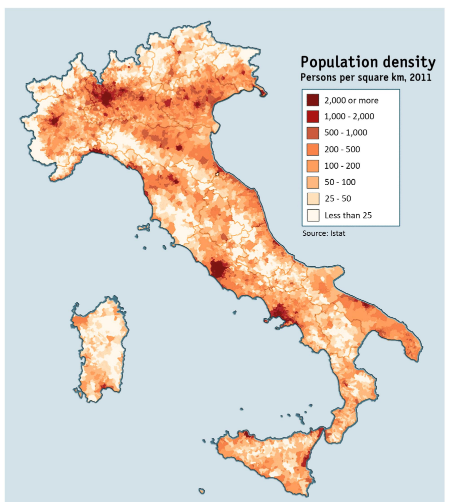
DDMCS 2022-23 Final Project

Simulating a SEIR Model in a Commuting Mobility Network



Application in Italian Commuting Networks:
Lazio
Puglia
North Italy

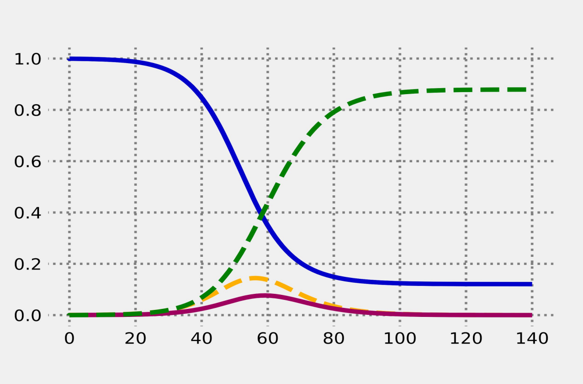
Ludovico Lentini

How it works: SEIR

1. Variant of the SIR Epidemic Model

Divides a population in

- **S -> Susceptible**
- **E -> Exposed**
- **I -> Infected**
- **R -> Recovered**



2. Models the **evolution** of SEIR values in time

$$\frac{dS}{dt} = -\beta \frac{SI}{N}$$

$$\frac{dE}{dt} = \beta \frac{SI}{N} - \sigma E$$

$$\frac{dI}{dt} = \sigma E - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

$$N = S + E + I + R,$$

3. Parameters:

- β Transition rate between Susceptible and Exposed.
- σ Rate of becoming infected
- γ Gamma is inverse of Recovery time.

How it works: SEIR Network

SEIR Model assumption: each element of the population is in contact with each other.

SEIR Network Model:

- Divide in subpopulations connected by a network.
- Treat each subpopulation as SEIR
- **Adds spreading through a directed network**

Number of new Exposed at location j

$$E_{j,t+1} = E_{j,t} + \frac{\beta_{j,t} S_{j,t} I_{j,t}}{N_j} + \frac{S_{j,t} \sum_k m^t_{j,k} x_{k,t} \beta_{k,t}}{N_j + \sum_k m^t_{j,k}},$$

Infected arriving from other locations

Infected at the location j

Kuhl, E. (2021). The network SEIR model. In: Computational Epidemiology. Springer, Cham. https://doi.org/10.1007/978-3-030-82890-5_10

Data and Implementation

Handled data to get a main dataframe with:

- Residence of the commuters

- Destination of the commuters

- Flux weight

Precision: Municipality

Resid	Dest	Flux
1005	96004	1
1006	1006	1186
1006	1272	661
1006	1013	254
1006	1219	229
1006	1303	85
1006	1115	72
1006	1189	61
1006	1120	56
1006	1045	54
1006	1270	51
1006	1008	48

Commuting mobility matrix from Istat

https://www.istat.it/it/archivio/139381

- **Municipalities = Nodes**
- **Edges represent people traveling between two municipalities**

- Edges are directed
- Edges are weighted according to the number of people traveling

SEIR Network implementation:

- **Using OD Matrix derived from df**
- **Cycle of SEIR evolution for every municipality**

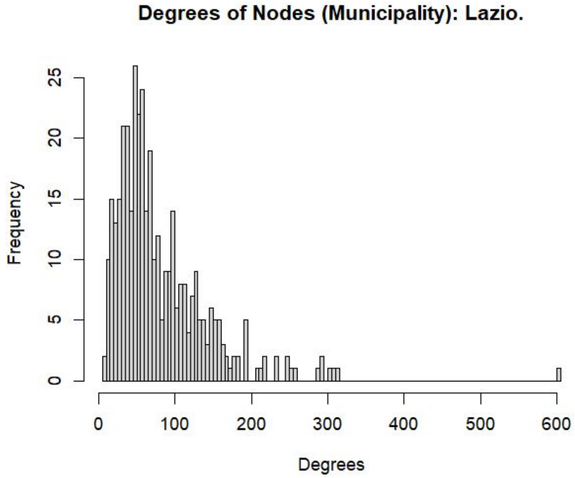
Used some code from:
https://www.databentobox.com/2020/03/28/covid19_city_sim_seir/

First applications

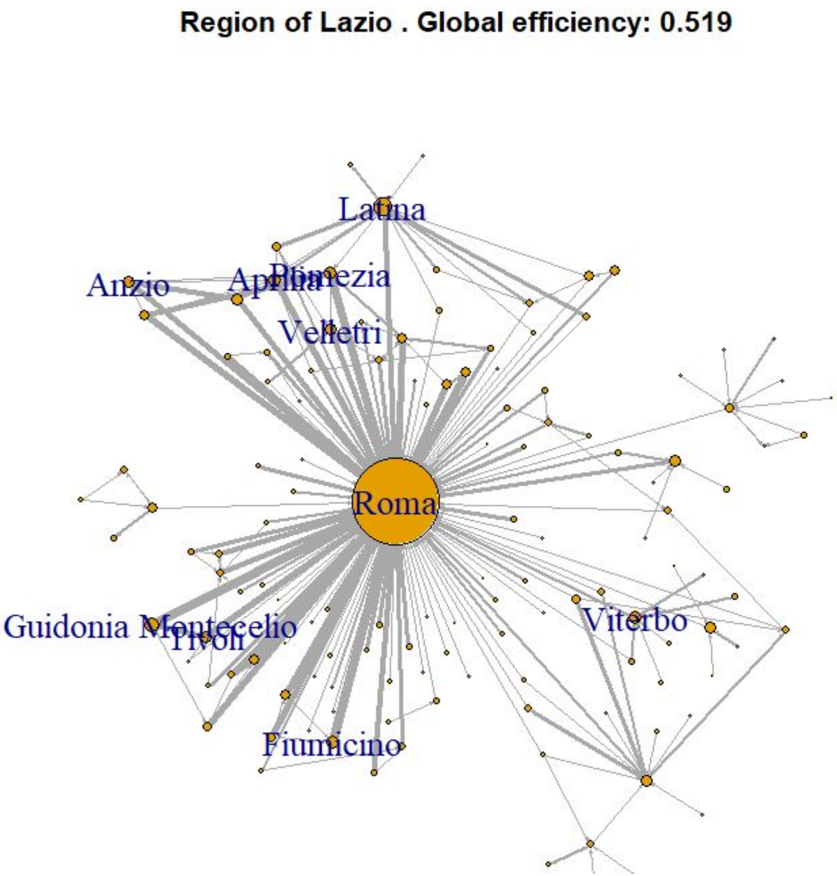
Lazio Region

Graph Structure

378 Nodes
15411 Edges



- Approaches a small-world network.
- There are not many nodes with a degree particularly small.
- There is one big hub, few intermediate.

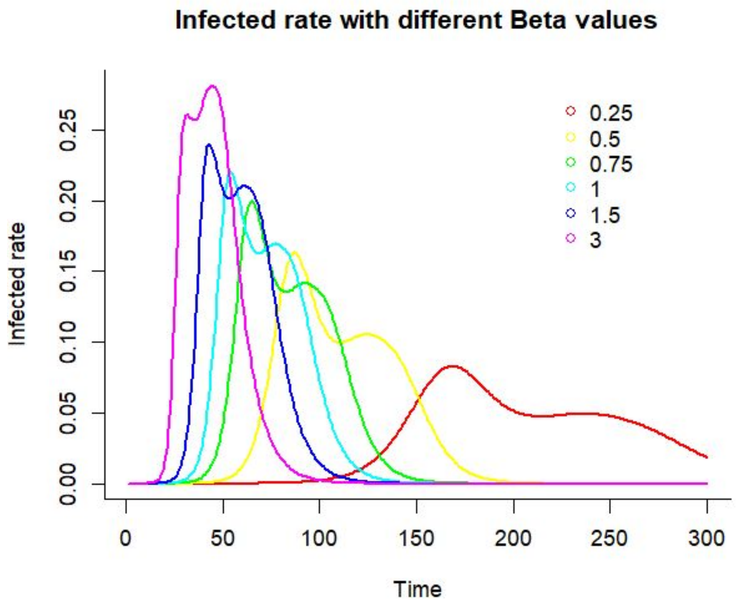


First results

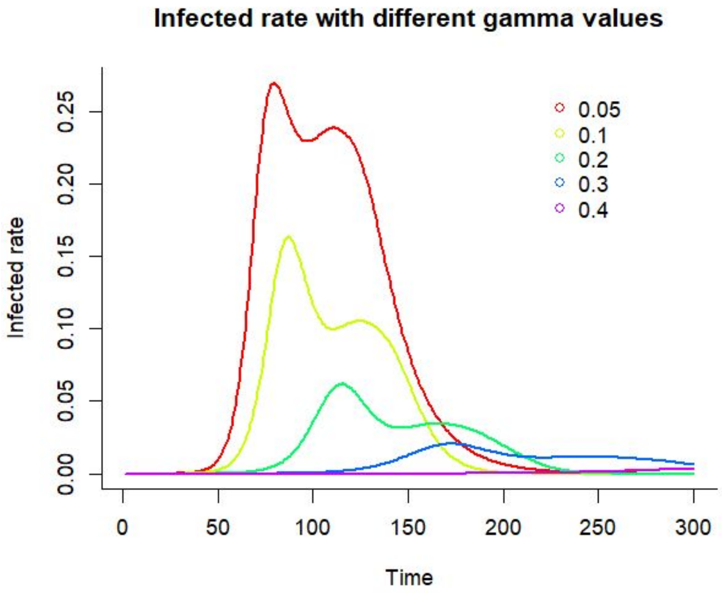
Parameter testing

Using as baseline Lazio network with Rome as start of infection.

Beta: the parameter controlling how often a susceptible-infected contact results in a new exposure



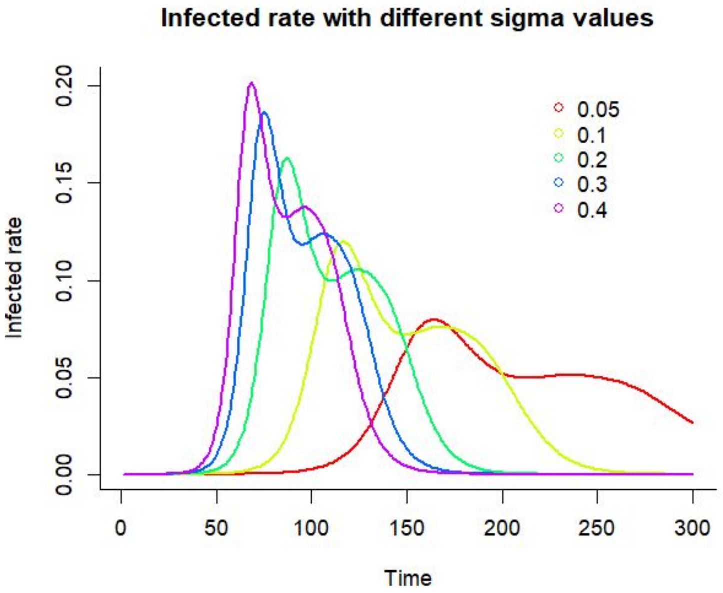
Gamma: the rate an infected recovers and moves into the resistant phase (1/Recovery_Time)



First results

Parameter testing

Sigma: the rate at which an exposed person becomes infective (1/Incubation_Time)



SEIR Network parameters testing confirms that:

1. Beta controls how **quick** an epidemic can outbreak.
2. Gamma, as connected to the Recovery time, can model the **intensity**.
3. Sigma represents the **dilation** in time of the infected peak.

First applications

Lazio Region

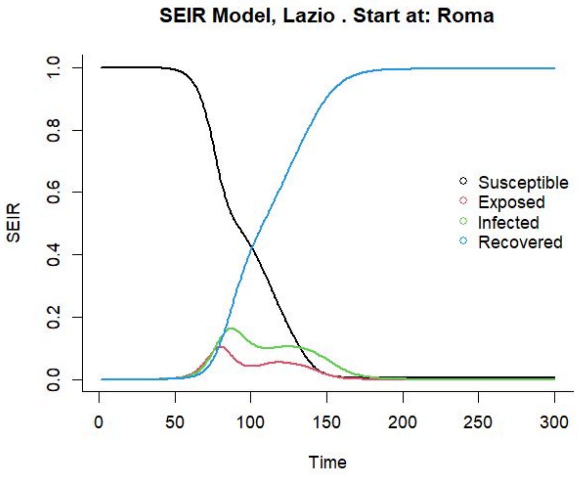
Observations:

Starting at the location with max degree **speeds up** the Infection curve.

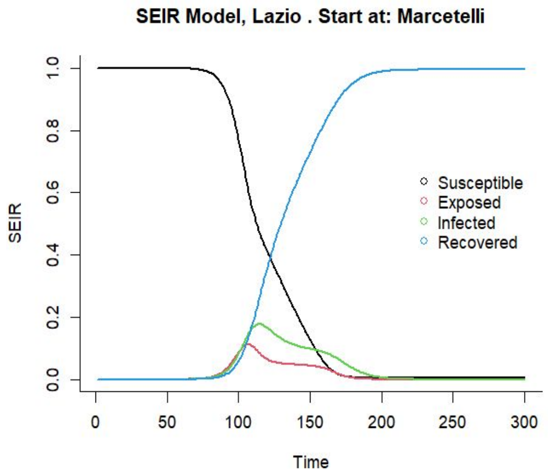
Starting at the location with min degree **is not always the most effective way to slow down** the infection curve.

Why?

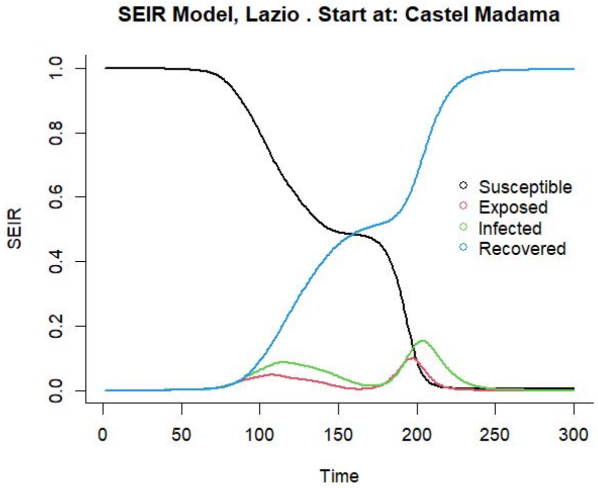
Start at max node degree: Roma.



Start at min node degree: Marcetelli



Start at other location



Why other locations:

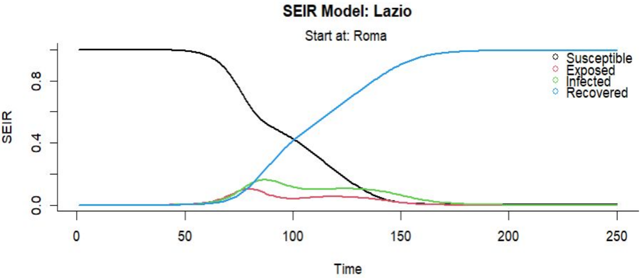
Lazio Region

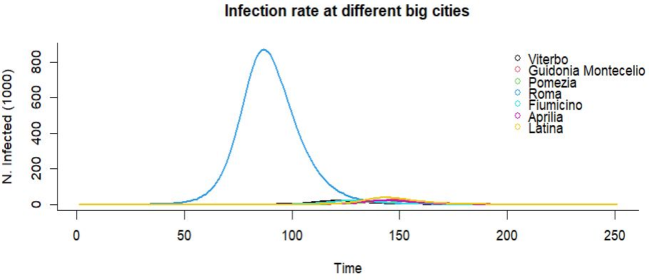
Add City visualization

There are other locations that **'hold' better** the contact with the hubs and slow more the infection.

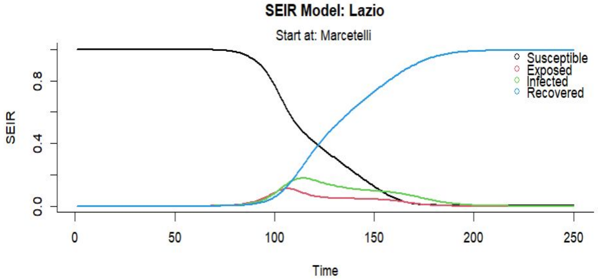
In this case starting **Castel Madama** spread the desease in other smaller hubs and later in Rome.

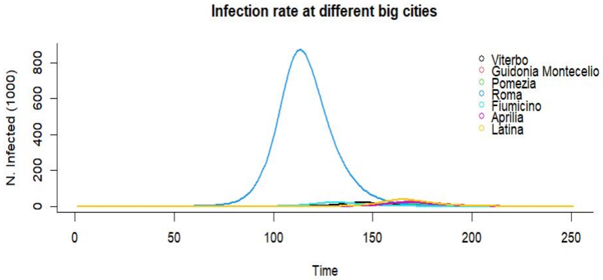
Start at max node degree: Roma



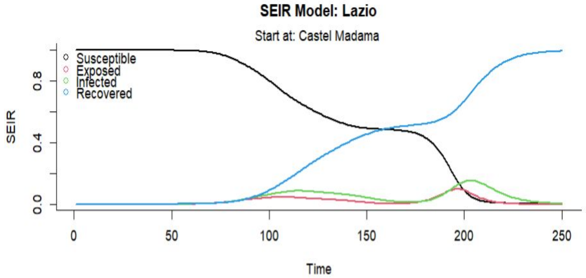


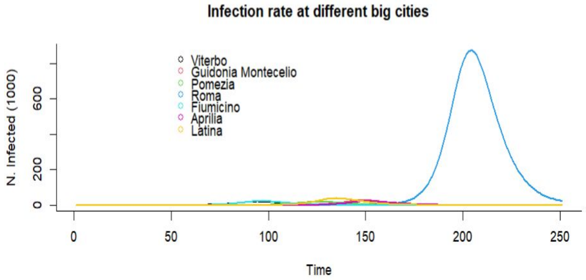
Start at min node degree: Marcetelli





Start at other location





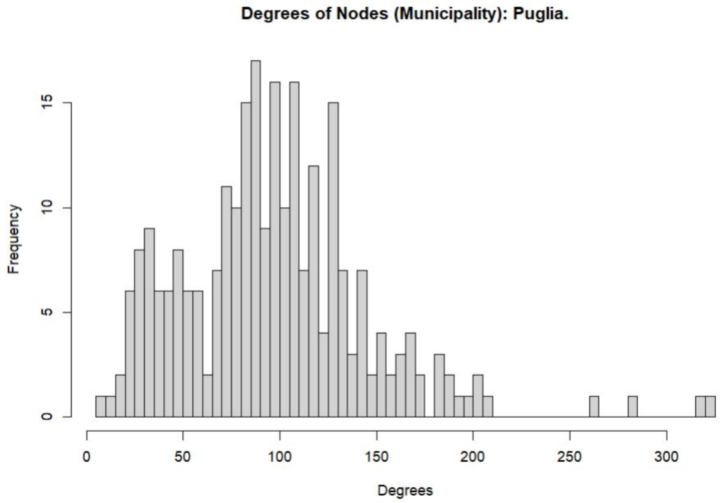
Second application

Puglia Region

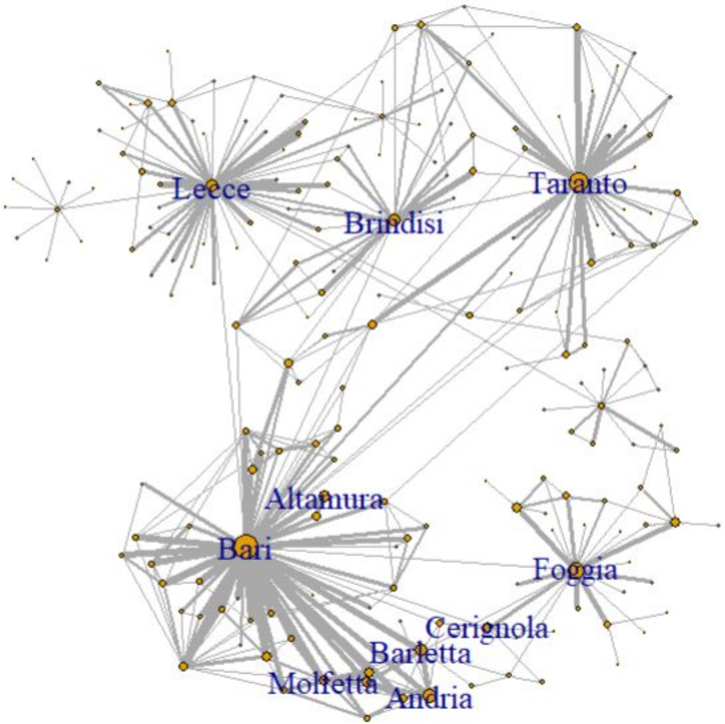
Graph Structure

258 Nodes
12559 Edges

- No single Hub like Rome, but multiples.
- More intermediate nodes.
- More clustered



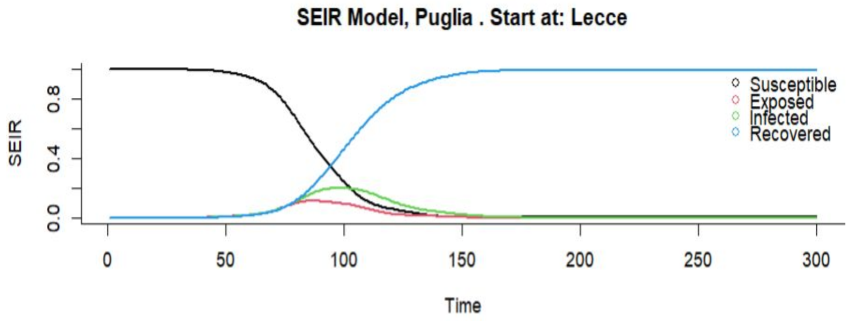
Region of Puglia . Global efficiency: 0.554

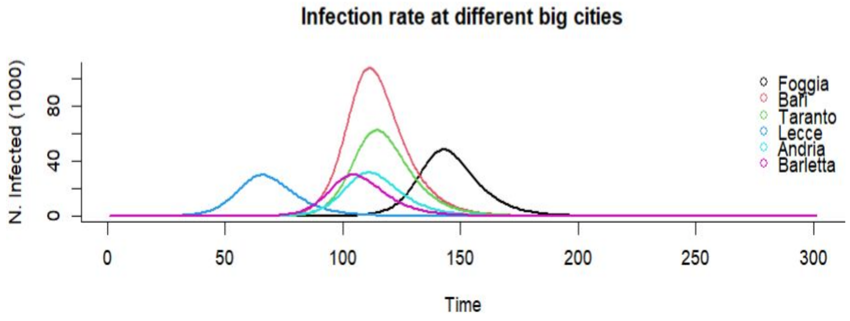


Second application

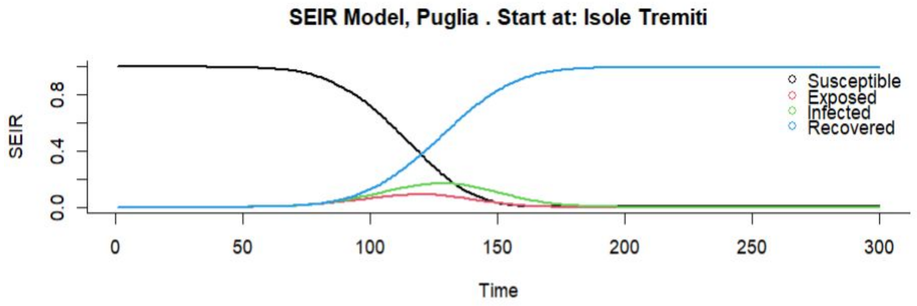
Puglia Region

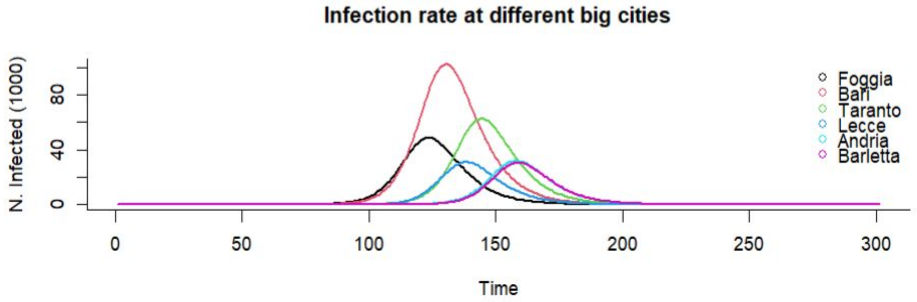
Start at max node degree: Lecce





Start at min node degree: Isole Tremiti



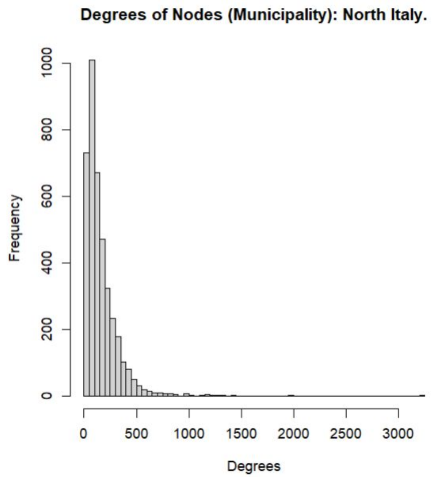


Bigger area

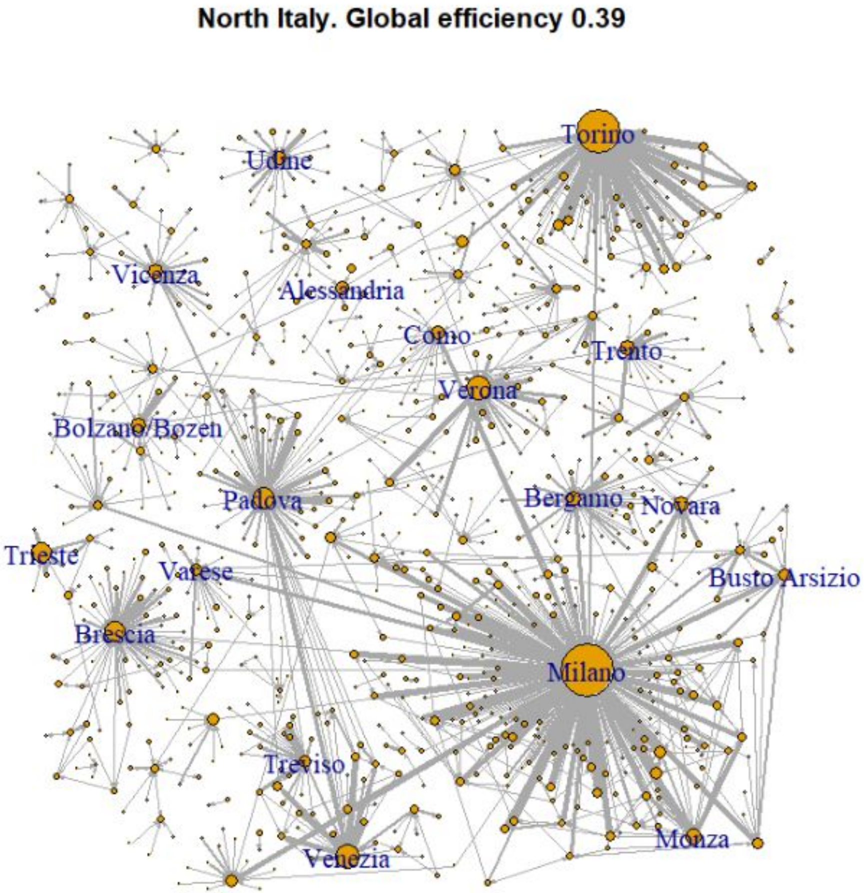
North Italy

Graph Structure

3956 Nodes
318380 Edges



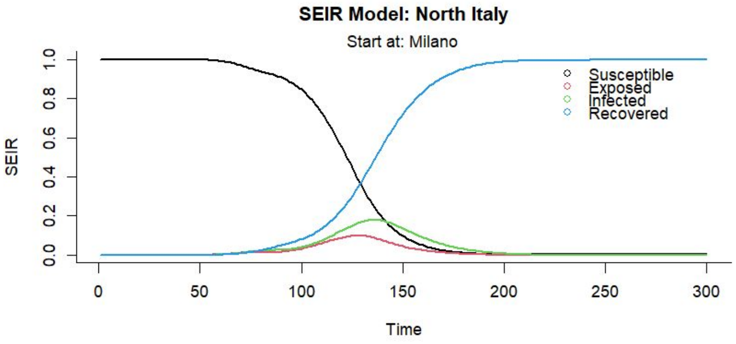
Regions:
Val d'Aosta, Piemonte, Lombardia, Veneto, Trentino, Friuli

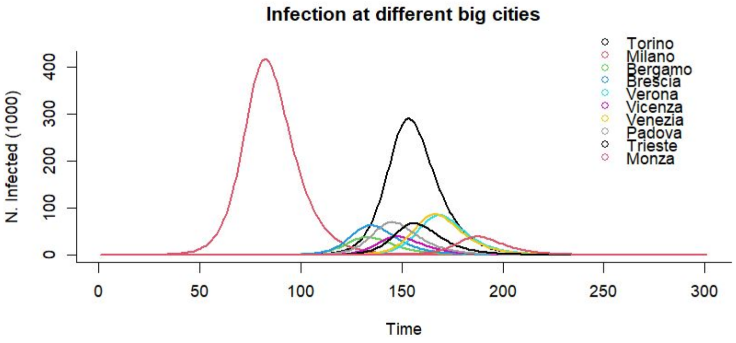


Bigger area

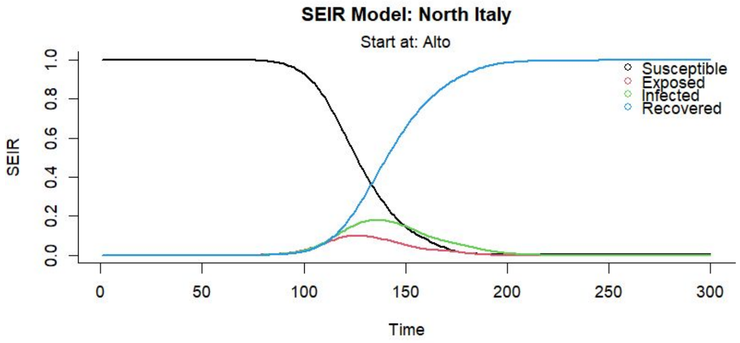
North Italy

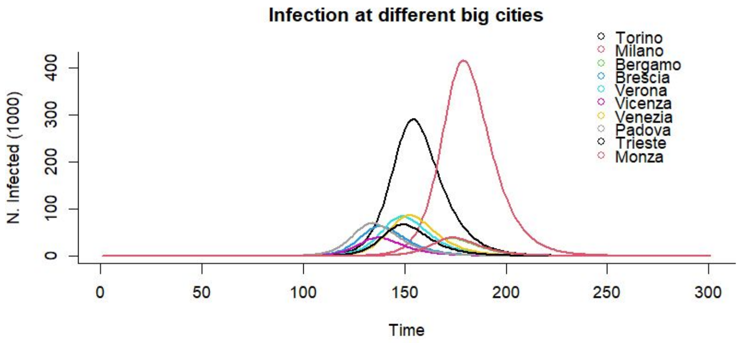
Start at max node degree: Milano





Start at min node degree: Isole Tremiti

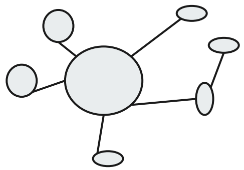




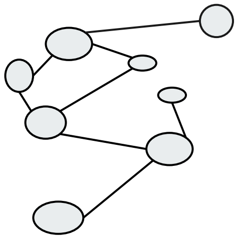
Conclusions

Parameter Testing confirms the Beta, Gamma and Sigma function in the SEIR Model.

Lazio
In a region with only a big Hub and some intermediate hubs, there is diverse spreading of the disease depending on where and when the infection reach the big Hub (Rome).



Puglia
Due to medium hubs of smaller dimension, the disease spreads slowly if starting in a low degree node.



North Italy
In a bigger area and with more diverse important hubs and good connection, there is no difference in the peak infection overall, around 150's day, even when started in lower degree nodes.