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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**IMPORTANT**

**You MUST include the ETH declaration of originality here; it is available for download on the course website or at**

**http://www.ethz.ch/faculty/exams/plagiarism/index\_EN;**

**It can be printed as pdf and should be filled out in handwriting.**

**Agreement for free-download**

We hereby agree to make our source code of this project freely available for download from the web pages of the SOMS chair. Furthermore, we assure that all source code is written by ourselves and is not violating any copyright restrictions.

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# Abstract

# 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.

# Introduction and Motivations

Surveillance and simulation of infectious disease are necessary to predict possible outbreaks of epidemics. The aim of this study is to follow the time evolution of discrete numbers of persons who are either susceptible or infected.

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?
* What happens if we implement a healing rate?

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.

# Description of the Model

The continuous disease model

Our model is basically a simplification of the SIR model proposed by Kermack and McKendrick[[1]](#footnote-1). 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 persons. In the equations below susceptible persons are labelled S and infected persons 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 persons per time unit depends on the availability of susceptible persons and their meetings with infected persons. The contact rate β is the rate at which susceptible persons 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.

The stochastic disease model

Since the goal of this study is to follow discrete numbers of infected persons 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 persons.

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 meetings between susceptible and infected persons as well as on the rate of successful infections after meetings.

# Implementation

# Simulation Results and Discussion

# Summary and Outlook

# References

1. [↑](#footnote-ref-1)