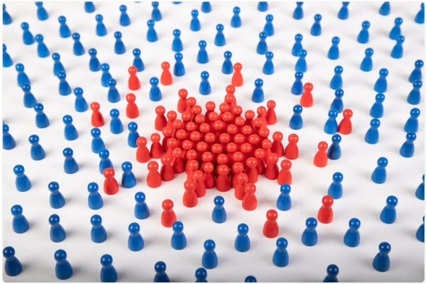
LECTURE 4

The SIR epidemic model on dense dynamic random graphs

Basic version of SIR model

- S: Susceptible, I: Infected, R: Recovered
- Homogeneous mixing: every individual is equally like to come into contact with every other individual
- Static network: the network does not evolve in response to the epidemic



Related works for static graphs

- FLLN for the proportion of S,I,R on sparse static configuration model
  Volz 2008
  Bohman, Picollelli 2012
  Barbour, Reinert 2013
  Decreusefond, Dhersin, Moyal, Tran 2012
  Janson, Luczak, Windridge 2014

- FLLN for the proportion of S,I,R in dense static random graphs
  Delmas, Frasca, Garin, Tran, Velleret, Zitt 2024
  Keliger, Horváth, Takács 2022 Pang, Pardoux, Velleret 2025

The SIR model on dynamic random graphs

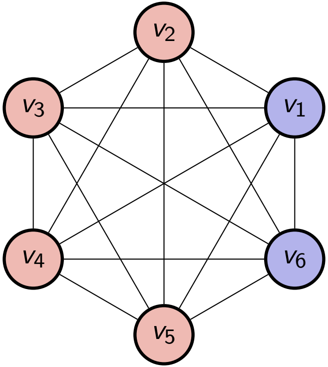
- Heterogeneous mixing: number of edges scales roughly as n^2 (dense regime)
- Dynamic network: connections appear and disappear over time (co–evolution)
- Two types of co–evolution: Local and Global

Related works for dynamic graphs

- FLLN for the proportion of S,I,R on sparse dynamic random graphs
  Ball, Britton, Leung, Sirl 2019
  Ball, Britton 2022
  Chen, Hou, Yao 2025
  Jiang, Kassem, York, Junge, Durrett 2019

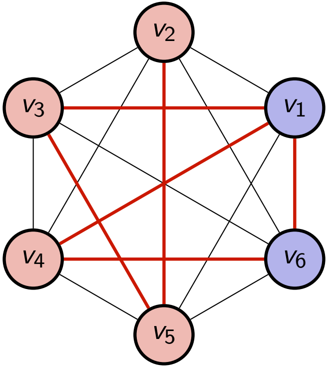
- FLLN for the proportion of S,I,R on dense dynamic random graphs
  Huang, Röllin 2024: dynamic stochastic block model (no co-evolution)

Definition of the model



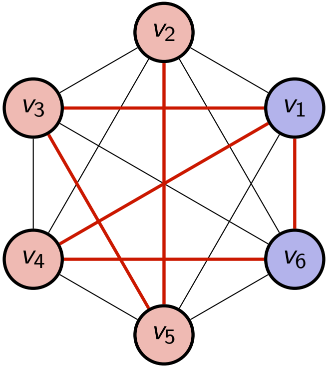
At time $t = 0$ *each vertex is infected with probability* $q_0 \in (0, 1)$
and it is susceptible with probability $1 - q_0$*, independently of everything else*

Definition of the model



At time $t = 0$ we start with the complete graph
and the active edges are chosen independently with probability p_0.

Definition of the model



Each susceptible vertex x has a rate-$\frac{\lambda}{n}\mathcal{N}_x^I$ Poisson clock;
when this rings, the vertex becomes infected.

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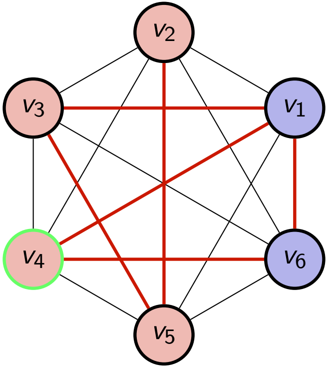

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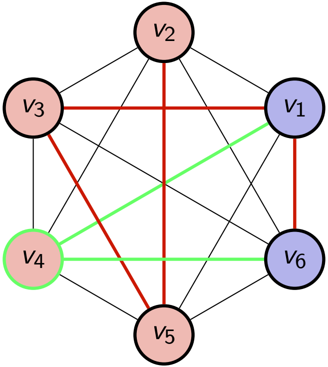

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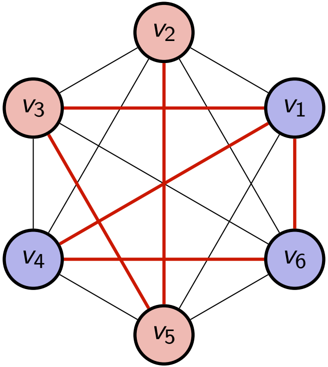
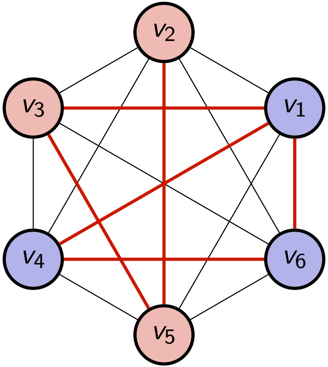


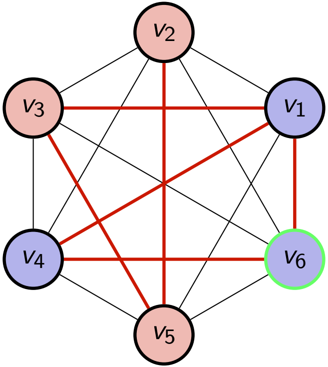
Each susceptible vertex x has a rate–$\frac{\lambda}{n}\mathcal{N}_x^I$ Poisson clock; when this rings, the vertex becomes infected.

Definition of the model



Each infected *vertex* x *has a rate*-1 *Poisson clock;*
when this rings, the vertex becomes recovered.

Definition of the model



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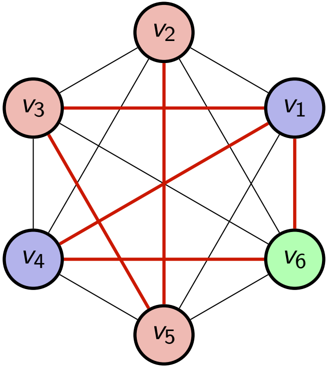

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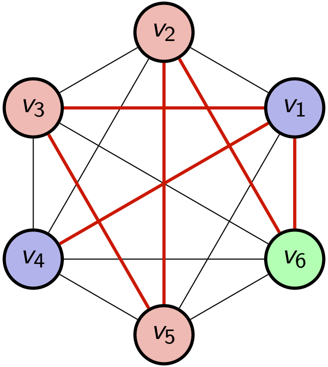

Each edge has a rate–γ Poisson clock; when this rings, the edge is active with a probability funtion that depends on connected vertices ($\pi_{SS}, \pi_{SI}, \pi_{II}$).

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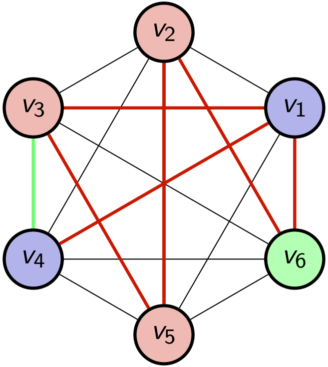

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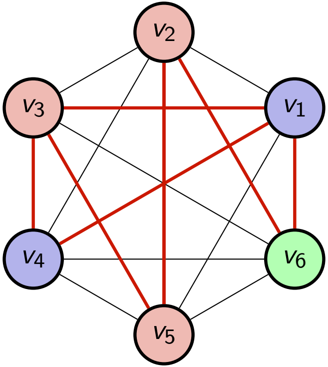

Each edge has a rate–γ Poisson clock; when this rings, the edge is active with a probability funtion that depends on connected vertices ($\pi_{SS}, \pi_{SI}, \pi_{II}$).

Assumptions on the parameters

- $\pi_{SS} = \pi_{SS}(F_n(t;\cdot))$
- $\pi_{SI} = \pi_{SI}(y_{\cdot}(t), F_n(t;\cdot))$
- $\pi_{II} = \pi_{II}(y_i(t), y_j(t), F_n(t;\cdot))$
- Assume Lipschitz continuity on π_{II}: there exists $L_{II} < \infty$ such that for any a_1, a_2, b_1, b_2 and all distribution fucntions F_1, F_2,

$$|\pi_{\mathrm{II}}(a_1, b_1, F_1) - \pi_{\mathrm{II}}(a_2, b_2, F_2)| \leq L_{\mathrm{II}}[|a_1 - a_2| + |b_1 - b_2| + d_L(F_1, F_2)],$$

  where d_L is the Lévy metric. We also impose analogous Lipschitz continuity assumptions on π_{SI} and π_{SS}

Key quantities of the model

- $x_i(t)$ is the state of vertex i at time t

- Keeping track of the states of vertices only is not enough to capture the structure of the resulting graph.

- $y_i(t) = \begin{cases} -1 & \text{if } x_i(t) = S, \\ t - t_i^I & \text{if } x_i(t) = I, \\ T + 1 & \text{if } x_i(t) = R, \end{cases}$ is the type of vertex i at time t

- $X_i(t) = (x_i(t), y_i(t))$ is the generalised type of vertex i at time t

Main results

- $F_n(t; y) = \frac{1}{n} \sum_{i=1}^{n} \mathbf{1}\{y_i(t) \leq y\}$ is the empirical type process.

- $$F(t; y) = \begin{cases} 0 & \text{if } y < -1, \\ p_{\mathrm{S}}(t) & \text{if } y \in [-1, 0), \\ p_{\mathrm{S}}(t) + \int_0^y f_{\mathrm{I}}(t; u)\,\mathrm{d}u & \text{if } y \in [0, t), \\ p_{\mathrm{S}}(t) + p_{\mathrm{I}}(t) & \text{if } y \in [t, T+1), \\ 1 & \text{if } y \geq T+1, \end{cases}$$

  with $f_{\mathrm{I}}(t; u)\,\mathrm{d}u = \mathbb{P}(X_i(t) \in (I, \mathrm{d}u))$.

The probability to have an active edge at time t between two vertices can be expressed in terms of their types only

$$\begin{aligned} p_{ij}(t) &= \mathrm{e}^{-\gamma t} p_0 + \gamma \int_0^t \mathrm{d}s\, \mathrm{e}^{-\gamma s} \pi_{x_i(t-s), x_j(t-s)}(\cdot) \\ &= \mathrm{e}^{-\gamma t} p_0 + \gamma \int_0^t \mathrm{d}s\, \mathrm{e}^{-\gamma (t-s)} \pi_{x_i(s), x_j(s)}(\cdot) \end{aligned}$$

If $x_i(t) = x_j(t) = S$, then

$$p_{ij}(t) = \mathrm{e}^{-\gamma t} p_0 + \gamma \int_0^t \mathrm{d}s\, \mathrm{e}^{-\gamma (t-s)} \pi_{SS}(F_n(s; \cdot))$$

We can do a similar computations for the other cases. We set $H(t; u, v, F_n(t; \cdot))$ the probability of having an active edge between two vertices of type u and v at time t

Definition of the mimicking process $(G_n^*(t))_{t\in[0,T]}$

- The edge dynamics is the same as the co-evolutionary model
- The vertex dynamics in the mimicking process is defined as follows. The infected and recovered vertices behave as in the original model. At any time $t \in [0, T]$, each susceptible vertex becomes infected at rate $\lambda \mathcal{J}(t)$
- The expression of $\mathcal{J}(t)$ will be specified later to make the mimicking process asymptotically equivalent to the original model as $n \to \infty$

The infinitesimal generator of the mimicking process is

$$(\mathcal{L}_t f)(x,y) = \left(\lambda \mathcal{J}(t)\,\mathbf{1}_{\{x=\mathrm{S}\}} + \mathbf{1}_{\{x=\mathrm{I}\}}\right)[f(x',y) - f(x,y)] + b(x,y)\,\frac{\partial}{\partial y} f(x,y),$$

where x' is the state of the selected vertex after changing its state x at time t. Here $b(x,y)$ is characterized as follows: (i) $b(x,y) = 0$ for $x \in \{\mathrm{S}, \mathrm{R}\}$, because the type of a susceptible or recovered vertex does not change in time if its state does not, and (ii) $b(\mathrm{I}, y) = 1$, indeed, if vertex i has state I during the entire time interval $(t, t + \mathrm{d}t)$, then

$$y_i^*(t + \mathrm{d}t) = y_i^*(0) + t + \mathrm{d}t - t_i^{\mathrm{I}} = y_i^*(t) + \mathrm{d}t.$$

This gives rise to the following Kolmogorov forward equations that characterise F:

$$
\begin{aligned}
\frac{\partial}{\partial t} p_{\mathrm{S}}(t) &= -\lambda \mathcal{J}(t)\, p_{\mathrm{S}}(t), \\
\frac{\partial}{\partial t} f_{\mathrm{I}}(t;u) + \frac{\partial}{\partial u} f_{\mathrm{I}}(t;u) &= -f_{\mathrm{I}}(t;u), \qquad u > 0, \\
f_{\mathrm{I}}(t;0) &= \lambda \mathcal{J}(t)\, p_{\mathrm{S}}(t), \\
\frac{\partial}{\partial t} p_{\mathrm{R}}(t) &= p_{\mathrm{I}}(t),
\end{aligned}
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\end{aligned}
$$

Theorem (FLLN for the densities of opinions) $(F_n(t;\cdot))_{t\in[0,T]}$ converges weakly to $(F(t;\cdot))_{t\in[0,T]}$ as $n \to \infty$ on $D((\mathcal{M}, d_L), [0, T])$.

Main results

Define the generalized inverse function of F as $\bar{F}(t;x) = \inf\{u : F(t;u) > x\}$ and the limiting graphon as

$$g^{[F]}(t;x,y) = H(t;\bar{F}(t;x),\bar{F}(t;y),(F(t;\cdot))_{t\in[0,T]})$$

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$$g^{[F]}(t;x,y) = H(t;\bar{F}(t;x),\bar{F}(t;y),(F(t;\cdot))_{t\in[0,T]})$$

Theorem (FLLN for the dynamic random graph) $(h^{G_n(t)}(\cdot,\cdot))_{t\in[0,T]}$ converges weakly to $(g^{[F]}(t;\cdot,\cdot))_{t\in[0,T]}$ as $n \to \infty$ on $D((W,d_\square),[0,T])$.

The mimicking process is close to the original process

In our case, the vertex dynamics in the mimicking process is defined as follows. The infected and recovered vertices behave as in the original model. At any time $t \in [0, T]$, each susceptible vertex becomes infected at rate $\lambda \mathcal{J}(t)$, where

$$\mathcal{J}(t) = \int_0^t \mathrm{d}F(t; u)\, H(t; -1, u, F(t; \cdot))$$

can be interpreted as the limiting rate (as $n \to \infty$) at which susceptible individuals become infected at time t

The discrepancies between the mimicking process and the co-evoultionary model during the time interval $[0, T]$ have a sufficiently small probability

Dynamics without global feedback

- $\pi_{SS} = p_0$: susceptible individuals are connect with probability p_0 at any time t
- $\pi_{SI}(u, F) = \pi_{SI}(u)$: there is no global co-evolutionary feedback

An individual who was infected u time units ago is connected to any susceptible individual with probability

$$p_{\mathrm{SI}}(u) = p_0 \mathrm{e}^{-\gamma u} + \int_0^u \mathrm{d}s \, \gamma \mathrm{e}^{-\gamma s} \, \pi_{\mathrm{SI}}(u - s)$$

The probability that the infected individual infects any susceptible individual during his lifetime is

$$\int_0^\infty \mathrm{d}u \, p_{\mathrm{SI}}(u) \, \frac{\lambda}{n} \, \mathrm{e}^{-u}$$

Considering the expected number of infections caused by a single infected individual among a large number (i.e., $n \to \infty$) of susceptible individuals, we then obtain the basic reproduction number

$$R_0 = \int_0^\infty \mathrm{d}u \, p_{\mathrm{SI}}(u) \, \lambda \, \mathrm{e}^{-u}$$

An initially susceptible individual does not ever get infected with probability $p_{\mathrm{S}}(\infty)/(1 - q_0)$, and if it remains susceptible, then it does not get infected by any of the $n(1 - s(\infty))$ individuals that get infected at some point. Consequently

$$\begin{aligned} \frac{p_{\mathrm{S}}(\infty)}{1 - q_0} &= \lim_{n\to\infty} \left(1 - \int_0^\infty \mathrm{d}u \, p_{\mathrm{SI}}(u) \, \frac{\lambda}{n} \, \mathrm{e}^{-u}\right)^{n(1-p_{\mathrm{S}}(\infty))} \\ &= \lim_{n\to\infty} \left(1 - \frac{R_0(1 - p_{\mathrm{S}}(\infty))}{n(1 - p_{\mathrm{S}}(\infty))}\right)^{n(1-p_{\mathrm{S}}(\infty))} = \mathrm{e}^{-R_0(1-p_{\mathrm{S}}(\infty))} \end{aligned}$$

$p_{S,n}(t)$ = proportion of S at time t in a system with n individuals

If $p_S(\infty) = \lim_{t\to\infty} \lim_{n\to\infty} p_{S,n}(t)$, then $p_S(\infty)$ satisfies the above equation. However, the limiting proportion of susceptible individuals is most naturally expressed as $p_S(\infty) = \lim_{n\to\infty} \lim_{t\to\infty} p_{S,n}(t)$.

The required interchange of limits is generally justified by dominating the epidemic process with a subcritical branching process after some large time t (see e.g. Borgs, Huang, Ikeokwu 2024).

Here, we encounter two challenges:

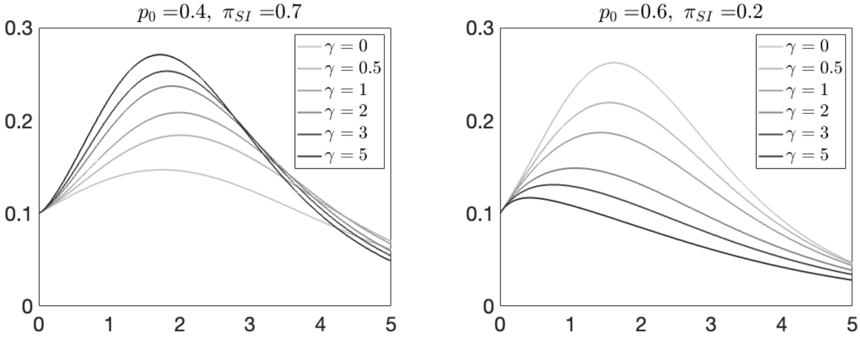
- The vertex types are continuous, which would likely require working with a dominating branching process with a continuous type space
- The dynamic nature of the edges complicates the construction of such a dominating branching process.

What can we say about the peak of the epidemic $i_{\max} := \max_{t \geq 0} p_{\mathrm{I}}(t)$?

A classical result for the conventional SIR model is (Huang, Röllin 2024)

$$i_{\max} = 1 - R_0^{-1} + R_0^{-1} \log R_0^{-1}.$$

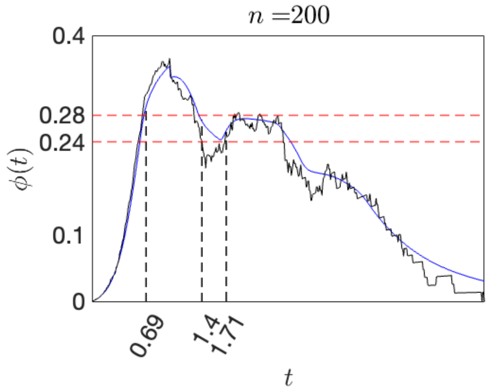
In our setting, deriving an analogous formula is challenging. Nevertheless, we can illustrate how γ, which defines the timescale of the edge dynamics, influences $i_{\max}$



Dynamics with global feedback

We assume that π_{SS} and π_{SI} depend on the infection level averaged over the recent past. For $a > 0$, define the proportion of individuals who were infected at most a time units ago and who are still infectious at time t as

$$\phi(t) = \int_0^a \mathrm{d}s\, f_{\mathrm{I}}(t;s) = F_n(t;a) - F_n(t;0)$$



For $0 < \phi_1 < \phi_2 < \infty$, define the piecewise linear function

$$d(\phi) = \begin{cases} 0.1 & \text{if } \phi \leq \phi_1, \\ 0.1 + 0.8\dfrac{\phi - \phi_1}{\phi_2 - \phi_1} & \text{if } \phi_1 < \phi < \phi_2, \\ 0.9 & \text{if } \phi \geq \phi_2, \end{cases}$$

which is a behavioral control function, representing how strongly the population is distancing: $d(\phi) \approx 0.9$ (resp. $d(\phi) \approx 0.1$) means that the system is in 'distancing mode' (resp. 'normal mode')

We put

$$\begin{aligned} \pi_{\mathrm{SS}}(\phi) &= (1 - d(\phi))\, p_{\mathrm{SS}}^{\mathrm{norm}} + d(\phi)\, p_{\mathrm{SS}}^{\mathrm{dist}}, \\ \pi_{\mathrm{SI}}(\phi) &= (1 - d(\phi))\, p_{\mathrm{SI}}^{\mathrm{norm}} + d(\phi)\, p_{\mathrm{SI}}^{\mathrm{dist}}, \end{aligned}$$

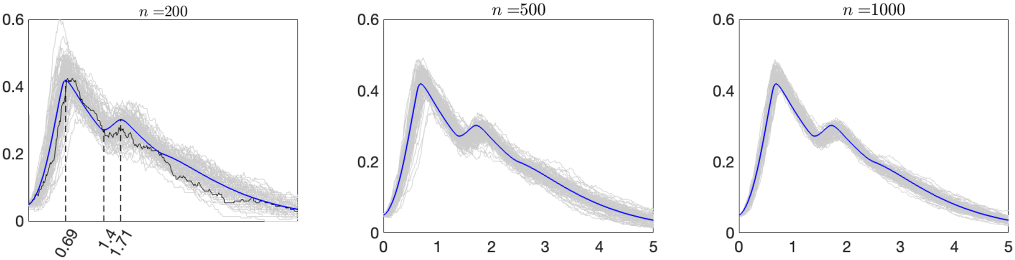
for given numbers $p_{\mathrm{SS}}^{\mathrm{norm}}$, $p_{\mathrm{SS}}^{\mathrm{dist}}$, $p_{\mathrm{SI}}^{\mathrm{norm}}$, $p_{\mathrm{SI}}^{\mathrm{dist}}$, where $p_{\mathrm{SS}}^{\mathrm{norm}} > p_{\mathrm{SS}}^{\mathrm{dist}}$ and $p_{\mathrm{SI}}^{\mathrm{norm}} > p_{\mathrm{SI}}^{\mathrm{dist}}$

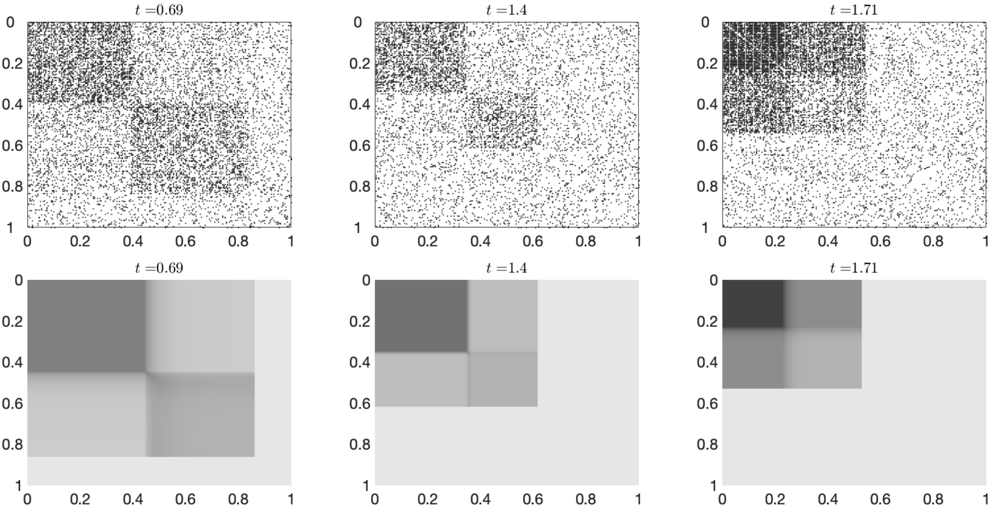
We have thus constructed a simplified model of 'behavioural response' (e.g., by government interventions or voluntary distancing), enforcing that contact rates drop when people perceive high infection

Global feedback: Numerical simulations for the graphons

In the numerical illustrations, we have chosen the parameters:

$$p_0 = 0.1, \quad q_0 = 0.05, \quad \phi_1 = 0.24, \quad \phi_2 = 0.28, \quad \gamma = 20, \quad \lambda = 10,$$
$$p_{\mathrm{SS}}^{\mathrm{norm}} = 0.9, \quad p_{\mathrm{SS}}^{\mathrm{dist}} = 0.3, \quad p_{\mathrm{SI}}^{\mathrm{norm}} = 0.6, \quad p_{\mathrm{SI}}^{\mathrm{dist}} = 0.01, \quad \pi_{\mathrm{II}} = 0.3, \quad a = 1$$




$t = 0.69$
$t = 1.4$
$t = 1.71$
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$t = 1.4$
$t = 1.71$
0
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1