A randomized k-centrality measure & applications to Networks Node Immunization

Luca Avena (Leiden, The Netherlands)



#### A day on random graphs, TorVergata, 30/05/2022 joint with Michael Emmerich, Alexandre Gaudillière and Irina Gurewitsch

Luca Avena (Mathematics, Leiden)

k-node Immunization

- **2** Multiple-node immunization
- **Our method: rooted forests & randomized** *k***-centrality**
- **4** Experiments: the geometry of contagion

#### Epidemic spread: a very brief modelling overview

# Epidemic spread: a very brief modelling overview

- **Compartmental models :** Population of *n* individuals **divided into interacting compartments** (e.g. infected, susceptible, recovered, immune).
- **Historical note** : First models back to **D. Bernoulli (1760)**; "mature" multidisciplinary area in the XX century **Kermack-McKendrick theory** (1927); from the '90 on (*theory developments* + *data fitting*).

# Epidemic spread: a very brief modelling overview

- **Compartmental models :** Population of *n* individuals **divided into interacting compartments** (e.g. infected, susceptible, recovered, immune).
- **Historical note** : First models back to **D. Bernoulli (1760)**; "mature" multidisciplinary area in the XX century **Kermack-McKendrick theory** (1927); from the '90 on (theory developments + data fitting).

# Epidemic spread: a very brief modelling overview

- Compartmental models : Population of *n* individuals divided into interacting compartments (e.g. infected, susceptible, recovered, immune).
- **Historical note**: First models back to **D. Bernoulli (1760)**; "mature" multidisciplinary area in the XX century **Kermack-McKendrick theory** (1927); from the '90 on (theory developments + data fitting).

SIS model (2-compartments)

I =Infected, S =Susceptible.

 $\beta =$ Infection rate,  $\mu =$ Recovery rate.

Interaction as "chemical reactions":

$$S+I \xrightarrow{\beta} 2I, \qquad I \xrightarrow{\mu} S.$$

# Epidemic spread: a very brief modelling overview

- Compartmental models : Population of *n* individuals divided into interacting compartments (e.g. infected, susceptible, recovered, immune).
- **Historical note :** First models back to **D. Bernoulli (1760)**; "mature" multidisciplinary area in the XX century **Kermack-McKendrick theory** (1927); from the '90 on (theory developments + data fitting).

#### SIS model (2-compartments)

$$I =$$
Infected,  $S =$ Susceptible.

 $\beta =$ Infection rate,  $\mu =$ Recovery rate.

Interaction as "chemical reactions":

$$S + I \xrightarrow{\beta} 2I, \qquad I \xrightarrow{\mu} S.$$

# Epidemic spread: a very brief modelling overview

- Compartmental models : Population of *n* individuals divided into interacting compartments (e.g. infected, susceptible, recovered, immune).
- **Historical note**: First models back to **D. Bernoulli (1760)**; "mature" multidisciplinary area in the XX century **Kermack-McKendrick theory** (1927); from the '90 on (theory developments + data fitting).

#### SIS model (2-compartments)

$$I = Infected,$$
  $S = Susceptible.$   
 $\beta = Infection rate,$   $\mu = Recovery rate.$ 

Interaction as "chemical reactions":

$$S + I \xrightarrow{\beta} 2I, \qquad I \xrightarrow{\mu} S.$$

**Basic Reprod.** Nr.  $\Rightarrow$   $r := \beta/\mu =$  infect. rate  $\times$  av. durat. infectiousness

# Epidemic spread: a very brief modelling overview

- Compartmental models : Population of *n* individuals divided into interacting compartments (e.g. infected, susceptible, recovered, immune).
- **Historical note :** First models back to **D. Bernoulli (1760)**; "mature" multidisciplinary area in the XX century **Kermack-McKendrick theory** (1927); from the '90 on (theory developments + data fitting).

#### SIS model (2-compartments)

$$I =$$
Infected,  $S =$ Susceptible.  
 $\beta =$ Infection rate,  $\mu =$ Recovery rate.

Interaction as "chemical reactions":

$$S+I \xrightarrow{\beta} 2I, \qquad I \xrightarrow{\mu} S.$$

**Basic Reprod.** Nr.  $\Rightarrow$   $r := \beta/\mu =$  infect. rate  $\times$  av. durat. infectiousness

**Network:**  $\mathcal{G} = (\mathcal{V}, \mathcal{E}), |\mathcal{V}| = n$ , undirected finite graph with adjacency  $\mathcal{A} := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = \mathbb{1}_{\{x \sim y\}}$ .

**Network:**  $\mathcal{G} = (\mathcal{V}, \mathcal{E}), |\mathcal{V}| = n$ , undirected finite graph with adjacency  $\mathcal{A} := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = \mathbb{1}_{\{x \sim y\}}$ .

**Network:**  $\mathcal{G} = (\mathcal{V}, \mathcal{E}), |\mathcal{V}| = n$ , undirected finite graph with adjacency  $\mathcal{A} := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = \mathbb{1}_{\{x \sim y\}}$ .

Definition (**SIS evolution** (a non-linear system of *n* diff. eqs.))

**Network:**  $\mathcal{G} = (\mathcal{V}, \mathcal{E}), |\mathcal{V}| = n$ , undirected finite graph with adjacency  $\mathcal{A} := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = \mathbb{1}_{\{x \sim y\}}$ .

Definition (**SIS evolution** (a non-linear system of *n* diff. eqs.))

**Network:**  $\mathcal{G} = (\mathcal{V}, \mathcal{E}), |\mathcal{V}| = n$ , undirected finite graph with adjacency  $\mathcal{A} := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = \mathbb{1}_{\{x \sim y\}}$ .

Definition (**SIS evolution** (a non-linear system of *n* diff. eqs.))

Set  $\rho_{\mathbf{x}}(\mathbf{t}) := \mathbb{P}(\text{ node } \mathbf{x} \text{ is infected at time } \mathbf{t}), \mathbf{x} \in \mathcal{V}, \text{ and fix}$ Infection rate  $= \beta > 0$ , Recovery rate  $= \mu > 0$ :

**Network:**  $\mathcal{G} = (\mathcal{V}, \mathcal{E}), |\mathcal{V}| = n$ , undirected finite graph with adjacency  $\mathcal{A} := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = \mathbb{1}_{\{x \sim y\}}$ .

Definition (**SIS evolution** (a non-linear system of *n* diff. eqs.))

Set  $\rho_{\mathbf{x}}(\mathbf{t}) := \mathbb{P}(\text{ node } \mathbf{x} \text{ is infected at time } \mathbf{t}), \mathbf{x} \in \mathcal{V}, \text{ and fix}$ Infection rate  $= \beta > 0$ , Recovery rate  $= \mu > 0$ :

**Network:**  $\mathcal{G} = (\mathcal{V}, \mathcal{E}), |\mathcal{V}| = n$ , undirected finite graph with adjacency  $\mathcal{A} := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = \mathbb{1}_{\{x \sim y\}}$ .

Definition (**SIS evolution** (a non-linear system of *n* diff. eqs.))

Set  $\rho_{\mathbf{x}}(\mathbf{t}) := \mathbb{P}(\text{ node } \mathbf{x} \text{ is infected at time } \mathbf{t}), \mathbf{x} \in \mathcal{V}, \text{ and fix}$ Infection rate  $= \beta > 0$ , Recovery rate  $= \mu > 0$ :

$$rac{\partial 
ho_{\mathsf{x}}(t)}{\partial t} = -\mu 
ho_{\mathsf{x}}(t) + \beta [1 - 
ho_{\mathsf{x}}(t)] \sum_{\mathsf{y} \in \mathcal{Y}} \mathsf{a}_{\mathsf{x},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

with some in. cond.  $\vec{\rho}(0) := (\rho_1(0), \dots, \rho_n(0)).$ 

**Network:**  $\mathcal{G} = (\mathcal{V}, \mathcal{E}), |\mathcal{V}| = n$ , undirected finite graph with adjacency  $\mathcal{A} := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = \mathbb{1}_{\{x \sim y\}}$ .

Definition (**SIS evolution** (a non-linear system of *n* diff. eqs.))

Set  $\rho_{\mathbf{x}}(\mathbf{t}) := \mathbb{P}(\text{ node } \mathbf{x} \text{ is infected at time } \mathbf{t}), \mathbf{x} \in \mathcal{V}, \text{ and fix}$ Infection rate  $= \beta > 0$ , Recovery rate  $= \mu > 0$ :

$$rac{\partial 
ho_{\mathsf{x}}(t)}{\partial t} = -\mu 
ho_{\mathsf{x}}(t) + eta [1 - 
ho_{\mathsf{x}}(t)] \sum_{\mathsf{y} \in \mathcal{V}} \mathsf{a}_{\mathsf{x},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

with some in. cond.  $\vec{\rho}(0) := (\rho_1(0), ..., \rho_n(0)).$ 

**Network:**  $\mathcal{G} = (\mathcal{V}, \mathcal{E}), |\mathcal{V}| = n$ , undirected finite graph with adjacency  $\mathcal{A} := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = \mathbb{1}_{\{x \sim y\}}$ .

Definition (**SIS evolution** (a non-linear system of *n* diff. eqs.))

Set  $\rho_{\mathbf{x}}(\mathbf{t}) := \mathbb{P}(\text{ node } \mathbf{x} \text{ is infected at time } \mathbf{t}), \mathbf{x} \in \mathcal{V}, \text{ and fix}$ Infection rate  $= \beta > 0$ , Recovery rate  $= \mu > 0$ :

$$rac{\partial 
ho_{\mathsf{x}}(t)}{\partial t} = -\mu 
ho_{\mathsf{x}}(t) + eta [1 - 
ho_{\mathsf{x}}(t)] \sum_{\mathsf{y} \in \mathcal{Y}} \mathsf{a}_{\mathsf{x},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

with some in. cond.  $\vec{\rho}(0) := (\rho_1(0), ..., \rho_n(0)).$ 

Remark:

Contact process on  $\{0,1\}^V$  = microscopic Markovian version of SIS

**Network:**  $\mathcal{G} = (\mathcal{V}, \mathcal{E}), |\mathcal{V}| = n$ , undirected finite graph with adjacency  $\mathcal{A} := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = \mathbb{1}_{\{x \sim y\}}$ .

Definition (**SIS evolution** (a non-linear system of *n* diff. eqs.))

Set  $\rho_{\mathbf{x}}(\mathbf{t}) := \mathbb{P}(\text{ node } \mathbf{x} \text{ is infected at time } \mathbf{t}), \mathbf{x} \in \mathcal{V}, \text{ and fix}$ Infection rate  $= \beta > 0$ , Recovery rate  $= \mu > 0$ :

$$rac{\partial 
ho_{\mathsf{x}}(t)}{\partial t} = -\mu 
ho_{\mathsf{x}}(t) + eta [1 - 
ho_{\mathsf{x}}(t)] \sum_{\mathsf{y} \in \mathcal{Y}} \mathsf{a}_{\mathsf{x},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

with some in. cond.  $\vec{\rho}(0) := (\rho_1(0), ..., \rho_n(0)).$ 

#### Remark:

Contact process on  $\{0,1\}^V$  = microscopic Markovian version of SIS

#### Endemic state & largest eigenvalue

#### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$ 

# Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$ 

# Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_{x}(t)}{\partial t} = -\rho_{x}(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{y}(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{x}(t) \rho_{y}(t)$$

#### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_{x}(t)}{\partial t} = -\rho_{x}(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{y}(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{x}(t) \rho_{y}(t)$$

#### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_x(t)}{\partial t} = -\rho_x(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_y(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_x(t) \rho_y(t)$$

Outbreak threshold estimate (linearization) :

$$\frac{\partial \rho_{x}(t)}{\partial t} \leq -\rho_{x}(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{y}(t)$$

#### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_{x}(t)}{\partial t} = -\rho_{x}(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{y}(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{x}(t) \rho_{y}(t)$$

Outbreak threshold estimate (linearization) :

$$rac{\partial 
ho_{\mathsf{X}}(t)}{\partial t} \leq -
ho_{\mathsf{X}}(t) + r\sum_{\mathsf{y}\in\mathcal{V}} \mathsf{a}_{\mathsf{x},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

#### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_x(t)}{\partial t} = -\rho_x(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_y(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_x(t) \rho_y(t)$$

Outbreak threshold estimate (linearization) :

$$rac{\partial 
ho_{\mathsf{X}}(t)}{\partial t} \leq -
ho_{\mathsf{X}}(t) + r\sum_{\mathsf{y}\in\mathcal{V}} \mathsf{a}_{\mathsf{x},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

From which, if  $\vec{\rho}(t) := (\rho_1(t), \dots, \rho_n(t))$ 

#### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_x(t)}{\partial t} = -\rho_x(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_y(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_x(t) \rho_y(t)$$

Outbreak threshold estimate (linearization) :

$$rac{\partial 
ho_{\mathsf{x}}(t)}{\partial t} \leq -
ho_{\mathsf{x}}(t) + r \sum_{\mathsf{y} \in \mathcal{V}} \mathsf{a}_{\mathsf{x},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

From which, if  $\vec{\rho}(t) := (\rho_1(t), \dots, \rho_n(t))$ 

#### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_{x}(t)}{\partial t} = -\rho_{x}(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{y}(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{x}(t) \rho_{y}(t)$$

Outbreak threshold estimate (linearization) :

$$rac{\partial 
ho_{\mathsf{X}}(t)}{\partial t} \leq -
ho_{\mathsf{X}}(t) + r \sum_{\mathsf{y} \in \mathcal{V}} \mathsf{a}_{\mathsf{X},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

From which, if  $\vec{\rho}(t) := (\rho_1(t), \dots, \rho_n(t)) \Rightarrow \vec{\rho}(t) \le \vec{\rho}(0) e^{(r\mathcal{A} - \mathsf{Id}_n)t}$ 

#### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_x(t)}{\partial t} = -\rho_x(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_y(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_x(t) \rho_y(t)$$

Outbreak threshold estimate (linearization) :

$$rac{\partial 
ho_{\mathsf{x}}(t)}{\partial t} \leq -
ho_{\mathsf{x}}(t) + r \sum_{\mathsf{y} \in \mathcal{V}} \mathsf{a}_{\mathsf{x},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

From which, if  $\vec{\rho}(t) := (\rho_1(t), \dots, \rho_n(t)) \Rightarrow \vec{\rho}(t) \le \vec{\rho}(0)e^{(r\mathcal{A} - \mathsf{Id}_n)t}$ 

### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_{x}(t)}{\partial t} = -\rho_{x}(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{y}(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{x}(t) \rho_{y}(t)$$

Outbreak threshold estimate (linearization) :

$$rac{\partial 
ho_{\mathsf{x}}(t)}{\partial t} \leq -
ho_{\mathsf{x}}(t) + r \sum_{\mathsf{y} \in \mathcal{V}} \mathsf{a}_{\mathsf{x},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

From which, if  $\vec{\rho}(t) := (\rho_1(t), \dots, \rho_n(t)) \Rightarrow \vec{\rho}(t) \le \vec{\rho}(0)e^{(r\mathcal{A} - \mathsf{Id}_n)t}$ Max eigenvalue  $\lambda_{max}$  of  $\mathcal{A}$ :

If  $r\lambda_{max} - 1 < 0 \Rightarrow \rho_x(t)$  decays exponentially fast to 0, for any  $x \in \mathcal{V}$ .

### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_{x}(t)}{\partial t} = -\rho_{x}(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{y}(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{x}(t) \rho_{y}(t)$$

Outbreak threshold estimate (linearization) :

$$rac{\partial 
ho_{\mathsf{x}}(t)}{\partial t} \leq -
ho_{\mathsf{x}}(t) + r \sum_{\mathsf{y} \in \mathcal{V}} \mathsf{a}_{\mathsf{x},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

From which, if  $\vec{\rho}(t) := (\rho_1(t), \dots, \rho_n(t)) \Rightarrow \vec{\rho}(t) \le \vec{\rho}(0)e^{(r\mathcal{A} - \mathsf{Id}_n)t}$ Max eigenvalue  $\lambda_{max}$  of  $\mathcal{A}$ :

If  $r\lambda_{max} - 1 < 0 \Rightarrow \rho_x(t)$  decays exponentially fast to 0, for any  $x \in \mathcal{V}$ .

#### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_{x}(t)}{\partial t} = -\rho_{x}(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{y}(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{x}(t) \rho_{y}(t)$$

Outbreak threshold estimate (linearization) :

$$rac{\partial 
ho_{\mathsf{X}}(t)}{\partial t} \leq -
ho_{\mathsf{X}}(t) + r \sum_{\mathsf{y} \in \mathcal{V}} \mathsf{a}_{\mathsf{X},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

From which, if  $\vec{\rho}(t) := (\rho_1(t), \dots, \rho_n(t)) \Rightarrow \vec{\rho}(t) \le \vec{\rho}(0)e^{(r\mathcal{A} - \mathsf{Id}_n)t}$ Max eigenvalue  $\lambda_{max}$  of  $\mathcal{A}$ :

If  $r\lambda_{max} - 1 < 0 \Rightarrow \rho_x(t)$  decays exponentially fast to 0, for any  $x \in \mathcal{V}$ .  $\Rightarrow$  critical parameter for the endemic state:

$$r_{c} \geq 1/\lambda_{max}.$$

#### Endemic state & largest eigenvalue

**SIS evolution**  $\rho_x(t) := \mathbb{P}(\text{ node } x \text{ is infected at time } t), \forall x \in \mathcal{V},$  rescaling time by  $1/\mu$  and setting  $\mathbf{r} := \beta/\mu$ :

$$\frac{\partial \rho_{x}(t)}{\partial t} = -\rho_{x}(t) + r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{y}(t) - r \sum_{y \in \mathcal{V}} a_{x,y} \rho_{x}(t) \rho_{y}(t)$$

Outbreak threshold estimate (linearization) :

$$rac{\partial 
ho_{\mathsf{X}}(t)}{\partial t} \leq -
ho_{\mathsf{X}}(t) + r \sum_{\mathsf{y} \in \mathcal{V}} \mathsf{a}_{\mathsf{X},\mathsf{y}} 
ho_{\mathsf{y}}(t)$$

From which, if  $\vec{\rho}(t) := (\rho_1(t), \dots, \rho_n(t)) \Rightarrow \vec{\rho}(t) \le \vec{\rho}(0)e^{(r\mathcal{A} - \mathsf{Id}_n)t}$ Max eigenvalue  $\lambda_{max}$  of  $\mathcal{A}$ :

If  $r\lambda_{max} - 1 < 0 \Rightarrow \rho_x(t)$  decays exponentially fast to 0, for any  $x \in \mathcal{V}$ .  $\Rightarrow$  critical parameter for the endemic state:

$$r_c \geq 1/\lambda_{max}.$$

Multiple-node immunization

### Multiple-node immunization & max eigendrop

## Multiple-node immunization & max eigendrop

• **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".

## Multiple-node immunization & max eigendrop

• **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".

## Multiple-node immunization & max eigendrop

- **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".
- Problem not well-posed: 1) limited rigorous analysis 2) heuristics ideas based on simulations with lots of other problems 3) choosing maximal degree nodes is not justified already for k = 1.

- **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".
- Problem not well-posed: 1) limited rigorous analysis 2) heuristics ideas based on simulations with lots of other problems 3) choosing maximal degree nodes is not justified already for k = 1.

- **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".
- Problem not well-posed: 1) limited rigorous analysis 2) heuristics ideas based on simulations with lots of other problems 3) choosing maximal degree nodes is not justified already for k = 1.
- Max eigendrop of adjacency: since r<sub>c</sub> ≥ 1/λ<sub>max</sub>, good strategy: look for sets of k−nodes from which after removal the reduced network has minimal largest eigenvalue.

- **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".
- Problem not well-posed: 1) limited rigorous analysis 2) heuristics ideas based on simulations with lots of other problems 3) choosing maximal degree nodes is not justified already for k = 1.
- Max eigendrop of adjacency: since r<sub>c</sub> ≥ 1/λ<sub>max</sub>, good strategy: look for sets of k-nodes from which after removal the reduced network has minimal largest eigenvalue.

- **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".
- Problem not well-posed: 1) limited rigorous analysis 2) heuristics ideas based on simulations with lots of other problems 3) choosing maximal degree nodes is not justified already for k = 1.
- Max eigendrop of adjacency: since r<sub>c</sub> ≥ 1/λ<sub>max</sub>, good strategy: look for sets of k-nodes from which after removal the reduced network has minimal largest eigenvalue. Equivalently: find S ⊂ V, with |S| = k maximising

 $\Delta_k \lambda(\mathcal{S}) := \lambda_{max}(\mathcal{V}) - \lambda_{max}(\mathcal{V} \setminus \mathcal{S}) = \mathbf{k} - \mathbf{eigendrop}$ 

- **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".
- Problem not well-posed: 1) limited rigorous analysis 2) heuristics ideas based on simulations with lots of other problems 3) choosing maximal degree nodes is not justified already for k = 1.
- Max eigendrop of adjacency: since r<sub>c</sub> ≥ 1/λ<sub>max</sub>, good strategy: look for sets of k-nodes from which after removal the reduced network has minimal largest eigenvalue. Equivalently: find S ⊂ V, with |S| = k maximising

$$\Delta_k \lambda(\mathcal{S}) := \lambda_{max}(\mathcal{V}) - \lambda_{max}(\mathcal{V} \setminus \mathcal{S}) = \mathbf{k} - \mathbf{eigendrop}$$

- **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".
- Problem not well-posed: 1) limited rigorous analysis 2) heuristics ideas based on simulations with lots of other problems 3) choosing maximal degree nodes is not justified already for k = 1.
- Max eigendrop of adjacency: since r<sub>c</sub> ≥ 1/λ<sub>max</sub>, good strategy: look for sets of k-nodes from which after removal the reduced network has minimal largest eigenvalue. Equivalently: find S ⊂ V, with |S| = k maximising

$$\Delta_k \lambda(\mathcal{S}) := \lambda_{max}(\mathcal{V}) - \lambda_{max}(\mathcal{V} \setminus \mathcal{S}) = \mathsf{k} - \mathsf{eigendrop}$$

Computational issues with max eigendrop:

• No poly exact algorithm for such an optimization problem.

- **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".
- Problem not well-posed: 1) limited rigorous analysis 2) heuristics ideas based on simulations with lots of other problems 3) choosing maximal degree nodes is not justified already for k = 1.
- Max eigendrop of adjacency: since r<sub>c</sub> ≥ 1/λ<sub>max</sub>, good strategy: look for sets of k-nodes from which after removal the reduced network has minimal largest eigenvalue. Equivalently: find S ⊂ V, with |S| = k maximising

$$\Delta_k \lambda(\mathcal{S}) := \lambda_{max}(\mathcal{V}) - \lambda_{max}(\mathcal{V} \setminus \mathcal{S}) = \mathbf{k} - \mathbf{eigendrop}$$

#### Computational issues with max eigendrop:

• No poly exact algorithm for such an optimization problem.

- **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".
- Problem not well-posed: 1) limited rigorous analysis 2) heuristics ideas based on simulations with lots of other problems 3) choosing maximal degree nodes is not justified already for k = 1.
- Max eigendrop of adjacency: since r<sub>c</sub> ≥ 1/λ<sub>max</sub>, good strategy: look for sets of k-nodes from which after removal the reduced network has minimal largest eigenvalue. Equivalently: find S ⊂ V, with |S| = k maximising

$$\Delta_k \lambda(\mathcal{S}) := \lambda_{max}(\mathcal{V}) - \lambda_{max}(\mathcal{V} \setminus \mathcal{S}) = \mathbf{k} - \mathbf{eigendrop}$$

#### Computational issues with max eigendrop:

- No poly exact algorithm for such an optimization problem.
- Chen Chen et al. (2016) proved approx. equivalence with so-called Shield-Value optimization which is NP complete.

Luca Avena (Mathematics, Leiden)

k-node Immunization

- **Goal:** Identify & remove set of *k*-nodes to empede the "*endemic outbreak*".
- Problem not well-posed: 1) limited rigorous analysis 2) heuristics ideas based on simulations with lots of other problems 3) choosing maximal degree nodes is not justified already for k = 1.
- Max eigendrop of adjacency: since r<sub>c</sub> ≥ 1/λ<sub>max</sub>, good strategy: look for sets of k-nodes from which after removal the reduced network has minimal largest eigenvalue. Equivalently: find S ⊂ V, with |S| = k maximising

$$\Delta_k \lambda(\mathcal{S}) := \lambda_{max}(\mathcal{V}) - \lambda_{max}(\mathcal{V} \setminus \mathcal{S}) = \mathbf{k} - \mathbf{eigendrop}$$

#### Computational issues with max eigendrop:

- No poly exact algorithm for such an optimization problem.
- Chen Chen et al. (2016) proved approx. equivalence with so-called Shield-Value optimization which is NP complete.

## Max *k*-eigendrop, ShieldValue & Netshield (Chen Chen et al. (2016))

## Max *k*-eigendrop, ShieldValue & Netshield (Chen Chen et al. (2010))

• Shield Value : for  $S \subset V$ , with |S| = k define

$$SV_k(S) := 2\lambda_{max} \sum_{x \in S} u^2(x) - \sum_{x,y \in S} a_{x,y} u(x) u(y)$$

("eingescore" – "repellence"),

with *u* principal eigenvector  $(Au = \lambda_{max}u)$ .

• Shield Value : for  $\mathcal{S} \subset \mathcal{V}$ , with  $|\mathcal{S}| = k$  define

$$SV_k(S) := 2\lambda_{max} \sum_{x \in S} u^2(x) - \sum_{x,y \in S} a_{x,y} u(x) u(y)$$

("eingescore" – "repellence"),

with u principal eigenvector ( $Au = \lambda_{max}u$ ).

• Shield Value : for  $\mathcal{S} \subset \mathcal{V}$ , with  $|\mathcal{S}| = k$  define

$$SV_k(S) := 2\lambda_{max} \sum_{x \in S} u^2(x) - \sum_{x,y \in S} a_{x,y} u(x) u(y)$$

("eingescore" – "repellence"),

with u principal eigenvector ( $Au = \lambda_{max}u$ ).

• Shield Value approximates max *k*-eigendrop:

 $\Delta_k \lambda(S) \approx SV_k(S).$ 

• Maximising shieldvalue is NP-complete problem.

• Shield Value : for  $\mathcal{S} \subset \mathcal{V}$ , with  $|\mathcal{S}| = k$  define

$$SV_k(S) := 2\lambda_{max} \sum_{x \in S} u^2(x) - \sum_{x,y \in S} a_{x,y} u(x) u(y)$$

("eingescore" – "repellence"),

with u principal eigenvector ( $Au = \lambda_{max}u$ ).

• Shield Value approximates max *k*-eigendrop:

$$\Delta_k \lambda(S) \approx SV_k(S).$$

• Maximising shieldvalue is NP-complete problem.

• Shield Value : for  $\mathcal{S} \subset \mathcal{V}$ , with  $|\mathcal{S}| = k$  define

$$SV_k(S) := 2\lambda_{max} \sum_{x \in S} u^2(x) - \sum_{x,y \in S} a_{x,y} u(x) u(y)$$

("eingescore" – "repellence"),

with u principal eigenvector ( $Au = \lambda_{max}u$ ).

• Shield Value approximates max *k*-eigendrop:

$$\Delta_k \lambda(S) \approx SV_k(S).$$

- Maximising shieldvalue is NP-complete problem.
- Netshield : greedy fast algorithm which finds near-to-optimal solutions in

O(nk + m) running time,

with m = number of edges.

• Shield Value : for  $\mathcal{S} \subset \mathcal{V}$ , with  $|\mathcal{S}| = k$  define

$$SV_k(S) := 2\lambda_{max} \sum_{x \in S} u^2(x) - \sum_{x,y \in S} a_{x,y} u(x) u(y)$$

("eingescore" – "repellence"),

with u principal eigenvector ( $Au = \lambda_{max}u$ ).

• Shield Value approximates max *k*-eigendrop:

$$\Delta_k \lambda(S) \approx SV_k(S).$$

- Maximising shieldvalue is NP-complete problem.
- Netshield : greedy fast algorithm which finds near-to-optimal solutions in

$$O(nk + m)$$
 running time,

with m = number of edges.

# Our randomized immunization method: Random Rooted Spanning Forests & randomized k-centrality

## Graph Laplacian and associated RW

Weighted Directed Network:  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , with  $|\mathcal{V}| = n$  and weighted adjacency  $\mathcal{A}_w := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = w(x, y) \mathbb{1}_{\{x \neq y\}}$ .

## Graph Laplacian and associated RW

Weighted Directed Network:  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , with  $|\mathcal{V}| = n$  and weighted adjacency  $\mathcal{A}_w := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = w(x, y) \mathbb{1}_{\{x \neq y\}}$ .

#### Definition (Graph Laplacian)

It is the  $n \times n$  matrix  $-\mathcal{L}_w$  with :

$$\mathcal{L}_w(x,y) = \begin{cases} w(x,y) & \text{if } x \neq y \in \mathcal{V}, \\ -\sum_{z \neq x} w(x,z) & \text{on the diagonal.} \end{cases}$$

In particular,  $\mathcal{L}_w = \mathcal{A}_w - \mathcal{D}_w = (weighted)$  "adjacency" – "degree"

## Graph Laplacian and associated RW

Weighted Directed Network:  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , with  $|\mathcal{V}| = n$  and weighted adjacency  $\mathcal{A}_w := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = w(x, y) \mathbb{1}_{\{x \neq y\}}$ .

#### Definition (Graph Laplacian)

It is the  $n \times n$  matrix  $-\mathcal{L}_w$  with :

$$\mathcal{L}_w(x,y) = egin{cases} w(x,y) & ext{if } x 
eq y \in \mathcal{V}, \ -\sum_{z 
eq x} w(x,z) & ext{on the diagonal.} \end{cases}$$

In particular,  $\mathcal{L}_w = \mathcal{A}_w - \mathcal{D}_w =$  (weighted) "adjacency" - "degree"

## Graph Laplacian and associated RW

Weighted Directed Network:  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , with  $|\mathcal{V}| = n$  and weighted adjacency  $\mathcal{A}_w := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = w(x, y) \mathbb{1}_{\{x \neq y\}}$ .

#### Definition (Graph Laplacian)

It is the  $n \times n$  matrix  $-\mathcal{L}_w$  with :

$$\mathcal{L}_w(x,y) = \begin{cases} w(x,y) & \text{if } x \neq y \in \mathcal{V}, \\ -\sum_{z \neq x} w(x,z) & \text{on the diagonal.} \end{cases}$$

In particular,  $\mathcal{L}_w = \mathcal{A}_w - \mathcal{D}_w =$  (weighted) "adjacency" - "degree"

#### Definition (Associated Random Walk)

Let  $X = (X(t))_{t \ge 0}$  be the continuous-time Markov chain on  $\mathcal{V}$  with infinitesimal generator  $\mathcal{L}_w$ .

## Graph Laplacian and associated RW

Weighted Directed Network:  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , with  $|\mathcal{V}| = n$  and weighted adjacency  $\mathcal{A}_w := (a_{x,y})_{x,y \in \mathcal{V}}$  s.t.  $a_{x,y} = w(x, y) \mathbb{1}_{\{x \neq y\}}$ .

#### Definition (Graph Laplacian)

It is the  $n \times n$  matrix  $-\mathcal{L}_w$  with :

$$\mathcal{L}_w(x,y) = egin{cases} w(x,y) & ext{if } x 
eq y \in \mathcal{V}, \\ -\sum_{z 
eq x} w(x,z) & ext{on the diagonal.} \end{cases}$$

In particular,  $\mathcal{L}_w = \mathcal{A}_w - \mathcal{D}_w =$  (weighted) "adjacency" - "degree"

#### Definition (Associated Random Walk)

Let  $X = (X(t))_{t \ge 0}$  be the continuous-time Markov chain on  $\mathcal{V}$  with infinitesimal generator  $\mathcal{L}_w$ .

Luca Avena (Mathematics, Leiden)

## RW and a determinantal set of nodes

#### Definition (Set of Roots $\mathcal{R}_q$ of intesity q- A.G.

Given  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , and a parameter q > 0, let  $\mathcal{R}_q \subseteq \mathcal{V}$  be a random subset of nodes with law characterized by:

$$\mathbb{P}\left(\mathcal{A}\subseteq\mathcal{R}_q
ight)=\det\left[K_q
ight]_{\mathcal{A}},\qquad ext{for any }\mathcal{A}\subseteq\mathcal{V},$$

with

$$\mathcal{K}_q(x,y) := \mathbf{P}_x(X(T_q) = y) = q(q \operatorname{Id} - \mathcal{L}_w)^{-1}(x,y)$$

and  $T_q$  an independent exponential random variable of parameter q.

#### Definition (Set of Roots $\mathcal{R}_q$ of intesity q- A.G. (2018))

Given  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , and a parameter q > 0, let  $\mathcal{R}_q \subseteq \mathcal{V}$  be a random subset of nodes with law characterized by:

$$\mathbb{P}\left(\mathcal{A}\subseteq\mathcal{R}_{q}
ight)=\det\left[\mathcal{K}_{q}
ight]_{\mathcal{A}},\qquad ext{ for any }\mathcal{A}\subseteq\mathcal{V},$$

with

$$\mathcal{K}_q(x,y) := \mathbf{P}_x(X(\mathcal{T}_q) = y) = q(q \operatorname{Id} - \mathcal{L}_w)^{-1}(x,y)$$

and  $T_q$  an independent exponential random variable of parameter q.

#### Definition (Set of Roots $\mathcal{R}_q$ of intesity q- A.G. (2018))

Given  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , and a parameter q > 0, let  $\mathcal{R}_q \subseteq \mathcal{V}$  be a random subset of nodes with law characterized by:

$$\mathbb{P}\left(\mathcal{A}\subseteq\mathcal{R}_{q}
ight)=\det\left[K_{q}
ight]_{\mathcal{A}},\qquad ext{ for any }\mathcal{A}\subseteq\mathcal{V},$$

with

$$\mathcal{K}_q(x,y) := \mathbf{P}_x(X(\mathcal{T}_q) = y) = q(q \operatorname{Id} - \mathcal{L}_w)^{-1}(x,y)$$

and  $T_q$  an independent exponential random variable of parameter q.

**Repelling roots when** 
$$w(x, y) = w(y, x)$$
  
 $\mathbb{P}(\{x, y\} \subseteq \mathcal{R}_q) \le \mathbb{P}(x \in \mathcal{R}_q) \mathbb{P}(y \in \mathcal{R}_q)$ 

#### Definition (Set of Roots $\mathcal{R}_q$ of intesity q- A.G. (2018))

Given  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , and a parameter q > 0, let  $\mathcal{R}_q \subseteq \mathcal{V}$  be a random subset of nodes with law characterized by:

$$\mathbb{P}\left(\mathcal{A}\subseteq\mathcal{R}_{q}
ight)=\det\left[\mathcal{K}_{q}
ight]_{\mathcal{A}},\qquad ext{ for any }\mathcal{A}\subseteq\mathcal{V},$$

with

$$\mathcal{K}_q(x,y) := \mathbf{P}_x(X(\mathcal{T}_q) = y) = q(q \operatorname{Id} - \mathcal{L}_w)^{-1}(x,y)$$

and  $T_q$  an independent exponential random variable of parameter q.

**Repelling roots when** w(x, y) = w(y, x)

$$\mathbb{P}\left(\{x,y\}\subseteq\mathcal{R}_q
ight)\leq\mathbb{P}\left(x\in\mathcal{R}_q
ight)\mathbb{P}\left(y\in\mathcal{R}_q
ight)$$

### $\mathcal{R}_q$ from Random Rooted Forests

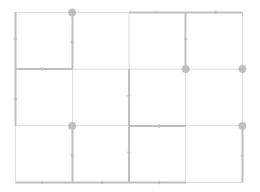
Forest Space: for  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , set

 $\mathcal{F}_{\mathcal{G}} := \{ \text{ spanning rooted forests on } \mathcal{G} \}$ 

### $\mathcal{R}_q$ from Random Rooted Forests

### Forest Space: for $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , set

$$\mathcal{F}_\mathcal{G}:=\{ ext{ spanning rooted forests on }\mathcal{G}\}$$



A spanning rooted forest on a square grid.

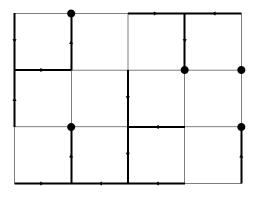
Luca Avena (Mathematics, Leiden)

k-node Immunization

## $\mathcal{R}_q$ from Random Rooted Forests

#### Forest Space: for $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , set

$$\mathcal{F}_\mathcal{G}:=\{ ext{ spanning rooted forests on }\mathcal{G}\}$$



A spanning rooted forest on a square grid.

Luca Avena (Mathematics, Leiden)

k-node Immunization

## $\mathcal{R}_q$ from Random Rooted Forests

Theorem (Random Forest with Determinantal Roots - A.G. (2018))

Fix q > 0 and  $\mathcal{G}$ . Consider the following probability measure on  $\mathcal{F}_{\mathcal{G}}$ :

$$u_q(F) := rac{q^{nr. \ of \ trees} \prod_{e \in F} w(e)}{Z(q)}, \quad F \in \mathcal{F}_\mathcal{G},$$

## $\mathcal{R}_q$ from Random Rooted Forests

Theorem (Random Forest with Determinantal Roots - A.G. (2018))

Fix q > 0 and  $\mathcal{G}$ . Consider the following probability measure on  $\mathcal{F}_{\mathcal{G}}$ :

$$u_q(F) := rac{q^{\textit{nr. of trees}} \prod_{e \in F} w(e)}{Z(q)}, \quad F \in \mathcal{F}_\mathcal{G},$$

Then,

the set of roots of the random forest with law  $\nu_q$ is the determinatal point process  $\mathcal{R}_q$  with kernel  $K_q$ 

Recall:

• 
$$\mathbb{P}\left(\mathcal{A}\subseteq\mathcal{R}_q\right)=\det\left[\mathcal{K}_q\right]_{\mathcal{A}},$$
 for any  $\mathcal{A}\subseteq\mathcal{V},$ 

•  $K_q(x, y) = \mathbf{P}_x(X(T_q) = y) = RW$  kernel observed at time-scale 1/q.

## $\mathcal{R}_q$ from Random Rooted Forests

Theorem (Random Forest with Determinantal Roots - A.G. (2018))

Fix q > 0 and  $\mathcal{G}$ . Consider the following probability measure on  $\mathcal{F}_{\mathcal{G}}$ :

$$u_q(F) := rac{q^{\textit{nr. of trees}} \prod_{e \in F} w(e)}{Z(q)}, \quad F \in \mathcal{F}_\mathcal{G},$$

Then,

the set of roots of the random forest with law  $\nu_q$ is the determinatal point process  $\mathcal{R}_q$  with kernel  $\mathcal{K}_q$ 

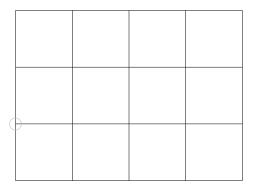
Recall:

• 
$$\mathbb{P}\left(\mathcal{A}\subseteq\mathcal{R}_q\right)=\det\left[\mathcal{K}_q\right]_{\mathcal{A}},$$
 for any  $\mathcal{A}\subseteq\mathcal{V},$ 

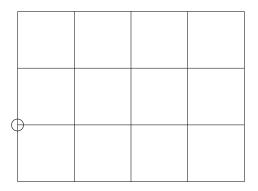
•  $K_q(x, y) = \mathbf{P}_x(X(T_q) = y) = RW$  kernel observed at time-scale 1/q.

#### Sampling $\mathcal{R}_q$ with Wilson's algorithm

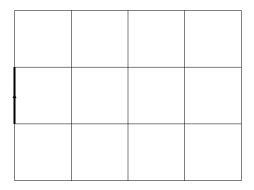
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



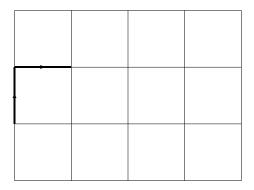
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



## Sampling $\mathcal{R}_q$ with Wilson's algorithm



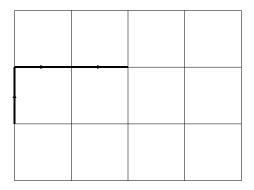
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



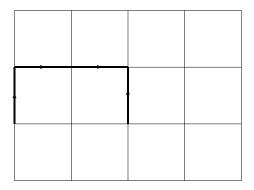
#### Build dynamically a rooted spanning forest using **loop-erased random walks** killed at rate *q*.

15 / 65

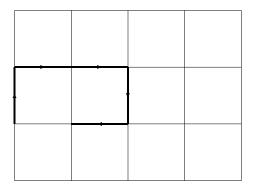
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



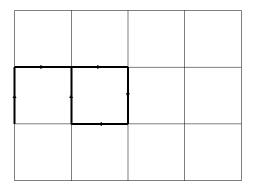
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



## Sampling $\mathcal{R}_q$ with Wilson's algorithm



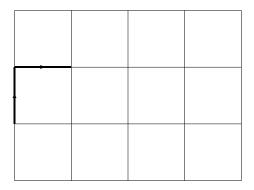
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



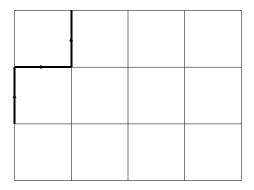
#### Build dynamically a rooted spanning forest using **loop-erased random walks** killed at rate *q*.

19 / 65

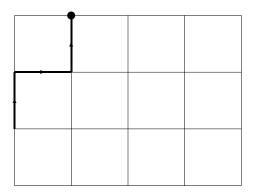
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



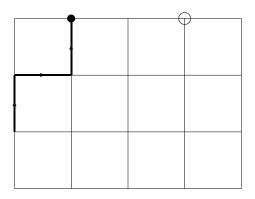
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



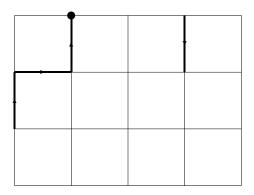
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



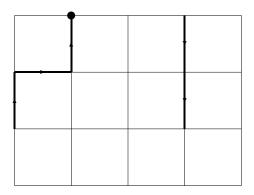
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



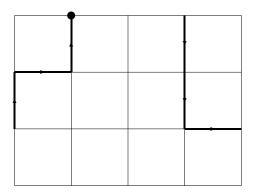
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



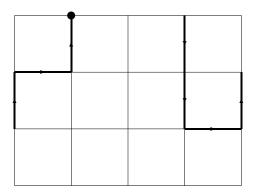
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



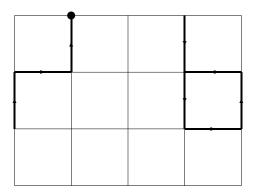
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



## Sampling $\mathcal{R}_q$ with Wilson's algorithm



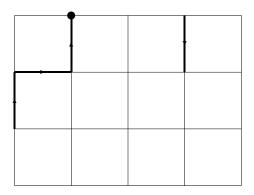
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



# Build dynamically a rooted spanning forest using loop-erased random walks killed at rate q.

28 / 65

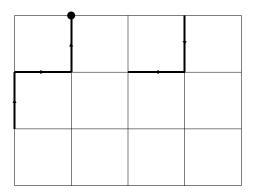
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



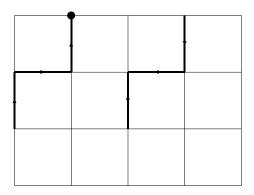
#### Build dynamically a rooted spanning forest using **loop-erased random walks** killed at rate *q*.

29 / 65

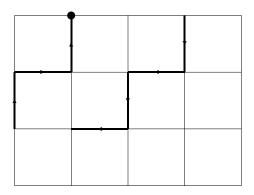
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



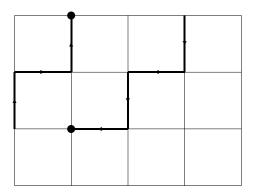
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



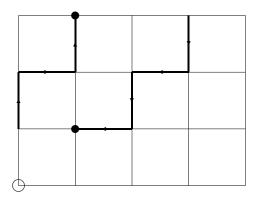
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



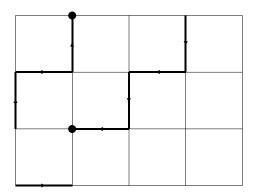
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



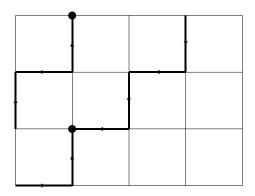
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



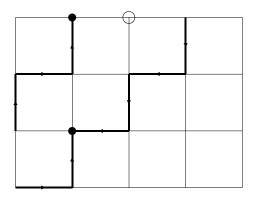
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



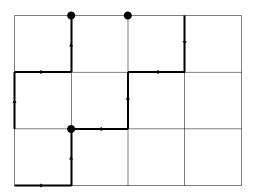
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



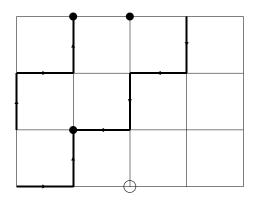
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



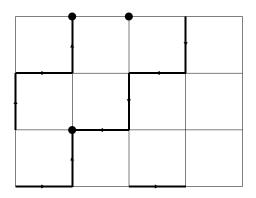
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



## Sampling $\mathcal{R}_q$ with Wilson's algorithm



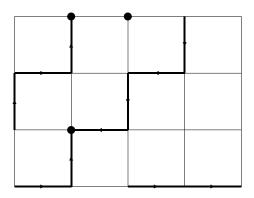
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



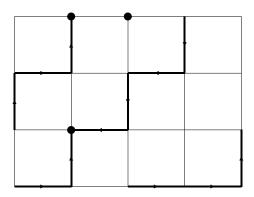
# Build dynamically a rooted spanning forest using **loop-erased random walks** killed at rate q.

40 / 65

## Sampling $\mathcal{R}_q$ with Wilson's algorithm



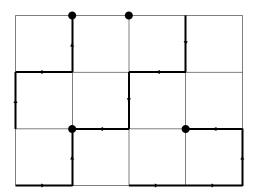
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



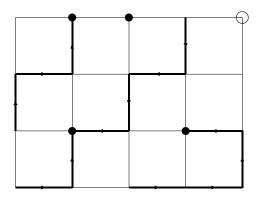
Build dynamically a rooted spanning forest using **loop-erased random walks** killed at rate q.

42 / 65

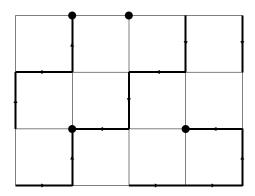
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



## Sampling $\mathcal{R}_q$ with Wilson's algorithm



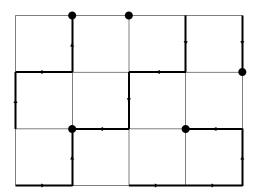
## Sampling $\mathcal{R}_q$ with Wilson's algorithm



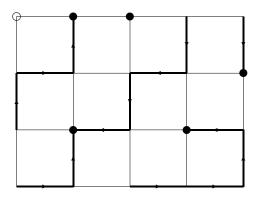
Build dynamically a rooted spanning forest using loop-erased random walks killed at rate q.

45 / 65

## Sampling $\mathcal{R}_q$ with Wilson's algorithm



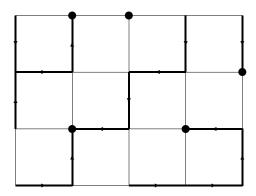
### Sampling $\mathcal{R}_q$ with Wilson's algorithm



Build dynamically a rooted spanning forest using loop-erased random walks killed at rate q.

47 / 65

### Sampling $\mathcal{R}_q$ with Wilson's algorithm



Build dynamically a rooted spanning forest using loop-erased random walks killed at rate q.

48 / 65

# $\mathcal{R}_q$ : a flexible set of well-distributed nodes

#### Theorem (Distribution of number of roots -

Given  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , consider the set of Roots  $\mathcal{R}_q$  with kernel  $K_q$ . Then its cardinality is a non-homogeneous Binomial :

$$|\mathcal{R}_q| = \sum_{i=1}^n Y_i, \qquad Y_i \sim Bernoulli\left(rac{q}{q+ heta_i}
ight)$$

with  $\theta_i$ 's eigenvalues of the graph Laplacian  $-\mathcal{L}_w$ .

#### Theorem (Distribution of number of roots - A.G. (2018))

Given  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , consider the set of Roots  $\mathcal{R}_q$  with kernel  $K_q$ . Then its cardinality is a non-homogeneous Binomial :

$$|\mathcal{R}_q| = \sum_{i=1}^n Y_i, \qquad Y_i \sim Bernoulli\left(rac{q}{q+ heta_i}
ight)$$

with  $\theta_i$ 's eigenvalues of the graph Laplacian  $-\mathcal{L}_w$ .

#### Theorem (Distribution of number of roots - A.G. (2018))

Given  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , consider the set of Roots  $\mathcal{R}_q$  with kernel  $K_q$ . Then its cardinality is a non-homogeneous Binomial :

$$|\mathcal{R}_q| = \sum_{i=1}^n Y_i, \qquad Y_i \sim Bernoulli\left(rac{q}{q+ heta_i}
ight)$$

with  $\theta_i$ 's eigenvalues of the graph Laplacian  $-\mathcal{L}_w$ .

**Note:**  $|\mathcal{R}_q| = n$  if  $q \to \infty$  and  $|\mathcal{R}_q| = 1$  if  $q \to 0$ .

#### Theorem (Distribution of number of roots - A.G. (2018))

Given  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , consider the set of Roots  $\mathcal{R}_q$  with kernel  $K_q$ . Then its cardinality is a non-homogeneous Binomial :

$$|\mathcal{R}_q| = \sum_{i=1}^n Y_i, \qquad Y_i \sim Bernoulli\left(rac{q}{q+ heta_i}
ight)$$

with  $\theta_i$ 's eigenvalues of the graph Laplacian  $-\mathcal{L}_w$ .

Note:  $|\mathcal{R}_q| = n$  if  $q \to \infty$  and  $|\mathcal{R}_q| = 1$  if  $q \to 0$ .

#### Theorem (Distribution of number of roots - A.G. (2018))

Given  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , consider the set of Roots  $\mathcal{R}_q$  with kernel  $K_q$ . Then its cardinality is a non-homogeneous Binomial :

$$|\mathcal{R}_q| = \sum_{i=1}^n Y_i, \qquad Y_i \sim Bernoulli\left(rac{q}{q+ heta_i}
ight)$$

with  $\theta_i$ 's eigenvalues of the graph Laplacian  $-\mathcal{L}_w$ .

**Note:**  $|\mathcal{R}_q| = n$  if  $q \to \infty$  and  $|\mathcal{R}_q| = 1$  if  $q \to 0$ .

Efficient sampling of exactly k roots

Wilson's algorithm allows to sample  $\mathcal{R}_q$  for fixed q, we developed

- a coupled algorithm to sample a trajectory  $(\mathcal{R}_q)_{q\in[0,\infty)}$ ,
- and  $\mathcal{R}_k := \mathcal{R}_q$  conditioned on having k roots ,
  - in O(n) running time if k is a fraction of n.

Luca Avena (Mathematics, Leiden)

#### Theorem (Distribution of number of roots - A.G. (2018))

Given  $\mathcal{G} = (\mathcal{V}, \mathcal{E}, w)$ , consider the set of Roots  $\mathcal{R}_q$  with kernel  $K_q$ . Then its cardinality is a non-homogeneous Binomial :

$$|\mathcal{R}_q| = \sum_{i=1}^n Y_i, \qquad Y_i \sim Bernoulli\left(rac{q}{q+ heta_i}
ight)$$

with  $\theta_i$ 's eigenvalues of the graph Laplacian  $-\mathcal{L}_w$ .

**Note:**  $|\mathcal{R}_q| = n$  if  $q \to \infty$  and  $|\mathcal{R}_q| = 1$  if  $q \to 0$ .

#### Efficient sampling of exactly k roots

Wilson's algorithm allows to sample  $\mathcal{R}_q$  for fixed q, we developed

- a coupled algorithm to sample a trajectory  $(\mathcal{R}_q)_{q \in [0,\infty)}$ ,
- and  $\mathcal{R}_k := \mathcal{R}_q$  conditioned on having k roots,
  - in O(n) running time if k is a fraction of n.

Luca Avena (Mathematics, Leiden)

#### A generalized Page-Rank *k*-centrality

#### Theorem (Roots are at local equilibrium -

Fix  $k \leq n$ , any partition  $\{B_1, \ldots, B_k\}$  of  $\mathcal{V}$  into k blocks, and any  $x_i \in B_i$ , for  $i = 1, \ldots, k$ . Then:

$$\mathbb{P}\Big(\mathcal{R}_k = \{x_1, \cdots, x_k\} \Big| \mathcal{P}_q = \{B_1, \ldots, B_k\}\Big) = \prod_{i=1}^{k} \mu_{B_i}(x_i),$$

where

•  $\mathcal{P}_q$  is the partition of  $\mathcal{V}$  induced by the forest with law  $\nu_q$ ,

•  $\mu_{B_i}$  is the invariant measure of the RW X restricted to  $B_i$ .

#### Theorem (Roots are at local equilibrium - A.G. (2018))

Fix  $k \leq n$ , any partition  $\{B_1, \ldots, B_k\}$  of  $\mathcal{V}$  into k blocks, and any  $x_i \in B_i$ , for  $i = 1, \ldots, k$ . Then:

$$\mathbb{P}\Big(\mathcal{R}_k = \{x_1, \cdots, x_k\} \Big| \mathcal{P}_q = \{B_1, \ldots, B_k\}\Big) = \prod_{i=1}^{\kappa} \mu_{B_i}(x_i),$$

where

- $\mathcal{P}_q$  is the partition of  $\mathcal{V}$  induced by the forest with law  $\nu_q$ ,
- $\mu_{B_i}$  is the invariant measure of the RW X restricted to  $B_i$ .

#### Theorem (Roots are at local equilibrium - A.G. (2018))

Fix  $k \leq n$ , any partition  $\{B_1, \ldots, B_k\}$  of  $\mathcal{V}$  into k blocks, and any  $x_i \in B_i$ , for  $i = 1, \ldots, k$ . Then:

$$\mathbb{P}\Big(\mathcal{R}_k = \{x_1, \cdots, x_k\} \Big| \mathcal{P}_q = \{B_1, \ldots, B_k\}\Big) = \prod_{i=1}^{\kappa} \mu_{B_i}(x_i),$$

where

- $\mathcal{P}_q$  is the partition of  $\mathcal{V}$  induced by the forest with law  $\nu_q$ ,
- $\mu_{B_i}$  is the invariant measure of the RW X restricted to  $B_i$ .

Note:

- For q ≈ 0 ⇒ P<sub>q</sub> = V and the unique root is distributed as the invariant measure µ of the RW.
- "Freedom to choose" the graph Laplacian.

#### Theorem (Roots are at local equilibrium - A.G. (2018))

Fix  $k \leq n$ , any partition  $\{B_1, \ldots, B_k\}$  of  $\mathcal{V}$  into k blocks, and any  $x_i \in B_i$ , for  $i = 1, \ldots, k$ . Then:

$$\mathbb{P}\Big(\mathcal{R}_k = \{x_1, \cdots, x_k\} \Big| \mathcal{P}_q = \{B_1, \ldots, B_k\}\Big) = \prod_{i=1}^k \mu_{B_i}(x_i),$$

where

- $\mathcal{P}_q$  is the partition of  $\mathcal{V}$  induced by the forest with law  $\nu_q$ ,
- $\mu_{B_i}$  is the invariant measure of the RW X restricted to  $B_i$ .

#### Note:

- For q ≈ 0 ⇒ P<sub>q</sub> = V and the unique root is distributed as the invariant measure µ of the RW.
- "Freedom to choose" the graph Laplacian.

### Forest-immunization (on undirected network)

♦ **Heuristic:** *k* best spreaders to be removed should be far from each other but also the remaining n - k susceptible ones ♦

# Forest-immunization (on undirected network)

♦ **Heuristic:** *k* best spreaders to be removed should be far from each other but also the remaining n - k susceptible ones ♦

### Forest-immunization (on undirected network)

♦ **Heuristic:** *k* best spreaders to be removed should be far from each other but also the remaining n - k susceptible ones ♦

# Forest-immunization (on undirected network)

♦ **Heuristic:** *k* best spreaders to be removed should be far from each other but also the remaining n - k susceptible ones ♦

Roots complement-set:  $\mathcal{R}_q^{\mathcal{C}} := \mathcal{V} \setminus \mathcal{R}_q$  is also determinantal set & it concentrates around max-degree sets.

Canidate set of k-spreaders to be removed: Sample R<sub>n-k</sub> roots for the susceptible ones & set its complement R<sup>C</sup><sub>k</sub> to be the candidate k-set of best spreaders.

# Forest-immunization (on undirected network)

♦ **Heuristic:** *k* best spreaders to be removed should be far from each other but also the remaining n - k susceptible ones ♦

Roots complement-set:  $\mathcal{R}_q^{\mathcal{C}} := \mathcal{V} \setminus \mathcal{R}_q$  is also determinantal set & it concentrates around max-degree sets.

Canidate set of k-spreaders to be removed: Sample R<sub>n-k</sub> roots for the susceptible ones & set its complement R<sup>C</sup><sub>k</sub> to be the candidate k-set of best spreaders.

# Forest-immunization (on undirected network)

♦ **Heuristic:** *k* best spreaders to be removed should be far from each other but also the remaining n - k susceptible ones ♦

- Canidate set of k-spreaders to be removed: Sample R<sub>n-k</sub> roots for the susceptible ones & set its complement R<sup>C</sup><sub>k</sub> to be the candidate k-set of best spreaders.
- Output: Provide the image of the image. The image of the image of

# Forest-immunization (on undirected network)

♦ **Heuristic:** *k* best spreaders to be removed should be far from each other but also the remaining n - k susceptible ones ♦

- Canidate set of k-spreaders to be removed: Sample R<sub>n-k</sub> roots for the susceptible ones & set its complement R<sup>C</sup><sub>k</sub> to be the candidate k-set of best spreaders.
- Output: Provide the image of the image. The image of the image of

### Forest-immunization (on undirected network)

♦ **Heuristic:** *k* best spreaders to be removed should be far from each other but also the remaining n - k susceptible ones ♦

- Canidate set of k-spreaders to be removed: Sample R<sub>n-k</sub> roots for the susceptible ones & set its complement R<sup>C</sup><sub>k</sub> to be the candidate k-set of best spreaders.
- **Output** Weight State (Constraint) Sample L many candidate k-sets {R<sup>C</sup><sub>k,i</sub> : i ≤ L} and compute their ShieldValue and Max-degree with L such that total running cost is as in Netshield O(m + nk).
- Sorest k-set S<sub>\*</sub> to be immunized: Among the L sampled k-sets. Pick the ones with max degree and max Shield Value. Take also the Netshield output set. Set S<sub>\*</sub> to be the set with maximal eigendrop among these 3 sets.

# Forest-immunization (on undirected network)

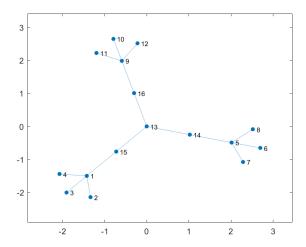
♦ **Heuristic:** *k* best spreaders to be removed should be far from each other but also the remaining n - k susceptible ones ♦

- Canidate set of k-spreaders to be removed: Sample R<sub>n-k</sub> roots for the susceptible ones & set its complement R<sup>C</sup><sub>k</sub> to be the candidate k-set of best spreaders.
- Output: Provide the image of the image. The image of the image of
- Forest k-set S<sub>\*</sub> to be immunized: Among the L sampled k-sets. Pick the ones with max degree and max Shield Value. Take also the Netshield output set. Set S<sub>\*</sub> to be the set with maximal eigendrop among these 3 sets.

# Forest immunization & the geometry of contagion in action: a few illustrative experiments.

52 / 65

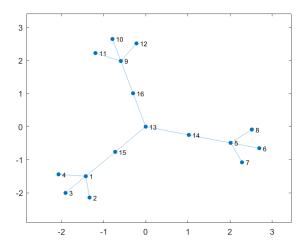
# A synthetic insightful example



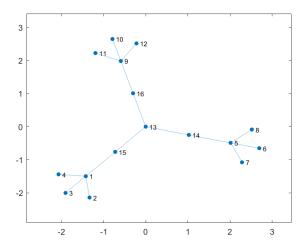
Luca Avena (Mathematics, Leiden)

53 / 65

#### A synthetic insightful example: k = 1



#### A synthetic insightful example: k = 1



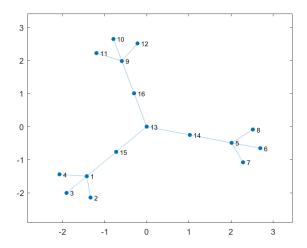
#### $\Rightarrow$ node with best eigendrop is {13}: not the highest degree node.

Luca Avena (Mathematics, Leiden)

k-node Immunization

Rome, May 30, 2022

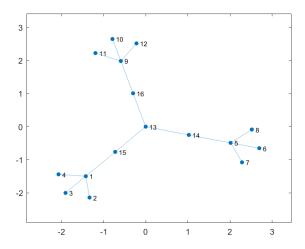
#### A synthetic insightful example: k = 1



 $\Rightarrow$  node with best eigendrop is {13}: not the highest degree node.

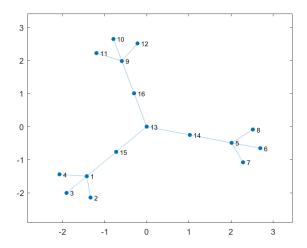
Luca Avena (Mathematics, Leiden)

#### A synthetic insightful example: k = 3



55 / 65

#### A synthetic insightful example: k = 3

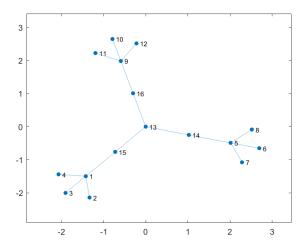


 $\Rightarrow$  best triple {14, 15, 16}: not the maximal degree set.

Luca Avena (Mathematics, Leiden)

k-node Immunization

#### A synthetic insightful example: k = 3

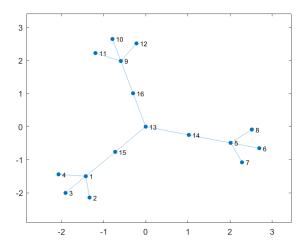


 $\Rightarrow$  best triple {14, 15, 16}: not the maximal degree set.

Luca Avena (Mathematics, Leiden)

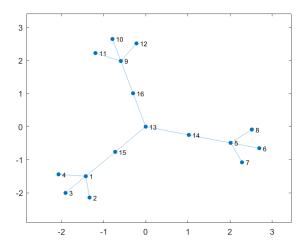
k-node Immunization

#### A synthetic insightful example: k = 4



56 / 65

#### A synthetic insightful example: k = 4

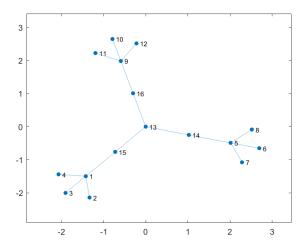


#### $\Rightarrow$ best quaduple {13, 1, 5, 9}: global + "periferial" centers.

Luca Avena (Mathematics, Leiden)

k-node Immunization

#### A synthetic insightful example: k = 4



 $\Rightarrow$  best quaduple {13, 1, 5, 9}: global + "periferial" centers.

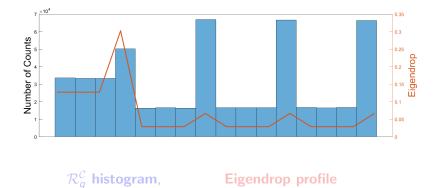
Luca Avena (Mathematics, Leiden)

k-node Immunization

Rome, May 30, 2022

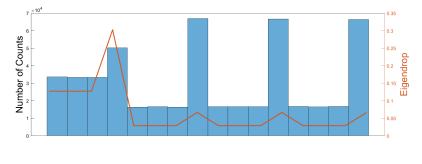
# A synthetic insightful example: $\mathcal{R}_{q}^{\mathcal{C}}$ for k = 1

# A synthetic insightful example: $\mathcal{R}_{q}^{\mathcal{C}}$ for k = 1



57 / 65

# A synthetic insightful example: $\mathcal{R}_{q}^{\mathcal{C}}$ for k = 1

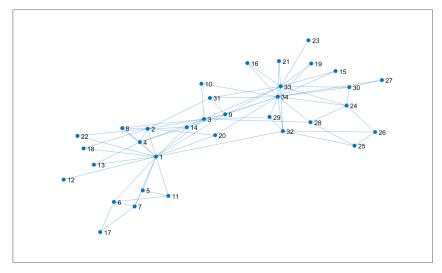


 $\mathcal{R}_{q}^{\mathcal{C}}$  histogram,

#### **Eigendrop profile**

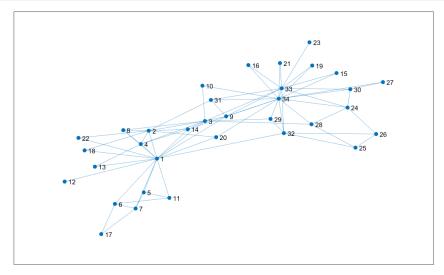
## The Karate club: "a fighting group"

## The Karate club: "a fighting group"



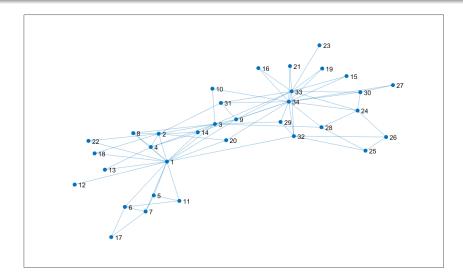
#### **President** $\{1\}$ Vs Instructor $\{34\}$ led to a split into 2 groups.

## The Karate club: "a fighting group"

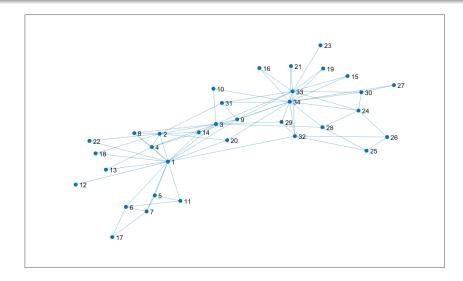


#### President $\{1\}$ Vs Instructor $\{34\}$ led to a split into 2 groups.

## The Karate club: k = 1



## The Karate club: k = 1

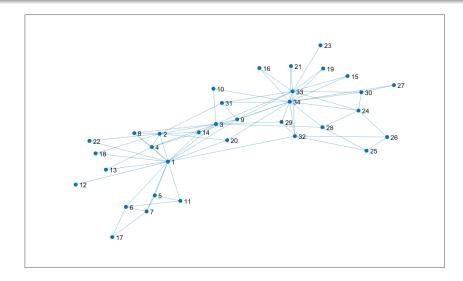


#### $\Rightarrow$ best node is {3}: neither the president nor the instructor.

Luca Avena (Mathematics, Leiden)

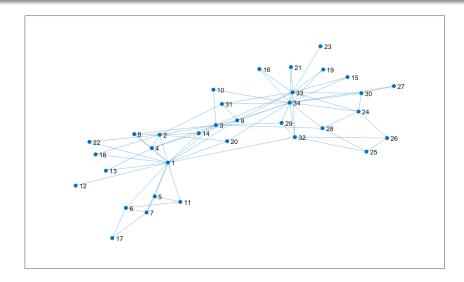
k-node Immunization

## The Karate club: k = 1



#### $\Rightarrow$ best node is {3}: neither the president nor the instructor.

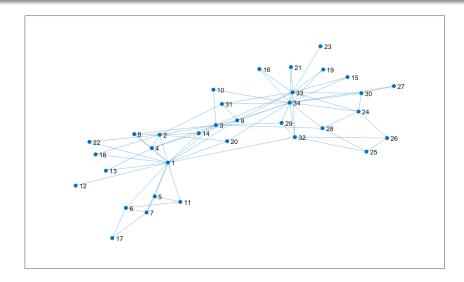
## The Karate club: k = 2



#### $\Rightarrow$ best pair is {1,34}: the president and the instructor.

Luca Avena (Mathematics, Leiden)

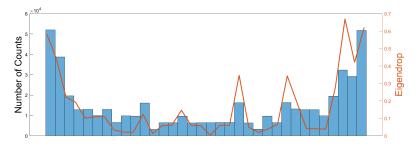
### The Karate club: k = 3



#### $\Rightarrow$ best triple is {1,3,34}: "the fighters and the philanthropist".

# The Karate club: $\mathcal{R}_q^{\mathcal{C}}$ for k = 1

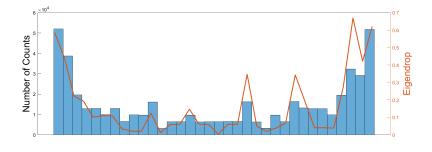
# The Karate club: $\mathcal{R}_q^{\mathcal{C}}$ for k = 1



 $\mathcal{R}_q^{\mathcal{C}}$  histogram,

#### **Eigendrop profile**

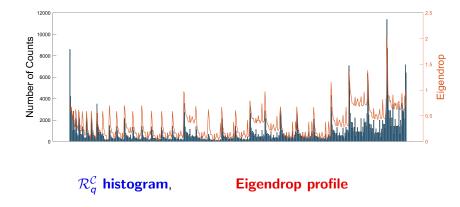
# The Karate club: $\mathcal{R}^{\mathcal{C}}_{a}$ for k = 1



 $\mathcal{R}_{q}^{\mathcal{C}}$  histogram,

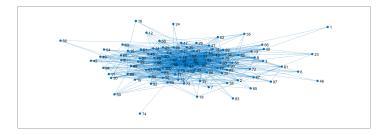
#### **Eigendrop profile**

# The Karate club: $\mathcal{R}_a^c$ for k = 2



## **Conference Interaction:** a weighted example

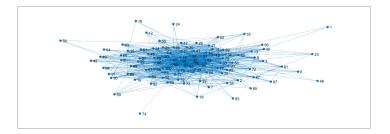
## **Conference Interaction:** a weighted example



 $|\mathcal{V}|=10^2$  individuals,  $|\mathcal{E}|pprox 10^3$  interactions in one day,

On such large non-regular networks benchmarks (and similar ones, e.g. airport, etc...) the forest-immunization can find better solutions than Nethsield in comparable running time.

## **Conference Interaction:** a weighted example



 $|\mathcal{V}|=10^2$  individuals,  $|\mathcal{E}|pprox 10^3$  interactions in one day,

On such large non-regular networks benchmarks (and similar ones, e.g. airport, etc...) the forest-immunization can find better solutions than Nethsield in comparable running time.

# **References & THANK YOU**

- (Survey on epidemics on networks) R. Pastor-Satorras, C. Castellano, P. Van Mieghem and A. Vespignani, *Epidemic processes in complex networks*, Reviews of Modern Physics 87 (2015).
- (Max eigenvalue for SIS and SIR) D. Chakrabarti, Y. Wang, C. Wang, J. Leskovec and C. Faloutsos, *Epidemic thresholds in real networks*, ACM Transactions on Information and System Security (2008).
- (Netshield) C. Chen, H. Tong, B. A. Prakash, C. E. Tsourakakis, T. Eliassi-Rad, C. Faloutsos and D. H. Chau, Node immunization on large graphs: theory and algorithms, IEEE Transactions on Knowledge and Data Engineering 28 (2016).
- (Roots theory) L. A. and A. Gaudillière, *Two applications of random spanning forests*, Journal of Theoretical Probability 31 (2018).
- (Survey on rooted forests) L. A., F. Castell, A. Gaudillière and C. Mélot, Random forests and networks analysis, Journal of Statistical Physics 173 (2018).
- (Forest immunization) L. A., M. Emmerich, A. Gaudillière and I. Gurewitsch to appear (2022+).