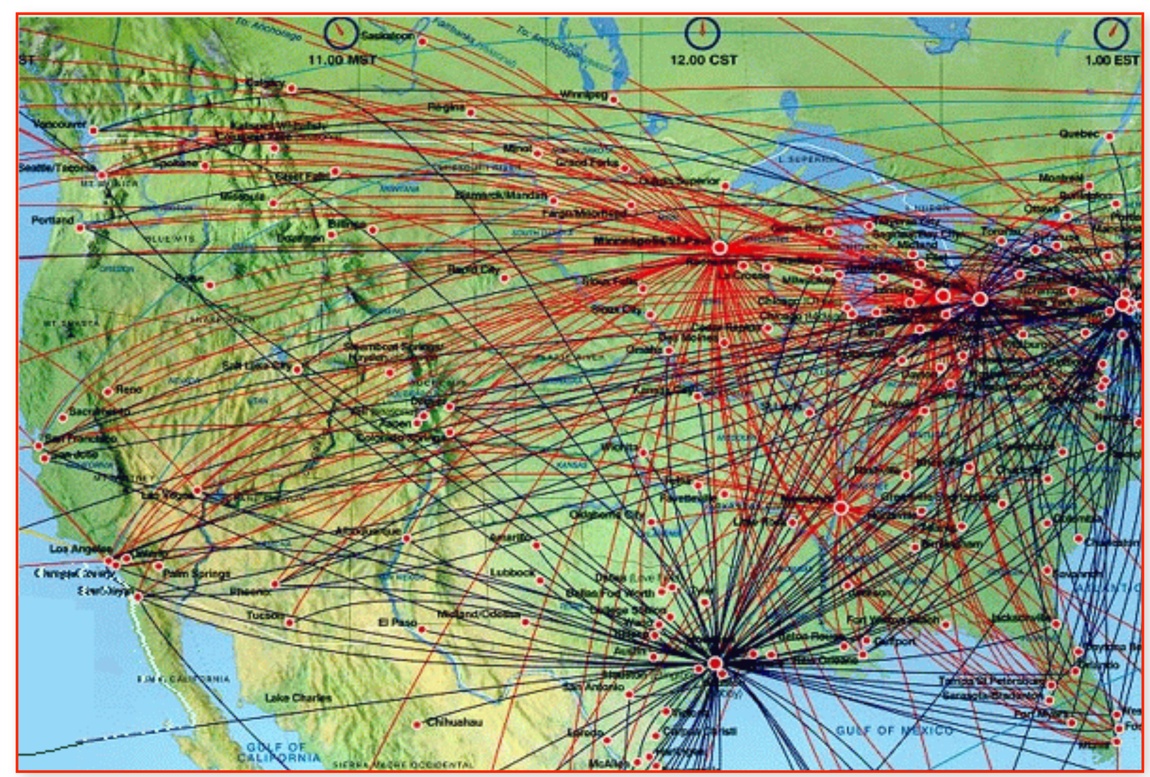
Poisson distribution



Power-law distribution

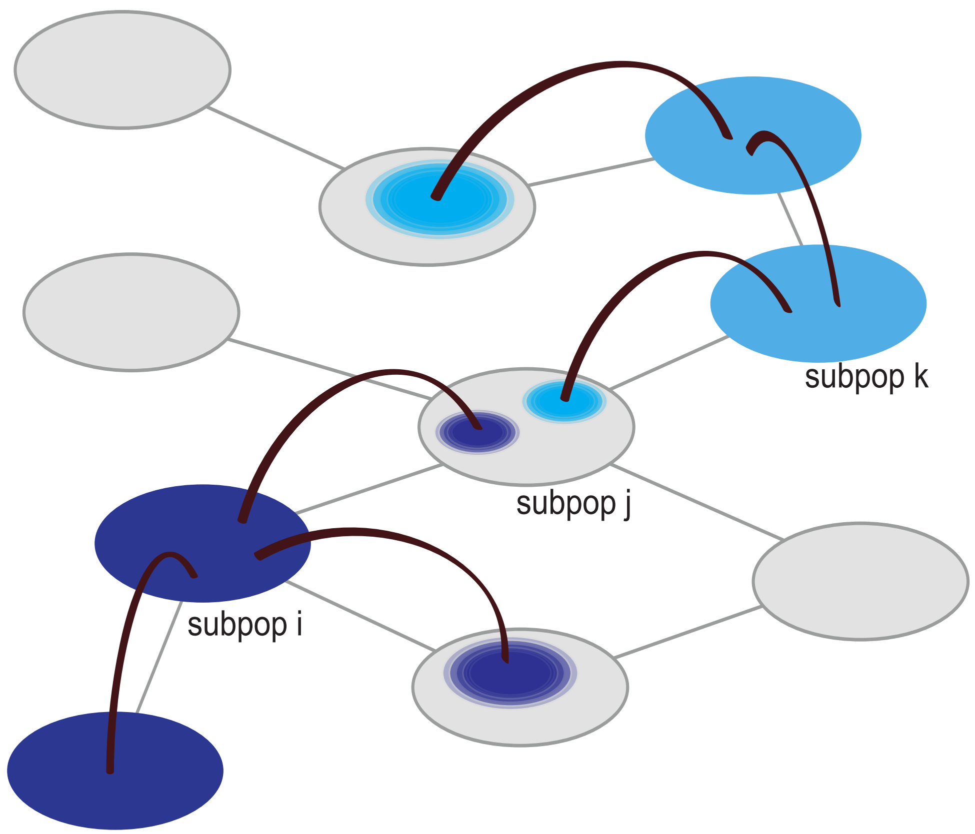


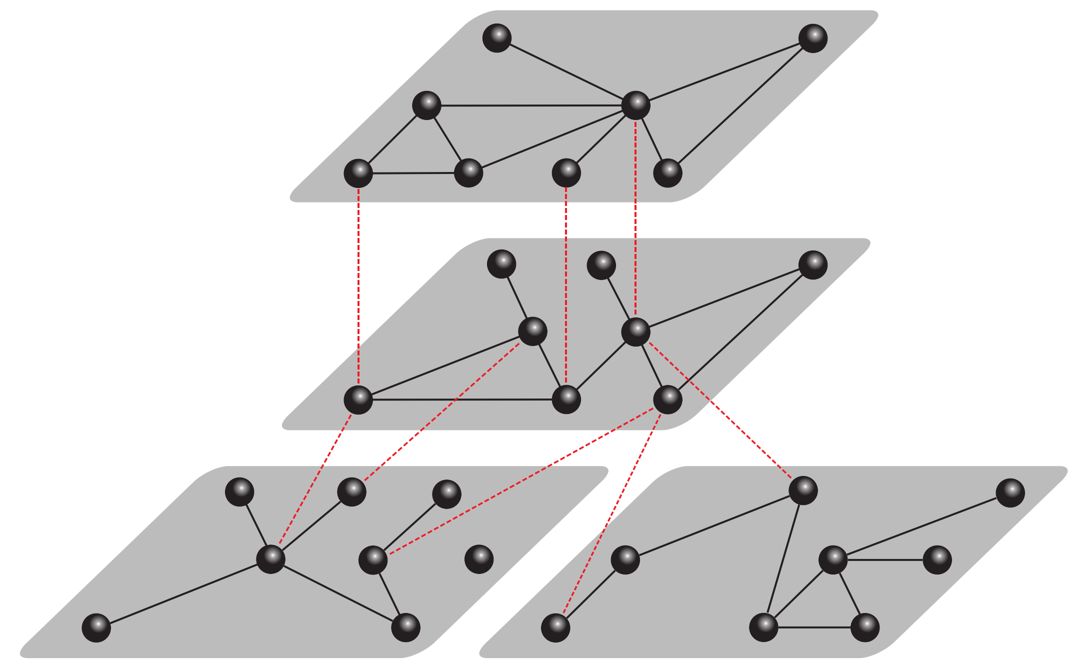
Exponential Network

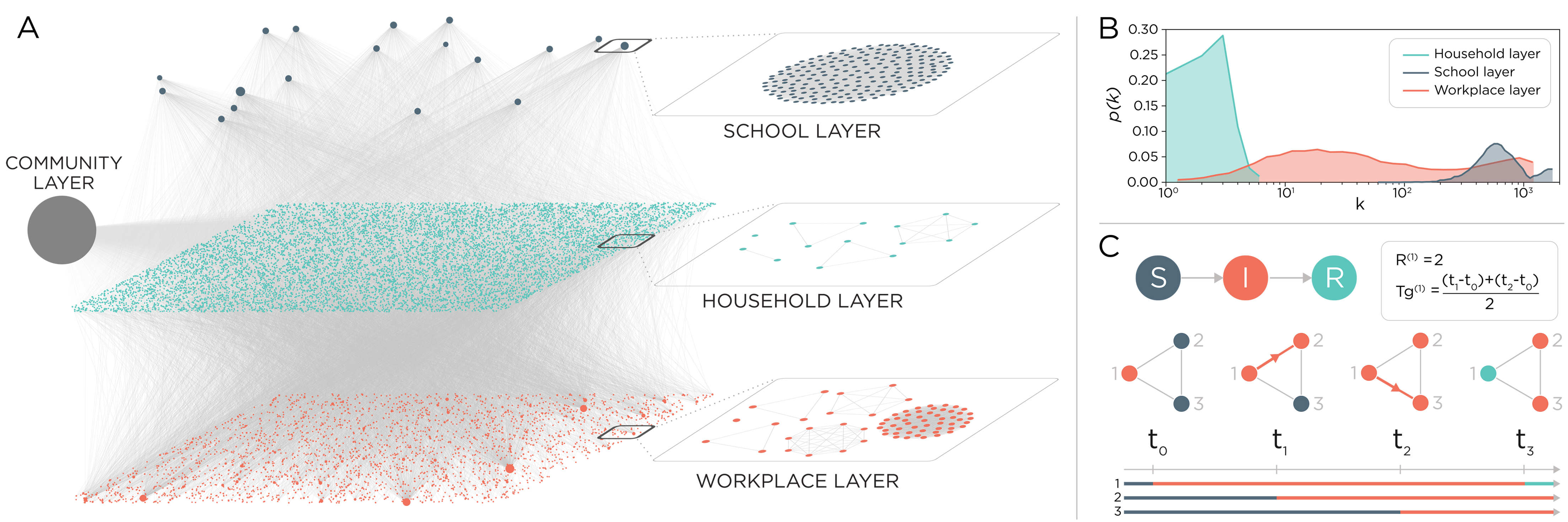


Scale-free Network

Structured Populations







Analytics

Complex Networks

Single Networks
(< 2011/ 12)

Structure

- Algorithms
- Metrics
- Real Networks
- Network Models

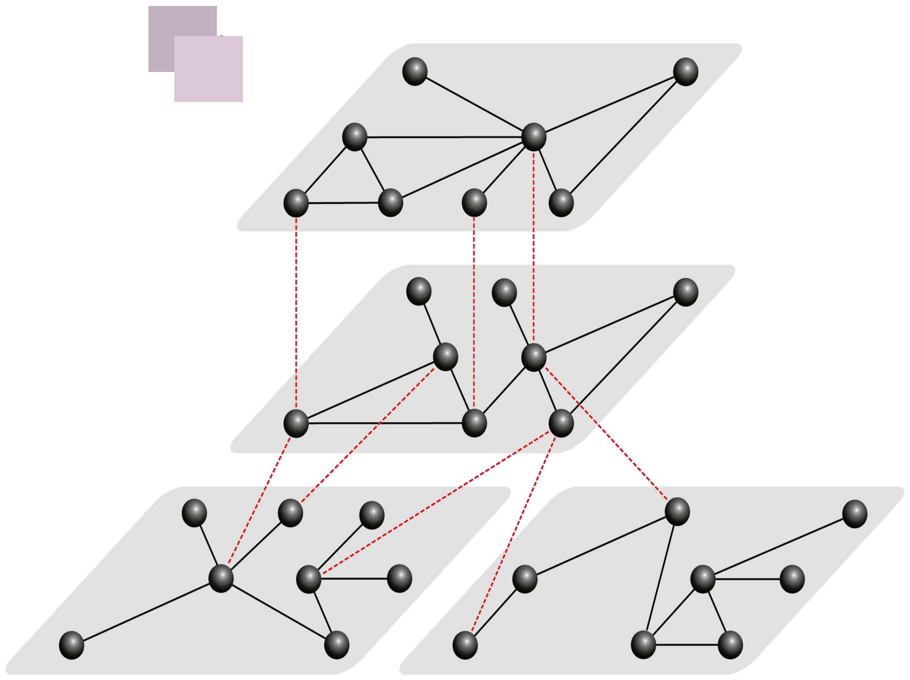
Dynamics

- Percolation
- Spreading Processes
- Diffusion
- Discrete

- Synchronization
- Reaction kinetics
- Signaling
- Evolutionary Game Dynamics

Multilayer Networks

State of the Art (> 2011-2012)



- New Theoretical Framework
- Characterization real networks
- New metrics
- (Simple) Dynamics: Diffusion, Percolation, Spreading

M. Kivela, A. Arenas, M. Barthelemy, J. P. Gleeson, **Y. Moreno**, and M. A. Porter, "**Multilayer Networks", Journal of Complex Networks 2**, 203-271 (2014).

A. Aleta and **Y. Moreno**, "**Multilayer Networks in a Nutshell",** to appear in **Annual Reviews of Condensed Matter Physics**, (2019).

G Bianconi,"**Multilayer Networks"**

E. Cozzo, G. F. de Arruda, F. A. Rodrigues and **Y. Moreno**,"**Multilayer Networks: basic formalisms and structural properties",** (2018).

Multilayer Networks in Biology: PPI networks

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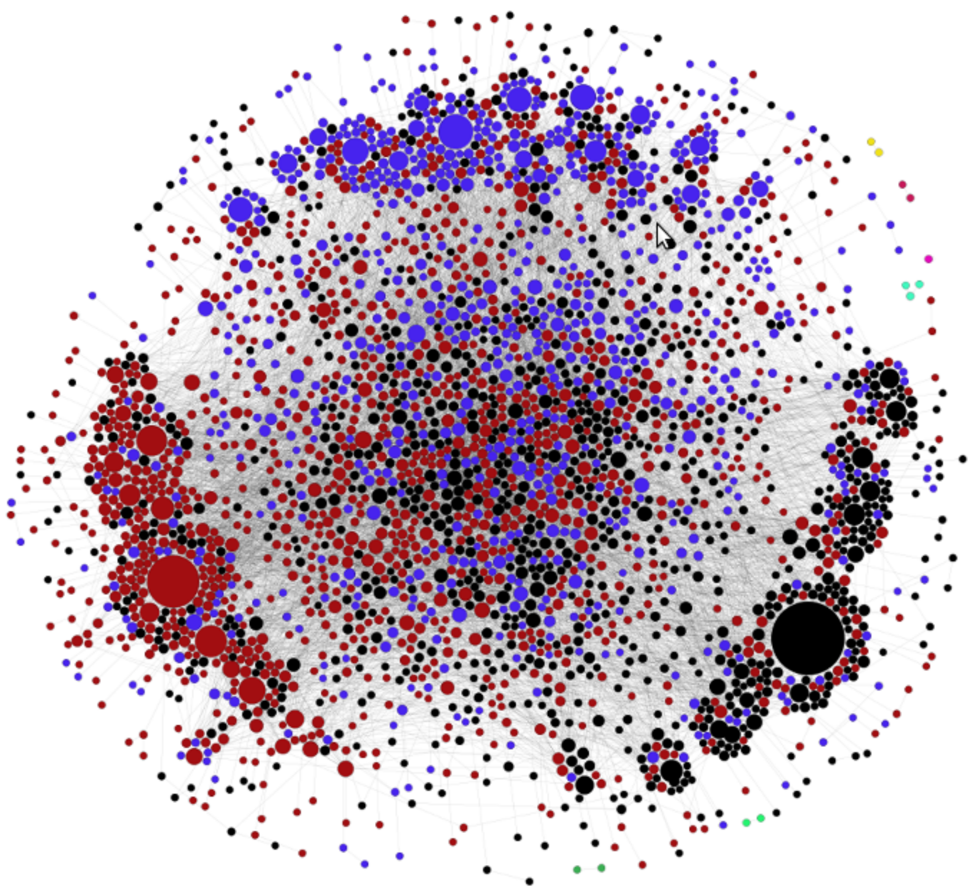
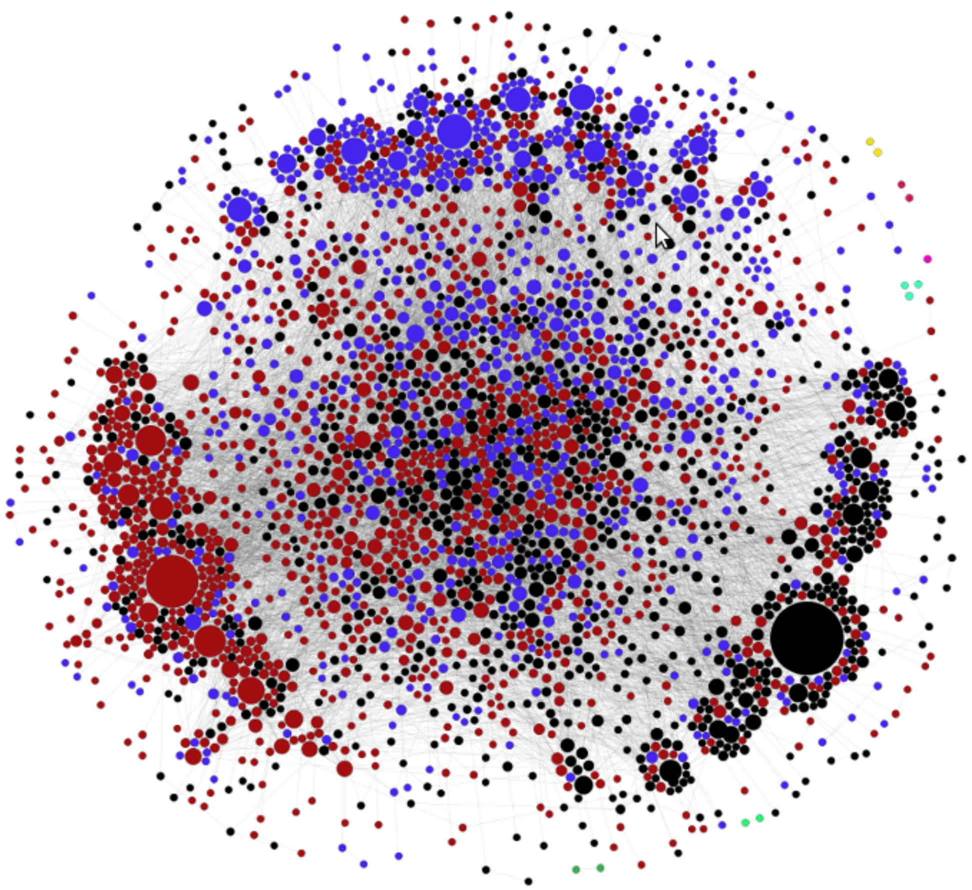
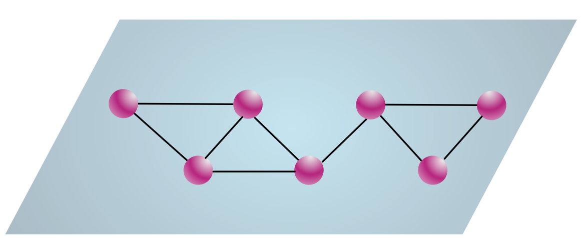
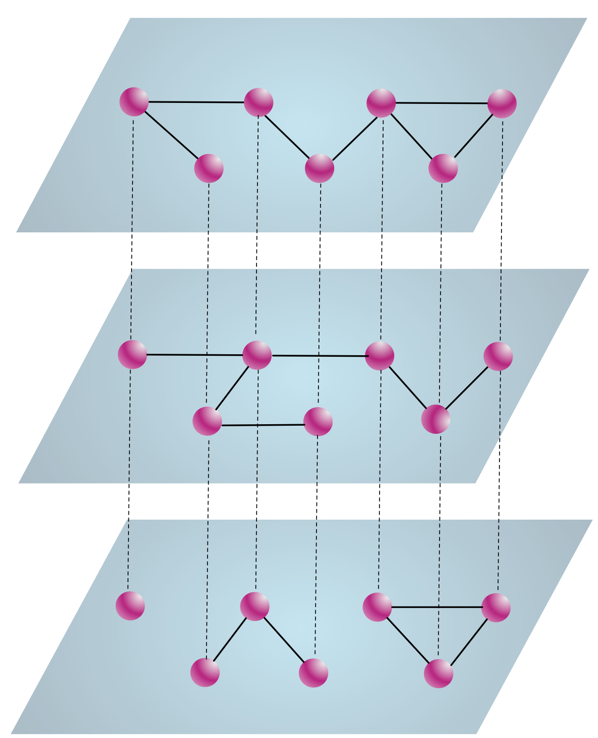


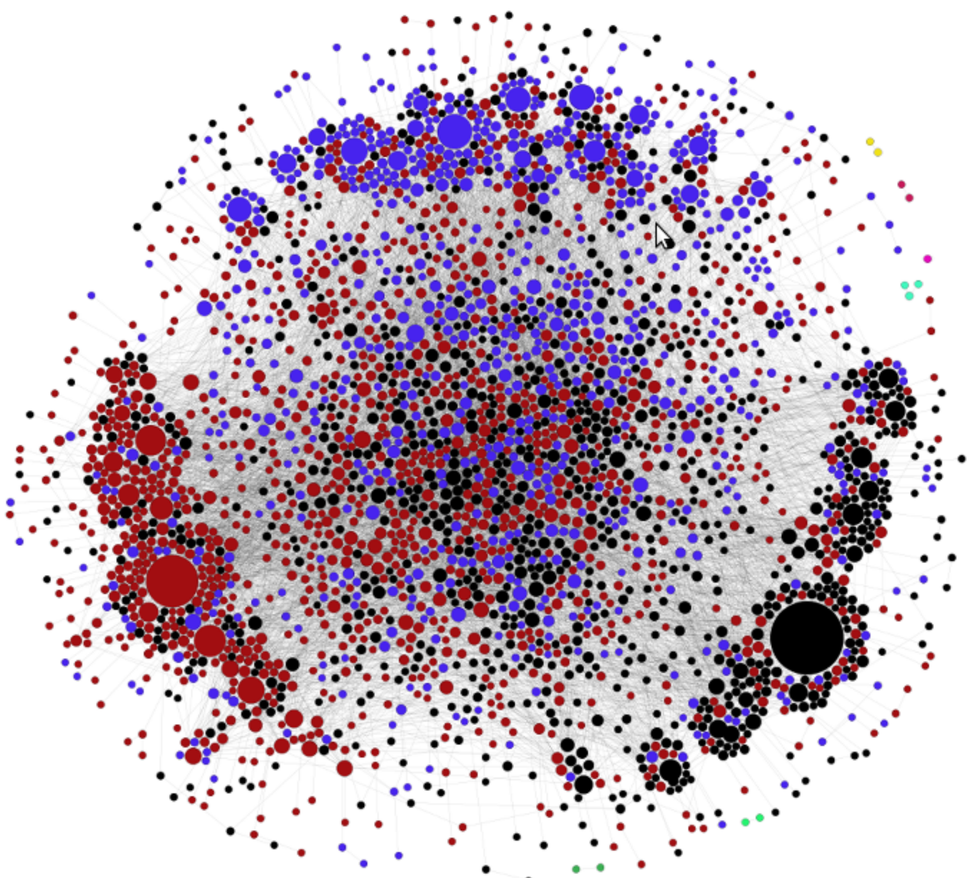
Multilayer Networks in Biology: PPI networks

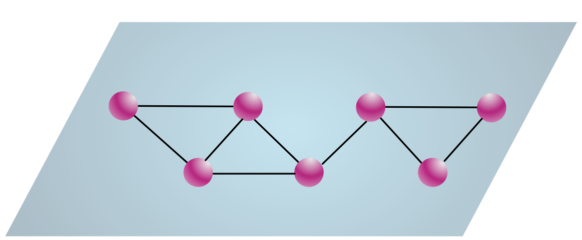


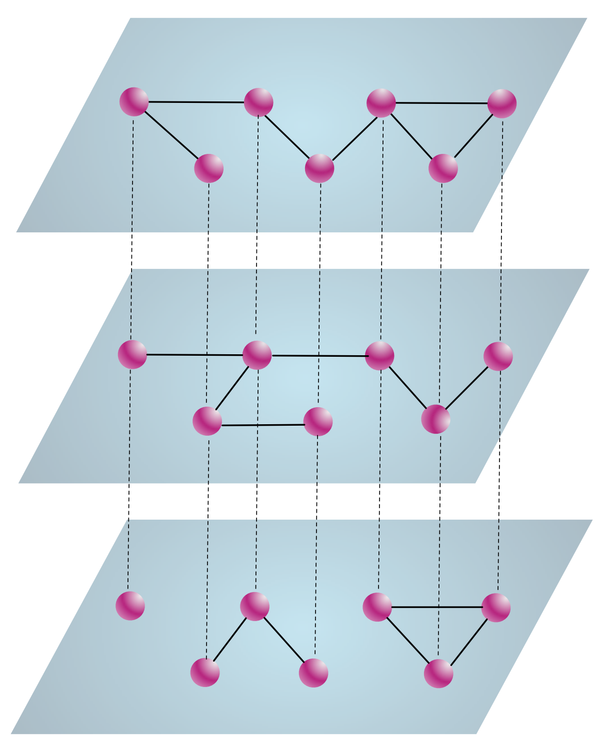


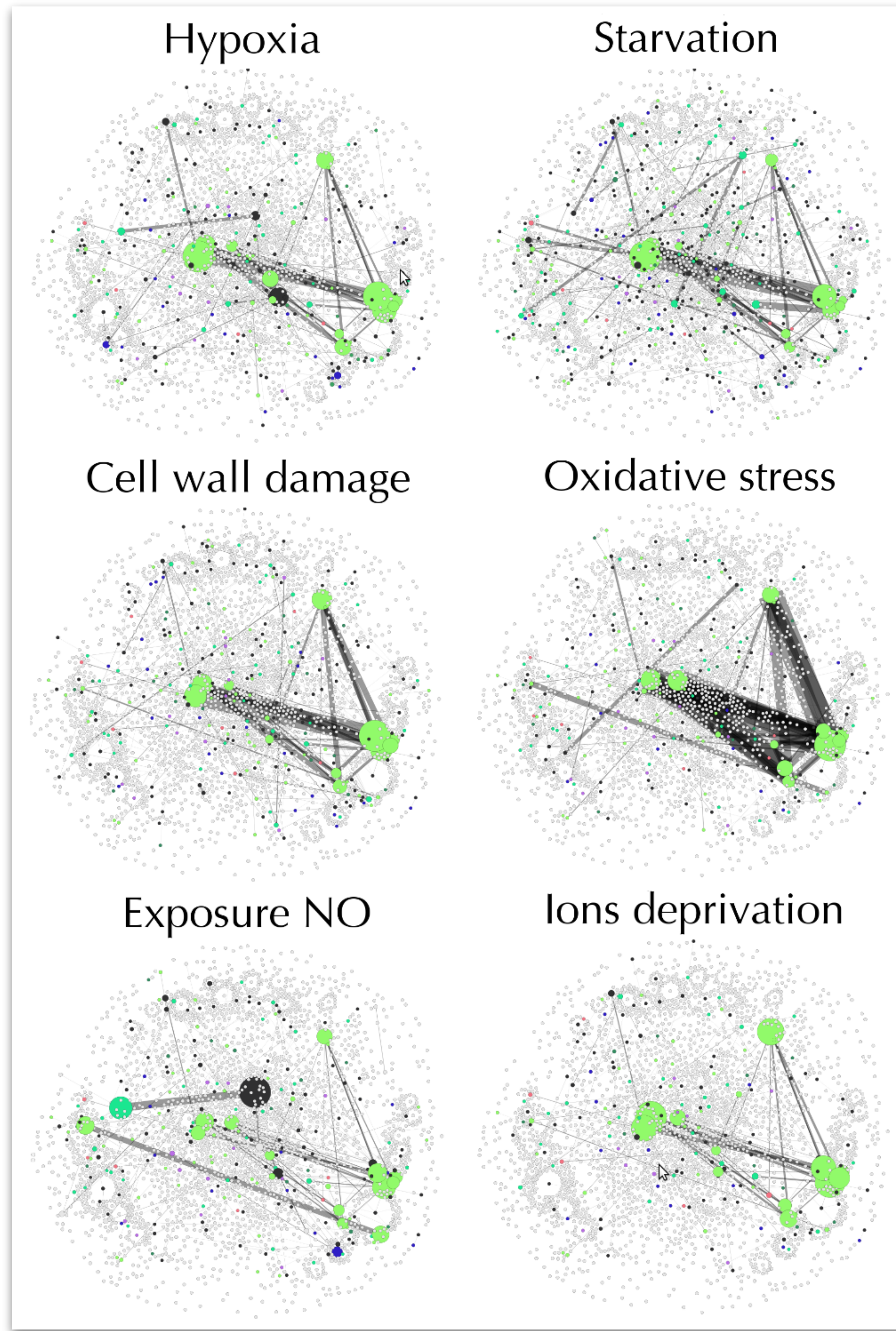


Multilayer Networks in Biology: PPI networks









Multilayer Networks in Biology: Ecology

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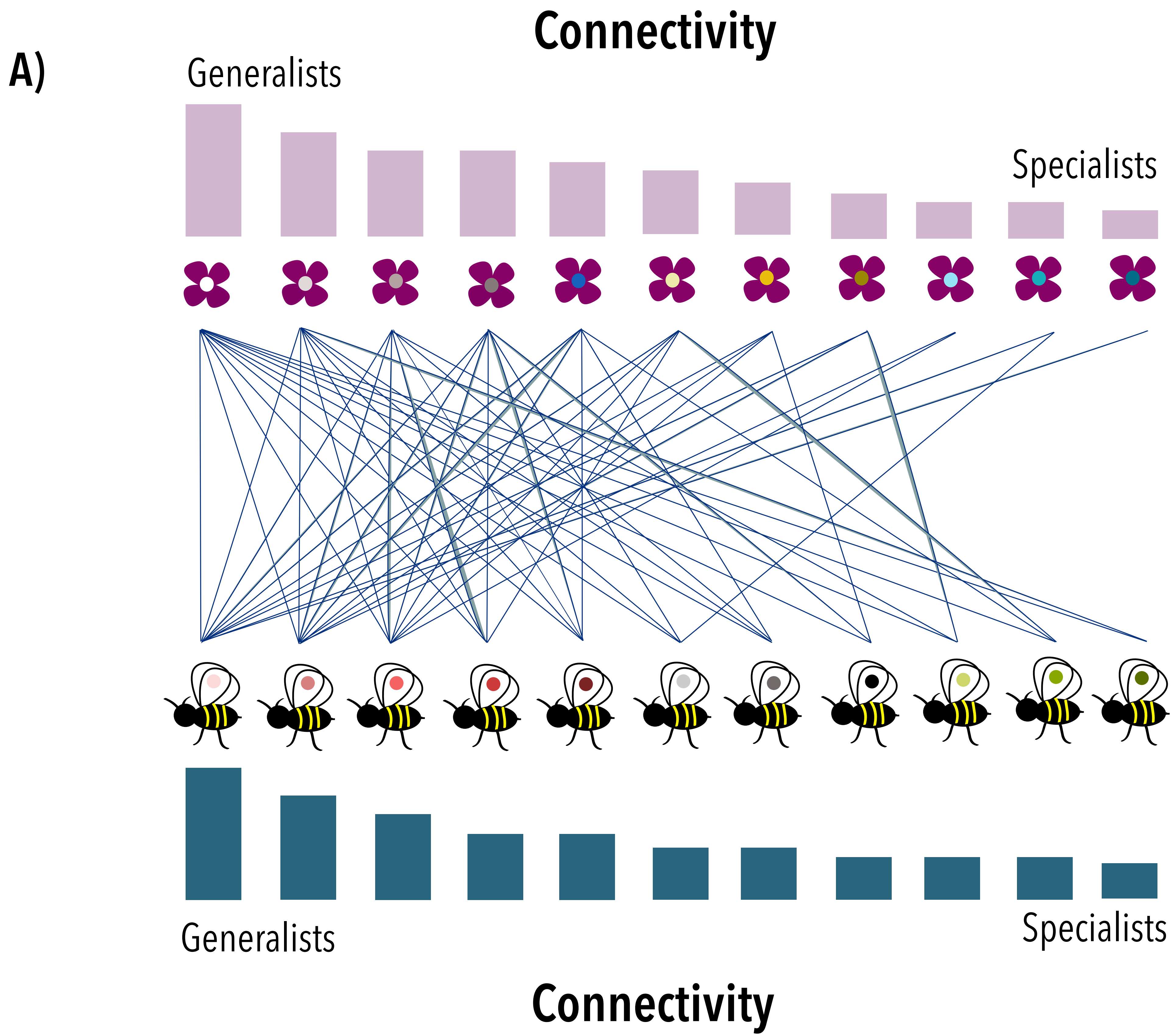
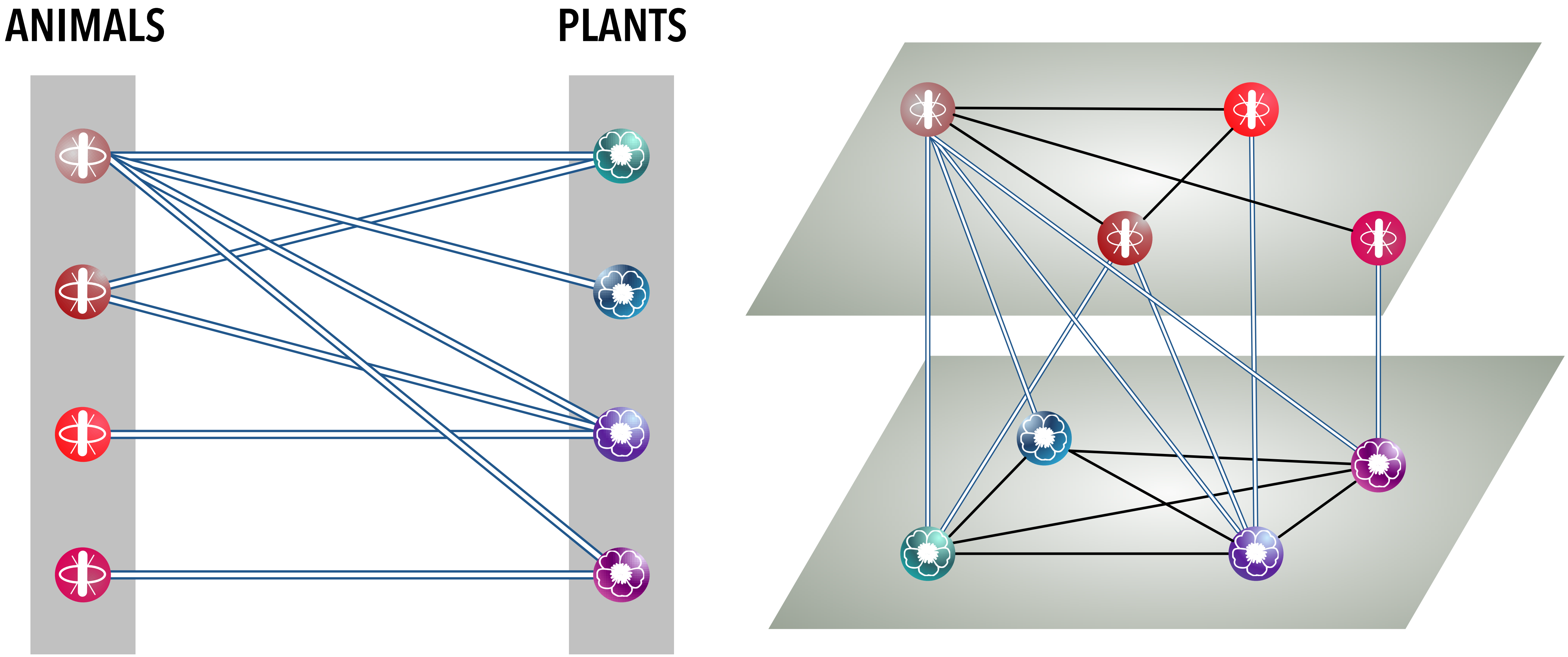


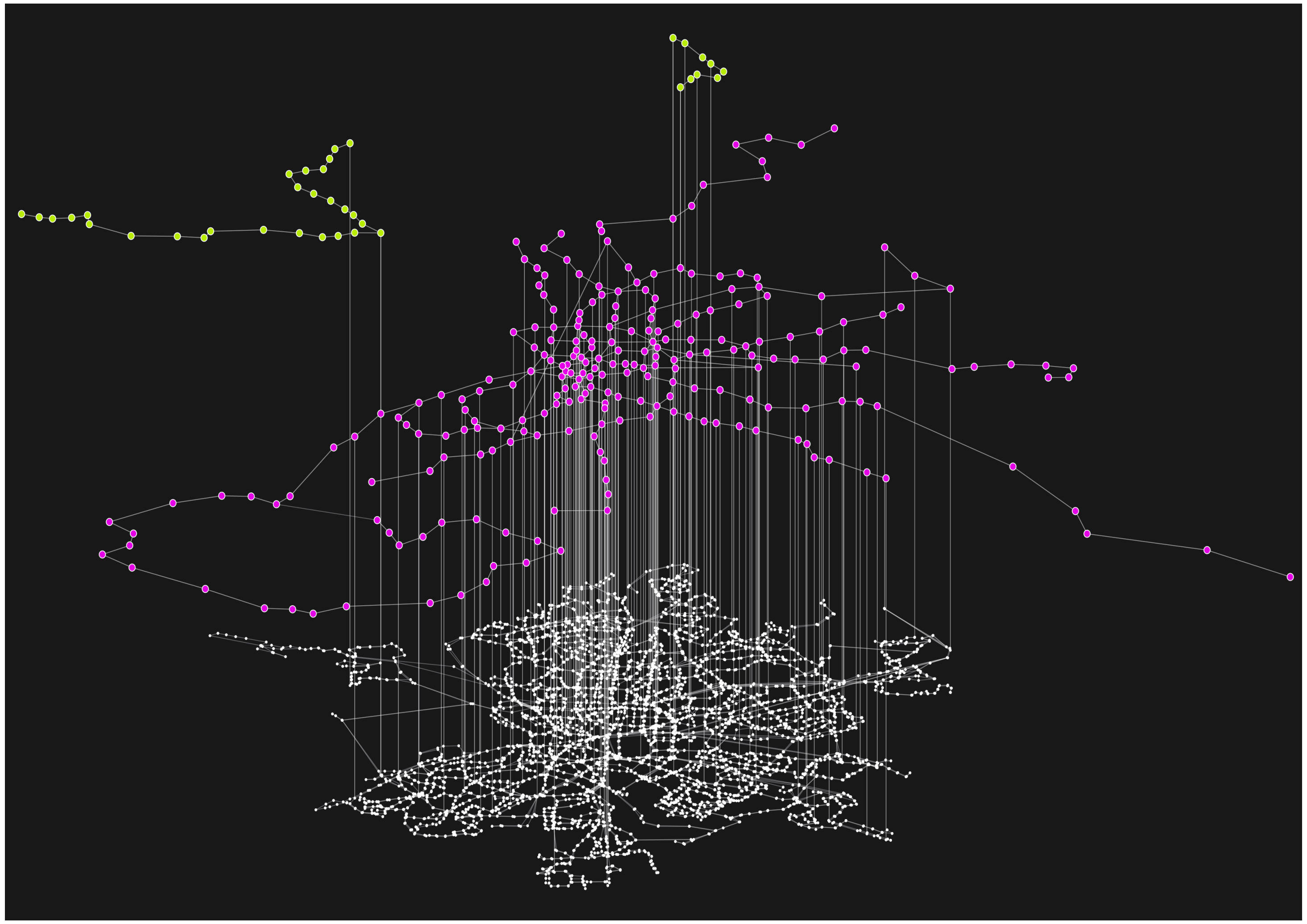
Multilayer Networks in Biology: Ecology

Multilayer Networks in Biology: Ecology

B)



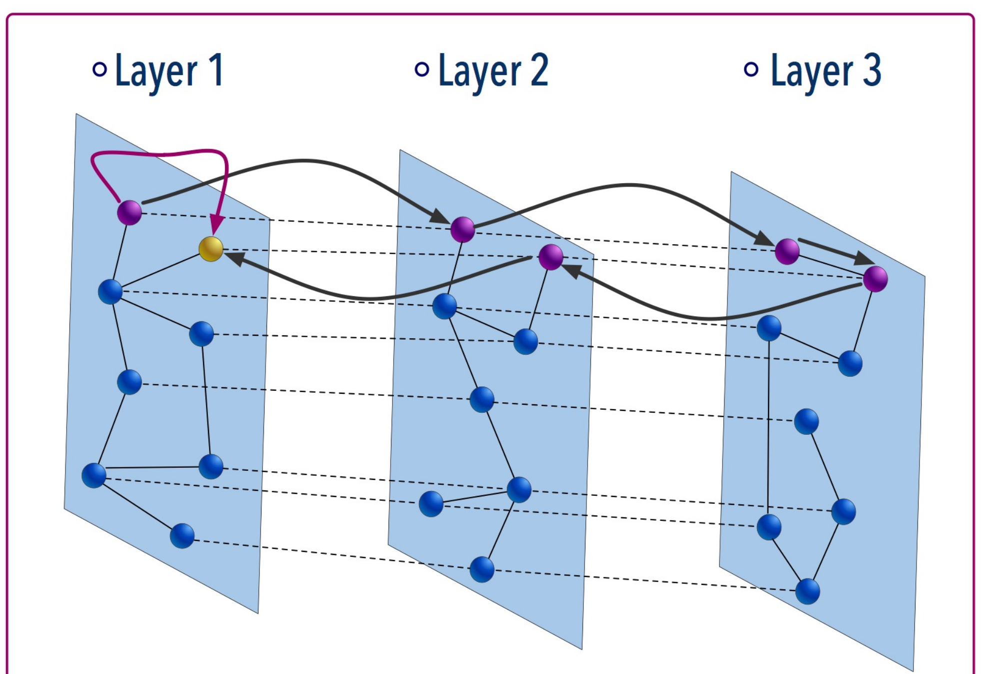
Multilayer Networks: Transportation

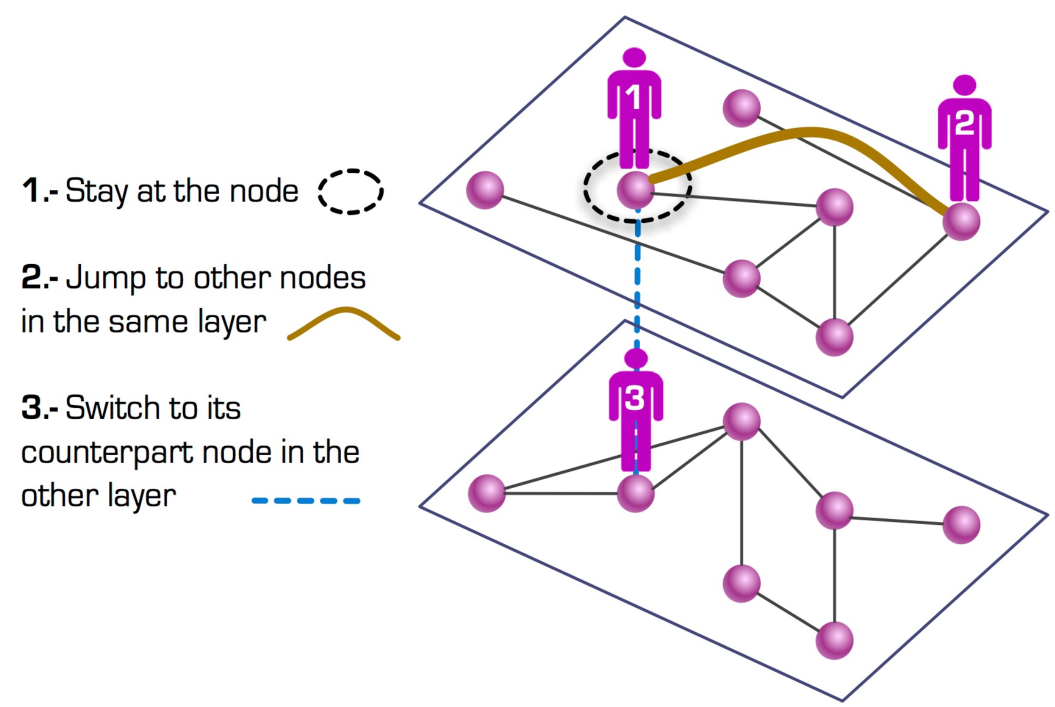


Tram

Metro

Bus



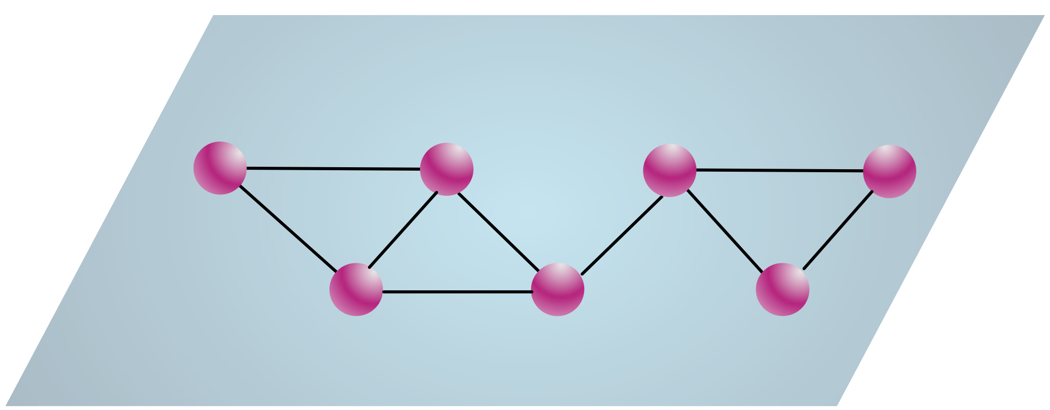


Q. Guo, E. Cozzo, Z. Zheng, and Y. Moreno, **"Lévy random walks on multiplex network"**, Scientific Reports 6:37641 (2016).

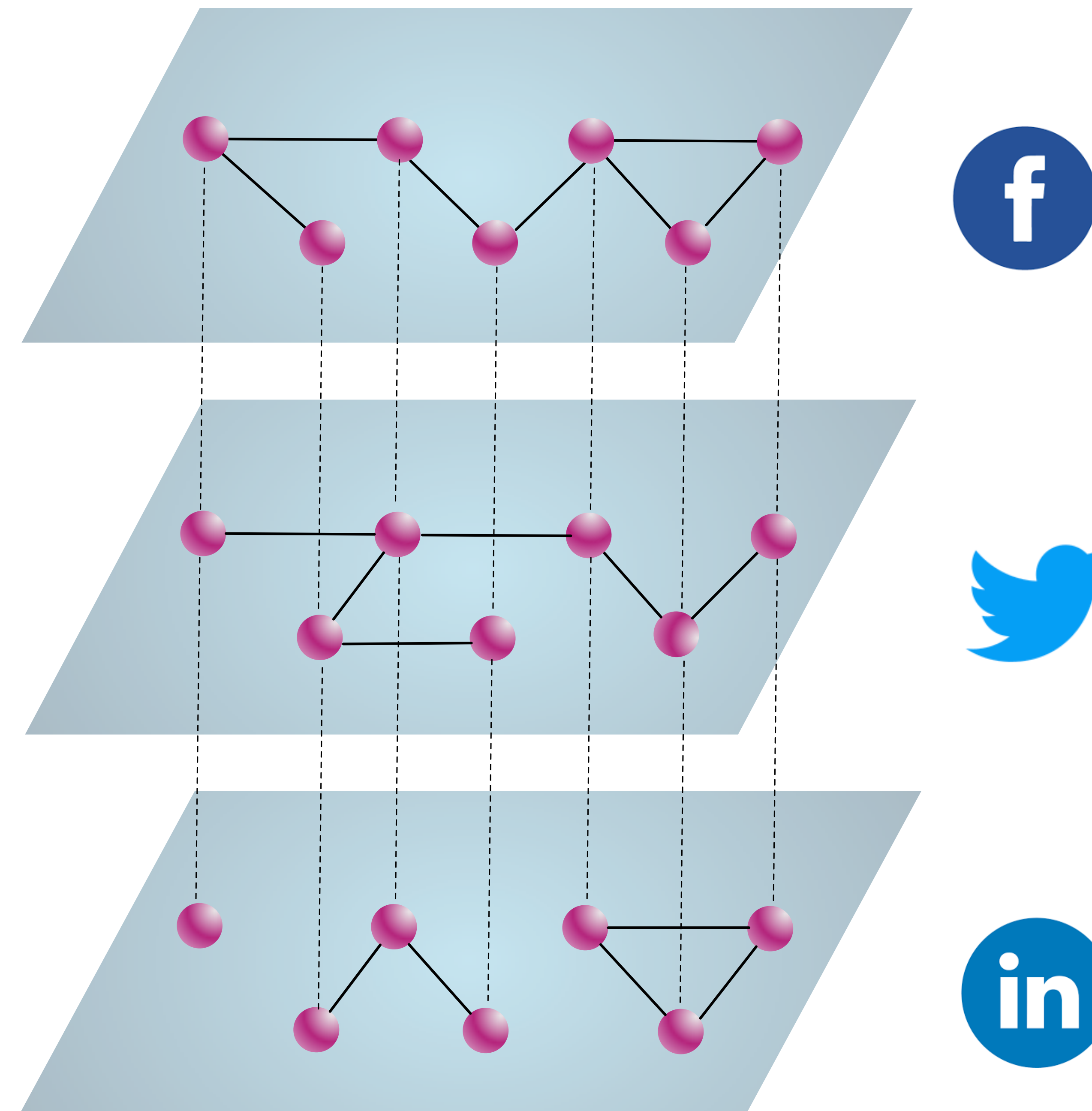
A. Aleta, S. Meloni, and Y. Moreno, **"A multilayer perspective for the analysis of urban transportation systems"**, **Scientific Reports 7:44359** (2017).

Multilayer Networks: Social Systems

Original, aggregate network

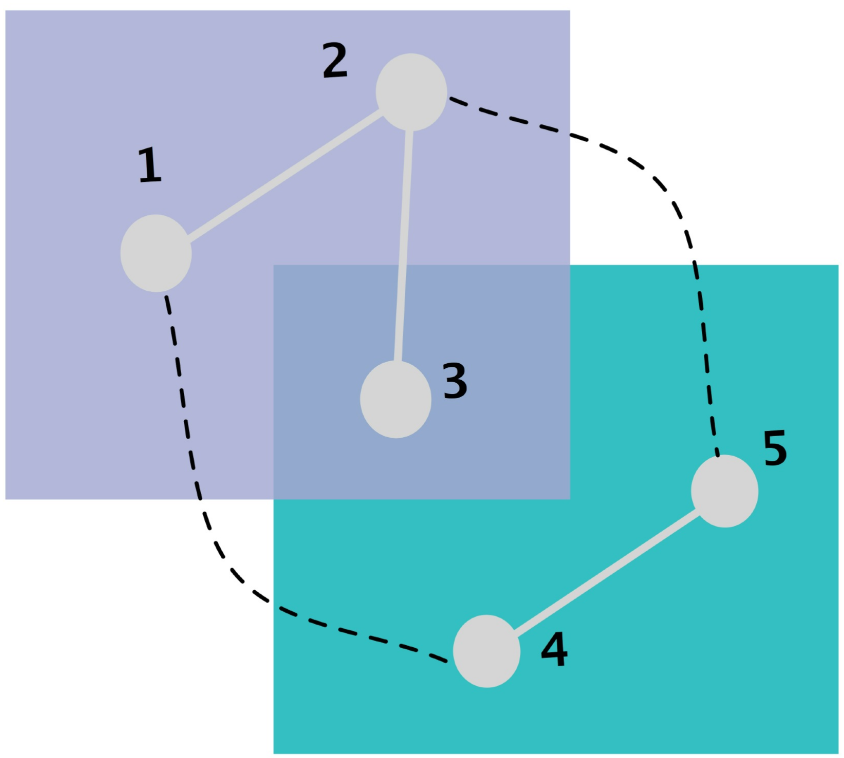


When unfolded, layers appear



Multilayer Networks: Representation

$$\bar{\mathcal{A}} = \bigoplus_{\alpha} \mathbf{A}^{\alpha} + \mathcal{C},$$



$$\bar{\mathbf{A}} = \begin{array}{c} \\ 1 \\ 2 \\ 3 \\ 4 \\ 5 \end{array} \begin{array}{c} \begin{array}{ccccc} 1 & 2 & 3 & 4 & 5 \end{array} \\ \left[\begin{array}{ccc|cc} 0 & 1 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 \\ 0 & 1 & 0 & 0 & 0 \\ \hline 1 & 0 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 & 0 \end{array}\right] \end{array} = \left[\begin{array}{c|c} A^1 & C_{12} \\ \hline C_{21} & A^2 \end{array}\right]$$

$$\mathbf{A} = \begin{bmatrix} A^1 & 0 \\ 0 & A^2 \end{bmatrix} \quad \mathscr{C} = \begin{bmatrix} 0 & C_{12} \\ C_{21} & 0 \end{bmatrix}$$

M. K., A. A., M. B, J. P. G., **Y. M.**, and M. A. P., "**Multilayer Networks**", Journal of Complex Networks 2, 203-271 (2014).

E. Cozzo, G. F. de Arruda, F. A. Rodrigues and **Y. Moreno**,"**Multilayer Networks: basic formalisms and structural properties",** (2018).

Competing and/or Interacting Diseases

A much less explored problem:

- **Theoretical models**

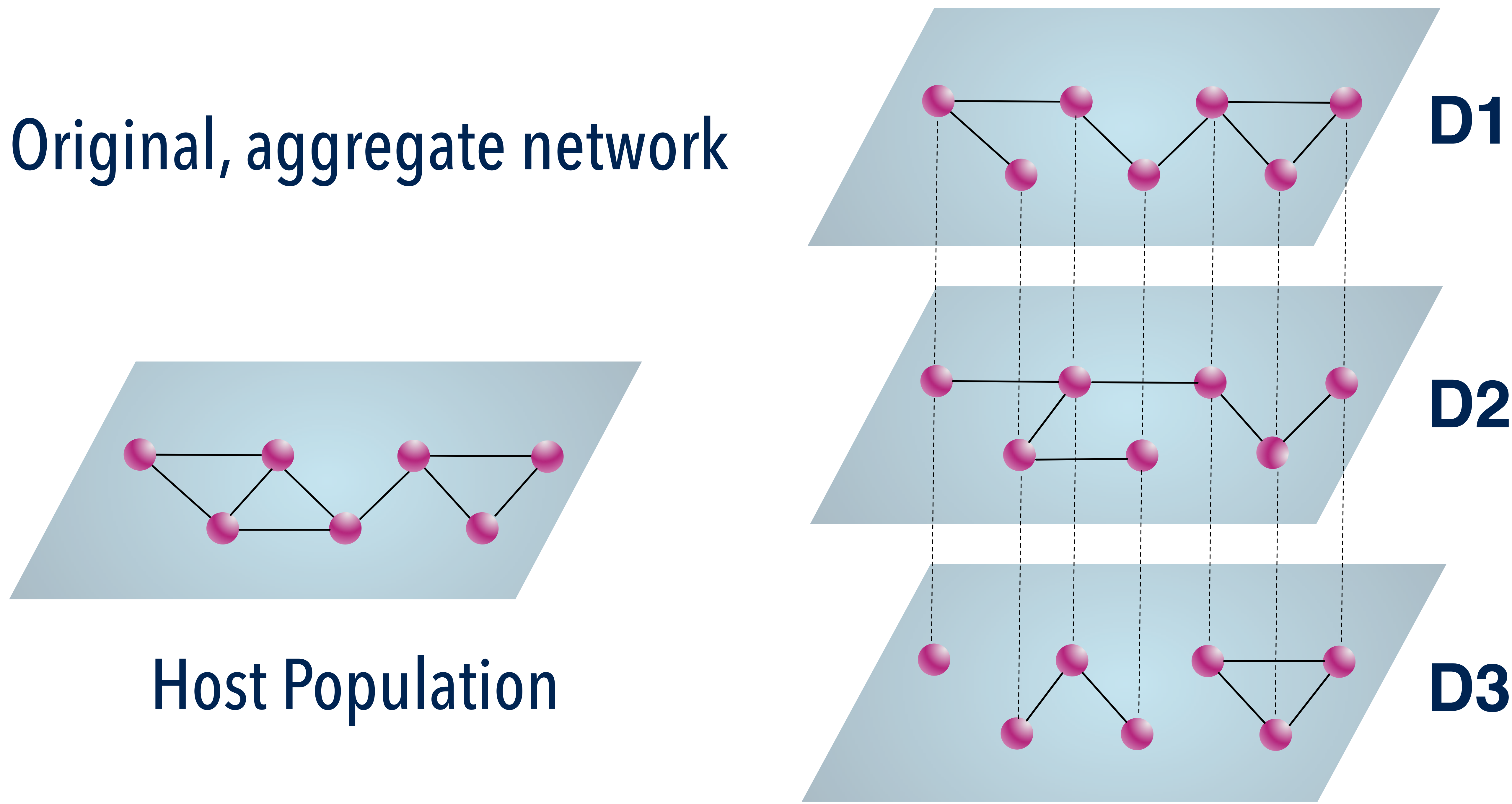
"Dynamics of Interacting Diseases"
(J. Sanz, C.-Y. Xia, S. Meloni, **Y. Moreno**, **Physical Review X 4**, 041005, 2014).

- **Meta-population**

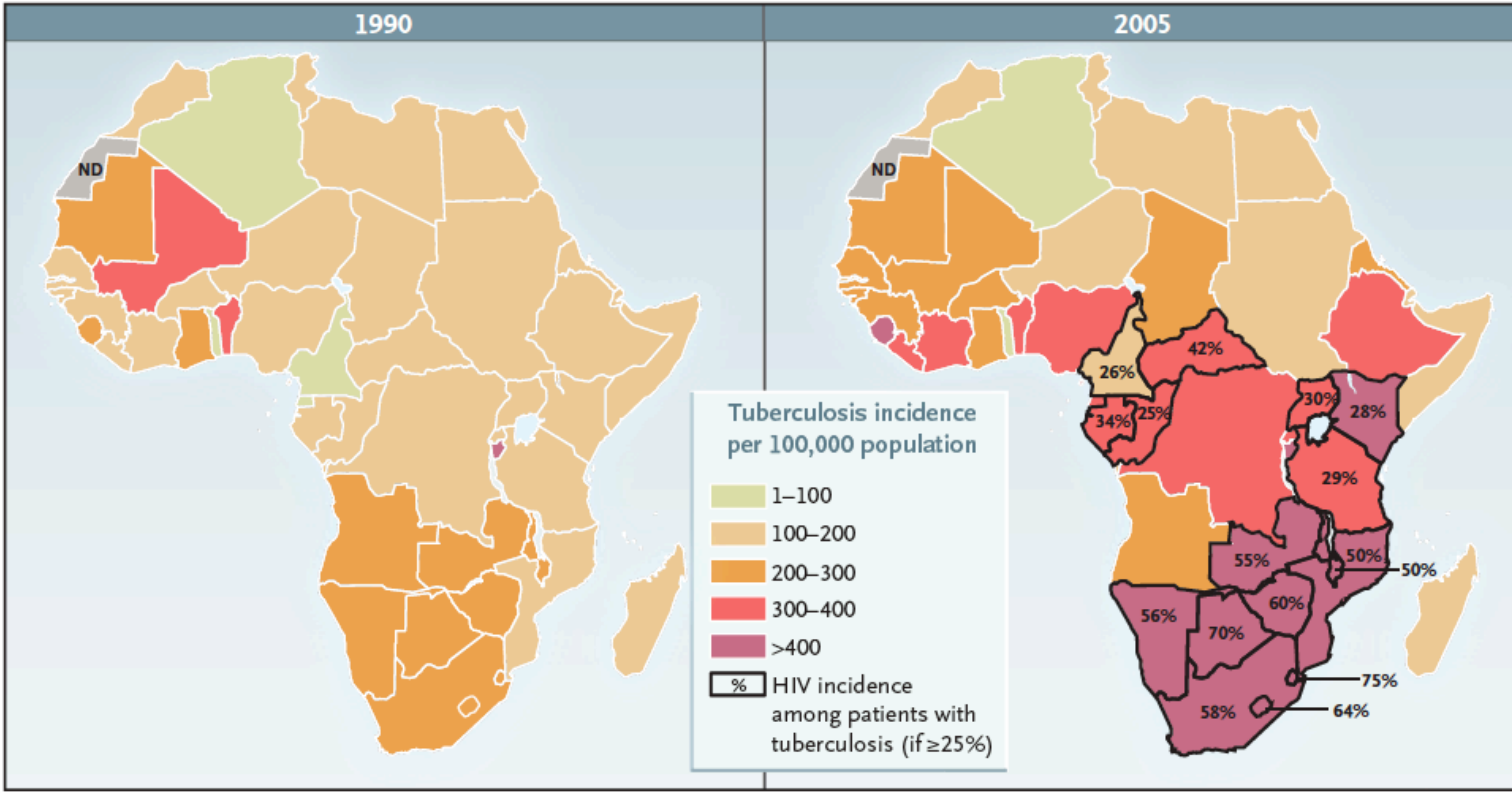
"Competing Strains on Structured Populations"
(C. Poletto, SM, V. Colizza, **Y. Moreno**, A. Vespignani, **PloS Comp. Bio. 9 (8)**: e1003169, 2013).

How to deal with the topology (NoC)?

Layers account for different networks of contacts through which diseases spread



Co-occurrence TB-HIV:



Estimated Incidence of Tuberculosis per 100,000 Population in African Countries in 1990 and 2005.
Data are from the World Health Organization. ND denotes no data.

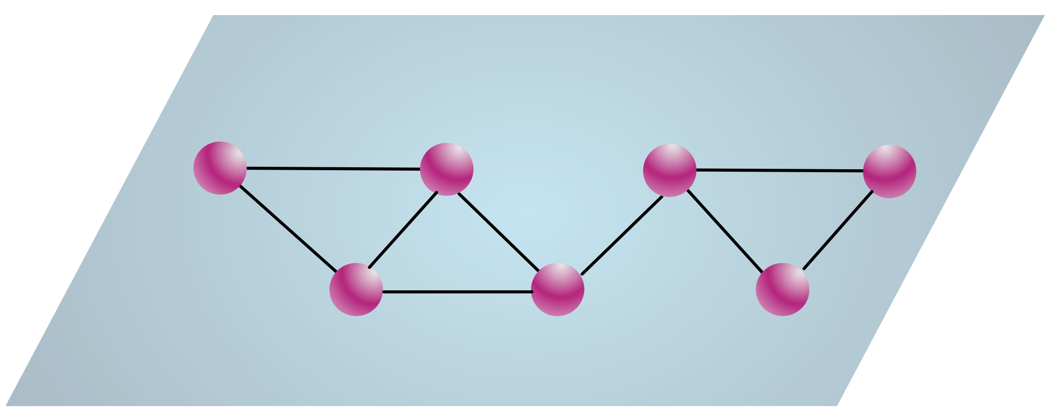
From "**Tuberculosis in Africa, combating an HIV-driven Crisis**" Chaisson, R.E. & Martinson, N.A., New Eng. J. Med., March 2008.

Social Contagion

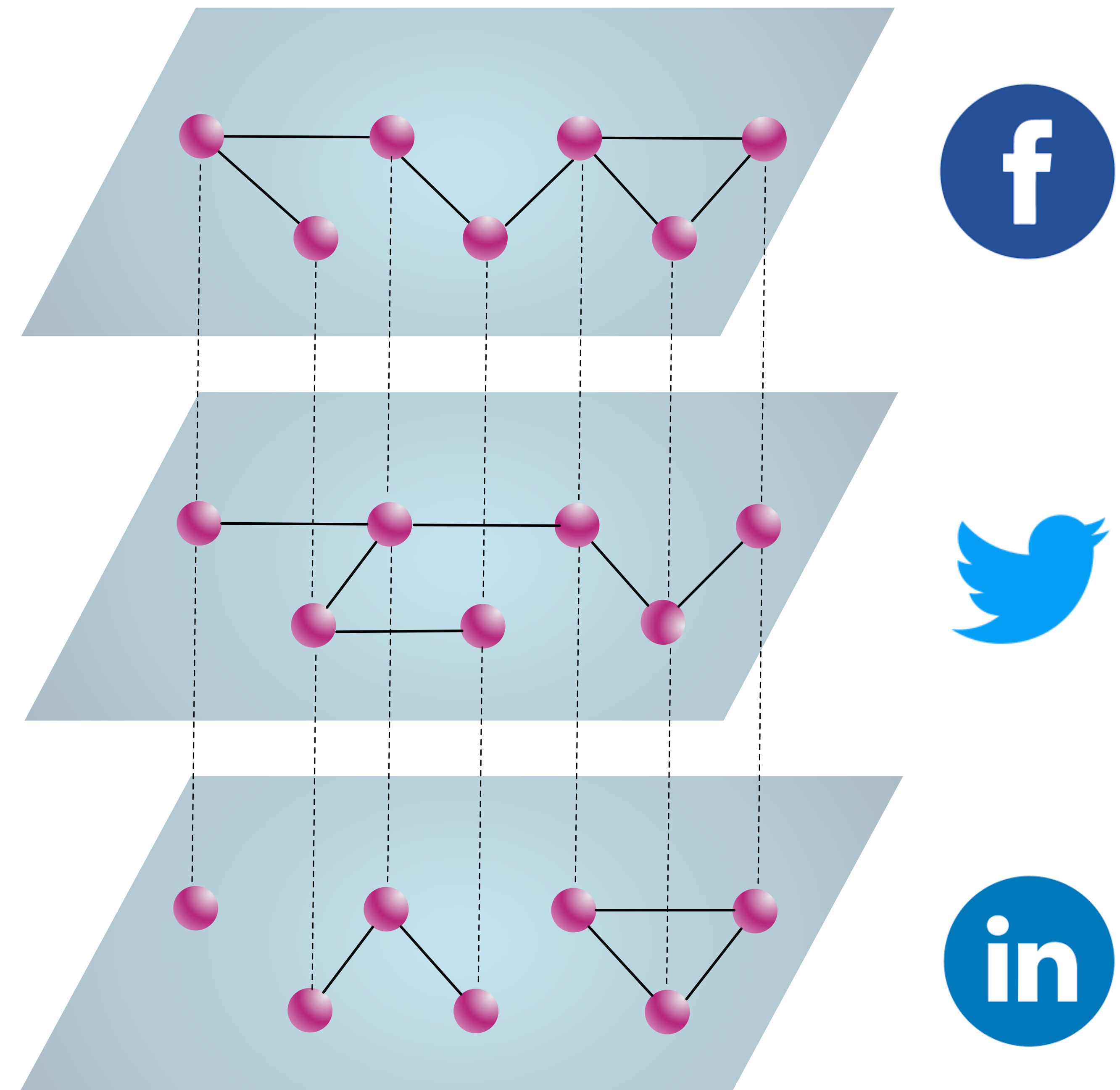
Social Movements | Belief Adoption | Viral spreading

Multilayer Networks: Social Systems

Original, aggregate network

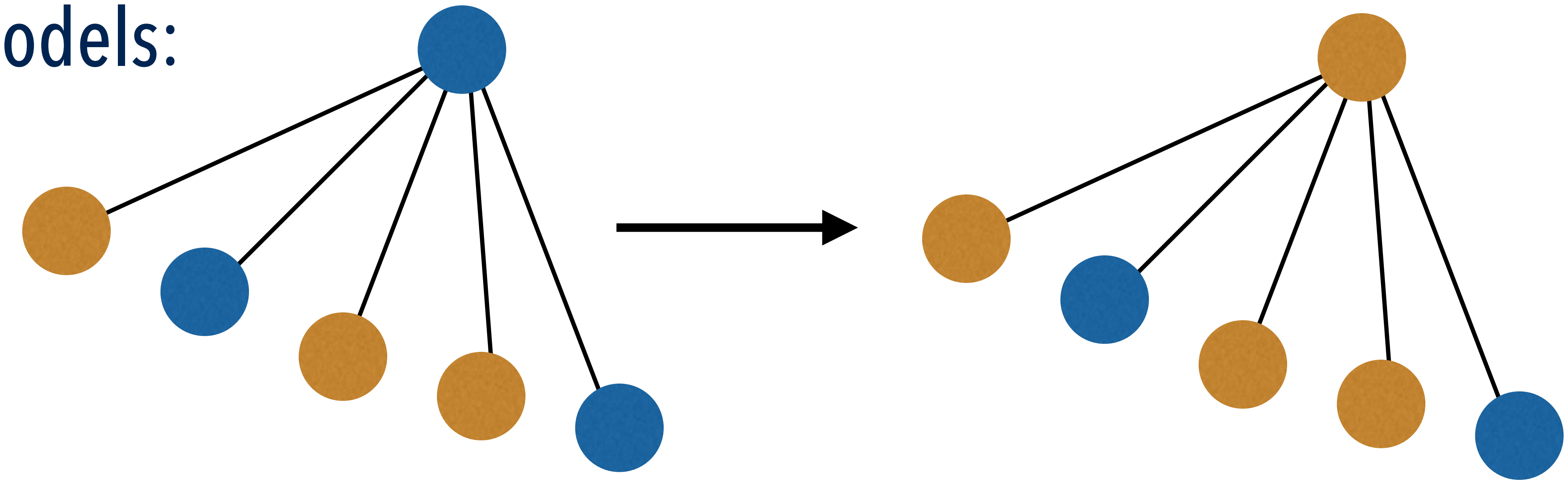


When unfolded, layers appear

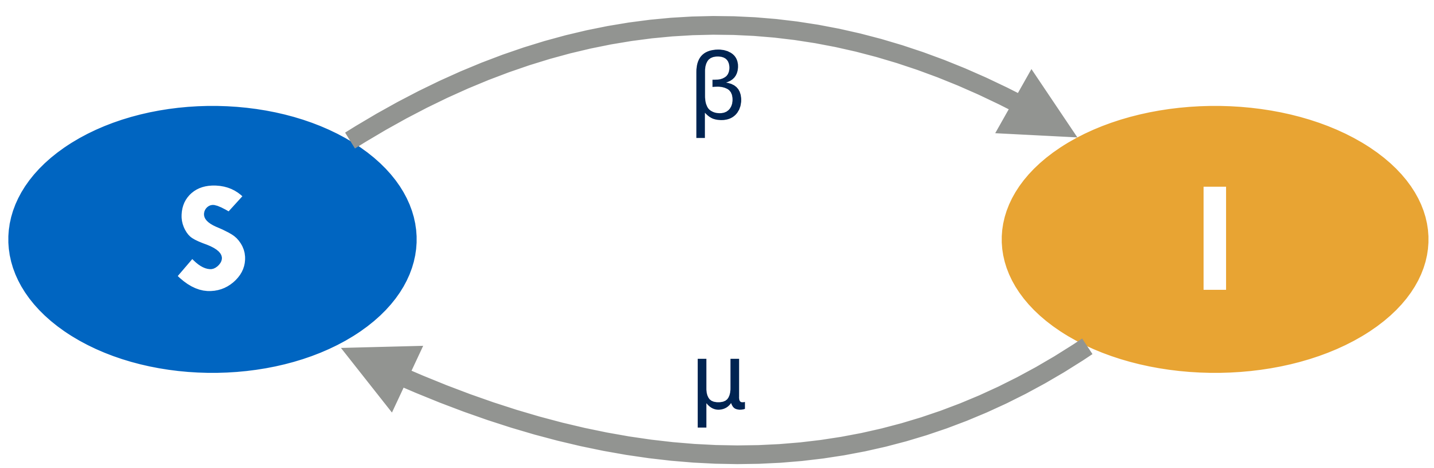


Models

- Threshold models:



Information like a pathogen: SIS



L. Weng, F. Menczer, Y.-Y. Ahn, **Virality Prediction and Community Structure in Social Networks**, Sci. Rep. 02522 (2013)

Single layer Microscopic Markov Chain

$$p_i(t+1) = (1-q_i(t))(1-p_i(t)) + (1-\mu)p_i(t) + \mu(1-q_i(t))p_i(t)$$

$$q_i(t) = \prod_{j=1}^{N}(1-\beta r_{ij}p_j(t))$$

$$r_{ij} = 1 - \left(1 - \frac{a_{ij}}{k_i}\right)^{\lambda_i}$$

S. Gómez et al., Europhys. Lett. 89, 38009 (2010)

Single layer Microscopic Markov Chain

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Probability of not being infected
by any neighbor

S. Gómez et al., Europhys. Lett. 89, 38009 (2010)

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Probability of not being infected by any neighbor

Contacts Matrix

S. Gómez et al., Europhys. Lett. 89, 38009 (2010)

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$$p_i(t+1) = (1-q_i(t))(1-p_i(t)) + (1-\mu)p_i(t) + \mu(1-q_i(t))p_i(t)$$

$$q_i(t) = \prod_{j=1}^{N}(1-\beta r_{ij} p_j(t))$$

$$r_{ij} = 1 - \left(1 - \frac{a_{ij}}{k_i}\right)^{\lambda_i}$$

Probability of not being infected by any neighbor

Contacts Matrix

Contacts per time

S. Gómez et al., Europhys. Lett. 89, 38009 (2010)

Single layer Microscopic Markov Chain

$$p_i(t+1) = (1 - q_i(t))(1 - p_i(t)) + (1 - \mu)p_i(t) + \mu(1 - q_i(t))p_i(t)$$

$$q_i(t) = \prod_{j=1}^{N}(1 - \beta r_{ij} p_j(t))$$

$$r_{ij} = 1 - \left(1 - \frac{a_{ij}}{k_i}\right)^{\lambda_i}$$

S. Gómez et al., Europhys. Lett. 89, 38009 (2010)

Single layer Microscopic Markov Chain

$$p_i(t+1) = (1-q_i(t))(1-p_i(t)) + (1-\mu)p_i(t) + \mu(1-q_i(t))p_i(t)$$

Threshold

$$q_i(t) = \prod_{j=1}^{N}(1-\beta r_{ij} p_j(t))$$

$$r_{ij} = 1 - \left(1 - \frac{a_{ij}}{k_i}\right)^{\lambda_i}$$

$$\left(\frac{\beta}{\mu}\right)_c = \frac{1}{\Lambda_{max}}$$

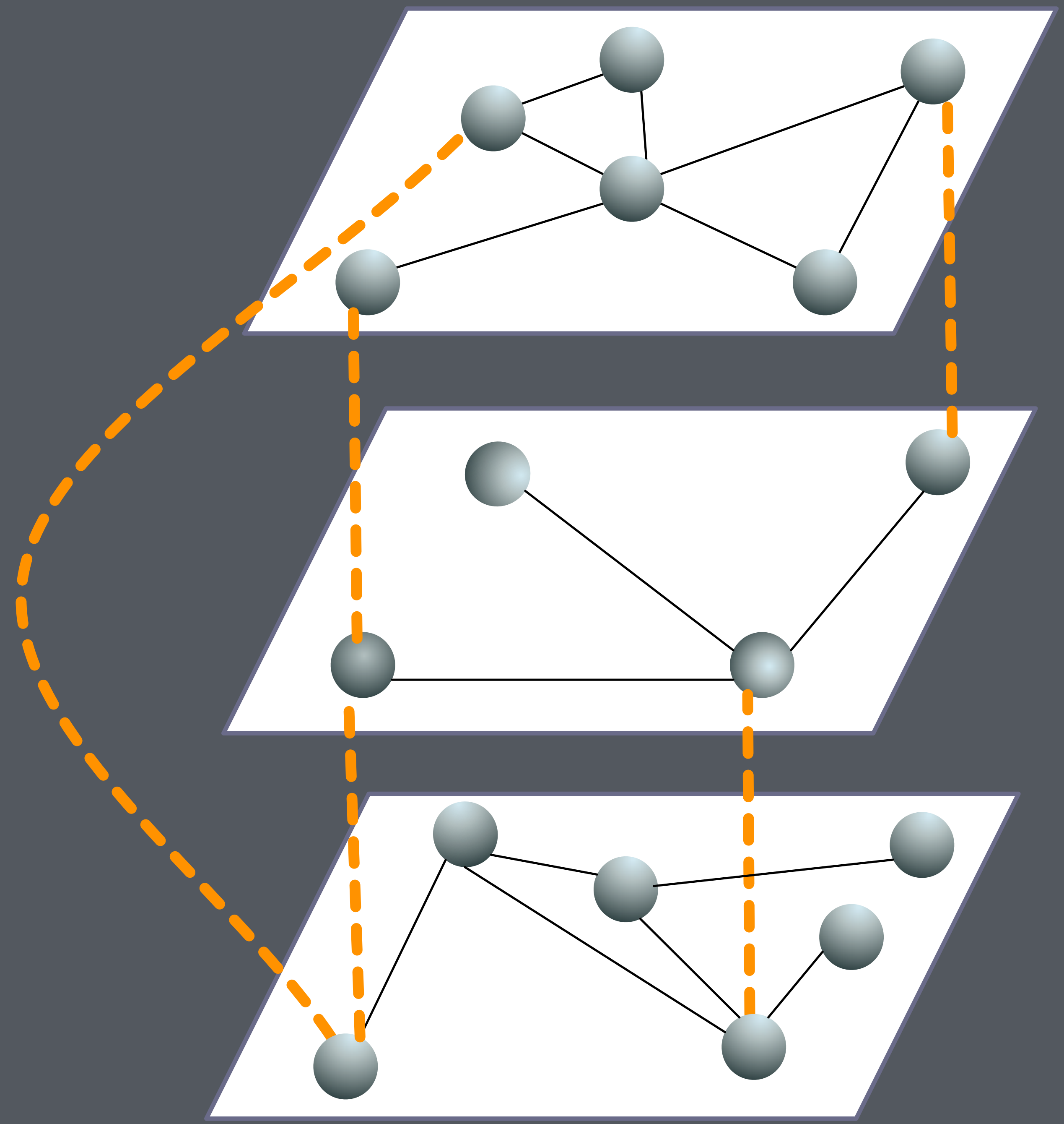
S. Gómez et al., Europhys. Lett. 89, 38009 (2010)

How to represent it

Supra-Adjacency Matrix

$$\bar{A} = \bigoplus_{\alpha} A_{\alpha} + C = A + C$$

$$\bar{A} = \left(\begin{array}{c|c|c} A_1 & C_{1,2} & C_{1,3} \\ \hline C_{2,1} & A_2 & C_{2,3} \\ \hline C_{3,1} & C_{3,2} & A_3 \end{array} \right)$$



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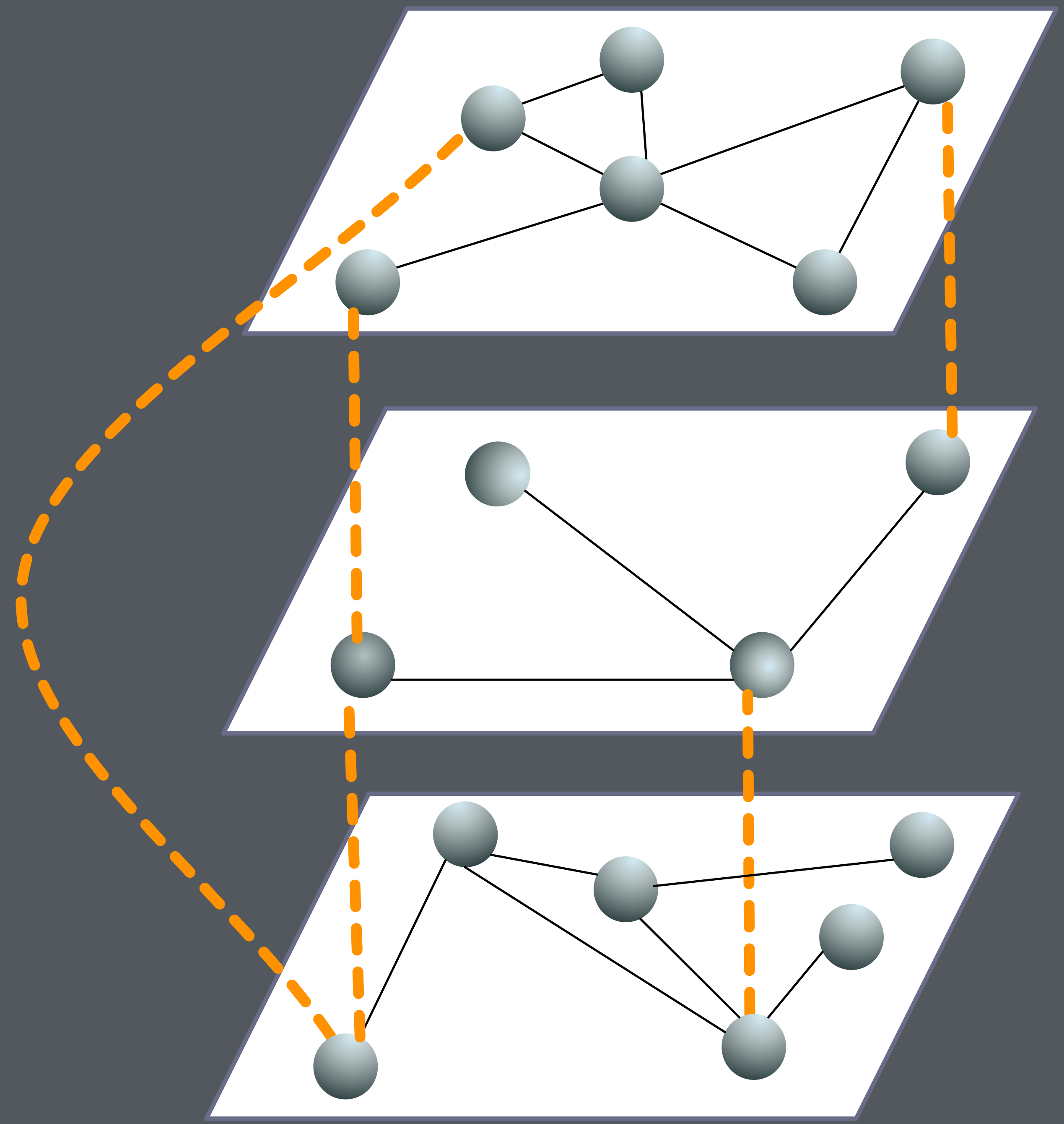

A_i Layer adjacency matrix

How to represent it

Supra-Adjacency Matrix

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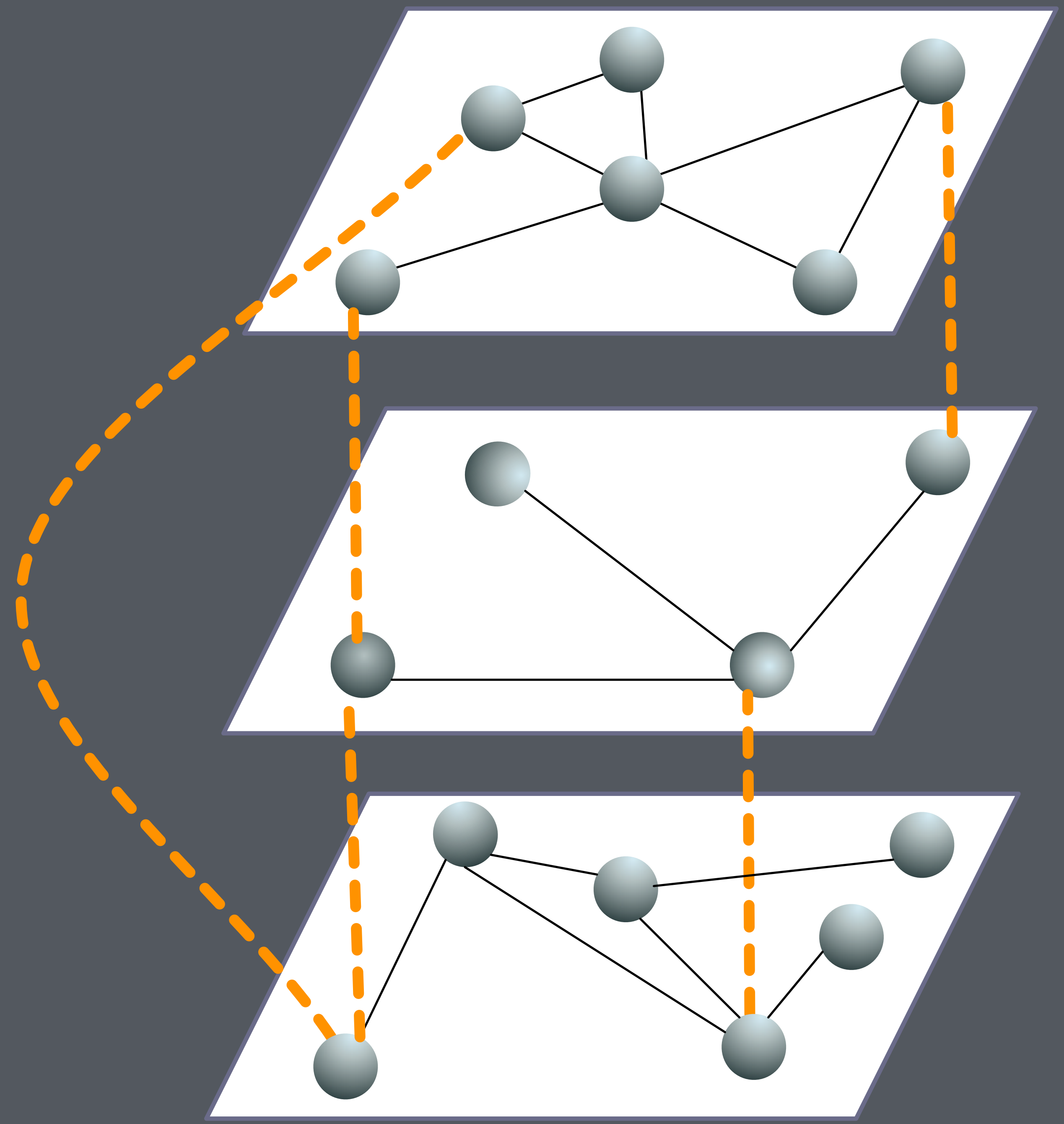


A_i Layer adjacency matrix

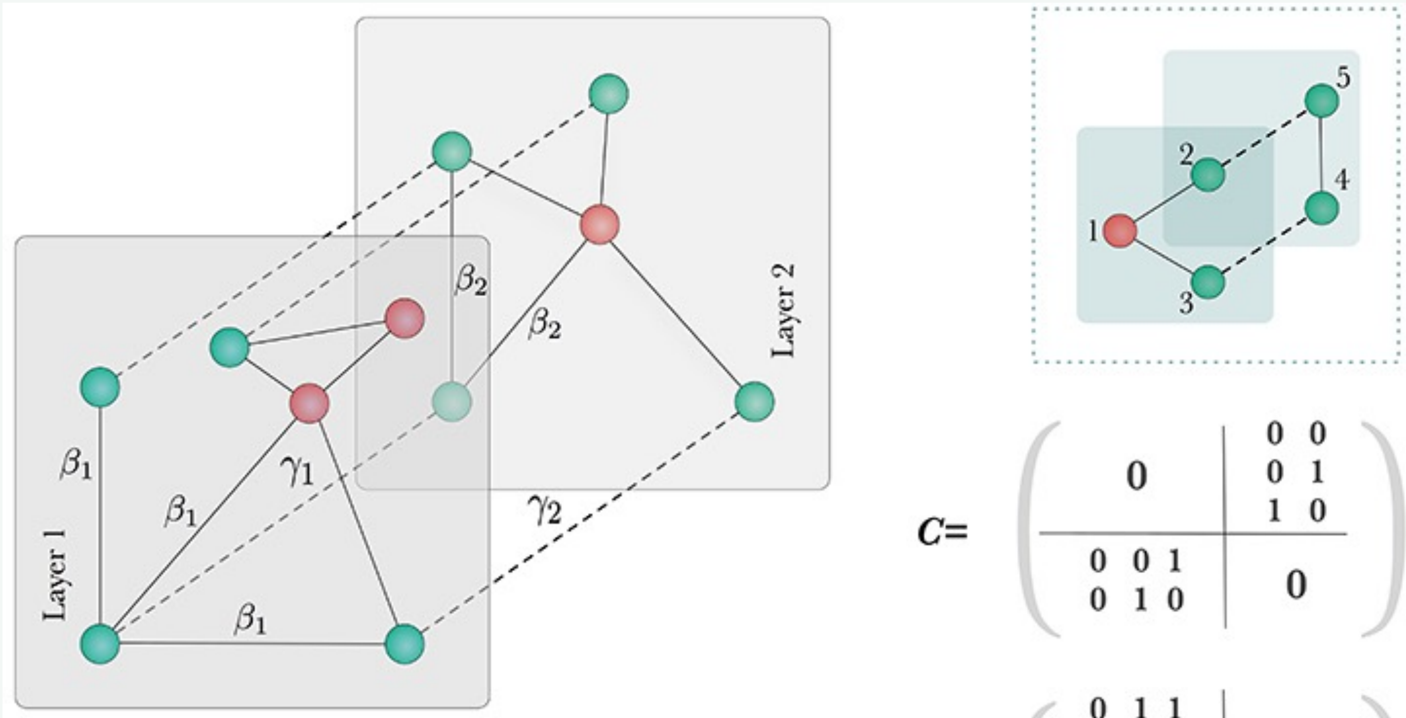
$C_{i,j}$ Coupling matrix

Microscopic Markov Chain on Multiplex

$$\vec{p}(t+1) = (\vec{1} - \vec{p}(t)) * (\vec{1} - \vec{q}(t)) + (\vec{1} - \vec{\mu}) * \vec{p}(t)\vec{\mu} * (\vec{1} - \vec{q}(t)) * \vec{p}(t)$$

Supra-Contacts Matrix

$$\bar{R} = \bigoplus_{\alpha} R_\alpha + \left(\frac{\vec{\gamma}}{\beta}\right)^T C$$



$$C = \left(\begin{array}{c|cc} \mathbf{0} & 0 & 0 \\ & 0 & 1 \\ & 1 & 0 \\ \hline 0\ 0\ 1 & & \\ 0\ 1\ 0 & \mathbf{0} & \end{array}\right)$$

$$A = \left(\begin{array}{ccc|c} 0 & 1 & 1 & \\ 1 & 0 & 0 & \mathbf{0} \\ 1 & 0 & 0 & \\ \hline & \mathbf{0} & & 0\ 1 \\ & & & 1\ 0 \end{array}\right)$$

$$(R_\alpha)_{ij} = 1 - \left(1 - \frac{(A_\alpha)_{ij}}{k_{\alpha i}}\right)^{\lambda_{\alpha i}}$$

Cozzo et al. Phys. Rev. E 88, 050801(R) (2013)

Microscopic Markov Chain on Multiplex

$$\vec{p}(t+1) = (\vec{1} - \vec{p}(t)) * (\vec{1} - \vec{q}(t)) + (\vec{1} - \vec{\mu}) * \vec{p}(t)\vec{\mu} * (\vec{1} - \vec{q}(t)) * \vec{p}(t)$$

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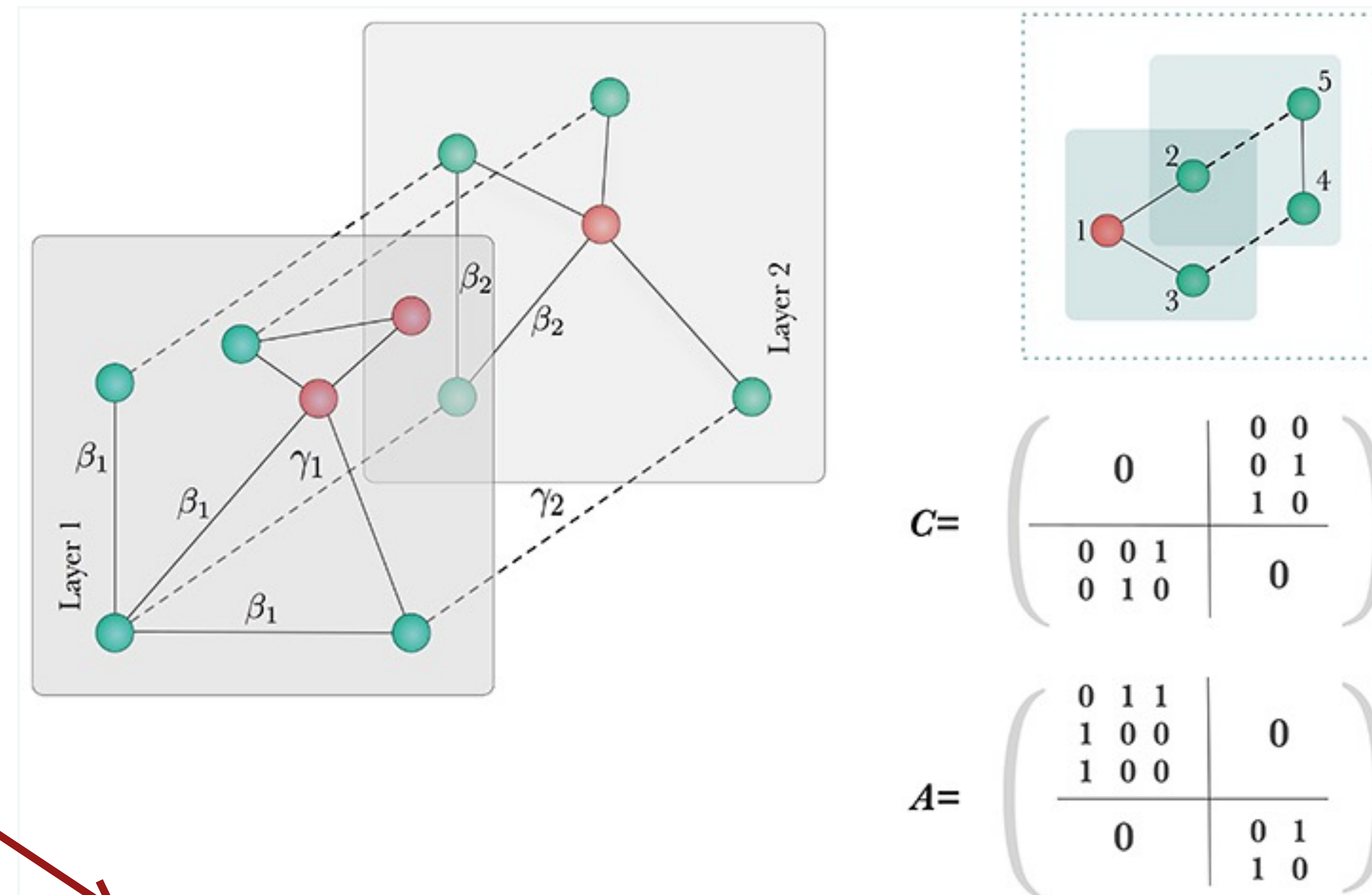

"self infection" probability

$$(R_\alpha)_{ij} = 1 - \left(1 - \frac{(A_\alpha)_{ij}}{k_{\alpha i}}\right)^{\lambda_{\alpha i}}$$

Cozzo et al. Phys. Rev. E 88, 050801(R) (2013)

Solving it

$$[\bar{R} - \frac{\mu}{\beta} I]p = 0$$

$$\left(\frac{\beta}{\mu}\right)_c = \frac{1}{\bar{\Lambda}_{max}}$$

The largest eigenvalue of $\bar{R}$ sets the critical value but…

What does $\bar{\Lambda}_{max}$ look like?

The largest eigenvalue of $\bar{R}$

Perturbative Analysis

$$\bar{R} = R + \epsilon C$$

$$\bar{\Lambda}_{max} \simeq \Lambda + \epsilon \triangle \Lambda$$

$$\bar{\Lambda}_{max} = \max_{\alpha} \{\Lambda_\alpha\}$$

$$\triangle \Lambda_{max} = \frac{\vec{v}^T C \vec{v}}{\vec{v}^T \vec{v}}$$

If $\Lambda_{1_{max}} >> \Lambda_{\alpha_{max}}$

$$\vec{v} = \left(\begin{array}{c} \vec{v}_{(1)} \\ 0 \end{array} \right) \rightarrow \triangle \Lambda = 0$$

At first order:

$$\bar{\Lambda}_{max} = \Lambda_{max}$$

The largest eigenvalue of $\bar{R}$

Perturbative Analysis

$$\bar{R} = R + \epsilon C$$

$$\bar{\Lambda}_{max} \simeq \Lambda + \epsilon \triangle \Lambda$$

$$\bar{\Lambda}_{max} = \max_{\alpha}\{\Lambda_{\alpha}\}$$

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At first order:

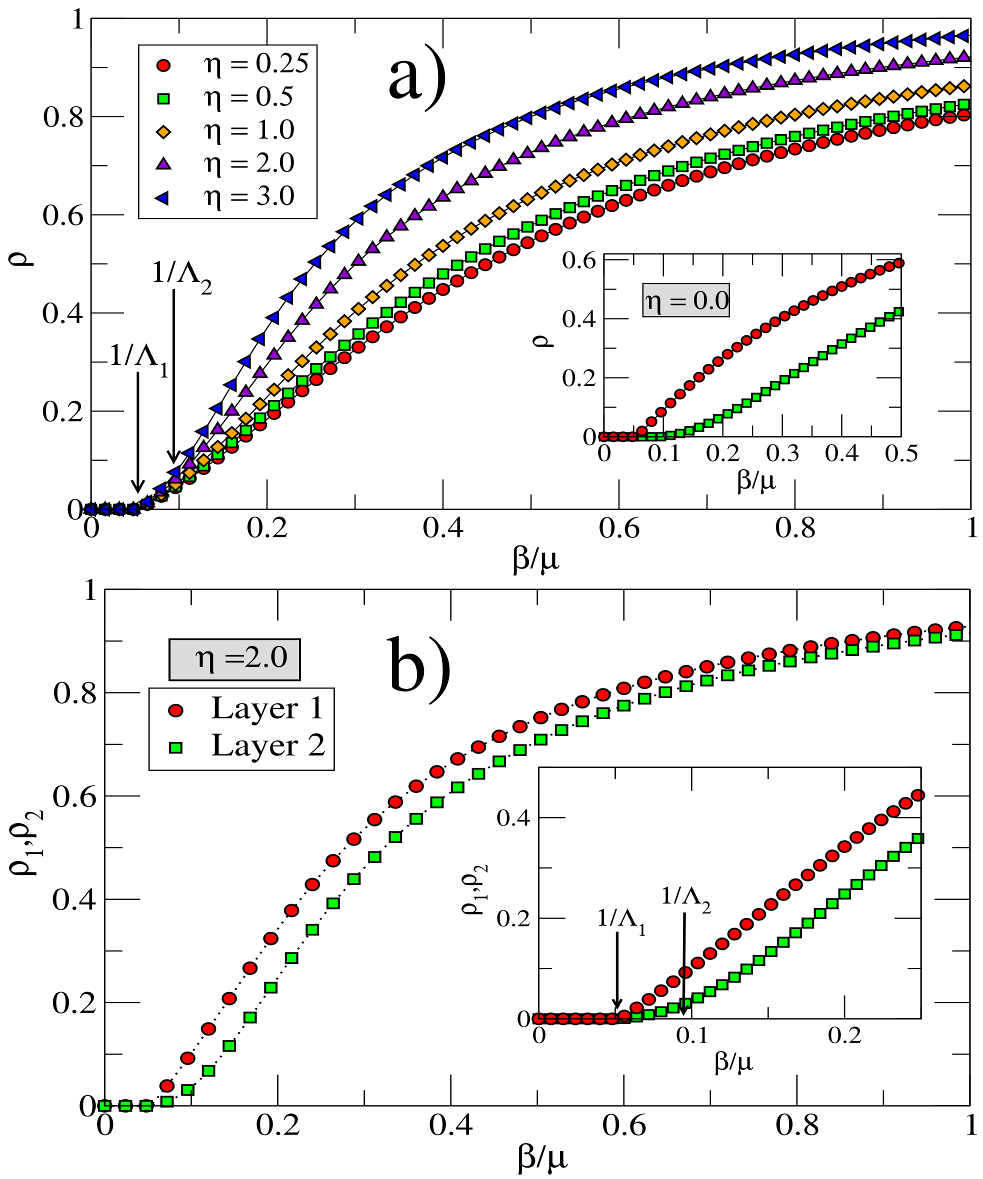
$$\bar{\Lambda}_{max} = \Lambda_{max}$$

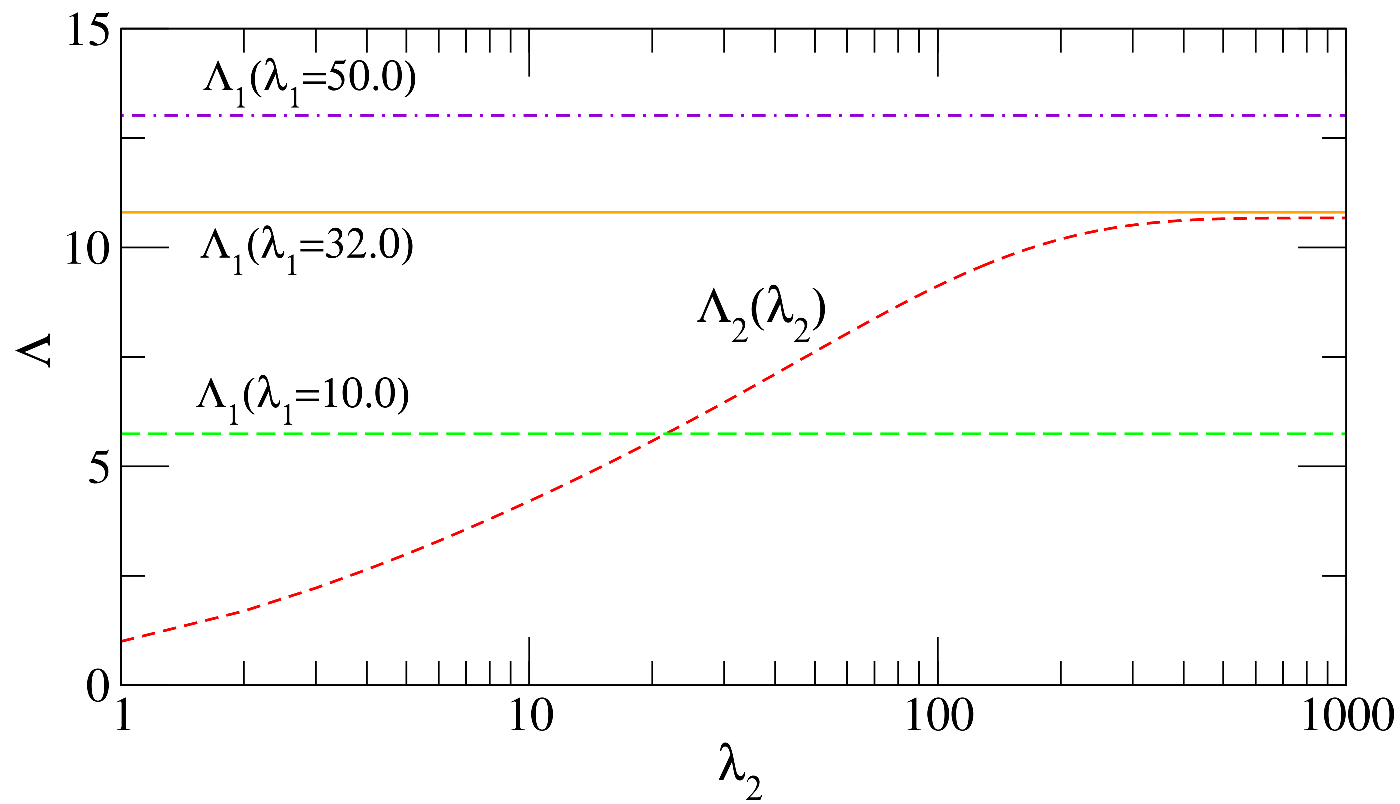
Dominant Layer

The Dominant Layer sets the critical point for the outbreak but…

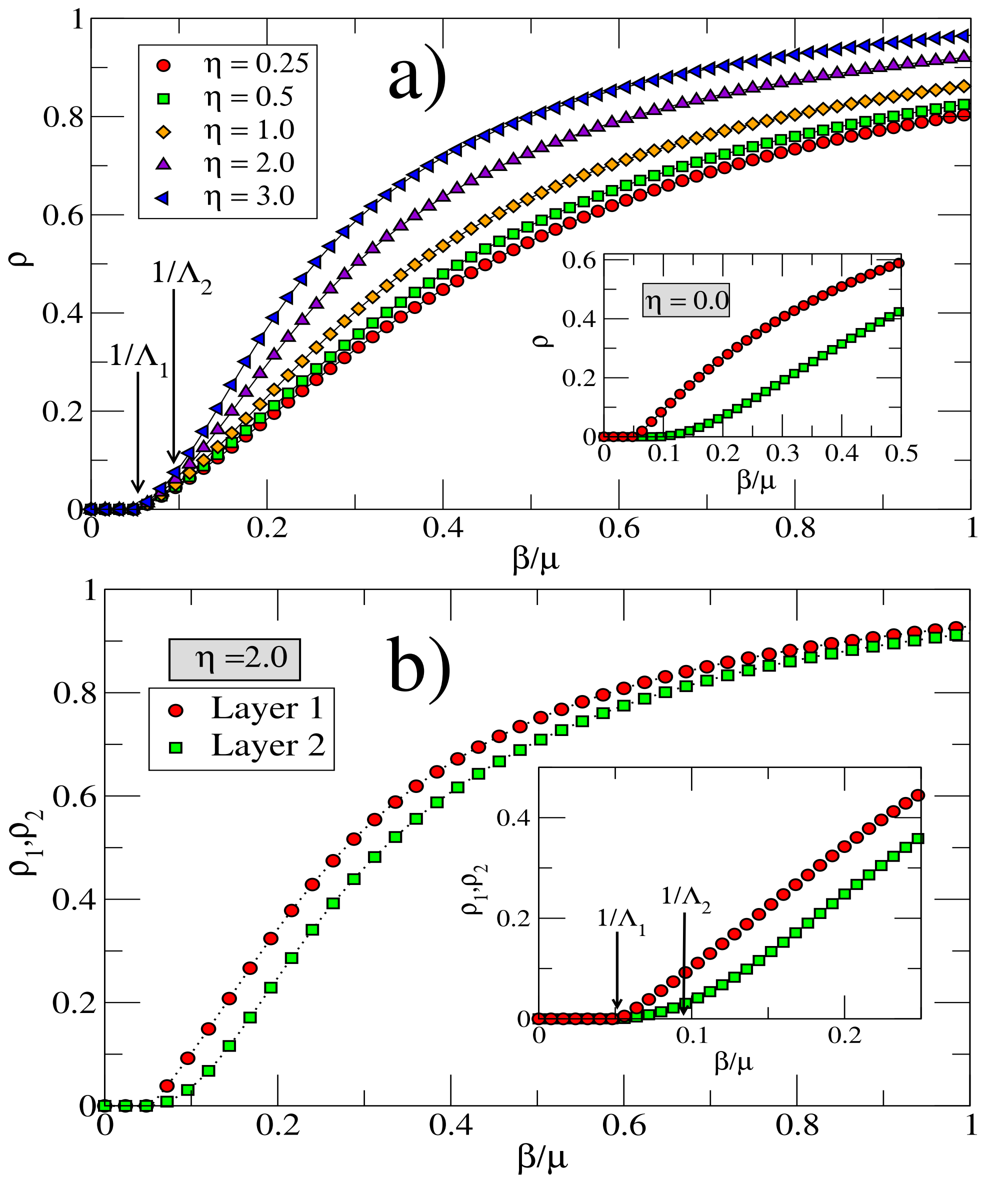
Dominance depends on both topology and activity

$$(R_\alpha)_{ij} = 1 - \left(1 - \frac{(A_\alpha)_{ij}}{k_{\alpha i}}\right)^{\lambda_{\alpha i}}$$



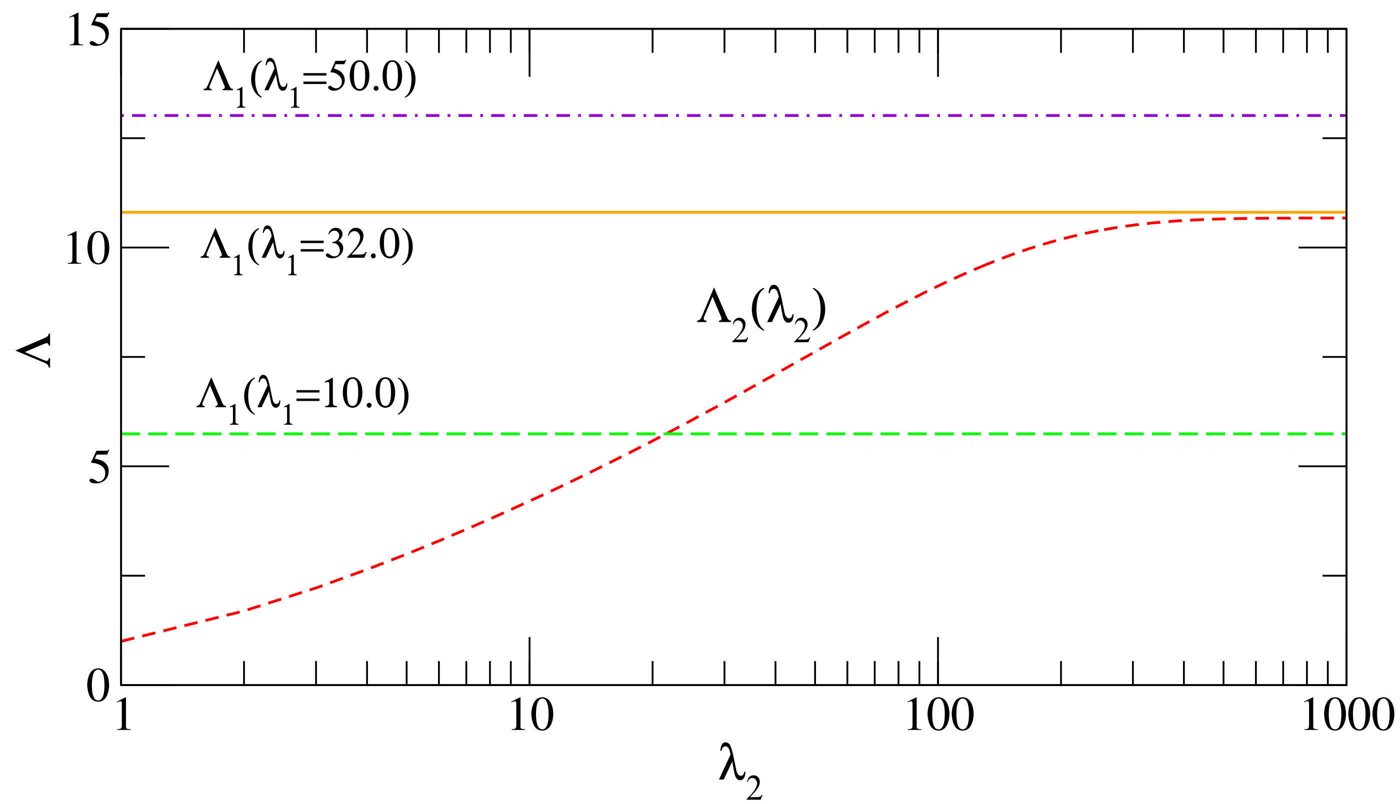


The Dominant Layer sets the critical point for the outbreak but…



Dominance depends on both topology and activity

$$(R_\alpha)_{ij} = 1 - \left(1 - \frac{(A_\alpha)_{ij}}{k_{\alpha i}}\right)^{\lambda_{\alpha i}}$$

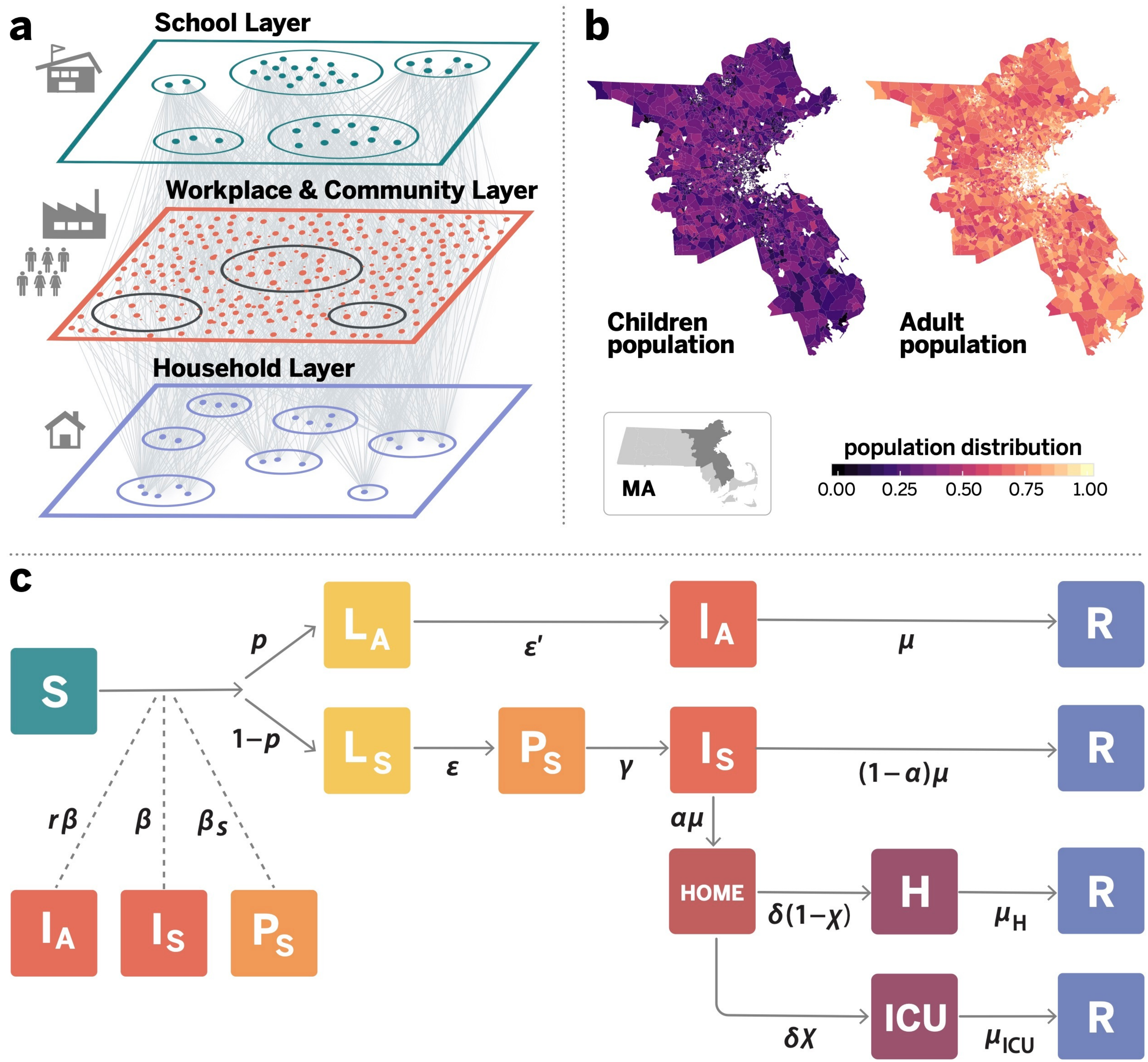


- Largest eigenvalue of R_α:
  a measure of the uncertainty of the interactions

- Dominant layer: least constrained interaction network

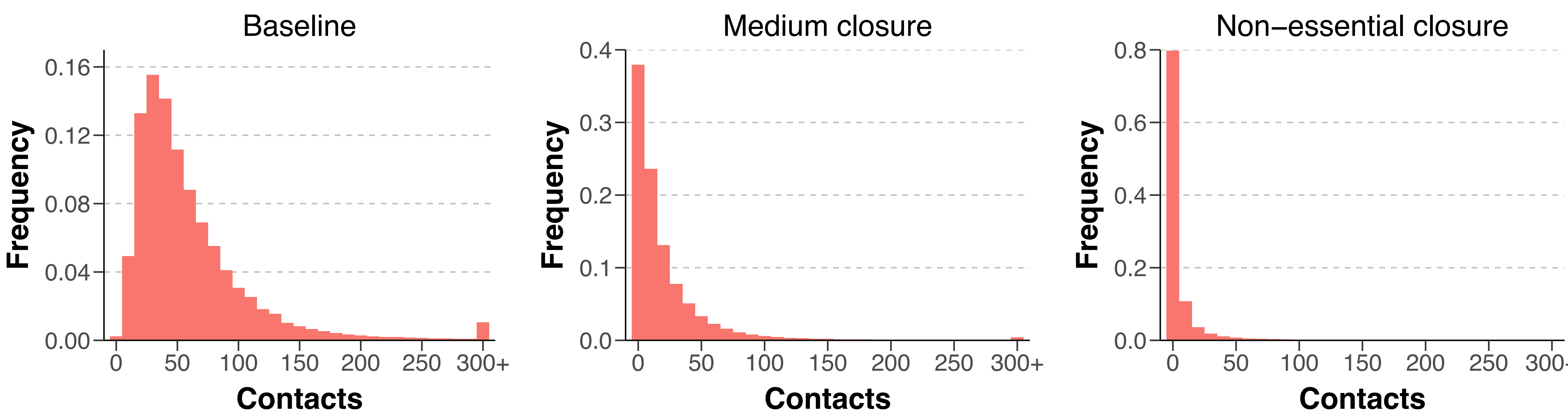
The least constrained interaction network drives the social contagion process

COVID-19: Boston,
more sophisticated model

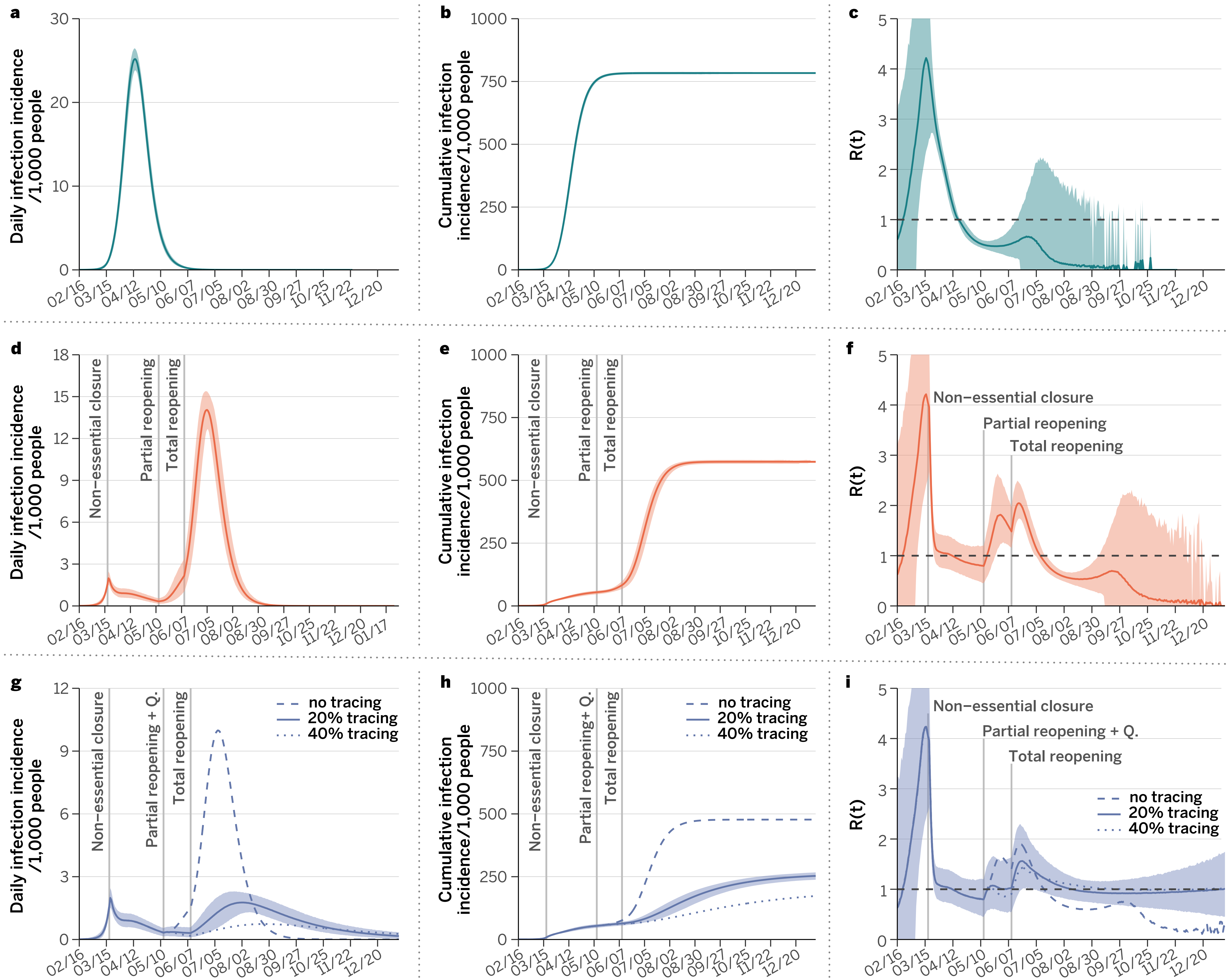


A. Aleta et al. **Nature Human Behaviour** 4, 964–971 (2020).

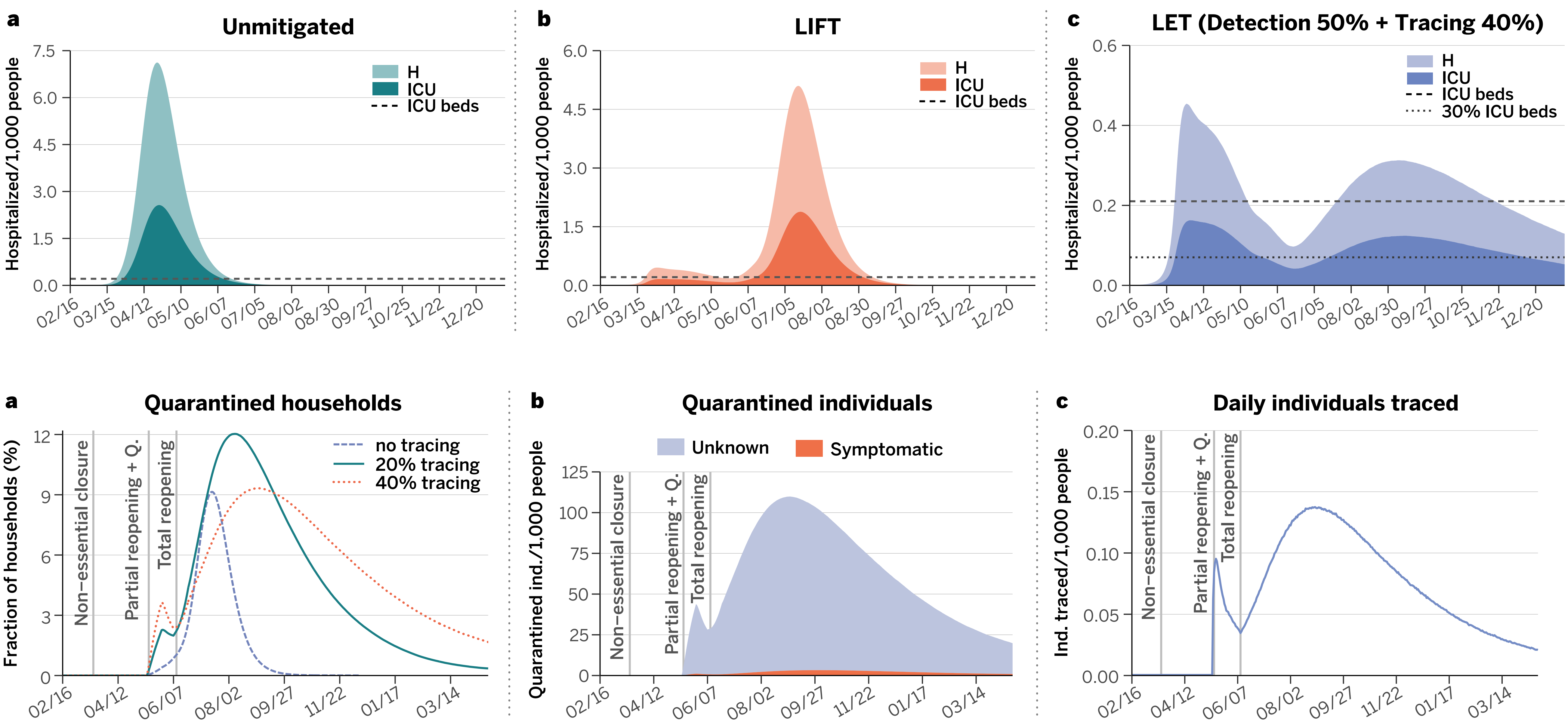
	Baseline		Medium clos.			Non-essential clos.		
Layers	Contacts	%.	Contacts	%	% Diff.	Contacts	%	% Diff.
Community	3,924,694	78	1,378,054	27.4	-72.6	357,144	7.1	-92.9
Households	160,748	3.2	160,748	3.2	0	160,748	3.2	0
Schools	944,446	18.8	0	0	-100	0	0	-100
Total	5,029,888	100	1,538,802	30.6	-69.4	517,892	10.3	-89.7



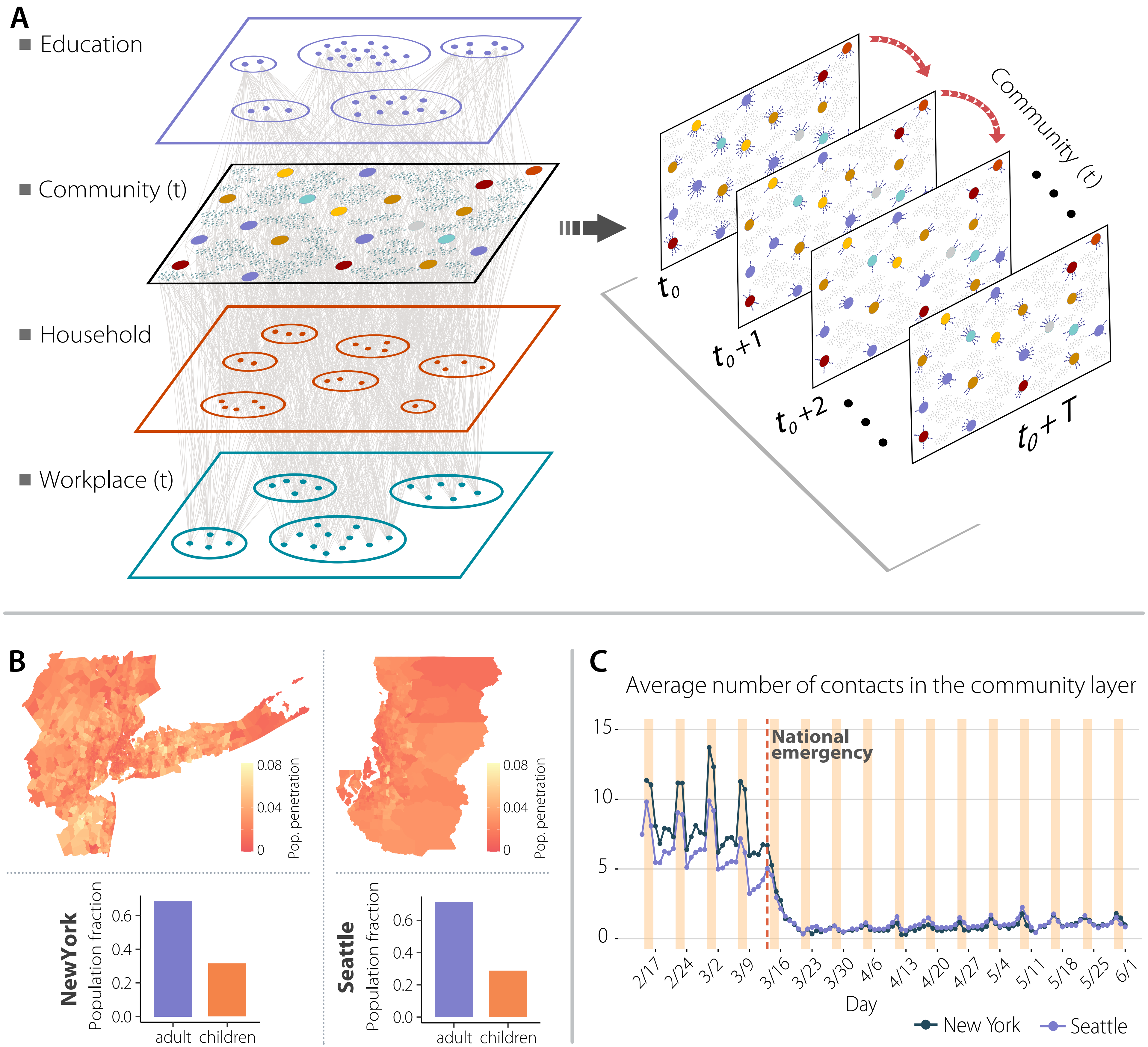
COVID-19: Boston, more sophisticated model



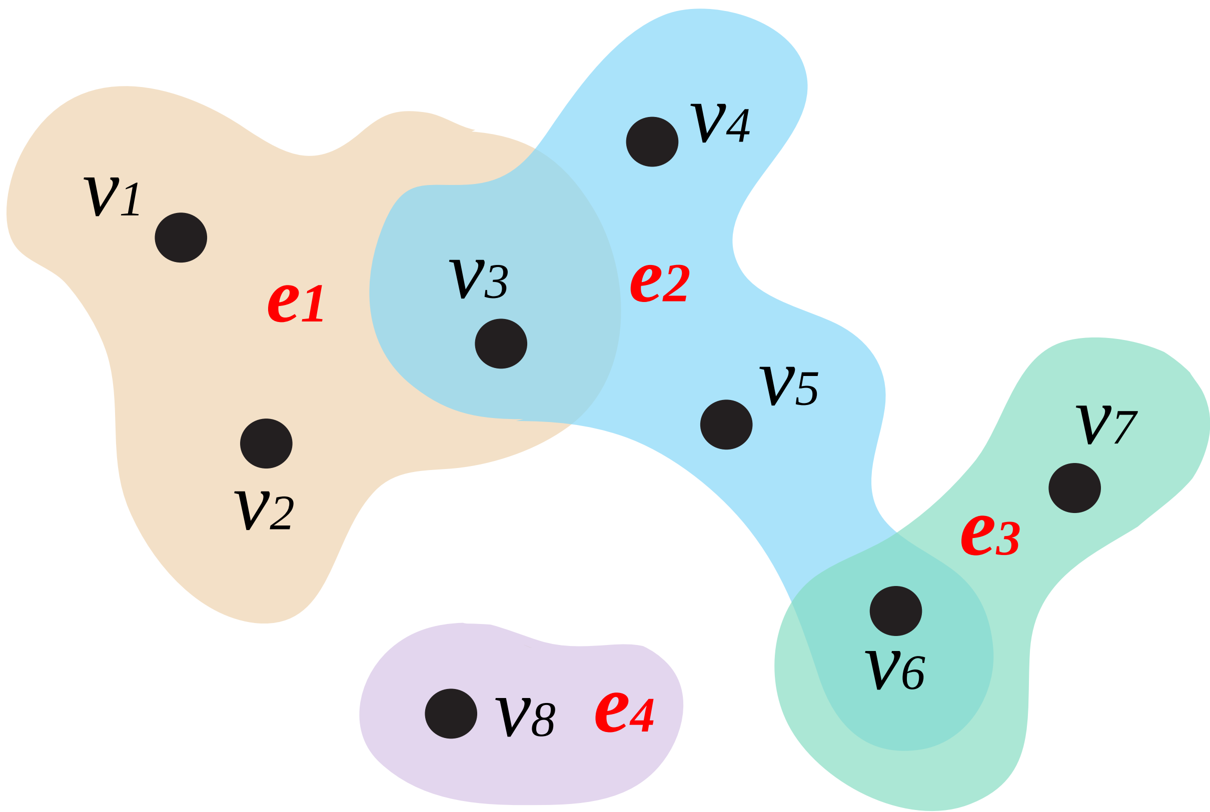
COVID-19: Boston, more sophisticated model

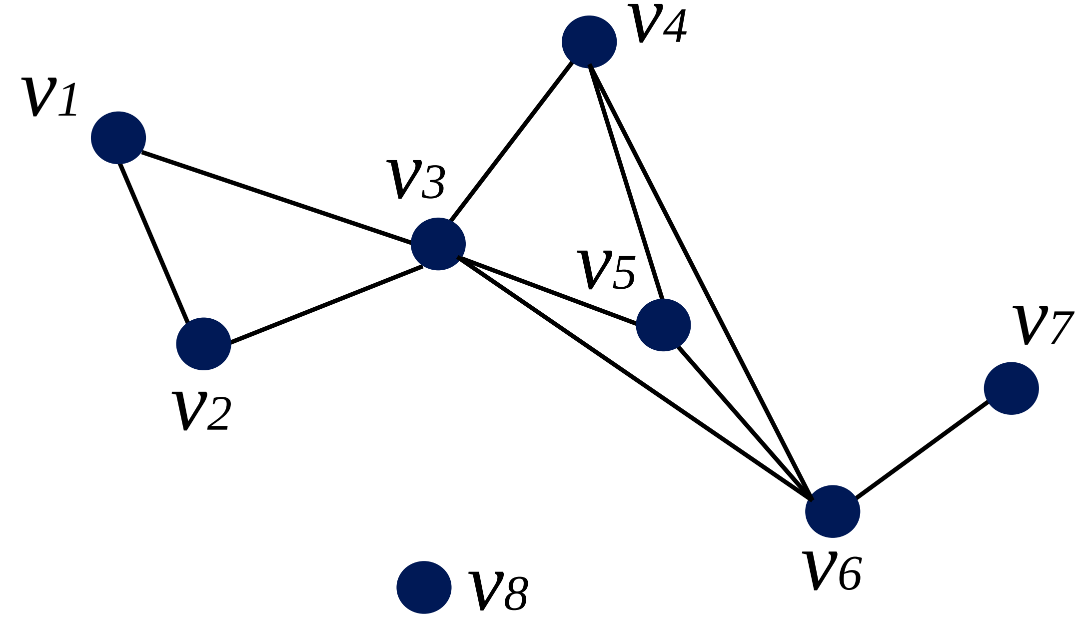


Super-spreaders events



Hypergraphs: basic definitions

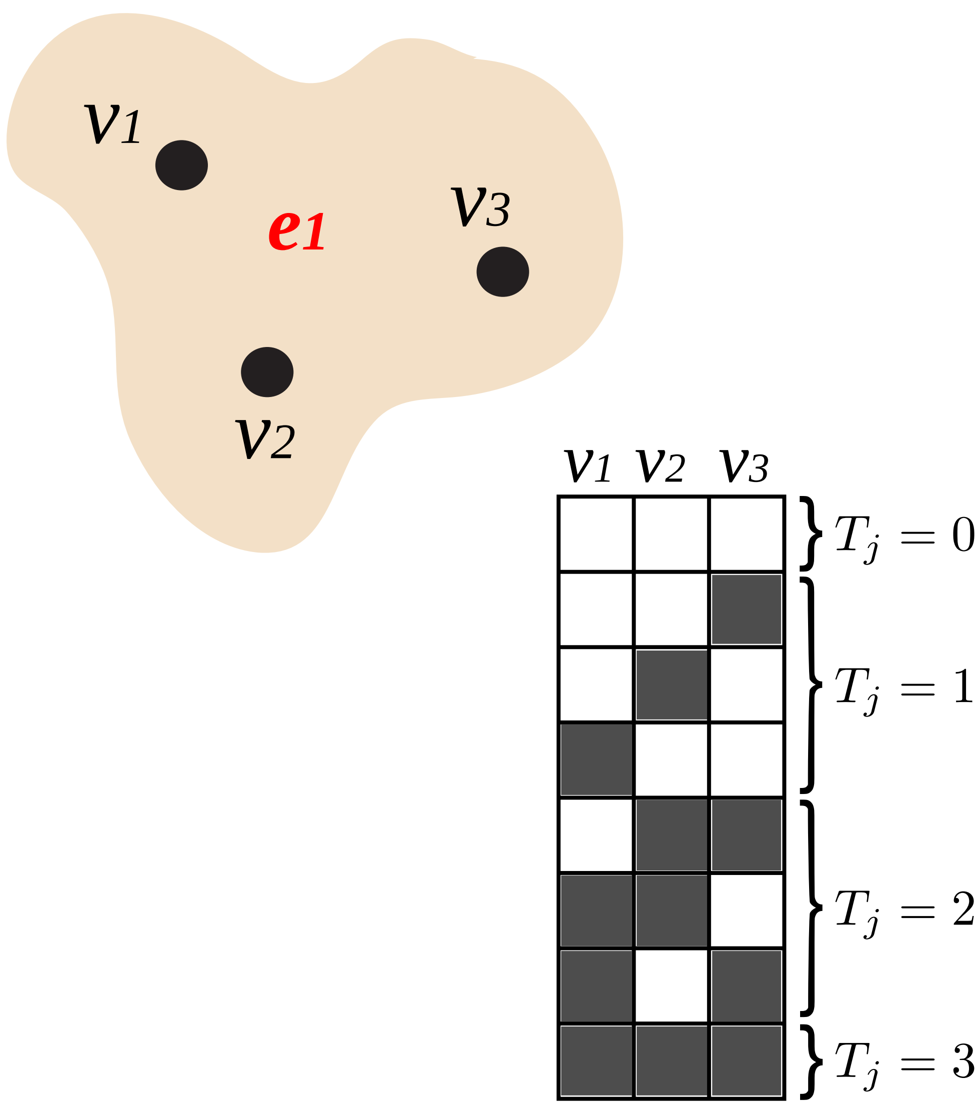




$$\mathcal{V} = \{v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8\}$$
$$\mathcal{E} = \{e_1, e_2, e_3, e_4\}$$
$$e_1 = \{v_1, v_2, v_3\},\ e_2 = \{v_3, v_4, v_5, v_6\},$$
$$e_3 = \{v_6, v_7\} \text{ and } e_4 = \{v_8\}$$

$$\mathcal{V} = \{v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8\}$$
$$\mathcal{E} = \{\{v_1, v_2\}, \{v_1, v_3\}, ..., \{v_6, v_7\}\}$$

Model definition: Hyperedge process construction



Bernoulli random variable:

$$Y_i = \begin{cases} 1, & \text{if } i \text{ is active} \\ 0, & \text{if } i \text{ is inactive} \end{cases}$$

Critical-mass dynamics:

$$\rightarrow T_j = \sum_{k \in e_j} Y_k$$
$$\rightarrow T_j > \Theta_j$$

Poisson binomial distribution:

$$\mathbb{P}\left(K = k\right) = \sum_{A \in F_k} \prod_{i \in A} p_i \prod_{j \in A^c} \left(1 - p_j\right)$$

DFT [1]:

$$\mathbb{P}_{e_j}\left(K = k\right) = \frac{1}{n+1} \sum_{l=0}^{n} C^{-lk} \prod_{m=1}^{n} \left(1 + (C^l - 1) y_m\right)$$

$$C = \exp\left(\frac{2i\pi}{n+1}\right)$$

[1] M. Fernandez and S. Williams, IEEE Trans. Aerosp. Electron. Syst. 46, 803 (2010)
Guilherme Ferraz de Arruda, Giovanni Petri, and Yamir Moreno, Phys. Rev. Research 2, 023032

Model definition: Arbitrary hypergraphs

→ Bernoulli random variable Y_i

→ Set of independent Poisson Processes:

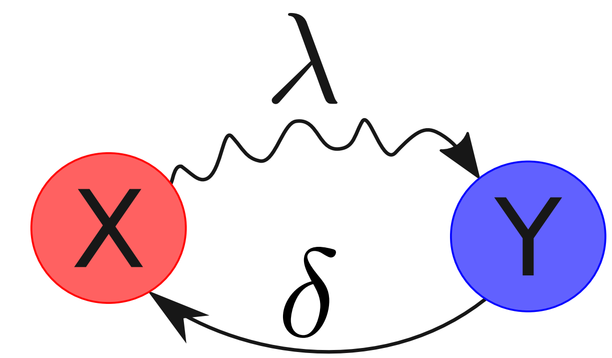
$$\{N_i^{\delta}, N_j^{\lambda_j}\}$$

Deactivation (spontaneous)

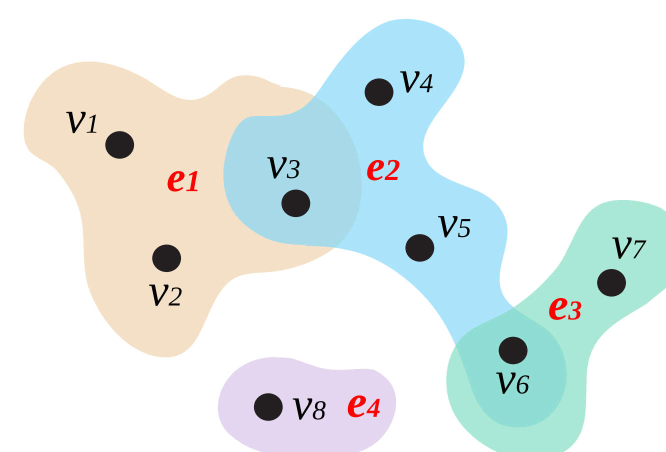
Critical-mass dynamics:

$\rightarrow T_j > \Theta_j$

$\rightarrow T_j = \sum_{k \in e_j} Y_k$



+



→ Exact Model:

$$\frac{d\mathbb{E}(Y_i)}{dt} = \mathbb{E}\left(-\delta Y_i + [1 - Y_i] \sum_{e_j \cap \{v_i\} \neq \emptyset} \lambda_j \sum_{B} \mathbb{1}_{\{Y_i = 0, T_j \geqslant \Theta_j\}} \right)$$

→ First-order approximation

$$\frac{dy_i}{dt} = -\delta y_i + \lambda \left(1 - y_i\right) \sum_{e_j \cap \{i\} \neq \emptyset} \sum_{k=\Theta_j}^{|e_j|} \lambda^*(|e_j|) \mathbb{P}_{e_j}\left(K = k\right)$$

$$\mathbb{P}_{e_j}\left(K = k\right) = \frac{1}{n+1} \sum_{l=0}^{n} C^{-lk} \prod_{m=1}^{n} \left(1 + (C^l - 1) y_m\right)$$

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Hyperblob: Analytical results II

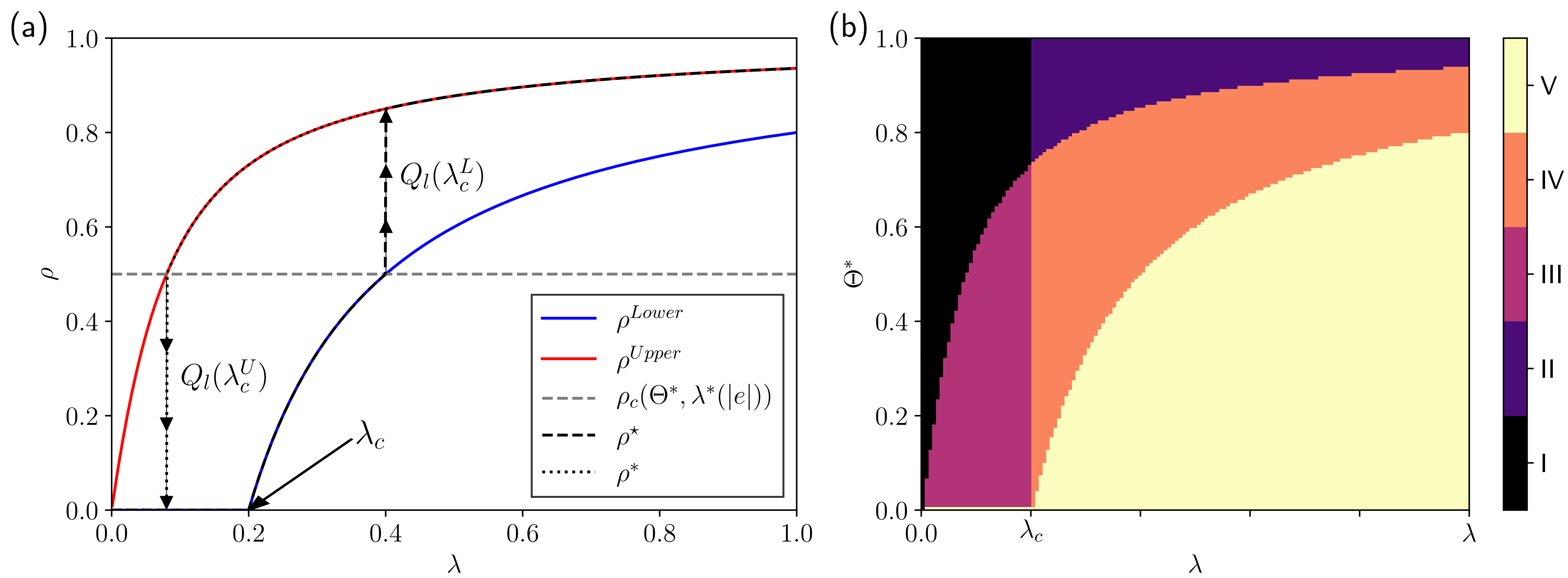

FIG. 2. Results for the hyperblob. Panel (a) shows the possible solutions for a fixed $\Theta^* = 0.5$. In red and blue, the upper and lower solutions (branches), respectively. The transition from the lower to the upper solution (upper to lower) occurs at the intersection of the lower (upper) solution with a value of ρ_c in which the upper solution became stable (unstable). The discontinuity is characterized by the latent heat, $Q_l(\lambda_c^L)$ or $Q_l(\lambda_c^U)$. At $\lambda_c = 0.2$, the lower solution shows a second-order phase transition. In (b) Schematic of the parameter space: Region I: the absorbing state for both the lower and upper solution; Region II: only the lower solution is stable (the global critical mass is not reached, $\rho < \rho_c$); Region III: ρ^{Upper} is stable and $\rho^{\text{Lower}} = 0$ (below the critical point); Region IV: $\rho^{Upper} > \rho^{Lower} > 0$ and both are stable (bi-stable); Region V: only the upper solution is stable (the global critical mass was reached, $\rho \geq \rho_c$).

Guilherme Ferraz de Arruda, Giovanni Petri, and Yamir Moreno, Phys. Rev. Research 2, 023032

Main messages

- Hypergraphs have virtually no structural constrains
- Social contagion models in hypergraphs present a vast parameter space
- **Real processes might present discontinuity, multistability, hysteresis**
- **Bimodal distribution of states, intermittency, hybrid transitions, ...**
- Pairwise interactions are a necessary condition for a second-order phase transition (special case)
- Motivate further research in higher-order social models