



Eidgenössische Technische Hochschule Zürich
Swiss Federal Institute of Technology Zurich

Lecture with Computer Exercises:
Modelling and Simulating Social Systems with MATLAB

Project Report

**Simulation of Information Spreading
in a Facebook Network**

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Zurich
December 2013

Agreement for free-download

We hereby agree to make our source code for 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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1 Abstract

2 Individual contributions

3 Introduction and Motivations

3.1 Introduction and fundamental questions

Social Networks like facebook and twitter are growing very fast. Most young people like students do have an account in one ore more of them. Many articles, pictures and videos on the internet have a direct "share" button. It is a very interesting question how information spreads in such networks. First, the internet may have become the fastest and sometimes most important source of "news" and information beside the "traditional" media and second, companies seem to be very interested in "informing" the right people with their commercials.

The simplest way to describe the information spreading uses similarities to epidemiology, which means that the flow of information of one person to another is looked at as an "infection". In this work, we implemented a simple model in a homogeneous way with a set of differential equations and their numeric solutions as well as an agent-based, heterogeneous model, using a real facebook network.

The fundamental questions of this work are:

- Are there relevant differences in the time evolution of the homogeneous and the agent-based network?
- Are there individuals which are more important to the spreading of information? Can they be recognized in the sense of position and connectivity in the network?

4 Description of the Model

The process of information spreading has many similarities with epidemiology, so the well known SIR-model was adapted[1]. The "susceptibles", are not aware of the information and are called "ignorants" within this work. "Infected" individuals know about the information and are willing to share it with other people, in other words they spread it and are therefore called "spreaders". The adaptation of the epidemiological term "recovered" is not that straightforward because it is not entirely clear, what that means in this context but they can be looked at persons that are aware of the information but don't want to tell it others. They are called "stiflers".

In the SIR-model as well as in the Agent-based model, the following set of “reaction equations” was used (I: Ignorant, S: Spreader, R: Stifler):

$$\begin{cases} I + S \xrightarrow{\lambda} 2S & (1) \\ S + R \xrightarrow{\alpha} 2R & (2) \\ S + S \xrightarrow{\alpha} S + R & (3) \end{cases}$$

The main difference to the standard SIR-model is that spreaders don’t become stiflers spontaneously but this change is only induced by meeting an other spreader or stifler. Also it can be shown that for $\frac{\lambda}{\alpha} > 0$, i.e. for any positive rate, the number of stiflers is non-zero for large times. That means that there is no epidemic threshold as in the standard SIR-model.

4.1 Homogeneous SIR model

In the mathematical treatment of the model in a homogeneous system, the set of differential equations is expressed in terms of the densities $i(t) = I(t)/N$, $s(t) = S(t)/N$ and $r(t) = R(t)/N$.

$$\begin{cases} \frac{di(t)}{dt} = -\lambda \cdot s(t)i(t) & (4) \\ \frac{ds(t)}{dt} = \lambda \cdot s(t)i(t) - \alpha \cdot s(t)[s(t) + r(t)] & (5) \\ \frac{dr(t)}{dt} = \alpha \cdot s(t)[s(t) + r(t)] & (6) \end{cases}$$

4.2 Agent-based model

In the inhomogeneous, agent-based model, the individuals are connected in a certain manner (facebook friends in this particular work). Only connected agents are able to meet. If a meeting occurs, transitions are induced at a certain probability depending on the relation between the agents (details are discussed later). Additional to the different degree of the agents, they also have a different activity, i.e. different probability to meet somebody. In total, the number of meetings in a certain time is proportional to the product of the degree (number of friends) and the activity. This has to be verified in the implementation of the model.

To convert the reaction equations into an agent-based model, time was discretized and in each time step a series of two steps is performed shown in Figure 1. First, the

Flow Chart of overall steps

Figure 1: Steps performed in each timestep.

agents randomly meet another agent they know or nobody. Only two-agent meetings are possible. In the second step, the status of the agents change corresponding to the situation. There are six possible combinations of ignorants, spreaders and stiflers. Three of them correspond to the “reactions” 1-3, the other ones (I+I, I+R and R+R) have no other influence than “occupying” the agents. The probability λ was chosen to be dependent on the number of common friends. For simplicity, α was a constant.

5 Implementation

5.1 How did we get the network

To get the data for our simulation, we used the so-called Facebook Graph API. What does Graph API mean? A Facebook Grpah API is a programming tool designed to support better access to conventions on the Facebook social media platform.¹

Unfortunately, there is no implementation for Matlab, so we programmed the data-fechting in python.

5.2 Coding

For the coding in python we used the facebook sdk².

5.2.1 Get access

First, one needs to get access to the social graph. Therefore, you need to enter an access token³.

```
1 token = raw_input('Enter your Access Token: ')
2 anonym = input('Do you want to anonymize your Data? Yes (1) or No (0)? ')
3 graph = facebook.GraphAPI(token)
```

¹<http://www.techopedia.com/definition/28984/facebook-graph-api>

²<https://github.com/pythonforfacebook/facebook-sdk>

³<https://developers.facebook.com/docs/facebook-login/access-tokens/>

5.2.2 Get graph

Having entered a valid token, we can now access all information this token provide us. For simplicity, we'll only discuss the non-anonymized case in details. [For more details on the anonymization, look at subsection anonymization]

```
1 profile = graph.get_object("me")
2 friends = graph.get_connections("me", "friends")
```

In our case, we're interested in data about our own profile, as well as all available information we get from our friends. The object friends is nothing else but an array that contains all id's of our friends. For each id there is another array, named data, that contains all (available) information about this specific friend.

```
1 friend_list = [friend['id'] for friend in friends['data']]
```

With this simple for-loop, one can now get a list of all friends. Since we're not primarily interested in our friends, but the connection in between them, we have to access at least the mutualfriends.

```
1 mutualfriends = graph.get_connections(tfriend, "mutualfriends")
```

The object mutualfriends provides us a list with all mutualfriends of "me" and friend "tfriend" (which is nothing else but one of the id's we have in the saved in "friend_list")

Repeat this procedure for all friends, and we'll get exactly what we're looking for - a graph of all connection between our friends.

5.2.3 Get activity

How did we define the parameter activity? We simply determine for each friend how many posts he makes on average per day. This gives us an indicator, how active a certain person is on facebook.

Again, this is done fairly quickly (using graph api).

```
1 statuses = graph.get_connections(tfriend, "statuses", fields="updated_time",
    limit="100")
```

This object provides us, all information we need (a list of all posts incl. a time stamp when it's been posted) to calculate the above mentioned quotient.

5.2.4 Get coordinates

urs will tell you!

5.3 Anonymization

The anonymization is acutally only a pseudo-anonymization. First all id's get arranged in order of size. Secondly, we create a list from 1 to n (number of friends). We then define a bijection between the two sets, such that the i-th element of the first set, maps to the i-th element of the second set.

Eventhough, this is not really anonymizing our data. It is more then sufficient for our purpose.

5.4 Homogeneous SIR-model

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5.5 Agent-based model

5.5.1 Initial condition

At the beginning of each simulation, all agents are ignorant but one, which is a spreader. In the biggest performed simulation, every one of the 384 nodes was the first spreader 10 times.

5.5.2 Determine the meetings

(See `talkstep.m` for details.)

In order to determine who meets who, the program goes through the vector of agents (1:N) randomly . With a probability corresponding to the activity of that agent, he may meet somebody . The person he meets is determined randomly and must be one he knows and one which is not already meeting another agent in this time step. Agents with more friends also have more meetings(If you don't take the activity into account).

5.5.3 Status changes in meetings

After the meetings are determined, the status of each agent has to change according to the model. In order to be able to determine who infected whom, and how many where infected, a list `infecpath` was created in each round containing the directed edges of infections.

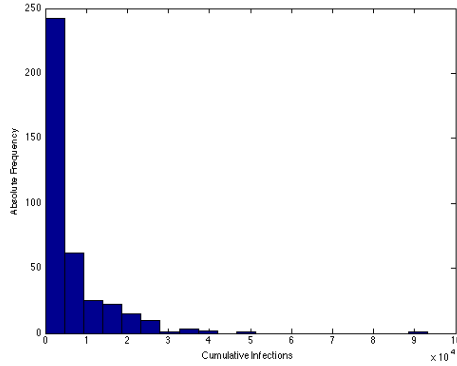


Figure 2: sdlhfa

5.5.4 cumulative infections

With a given `infecpath`, with the directed edges of infections, it is obviously easy to obtain the number of direct infections of every node and also relatively easy to get the number of "cumulative infections", which is the whole subtree of infections of each node. The ladder was obtained in a recursive manner in the following way:

```

1  L=length(infecpath(:,1));
2  for i=L:-1:1
3
4      p1=infecpath(i,1);
5      p2=infecpath(i,2);
6      cum_infections(p1)=1+cum_infections(p1)+cum_infections(p2);
7  end

```

6 Simulation Results and Discussion

6.1 Influentials

6.1.1 Existance and importance of influentials

To analyse the existence of influentials, we first need to define its meaning. We will use the definition given in Paper Cascade[?], which simply says that a person's importance is determined by the number of its cumulative infection (called casced).

Figure 2 is a simple histogram, that shows that the vast majority of people has only a small cumulative infection value. Whereas we see in Figure ?? (which again plots the cumulative infection, sorted from small to large), that there are only a few

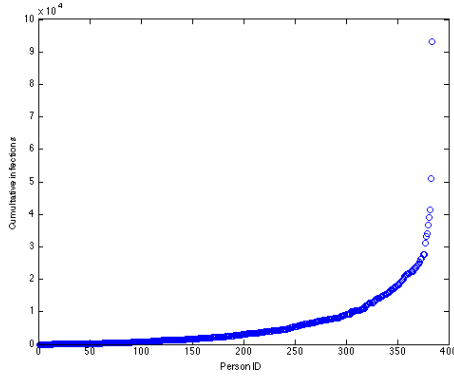


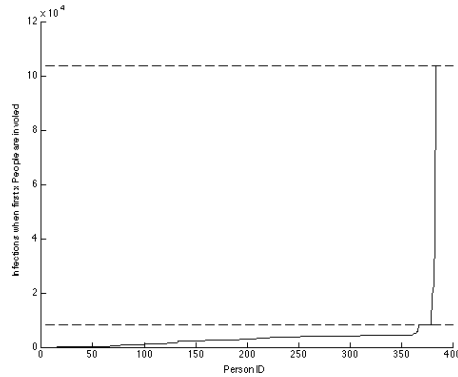
Figure 3: sdlhfa

with a very large cumulative infection value.

We can even go one step further and try to estimate the importance of those influentials on all infections that occur in total. In order to do so, we sort the people after their importance (defined as above). We then calculate the amount of infections conditioned that only the m least important person have been involved in the spreading process ($1 \leq m \leq 384$).

For instance, $m = 384$ implies all infections that occurred, when only the last (therefore most important) person has been excluded.

Given these results, we get that 94% of all infections, happen in the runs where the 1%-quantile of the most important people (in our case 4) have contributed (ie. were not excluded). This again indicates their importance.



According to the paper "Talk of the Network: A Complex Systems Look at the Underlying Process of Word-of-Mouth" the importance of influential often over-

estimated. Our simulation contradicts this statement.

Reasons might be, that our network is a) of relative small size, b) we kinda cut the network. We only look at mutualfriends ,but not all friends of friends. So we might underestimated some people.

6.1.2 Determine influentials

7 Summary and Outlook

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8 Appendix

References

- [1] A. Barrat, M. Barthlemy, A. Vespignani. Dynamical Processes on Complex Networks. Chapter 10.