ETHlogo

**Lecture with Computer Exercises:**

**Modelling and Simulating Social Systems with MATLAB**

Project Report

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| Stochastic Simulation of Epidemic Outbreak in a large Network |

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# Abstract

# 1 Individual contributions

We initially divided the programming part which was easily feasible since there were three main tasks. Pascal Stücheli was responsible for the epidemic model and its implementation, Christian Jordi familiarized himself in with GEPHI and was responsible for the network generation. Yannick Schmid wrote the transport function. At any time we assisted each other because we had to make sure that the functions worked well together. Further we had to increase the overall performance of our simulation, mainly by making approximation or changing the structure of certain functions. At this point it was important to discuss the possibilities and limitations of the approximations and all of us contributed ideas and concerns. The analysis and interpretation of the results and also the writing of the report was done in a cooperative manner.

# 2 Introduction and Motivations

Last winter, the movie Contagion*[[1]](#footnote-1)* came to the cinemas. In this movie the fates of some characters are shown during the outbreak of a deadly viral infection disease. The first infected person in the movie was a travelling business woman, who carried the virus across two continents such that the disease could spread over the whole world very rapidly. After seeing this movie we asked ourselves how a realistic disease would behave if no remedy or cure could be found. Inspired by this movie, we thought about a large network representing the big cities on the world, which are either connected by air route or other means of public transportation.

Surveillance and simulation of infectious disease are necessary to predict possible outbreaks of epidemics. At the moment there are of course already several epidemic simulation tools. Some of them also contain stochastic effects like example given FluTE*[[2]](#footnote-2)*. Therefore we do not claim to invent something new, but we wanted to see if we would be able to implement an epidemic simulation in a large network with ordinary computational power.

The aim of this study is to follow the time evolution of discrete numbers of people who are either susceptible or infected and the spreading of infected people among a large scale-free network.

We wanted to investigate the following questions:

* How does the number of total infected in a network vary for a given time of simulation?
* How does the time vary among the different simulation until the whole population in the network has been infected?
* What are the variations for certain cities with different degrees? What are the differences for hubs and leaves in the network?
* Are there tendencies in the regional spreading like for example towards hubs?
* Can we gain predictive power from our result? For example, can we predict the time until a city becomes infected depending on the degree of the first infected city? Or depending on the distance?

Additionally we were also interest if we could handle such an amount of data. Actually we spent a lot of time improving the performance of our simulation and exploring approximations. We want to emphasize that we tried to realize our own ideas to create a stochastic epidemic simulation.

# 3 Description of the Model

3.1 The continuous disease model

Our model is basically a simplification of the SIR model proposed by Kermack and McKendrick[[3]](#footnote-3). The major difference is we did not consider the state R that represents removed people which became immune or died after being infected.

To derive the disease model a city with N inhabitants is considered. The inhabitants are either susceptible for the disease or they already carry the disease and can therefore infect susceptible people. In the equations below susceptible people are labelled S and infected people I. At a constant birth rate B healthy (and therefore susceptible) children are born while dyeing is a first order process with a death rate d. The amount of newly infected people per time unit depends on the availability of susceptible people and their meetings with infected people. The contact rate β is the rate at which susceptible people become infected after a meeting with an infected person.

For further simplification we assume that the number of newborn balances the number of dyeing people per time unit in order to neglect the birth and death in the city.

3.2 The stochastic disease model

Since the goal of this study is to follow discrete numbers of infected people and to integrate noise, we obviously ended up with a stochastic model. For a proper stochastic simulation spatial homogeneity is assumed. This means the population in a city is well mixed and there are no spatial accumulations of either susceptible or infected people.

In the SI model there is only one transition possible.

Where s denotes a susceptible person j or k and i denotes an infected person j or k. The propensity a is the probability per time unit for a successful infection. The propensity depends on the meeting events between susceptible and infected people as well as on the rate of successful infections after meeting. The most accurate way in calculating dI for only discrete dI and dt would be to calculate in each time step for each infected the number of meetings and then for each meeting the probability whether it leads to an infection or not. With a uniformly distributed random variable then it could be decided whether or not an infection happened through this event. The formula for calculating the probability of a meeting to result in an infection looks as follows (where N is the population in a city).

Each outcome of this decision influences the following decisions. This is an extremely slow calculation for a high population and would not be possible to be calculated. Instead approximations could be used which work with normally, binomial or hyper geometrically distributed random variables. The binomial and hyper geometric distribution can be explained with a series of flipping a coin or drawing balls from which several have the desired colour. In the binomial distribution the different events are independent from the previous ones and in the hyper geometric distribution they are not. The fact that the normal distribution is calculated much faster than the binomial distribution, which is much faster calculated than the hyper geometric distribution, can be used to approximate slow functions with faster ones.

3.3 The network

Instead of modelling an existing city network an artificial scale free network was created. A scale free network was chosen, because its capability to form hubs, which we compared with metropoles that are highly interconnected and surrounded by more isolated cities of smaller size. Hence the network would at least be a sufficient model for the air traffic between the cities, as stated by M. Beliant et al.

The scale free network was generated using an implementation of the Barabási-Albert algorithm, which we learned in an exercise of Prof. D. Iber’s lecture on mathematical modelling. []

The idea of this algorithm is to create a network around a couple of seed nodes by adding new ones step by step. Thereby the probability to form an edge to target existing node j is given by:

In this way nodes with a high degree kj are more likely to be selected and a scale free network is created. [mamo]

Initially, a loop free version of the algorithm was tested but the created network did not look interconnected enough. Therefore, a loop forming version was used in the simulation (Fig. 1).

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| 100unlooped.png100loop.png |
| **Fig. 1** Two examples of 100 node networks generated by a Barabási-Albert Model. A: loop free version. B: loop forming version. Gephi 0.81 beta was used for graph visualization. |

Erklärung der Formel und Kennzahlen des NetzwerksIt is well known that the population of cities can be described by a power law (Zipf’s Law). Prof. Guido Spars et al [] determined the Zipf parameters of german cities with high accuracy. We assigned a population to each node according to its rank in the network and the value predicted by Zipf’s Law.

Our final network consisted out 10 000 cities and had a population of 93 Millions.

3.4 The transport

People from a city x are able to travel to city y if the nodes x and y are connected by an edge. However, we want the total population of a city to be constant. Therefore there the same number of people travel from city x to city y as vice versa while the composition of the travellers (susceptible or infected) can vary. If a fixed number of total travellers per simulation day are assumed – like for example seats in airplanes – the portion of infected travellers is hyper geometrically distributed. Txy corresponds to the total travellers on the edge between city x and city y and is equivalent to the number of drawings without laying back out of a population with Sx,y + Ix,y people and Ix,y as the number of infected people[[4]](#footnote-4).

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| **Fig. 2** Sketch of two cities x and y where S and I correspond to the number of susceptible or infected people. Edges are indicated as arrows. T denotes the total number of travellers along an edge and is the same in both directions of the edge. |

The number of total travellers along an edge should obviously not exceed the population of either city connected by the specific edge. It must also be ensured that cities with multiple edges do not have higher traveller fluxes than populations. Also a factor depending on the degrees k of the connected cities compared to the average degree in the network was included to contribute more transports between cities with many connections – intuitively that is like cities with more airports and stations have more transport capacity. Finally we included a factor to reduce the transport of infected people assuming that people who feel sick travel less.

Actually, it would have been nicer if the degree factor would be divided by two. However, since the transport rate is further reduced[[5]](#footnote-5), this flaw is corrected.

# 4 Implementation

*4.1 Network generation*

The function *networkepid2loops* was used to generated he scale free network. After the definition of the seed nodes and a seed edge list, a network of 10‘000 nodes was created, by introducing new nodes one after another. Each new node was enabled to form two edges to existing nodes. Hence loops could be formed. The targeted loops were chosen randomly and their pj was calculated. Thereafter, a random number between zero and one was generated and compared with pj. If the random number was smaller the edge was formed, otherwise a new target was chosen.

The edge list was saved as a nx2 matrix. Every row contains the two nodes connected by the edge. To import the matrix into the graph visualization tool Gephi, it had to be converted using the function *cell2csv*[[6]](#footnote-6)*.*

The nodes were stored in *cities.txt*, a mx3 matrix, where every row stands for a city in the network. The degrees of the nodes were stored in the first column of this matrix and then passed to the function *city\_size*

*city\_size* ranked the cities according to their degree and used Zipf’s law to assign a population size to each city. Thereby a variation of 1% was added to the predicted size to reduce the impact of the sequence on cities that have the same degree.

The whole process of generating the network was collected in the function *initialization.*

4.2 Simulation of the infection

As the name indicates, the function Simulate\_Infection computes the number of infections per city and per time step. Therefore the number of meetings between infected and healthy people is calculated according to an arbitrarily chosen mean and standard deviation of daily meetings with other people. Further, a Gaussian distributed error was included. As long as the number of infected people in a city is below a certain threshold the infection is simulated in a stochastic manner. The number of meetings which result in an infection is a hyper geometrically distributed number, as mentioned in section 3.1. Because MATLAB is very slow in drawing hyper geometrically distributed random numbers, a binomial distributed random number was used as an approximation. The drawback of the binomial distribution in this situation is that a person can be infected more than one time. However, by using small time steps, the probability to infect two times the same person becomes rather low. As soon as the number of infected people exceeds the threshold, the simulation works in a deterministic manner and is equal to the expected value.

4.3 Transport

According to section 3.4 the total number of travellers along every edge is calculated before the actual simulation. Then for every city and time step the number of infected travellers is simulated. The transport function uses the edges matrix and in order to avoid constraints from calculating always in the same order along the edges matrix, the rows of the matrix are shuffled in every time step. Again, we have hyper geometrical distribution for the number of infected travellers. So, the mean and the standard deviation of the hyper geometrical distribution are computed. This is done with the MATLAB function hygestat. A Gaussian distributed error is included to introduce noise in the transport. Finally, the number of infected people in the cities is updated due the change through transport.

4.4 Experiments

Three simulations were performed to characterize the epidemic outbreak in the scale-free network. To start each simulation, the first infected person was set randomly into a city – the seed. The parameters like infection probability and mean of daily meetings were chosen empirically and tested in smaller networks. Implementation of real parameter values would be interesting for further experiments and is discussed in the section 6.

In the first experiment 80 days were simulated and the number of cities with at least ten percent infected citizens was taken as output. Additionally, the ratio of total infected people over the whole network population was computed. The aim was to compare the time courses of the epidemic in multiple simulations and to measure the temporal variations.

The second experiment was performed to test the hypothesis that the epidemic spreads faster when started big cities with high degrees than in small cities. Since, we assumed a high influence of the nodes connected to the seed, the sum of the degrees of the direct neighbours was considered too. In every simulation, the time until at least twenty cities had at least one infected person was measured.

In the third experiment, in addition to the seed, a random target city was chosen. In order to find the number of edges in the shortest path connecting the seed with the target city, which is the distance, we used the MATLAB Graph theory tool box. The function graphshortestpath solves the shortest path problem. Then, the1 time until at least one infected person appeared in the target city was measured.

# 5 Simulation Results and Discussion

5.1 Simulating 80 days

The aim of this experiment was to follow the time course of the whole epidemic over a given time of 80 days and to see the impact of the stochastic effect among the different simulations. We were interested, on one hand in the regional progression of the disease, which we tried to show with the number of cities with at least ten percent infected citizens. On the other hand, in the temporal variations of the number of global infected people. For both, the ratio of global infected people and the number of cities with at least ten percent infected people the mean was calculated (Fig. 3 and Fig. 4 respectively). To show variations in time, either for a certain ratio or a number of cities with at least ten percent infection, the temporal expectation range was computed (Fig. 3 and Fig. 4 respectively). Further, the regional and the quantitative progress of the disease were compared (Fig. 5). To gain a quantitative value for the stochastic, the times until 1000 people in the network became infected were used to compute an expectation range, .

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| **Fig. 3** The mean of the time course of the disease for 80 days is shown as black line by plotting the average ratio of the total number of infected people vs. the time. Further, the expectation range of the time at which a certain ratio is reached, is shown as dashed blue lines. |

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| **Fig. 4** This figure provides the mean, black line, and the expectation range, dashed blue lines, of the time, which is needed to infect at least ten percent of the citizens of a certain number of cities. |

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| **Fig. 5** Simulations of the epidemic for 80 days. The mean of the number of cities with at least ten percent infected citizens after simulating 80 days is shown by the black line. In addition, the mean of the ratio of the total number of infected people over the total network population is represented by the blue line. The means were calculated from the data of 147 simulations. |

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| **Fig. 6** The time until at least 20 cities having at least 1 infected person vs. the sum of the degree of the seed and its first generation neighbors is shown in blue for 635 simulations. The black line represents the curve fit performed with MATLAB, assuming a power law dependency. Due the lack of measurement points between degrees of 400 to 900, the statistical power of the fit might be limited. Nevertheless, a certain tendency is observable. |

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| **Fig. 7** This figure provides the correlation of the distance and the time needed for the disease to reach the random target city. The distance is the shortest path from the seed (random city where the first infected person was set) to a random target city and corresponds exactly to the number of edges, since we used un-weighted edges in our network. The error bars and the mean are shown in blue. The black line is the result of the linear regression analysis of the time measurements city (). |

Expectancy range until infection of 1000 people = 18.2029 +/- 5

# 6 Summary and Outlook

Outlook

In our experiment a completely fictional network was used, so obviously, the next step would be to implement real data and an existing network. For the network it would make sense to take a continent or even the whole world as long as only the important cities are considered, such that the performance does not suffer too much. It would be interesting to weight the edges according to geographic distances and to include real transportation data. Furthermore, the integration of either a healing rate or an immunisation would extend the simulation and make it more realistic.

We assume that infection simulation will gain further importance for the understanding of the spreading in network. Either one can think of diseases like H1N1 or sexually transmitted diseases like HIV. But also the spreading of information or malware in computer networks could be simulated with programs, such as ours.

# References

1. Contagion. Dir. Steven Soderbergh. Perf. Matt Damon, Kate Winslet, Jude Law. Warner Bros. Pictures, 2011. [↑](#footnote-ref-1)
2. Chao DL, Halloran ME, Obenchain VJ, Longini IM Jr “FluTE, a Publicly Available Stochastic Influenza Epidemic Simulation Model.” PLoS Comput Biol **6**(1), 2010. [↑](#footnote-ref-2)
3. Kermack, WO and McKendrick, AG, "A Contribution to the Mathematical Theory of Epidemics." Proc. Roy. Soc. Lond. A **115**, 700-721, 1927. [↑](#footnote-ref-3)
4. The colon of Sx,y and Ix,y means „or“. [↑](#footnote-ref-4)
5. The factor is not shown in the equation above, but was included in the simulation (see the FINAL\_SIMULATION.m files). [↑](#footnote-ref-5)
6. Provided on the lecture site [↑](#footnote-ref-6)