

## Spatial Simulation Model for Infectious Viral Diseases with Focus on SARS and the Common Flu

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### Abstract

*This paper will focus on simulating the infectious process on a computer. To simulate how an infectious viral disease spreads not only shows how people get sick, it can also be a powerful tool in disease prevention. You can test actions such as to isolate people that get sick and analyze if the disease spread can be circumscribed or stopped. Special focus will be given to SARS and the Common Flu.*

### 1. Introduction

Simulations that show how diseases spread can be powerful tools in disease prevention. Most available simulations use abstract representations relying on well defined mathematical models. Commonly used parameters are infection rate, probability of getting ill, attack rate and duration of an infection. Age, family settings, school and work situation or geographic information are not considered in detail.

Furthermore, what happens if people stay home instead of going to school or work when they are sick? Can the disease spread be limited? What preventive methods such as vaccination are available and what is the effect of using these methods?

More questions arise. Where do people infect each other? How do family settings, school and work situation or geographical location of an individual change the likelihood of getting sick? How can infections be prevented? How can a disease spread be circumscribed or stopped?

This paper shows our approach in the design of an application that simulates the infectious process of a common viral disease. We allow not only input of commonly used parameter as described above but also allow to set age, family settings, school or work situation and spatial information. Our special focus will lie on the flu.

### 2. Related Work

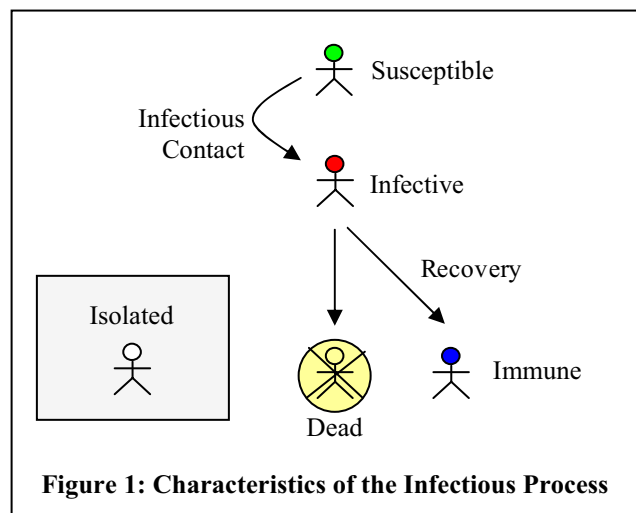
The field of Epidemiology is well established and sources of information are widely available.

#### 2.1. Characteristics of the Infectious Process

We now formulate the basic characteristics of a single disease as described in figure 1. We have five types of individuals:

- *Susceptible* – Neither infected nor immune.
- *Infective* – Infected with the disease.
- *Isolated* – Individual with no contact to others.
- *Immune* – Immune against the disease.
- *Dead* – Died because of the disease.

A Susceptible gets an Infective by an infectious



contact. He becomes a Removal if he either gets Immune or Dead. Isolated individuals have no contact to others, thus cannot get infected or cannot infect other individuals. By the model above only a single disease is considered. Furthermore individuals only infect each

other by contact. Supercarriers or agents for disease transmission are not considered either.

Parameters that have to be taken into consideration are the following:

- *Attack distance* – Max distance where an individual can infect somebody else.
- *Attacks per Time* – How many attacks does an individual execute per day. E.g. how many times does somebody cough and spread particles with the disease.
- *Attack rate* – Defines how likely it is for a susceptible to become infective by contact with an infective.
- *Infective period* – Duration for an individual to have the disease.
- *Recovery period* – Duration for an individual to recover.
- *Death rate* – Likelihood to die from the disease.

Furthermore we can put individuals into different groups based on their social function, age and family. Individuals that go to school have many more contacts with other people than individuals that stay home most of the time. The job that you are working in or the size of your family has a great impact on the probability of infection.

Geographically crowded areas such as big towns where many contacts between individuals are possible or less crowded areas might play an important in disease spread. So to model a disease we have to put the following items on our list to be taken into consideration:

- Age of an individual
- Number and type of people an individual is living with.
- School or work situation.
- Spatial information.

Furthermore, another area of interest is disease prevention. Actions that can be taken to limit or stop the spread of a disease:

- Vaccination
- Isolation of an individual. For example staying at home while infectious.
- Quarantine

## 2.2. Survey of Available Tools

Commonly available tools to simulate disease spread are largely based on mathematical formulas. Computer programs that model diseases related to real life situations are available rarely. The next following paragraphs give an overview of some selected tools for simulation of disease spread.

[11] describes different mathematical models to be used for simulation of infectious disease epidemics. Computer programs are given for the Fortran language.

“Epi Info” [15] by CDC [16] is a database and statistics software. It contains a series of programs for use by public health professionals in conducting outbreak investigations, managing databases for public health surveillance and other tasks, and general database and statistics applications. It allows different types of data to be inputted and analyzed, however it is not designed to simulate diseases.

“STELLA” [17] is a computer simulation based model building tool. It is designed as learning environment and for research and science. It can also be used for other fields than Epidemiology. Models have been created for the flu that are rather simplified and don’t go into details [18].

Another tool available is “SIMEX” [19] which enables a user to create micro population models. “SIMEX” is designed as a C++ library and somebody has to do programming in order to use the library package. Some rudimentary models have been created simulating the flu.

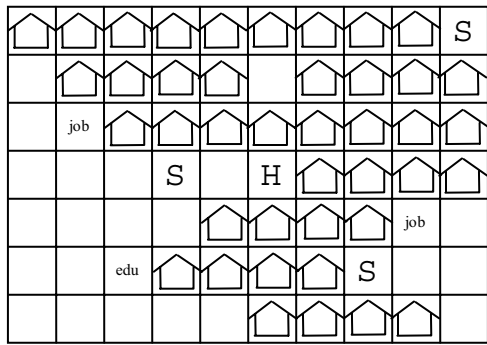
“NetLogo” [20] is a interesting tool that has the ability to model in 2D. Many models exist for different fields such as Biology, Chemistry, Mathematics and Social Science. “NetLogo” also allows to build own models. One model is available that simulates virus infection within a population.

The next section shows our approach in the design of an application that simulates diseases with special focus on the flu.

## 3. Simulation

For infectious diseases, mathematical models to calculate disease spread have a fundamental descriptive problem. However, mathematical models do not exactly simulate real life situations. A mathematical model is by its nature a simplification. It is abstract and ignores certain aspects of disease spread. It does not consider the environment in which people live. Spatial data such as the location of an individual at a certain time, buildings or locations of contagious contacts are left out.

Our approach in simulating a disease is embedded in an environment in which people can move around freely in 2D. The simulation uses stochastic interactions of people to determine disease spread. Consider figure 2. The environment can be arranged as grid with houses, stores, schools, work places and hospitals. The grid lines are designated as streets where individuals can move around from location to location.



- edu Educational Institute
- job Work Place
- S Store
- H Hospital
- Home

Figure 2: 2D Environment

Individual and disease(s) are described in figure 3. An individual has parameters such as age, gender, health and a current location. Furthermore an individual has a home and might have a work place or a school where he is going to. He does shopping and visits the hospital if he is ill.

A disease is modeled as virus and antibody pair. An individual can get infected by a disease using stochastic interaction. An individual gets a virus and builds up antibodies. The attack rate and number of contacts with a virus define the likelihood for an individual of getting

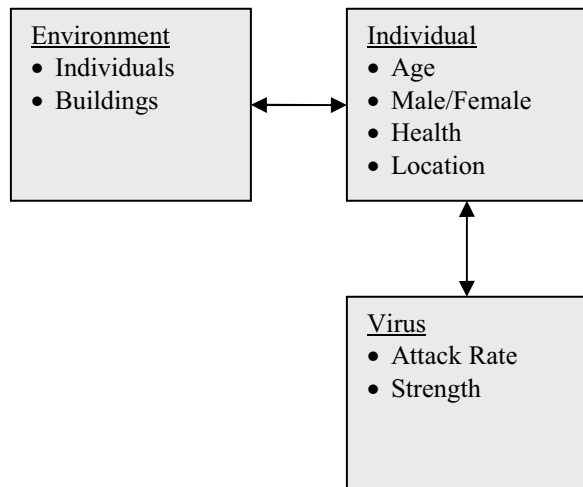


Figure 3: Environment, Individual and Virus

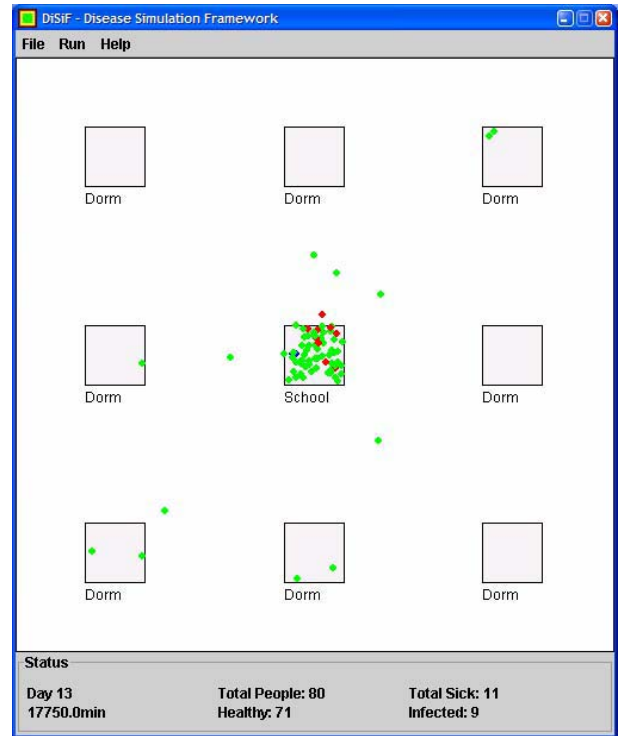


Figure 4: DiSiF Screenshot

infected.

Parameters play a role in deciding if somebody gets infected. How many people does somebody live with? Where does she go to school or work? How often does she stay at home? How many contacts does she have with her friends? How many times does she go out?

We built a simulation using the Java programming language to find out more about disease spread. The software is based on the model described in this section. We use a 2D environment where individuals can move around freely. The environment consists of buildings such as houses, schools, work places and hospitals. Individuals can have different viruses. Individuals can get infected, can recover, can die and can infect other individuals.

Figure 5 shows the parameters used for the stochastic, discrete simulation. *Infectious period*, *recovery period* and *body remaining time* can be inputted. *Body remaining period* donates the time where the virus still can infect other people. *Attack distance* donates the radius in which the virus can spread to other people. *Attacks per day* gives the number of time somebody is spreading out the virus, e.g. coughing. *Attack rate* donates the strength of an attack. Attack rate is the likelihood of getting infected when in contact with a virus.

| Virus Parameters          |      |
|---------------------------|------|
| Virus Name                | SARS |
| Infectious Period [d]     | 6    |
| Recovery Period [d]       | 7    |
| Body Remaining Period [d] | 120  |
| Attack Distance [m]       | 1.5  |
| Attack Rate [0.0, 1.0]    | 0.9  |
| Attacks Per Day           | 48   |
| Death Rate [0.0, 1.0]     | 0.05 |

Figure 5: Parameters

Information about the software framework is available upon request<sup>1</sup>. The next section shows the results obtained by the simulation.

#### 4. Results

Figure 4 shows a screenshot of the simulation implemented. The simulation functions in 2D, it has buildings and individuals that can move around inside. One disease can be simulated at a time.

Visible in figure 4 are eight buildings designated as dorms and a school in the middle. Individuals are represented as dots. The dots have three different colors based on their status of infection:

- Green ●: Never infected
- Red ●: Infected
- Blue ●: Previously infected and recovered

The software that runs the simulation executes the environment in discrete 60 second intervals. The individuals are executing simple tasks. They get up in the morning, go to school, move around in the school, go home in the evening, move around at home and go to sleep. Parameters can be set, so people stay at home when they are sick instead of going to school.

The created environment is simple, however it can be improved. More buildings can be created such as work places, hospitals and stores. The individuals can be changed to do more complex tasks.

Different tests have been done simulating the common flu and the SARS virus. Other viruses can be created and added to the simulation.

Figure 6 shows infections over time obtained by running the simulation, starting with only one individual infected by the flu. About 50% of all the individuals got infected in average.

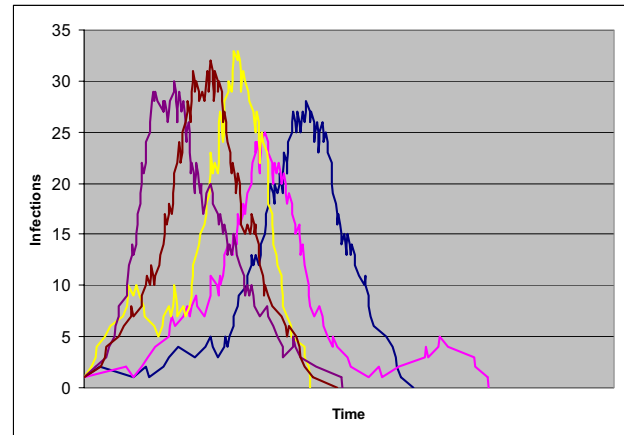


Figure 6: Common Flu

For the SARS virus various runs have been done. However, the infectious process and other parameters are not well known. Preliminary results show that in all the cases the infection spread to other individuals and infected about 90-95% of the people.

#### 5. Evaluation

The Disease Simulation Framework, in short DiSiF, has been implemented in Java. Thus it allows running the simulation on all major Computer Systems. The software is also implemented as Applet, therefore can be run from a web browser.

The application is implemented to enable simulation of diseases in 2D. The created environment is rather simple. The individuals execute easy tasks such as moving or sleeping. The viruses added are the Common Flu and SARS.

The simulation is designed to evaluate disease spread in areas such as small towns, single buildings or universities.

Results from various runs are not consistent with each other. Comparison to real outbreaks has not been done yet. Considering the facts, in a very well modeled environment, infectious disease spread prediction might be rather hard. Weather forecast even with the most sophisticated computer hardware is not perfect and can be wrong. Disease spread forecast seems to be even harder. It is not possible to know exactly what each individual is doing at a certain point of time. As for weather forecast, "*Does the Flap of a Butterfly's Wings in Brazil set off a Tornado in Texas?*" This is called the butterfly effect, which in turn can also apply for epidemics. Can disease spread ever be predicted accurately?

In order to improve the simulation, more complex environments have to be created. The individuals need to execute more realistic tasks than just going to school,

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going home and sleeping. So far only random tests have been done to evaluate the performance of the software.

## 6. Contributions and Future Directions

Preliminary results show that the software is working. It can be shown graphically what people are doing. Actions can be taken in order to prevent infection. However, the simulation is rather limited and cannot be used to determine disease spread.

First, the environment needs to be designed more complex. Streets, work places, stores and hospitals have to be added. The individuals need to be made aware of that and have to be changed to the new environment. Further it should be considered to implement the Disease Simulation Framework in 3D. Buildings have to be designed that have more than only one floor. Adding animals would allow simulating other disease such as Malaria or the Mad Cow Disease.

One interesting environment to be considered to be implemented could be a single island with people living on it. A closed environment is much simpler to implement than a whole continent because the ports of entries are well defined and allow control of people entering or leaving.

Other diseases of interest are HIV/AIDS. An abstract data type for viruses has been designed and allows adding any type of disease to the simulation.

Conclusive, still major changes and further test have to be done with the software.

## 7. Acknowledgements

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