

# Time-varying epidemic transmission in heterogeneous networks

Sara Sottile\*  
University of Trento

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\*Joint work with Prof. Xinzhi Liu - University of Waterloo

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- ▶ **Negligible incubation period:**  
no delay term in equations.

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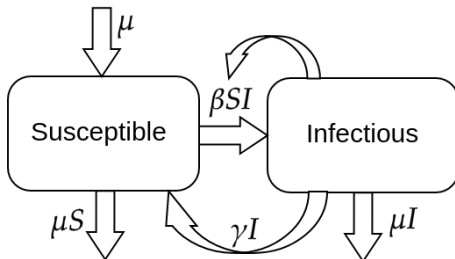
$$\begin{aligned}\textbf{Force of the infection} &= \text{contact rate} \times \text{risk of infection} \\ &\quad \times \text{proportion of infectious} \\ &= \text{transmission rate} \\ &\quad \times \text{proportion of infectious} \\ &= \beta \times \frac{I}{N}.\end{aligned}$$

**SIS Model**

$$\begin{cases} \frac{d}{dt} S(t) = \mu - \beta SI - \mu S + \gamma I, \\ \frac{d}{dt} I(t) = \beta SI - (\gamma + \mu)I. \end{cases}$$

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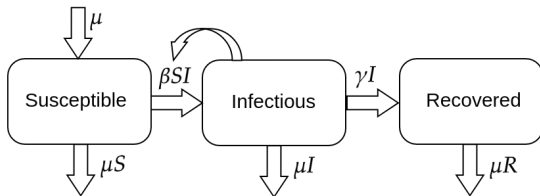


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Disease	BRN
Measles	12 - 18
Pertussis	12 - 17
Rubella	6 - 7
Influenza	1.5 - 1.8

In the epidemic models with demography the system admits always a **disease-free equilibrium**, that is the equilibrium point in which  $I^* = 0$ . Moreover, under certain conditions, it admits also an **endemic equilibrium**, that is the equilibrium in which the epidemic is persistent.



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It can be shown that the following result holds.

## Theorem

- ▶ *The disease-free equilibrium is globally asymptotically stable (g.a.s.) if  $\mathcal{R}_0 < 1$ .*
- ▶ *If  $\mathcal{R}_0 \geq 1$ , then the endemic equilibrium exists and it is g.a.s.*

**Goal:** *reduce the value of the BRN below the unity.*

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**Tools:** *quarantine, travel restrictions, vaccination.*

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Degree-based mean-field (DBMF): grouping nodes with respect to their state and degree.

We denote with  $K$  the set of all assumed degrees in the network and with  $X_k(t)$  the proportion of nodes of degree  $k$  at time  $t \geq 0$  in the compartment  $X$ .

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- ▶  $\Theta(t) = \frac{1}{\langle k \rangle} \sum_{k \in K} \varphi(k) p(k) I_k(t);$  (*uncorrelated network*)
- ▶  $\varphi(k)$  is the *infectivity*, that is the average number of links from which a node with degree  $k$  can transmit the disease.

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- ▶ Different BRNs for each subsystem.
- ▶ *Time-weighted average BRN*

$$\langle \mathcal{R}_\sigma \rangle = \sup_{t \geq h} \frac{1}{t} \sum_{i \in P} \mathcal{R}_{0,i} T_i(t), \quad \text{for some } h > 0.$$

where  $\{T_i(t)\}$  are the total activation times.

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**SEIR Model:** it is not possible to prove a result for  $\langle \mathcal{R}_\sigma \rangle$ .

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- ▶ **Peak every third years:**

$$\lambda_i(t) = \begin{cases} \lambda_1 & \text{every third years,} \\ \lambda_2 & \text{otherwise,} \end{cases}$$

with  $\lambda_1 \gg \lambda_2$ .

$$\begin{cases} \frac{d}{dt} S_k(t) = (1-p)\rho + (1-\chi)\alpha V_k - (\nu + \rho)S_k + \psi I_k S_k - \lambda_i k S_k \Theta, \\ \frac{d}{dt} V_k(t) = p\rho + \nu S_k - ((1-\chi)\alpha + \omega\chi + \rho)V_k + \psi I_k V_k, \\ \frac{d}{dt} E_k(t) = \lambda_i k S_k \Theta - \psi E_k I_k - (\sigma + \rho)E_k, \\ \frac{d}{dt} I_k(t) = \sigma E_k - (\gamma + \rho + \psi)I_k + \psi I_k^2, \end{cases}$$

where  $k \in K$  and  $i = 1, 2$ .

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Since the switching rule is periodic

$$\langle \mathcal{R}_0 \rangle = \frac{1}{\Omega} \sum_{i \in P} \mathcal{R}_{0,i} \tau_i.$$

In our model we find  $\Omega = 3$ ,  $\tau_1 = 1$  and  $\tau_2 = 2$ , then

$$\langle \mathcal{R}_0^{\text{SVEIR}} \rangle = \frac{1}{3} (\mathcal{R}_{0,1} + 2 \cdot \mathcal{R}_{0,2}).$$

- ▶ **Scale free-network.**

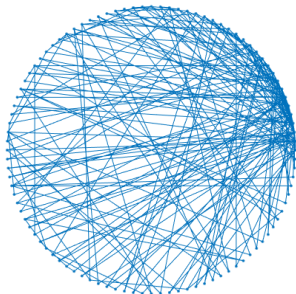
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- ▶ Network with 100 nodes,  $\langle k \rangle = 4.4823$  and  $\langle k^2 \rangle = 17.0203$ .  
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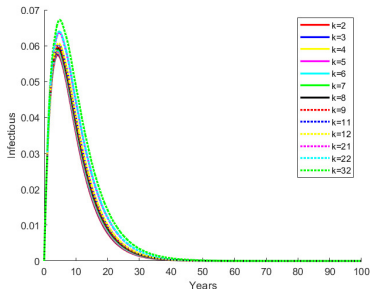
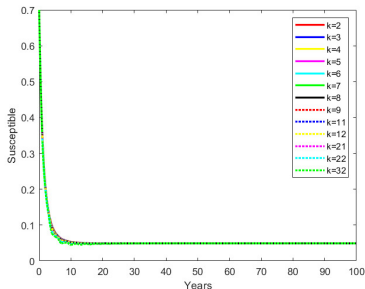


Both  $\mathcal{R}_{0,1}, \mathcal{R}_{0,2} \leq 1$  and  $\langle \mathcal{R}_{\sigma}^{\text{SVEIR}} \rangle < 1$ .

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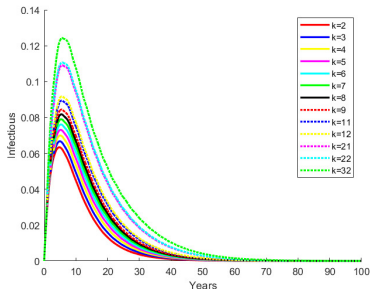
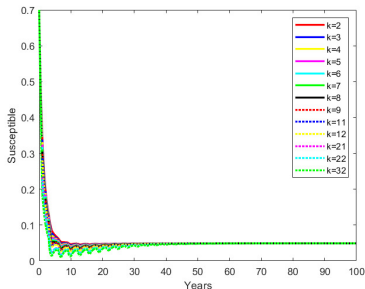


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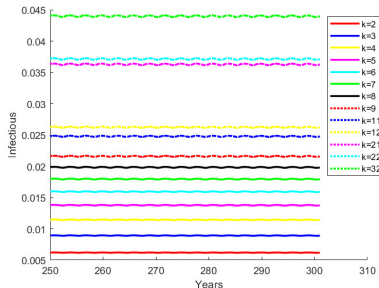
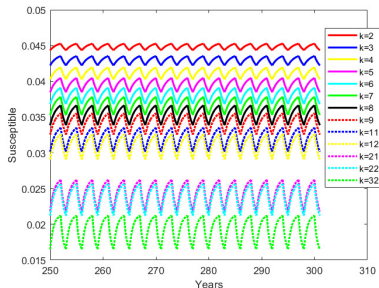


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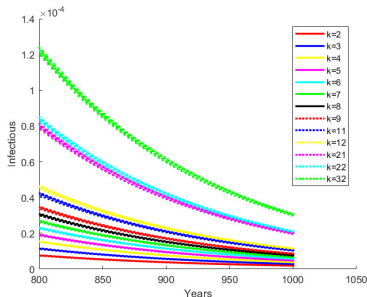
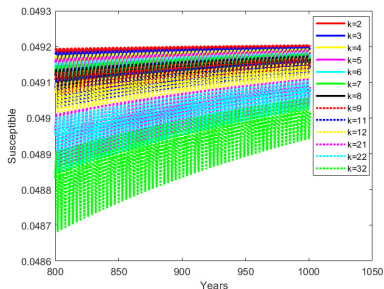


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- ▶ The higher the degree, the higher the number of the infectious in that compartment. The opposite happens with susceptible and vaccinated.



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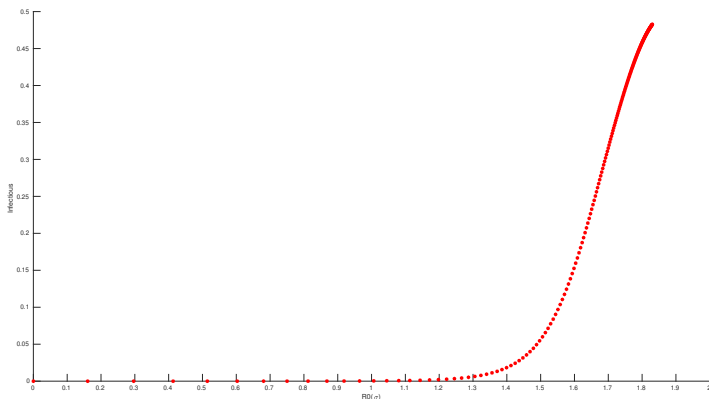
For simpler models (SIR, SIS, SIRS), the threshold's results on the time-weighted average BRN are the same as for the BRN in classic models.

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How does  $\langle \mathcal{R}_\sigma \rangle$  affect the total number of the infectious in the network? For the SEIR model we studied  $\langle \mathcal{R}_\sigma \rangle$  as a function of the parameters of the model and how its expression influences the total number of the infectious in the network. We found that the persistence of the disease occurs when  $\langle \mathcal{R}_\sigma \rangle \gtrsim 1.3$ .

For example, if we analyze the expression of  $\langle \mathcal{R}_\sigma \rangle$  as a function of the incubation period  $\sigma$ , simulations suggest that the eradication of the disease occurs also for values of  $\langle \mathcal{R}_\sigma \rangle > 1$ .



More details about this work can be found in: Sottile, S. and Liu, X. *Time-varying epidemic transmission in heterogeneous networks and applications to measles*, Journal of Biological Systems, Vol. 28, No. 4 (2020), pp. 1-26.

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Further works:

- ▶ consider also the infectivity changing according to a switching rule (for example to describe isolations or quarantines);
- ▶ using different switching rules than piecewise functions;
- ▶ applications to temporal networks.

Thank you for your attention