

# QUALITATIVE BEHAVIOUR OF EPIDEMIC MODELS IN DEGREE-BASED NETWORKS WITH TIME-VARYING INFECTION RATE

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## Introduction

Classic epidemic models are based on certain assumptions which make them easier to study. The most important hypothesis are:

1. homogenous mixing in the population (named “mass-mixing”);
2. all the parameters constant in time, ruling out possible effects of the seasonality.

The goal is to extend the approach in which time-varying transmission rate has been considered ([6, 5]) by using heterogeneous networks ([3, 4, 7]).

## Methodology

### Epidemic models in heterogeneous networks

Each person is a node and the degree  $k$  of a node is defined as the number of neighbourhood of an individual. In such models the transmission rate is replaced by the degree-dependent transmission rate denoted by  $\lambda \cdot k$  and the proportion of infectious is a time-dependent function  $\Theta(t)$ , where

$$\Theta(t) = \frac{1}{\langle k \rangle} \sum_{k \in K} kp(k)I_k(t).$$

### Time-varying transmission rate

The transmission rate has been considered as a piece-wise constant function, subject to the switching rule with a set of switching times  $\{t_k\}$ .

Thus  $\lambda(t) = \lambda_{i_k}$  and we obtain different subsystems, with their own BRN.

When the switching rule is periodic we can evaluate  $\mathcal{R}_0$  as

$$\mathcal{R}_0 = \frac{1}{\omega} \sum_{i \in P} \mathcal{R}_{0,i} \tau_i,$$

where  $\omega$  is the period of the function  $\sigma$ ,  $\tau_i = t_i - t_{i-1}$  and  $\tau_{i+m} = \tau_i$ , based on [2],[1].

## SEIR model

$$\begin{cases} S'_k(t) = \mu - \lambda_i k S_k \Theta - \mu S_k, \\ E'_k(t) = \lambda_i k S_k \Theta - \sigma E_k - \mu E_k, \\ I'_k(t) = \sigma E_k - \gamma I_k - \mu I_k, \\ R'_k(t) = \gamma I_k - \mu R_k, \end{cases}$$

where  $k \in K$  and  $i \in P$ .

## Results

There exists always a disease-free equilibrium  $E_0 = (1, 0, 0, 1, 0, 0, \dots, 1, 0, 0)$ .

The Basic Reproduction Numbers of all the subsystems are

$$\mathcal{R}_{0,i}^{\text{SEIR}} = \frac{\lambda_i \sigma}{(\sigma + \mu)(\gamma + \mu)} \frac{\langle k^2 \rangle}{\langle k \rangle}, \quad i \in P.$$

1. Assume that  $\mathcal{R}_{0,i}^{\text{SEIR}} \leq 1$  for all  $i \in P$ , then  $E_0$  is GAS in  $\Omega_{\text{SEIR}}$ .
2. The endemic equilibrium in the domain  $\Omega_{\text{SEIR}}$  exists if  $\mathcal{R}_{0,i}^{\text{SEIR}} > 1$  for all  $i \in P$ .
3. In the SIR model, if  $\mathcal{R}_0^{\text{SIR}} < 1$  then  $E_0$  is exponentially stable in the meaningful domain.

## Simulations

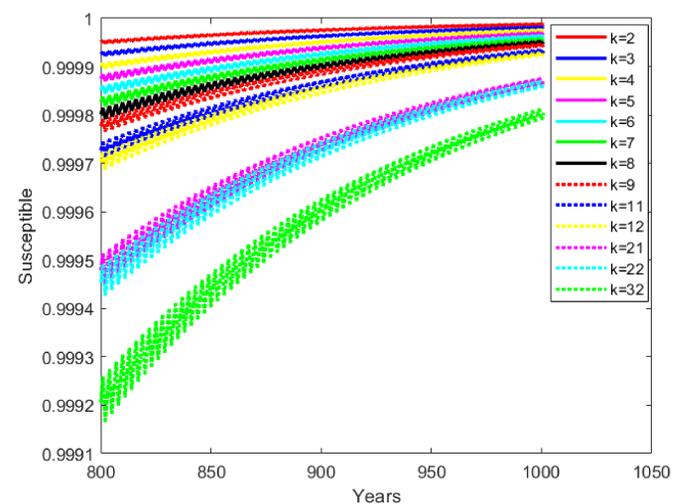
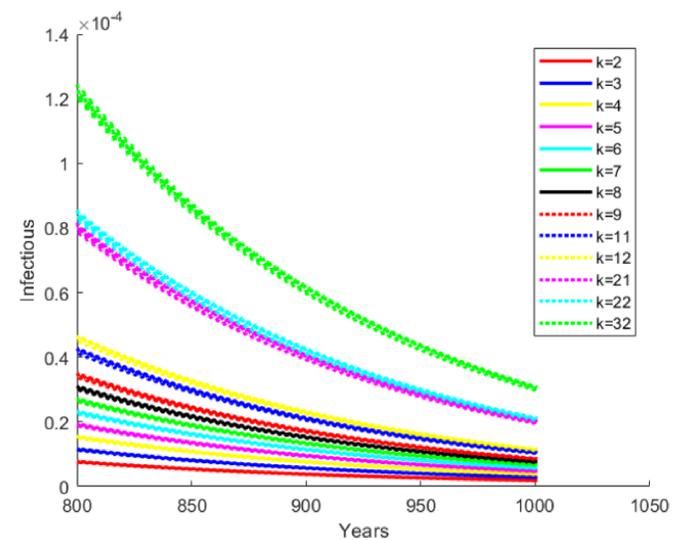
The considered network architecture is the scale-free network. We build a network with 100 nodes and 13 different degrees. The transmission rate is considered as follow changing every three years, switched between two values  $\lambda_1$  and  $\lambda_2$ , where  $\lambda_1 > \lambda_2$ . We obtain two subsystems, identified by their own BRNs. Since the periodicity of the switching rule, we can easily find the value of  $\mathcal{R}_0^{\text{SEIR}}$ .

Results:

1. When  $\mathcal{R}_{0,i} < 1$  over all time intervals  $T_i$ , solutions converge to the disease-free equilibrium.
2. If  $\mathcal{R}_{0,i} > 1$  over all time intervals  $T_i$ , then there is an endemic equilibrium and system converges to it.

3. If  $\mathcal{R}_0^{\text{SEIR}} < 1$  then the system converges to the disease-free equilibrium.
4. When  $\mathcal{R}_0^{\text{SEIR}} > 1$  but  $\mathcal{R}_{0,2}^{\text{SEIR}} < 1$  the system is approaching the disease-free equilibrium slowly, as shown in the following simulations.

### Simulations of the fourth case



## Open questions

1. Is the free-disease equilibrium exponentially stable when  $\mathcal{R}_0^{\text{SEIR}} < 1$ ?
2. Which type of stability has the endemic equilibrium, when it exists?
3. What happen if  $\mathcal{R}_0^{\text{SEIR}} > 1$  but there exists  $i \in P$  such that  $\mathcal{R}_{0,i}^{\text{SEIR}} < 1$ ?

## References

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