

CARE – Creative Application to Remedy Epidemics

R. KASPRZYK, B. LIPIŃSKI, K. WILKOS, M. WILKOS, C. BARTOSIAK
e-mail: rkasprzyk@wat.edu.pl

Institute of Information Systems
Cybernetics Faculty, Military University of Technology
Kaliskiego Str. 2, 00-908 Warsaw

The paper focuses special attention on a project named CARE. The developers of the project is *NosoiFighters* team, which consists of students of the Cybernetics Faculty in Military University of Technology. The system is a very creative software solution that takes advantage of pioneering sociological theories, graph/networks theory and the last but not least most advanced technologies. It has a very practical purpose, in particular nowadays: countering infectious diseases, for instance HIV/AIDS, malaria, SARS, etc. The paper demonstrates how the system can help us to nail epidemics. CARE has enormous practical potential in regions such as Africa, where there are not enough medicines to treat all who are at risk.

Keywords: complex networks, centrality, epidemic spreading, vaccination

1. Introduction

We define dynamic model for the spreading of infections on networks and build application to simulate and analyze many epidemic scenarios for various diseases. The idea for the project was born in order to participate in Imagine Cup Student Competition based on some Complex Networks researches [4] [5] [6] [7] conducted at the Military University of Technology.

The network of possible contacts between individuals determines which individuals can infect each other. We explore epidemic spreading in Social Networks modeled by Complex Networks. One of the most known mathematical models of social networks generators was a random graph [1]. Assuming equally probable and independent random connections made between any pair of vertices in initially not connected graph, they derived a model suffering unrealistically social network topology. Apparently Complex Networks have *Scale Free* [3] and *Small World* [2] features, what make them accurate model of social networks. These features, which appear to be very efficient for communication networks, favor at the same time the spreading of many diseases. What do the features mean? A *Small World* network is a type of graph in which most nodes are not neighbors of one another, but most of them can be reached from every other by a small number of steps. The *Scale Free* feature concerns to a network in which most of people have rather relatively small amount of contacts, but there are some individuals that

have huge amount of contacts. These individuals are called “*super-spreaders*”, because they have ability to spread diseases very fast. If such individual gets infected he can infect all of his numerous neighbors, what causes a sudden increase of sick people count. The application uses a few centrality measures [11] that help in finding the critical elements (e.g. degree centrality, radius centrality, closeness centrality or betweenness centrality) and finally suggests who should be immunized [14].

It is important to notice that we can determine the dynamic of epidemics if we know the network of possible contacts between people. Thus knowledge of such network topology makes possible to simulate spreading contagious diseases and effectively counteract them. The system is a new attempt in countering diseases spreading, because it uses the knowledge stated above and there is no similar solution, as nowadays epidemiologists choose people to vaccinate in most cases randomly and even they decide to vaccinate the whole population if they have enough vaccines number. Why the current methods are wrong? Unfortunately the most frequent situation is that we haven't enough vaccines count and random immunization is almost useless, because we have a very small chance to separate a social network into independent components. It is very characteristic for *Scale Free* networks that they remain connected even after up to 80% of their all nodes are removed (immunized or isolated) [10]. This suggests a simple solution: to immunize the “*super-spreaders*” in the first order, what may

slow or stop the spread. Unfortunately this solution is almost always impossible because in most cases the network topology is uncertain and incomplete.

So how the system uses the knowledge of social networks features? Well, it proposes a number of solutions. First of all it enables to create specific questionnaires (polls) which help in discover networks topologies. For example they may include a question that requires naming at least one acquaintance/ friend/ boy/ colleague etc. Individuals who are frequently named could be potential “*super-spreaders*” [13]. It also gives a possibility to generate social networks with the same statistical properties as real networks [12].

2. System overview

Application was implemented using Microsoft NET 3.5 platform with SP1 [15]. Originally the simulator was developed as desktop application. Our experiences with Web application cause entire modification of architecture. Now we use SOA (Services Oriented Architecture) with Web Services. The web user interface uses AJAX (Asynchronous JavaScript and XML) technology takes advantage of Microsoft Silverlight 2.0 solution [16].

The information is stored in MS SQL Server database which is divided into three parts: questionnaires and validated data from questionnaires; models of diseases and networks; and reports with simulation outcomes.

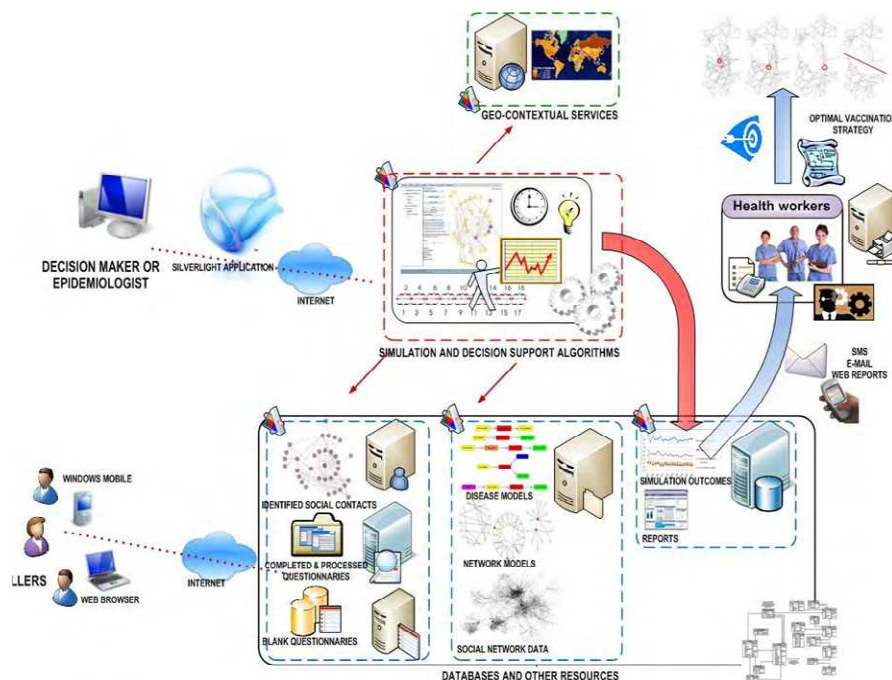


Fig. 1. CARE architecture overview

The system consists of a server and different types of clients. The server side contains a few components such as the database, web services, the simulation engine. At the moment there are two types of clients. Firstly web client accessible through the web browser, which contains diseases’ model editor, social network generators algorithms, interactive simulation with visualization subsystem and geo-contextual data relation with a help of MS Virtual Earth. Secondly mobile platform client which contains the poll application. Other developers can access web services designing completely new interface and/or create custom analysis.

3. CARE functionality

The application allows users:

- Model any kind of diseases based on knowledge from epidemiology field;
- Model and generate social network using Complex Network theory;
- Build special polls running on mobile devices to discover network topology;
- Identify the “*super-spreader*” and come up with the most efficient vaccination strategy;
- Simulate and visualize how the epidemic will spread in a given population;
- And assess the expected outcomes of different strategies.

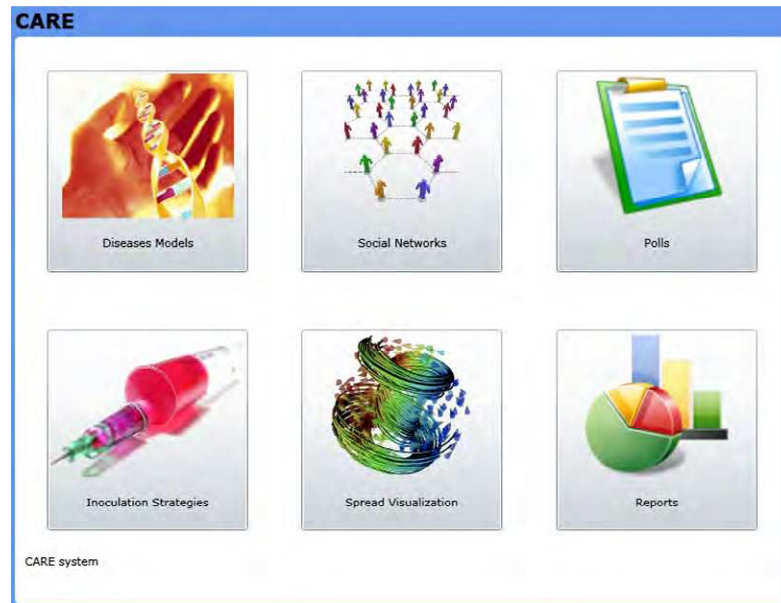


Fig. 1. CARE main screen

4. Poll application

The first step in fighting with some disease is to get information about social network, which is attacked by the disease. The CARE software helps sharing the special poll application directed to mobile platforms.

The application could be used for instance by missionaries in Africa to get information about people. Because *NosoiFighters* team has a very important purpose of decreasing costs of using the system, the poll application could be launched on PDA or simply mobile phone. There is also another problem with using the system, unfortunately in places like Africa internet access could be a problem, so application stores data in a local database (distributed with the application) and when the access is possible, the database is synchronized with the main database stored on the server. Fig. 2 presents how the application looks like at now:



Fig. 2. The poll application user interface

5. Network source

Now let's have a look at the Silverlight client. The first thing a potential user is asked to do is to load or generate some network. He can do this by importing an appropriate file or generating using predefined generators.

The system uses graphML network format to keep networks in the database and external sources (e.g. epidemiologists' sources). It is a very popular xml format that is used by many applications working with networks. The application couldn't have been an exception. Another interesting option is to use generators to generate some sample network with the same statistical properties as real social networks.

The algorithms generally make networks that are random graphs, *Small World* networks, *Scale Free* networks or their modifications. They all were defined in studies of people like Watts and Strogatz (who worked on the *Small World* model), Kleinberg (who explained using his own model why people are able to find the shortest paths between each other in *Small World* model very easily) or Barabasi and Albert (who introduced their model of networks as a result of two main assumptions: constant growth and preferential attachment, they worked on *Scale Free* model). Fig. 3 presents algorithms that are implemented in the system:

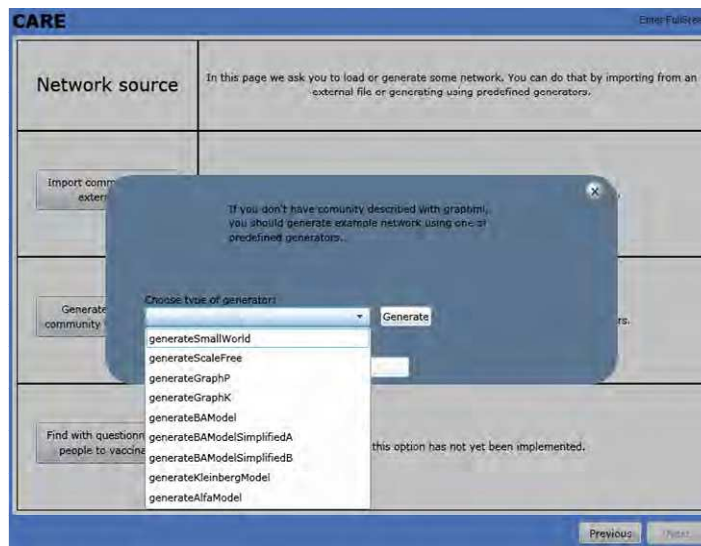


Fig. 3. The page with a network source choice

6. Disease source

The next step is to choose a disease model. The user has three possibilities: he can import it from external sources, create using the model editor or

open a model from the database. Options no. 1 and no. 3 mean simple load graphML file but the second option is a very interesting feature of the system.

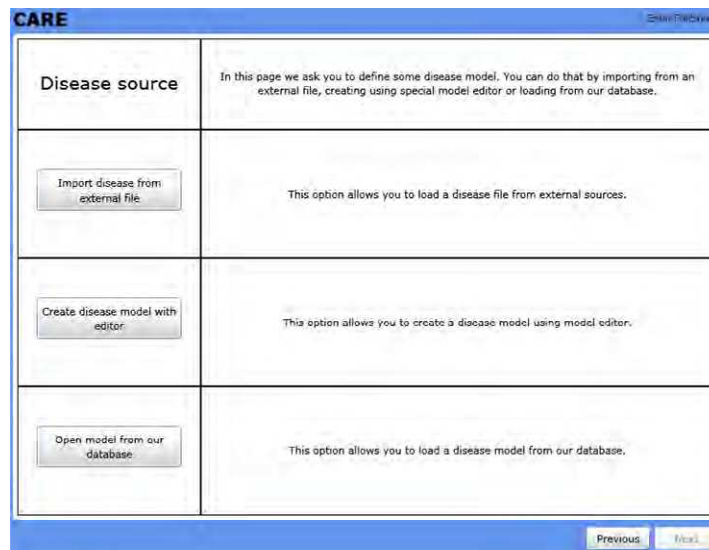


Fig. 4. The page with a disease source choice

It is a good moment to explain how the system defines a disease model. Generally it uses a State Machine approach. It means that every disease consists of a few states (e.g. susceptible, infected, carrier, immunized, dead etc.) which can be assigned to each individual and the system allows state to change as a result of social interactions (contacts). So underlying network topology is crucial problem in our simulator. For simulation we need at least two states S (Susceptible) and I (Infected). For realistic scenarios we make possible to define the model of disease with many more states and transitions

between them. In the classical theory of infectious diseases, the most extensively studies epidemic models are the SIR (Susceptible-Infected-Removed) and SIS (Susceptible-Infected-Susceptible) model.

We allow to build the models of diseases with any state in the editor we have proposed. There is also some transition probability, minimal/maximal time that individual spend in state and maximal number of neighbor that can be infected in simulation time step.

Fig. 5 presents AIDS model created using the model editor:

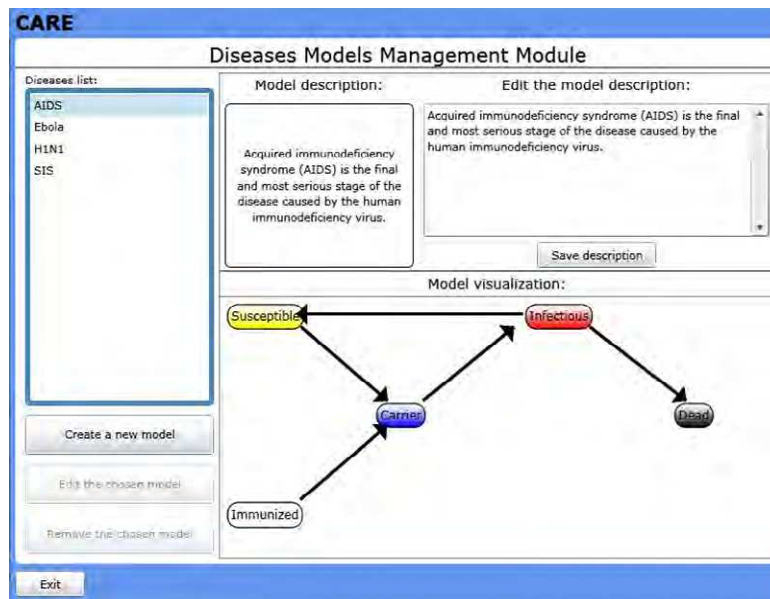


Fig. 5. AIDS model created with a help of the model editor

As we can see the model editor also allows the user exporting created model to the database for a further use.

7. Simulation setup

The next page is the simulation setup. In here the user can either do nothing or setup some

parameters: simulation steps (steps count of simulation) and state change strategies (he can add so many strategies as he wants. They will be fired in the same order he typed them. By “state change strategies” we should understand methods of changing states of individuals).

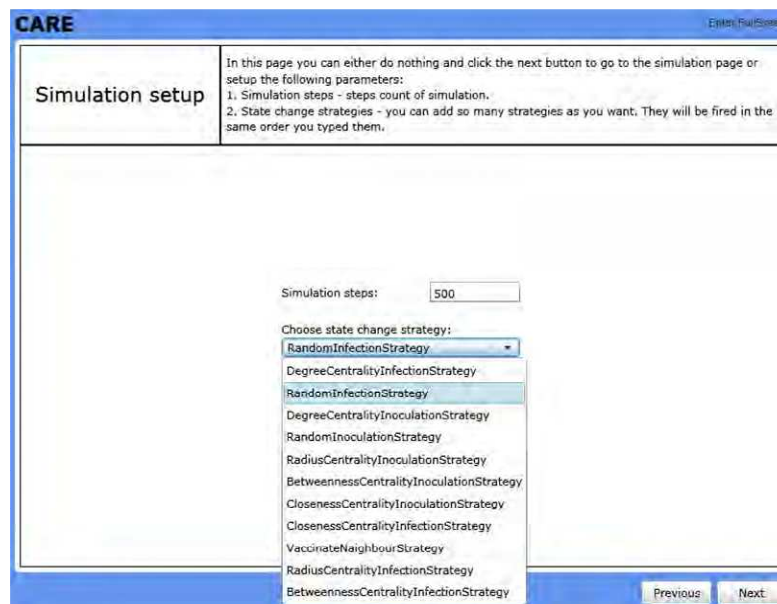


Fig. 6. In this page the user should setup the simulation

8. Simulation

This page is the most interesting step in the web client from the user point of view. It is an evidence for statement that interactive information visualization is important and how visual representation of information can be used to

demystify data and reveal otherwise hidden patterns by leveraging human visual capabilities to make sense of abstract information [8]. Generally the system proposes two ways of information visualization. The first way is called “Layout” and is presented below:

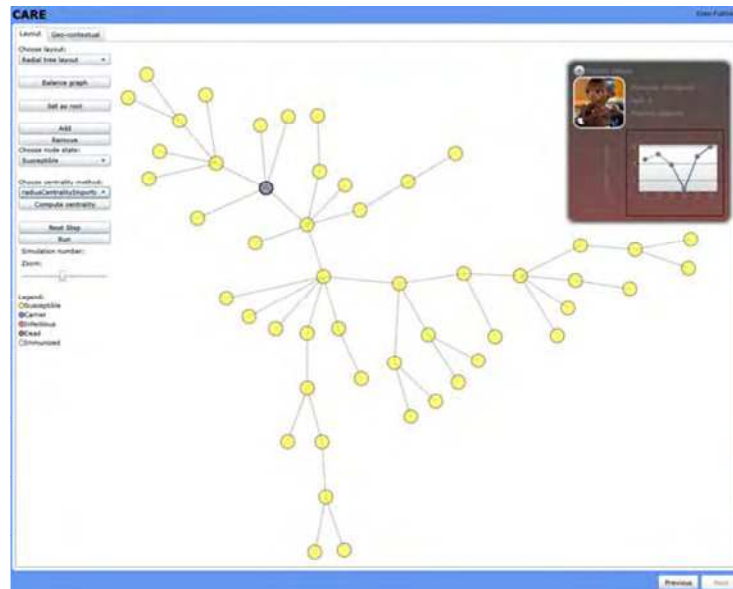


Fig. 6. The “Layout” view of the simulation page

Here the user can manipulate the network, in particular he can:

- change a position of each node;
- choose layout (what means choice of some graph balance algorithm);
- set some node as a root of layout (it’s a feature suitable for tree based layouts like e.g. radial tree layout visible in the picture above);
- remove nodes (what means e.g. isolating some individual);
- zoom layout for better view;
- start simulation, what is the most important option here.

In the right up corner of the picture we can see the patient details panel, which presents some important information about the current selected node (individual).

There is also an alternative way for visualize information. It is called “Geo-contextual”. This type of visualization makes easier to orientate in positions of each individual. It could be very useful for epidemiologists to see all the nodes on the world map and may help them to make decisions.

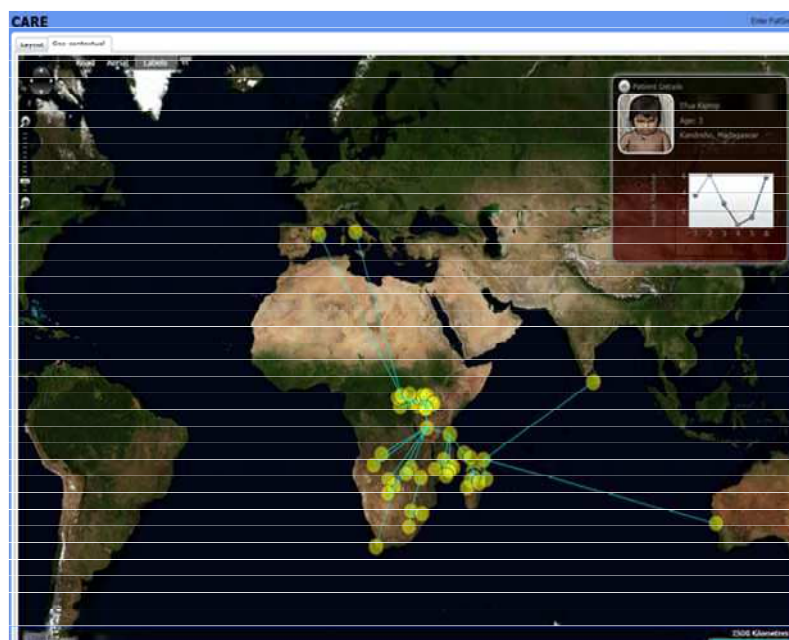


Fig. 7. The “geo-contextual” view of the simulation page

9. Reports

The last step is to analyse a report chart, which is created on the basis of the simulation. The x-axis represents simulation steps and the y-axis represents a count of individuals of each state in the appropriate step.

The user can estimate the results and the effectiveness of used state change strategies. In the future there will be also a possibility of getting the list of individuals which the system suggests to be vaccinated.

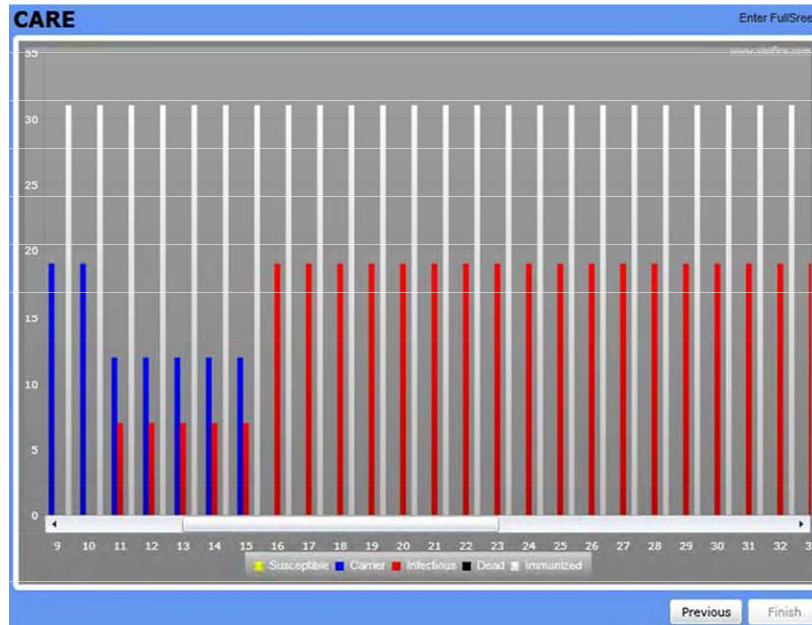


Fig. 8. The page with a report chart

10. Summary

The CARE software has enormous practical potential in such regions as Africa, where there are not enough medicines to fight against all dangerous diseases. It can be used in many various matters: the automatic notification of hospitals, rescue services, etc. about emergency situation e.g. risk of epidemic (with providing of coordinates and patient information). It could be also used by crisis management centers, epidemiology centers in the whole world to fight against not only terminal diseases, but also flu etc.

11. References

- [1] P. Erdős, A. Rényi: On random graphs, *Publ. Math Debrecen* 6 (1959), 290-297.
- [2] Watts Duncan J., Strogatz Steven H.: *Collective dynamics of „small-world” networks*, *Nature*, 393:440-442, 1998.
- [3] Barabási Albert László, Albert Réka: *Emergence of Scaling in Random Networks*, *Science*, 286:509-512, 1999.
- [4] Rafał Kasprzyk: *Complex networks in countering terrorism*, VII International Workshop for Candidates for a Doctor's Degree OWD, Wisła 22-25.10.2005.
- [5] Rafał Kasprzyk: *Fault and attack resistance of Complex Networks*, Military CIS Conference 2008, Kraków 22-24.09.2008.
- [6] Rafał Kasprzyk: *Modeling the evolution of Complex Networks with Small World and Scale Free features*, X International Workshop for Candidates for a Doctor's Degree OWD, Wisła 18-21.10.2008.
- [7] Rafał Kasprzyk: *Fault and attack resistance of Complex Networks*, X International Workshop for Candidates for a Doctor's Degree OWD, Wisła, 18-21.10.2008.
- [8] Brandes U., Kenis P., and Raab J.: *Explanation Through Network Visualization*, *Methodology* 2006, Vol. 2(1): 16-23.
- [9] Romualdo Pastor-Satorras & Alessandro Vespignani: *Epidemic Spreading in Scale-Free Networks*, *PRL Volume* 86, Number 14 p. 3200 (2 April 2001).
- [10] Paolo Crucitti, Vito Latora, Massimo Marchiori, Andrea Rapisarda: *Error and attack tolerance of complex networks*, *Physica A* 340 (2004), 388-394.
- [11] Stefan Wuchty, Peter F. Stadler: *Centers of complex networks*, *Journal of Theoretical Biology* 222 (2003), 45-53.
- [12] Barabási Albert László, Albert Réka, *Topology of Evolving Networks: Local Events*

and Universality, PRL Volume 85, Number 24 p. 5234 (11 December 2000).

- [13] Reuven Cohen, Shlomo Havlin, Daniel ben-Avraham: *Efficient Immunization Strategies for Computer Networks and Population*, PRL Volume 91 Number 24 p. 247901-1 (12 December 2003).
- [14] N. Madar, T. Kalisky, R. Cohen, D. ben-Avraham, S. Havlin: *Immunization and epidemic dynamics in complex networks*, Eur. Phys. J. B 38, 269-276 (2004).
- [15] <http://www.microsoft.com/NET/>
- [16] <http://silverlight.net/>