

H1N1 Influenza on Romania Territory

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Abstract: A pandemic is a worldwide epidemic of a disease. An influenza pandemic may occur when a new influenza virus appears against which the human population has no immunity. Epidemic propagation models have been applied on modeling the propagation of viruses. Some mathematical models and computer simulations deal with the spatial distribution of susceptible along a line, across a lattice or over a network to overcome the inaccuracies due to the assumption of random mixing of the population. The viral propagation is determined by intrinsic characteristics of the network. This work is focused on analyzing and fitting the classical SIR model to predict the course of pandemic H1N1 influenza on the Romania territory. An architectural system is proposed for implementing a web application for pandemic viruses that affected or can affect the Romania territory.

Keywords: Models, Parameter estimation, Analysis, Systems, Architectures.

1. INTRODUCTION

According to the World Health Organization (WHO), a pandemic can start when three conditions have been met:

- The emergence of a new disease to the population is increased.
- The agent infects humans, causing serious illness.
- The agent spreads easily and sustainably among humans.

The pandemic spread of some viruses depends on the specific characteristics of the disease, the number and structure of the population, its dynamics, the existence of infection foci and/or risk factors (animal farms or crowded people places with a high degree of insalubrity), the capacity of isolation for the infested area, the capacity to combat the disease's effects (the existence of well equipped hospitals in the contaminated area), the climate factors. It can be synthesized the fact that disease's spreading is achieved by three ways: proximity (a percentage of nearby population will get sick in time), by common transportation (primary and secondary service transportation on railway, public roads, with plane or ship) or, regarding diseases transmitted from animals, by their migration A.Doyle et al. (2006).

This work is focused on analyzing and fitting the classical SIR model to predict the course of pandemic H1N1 influenza on the Romania territory. An architectural system is proposed for implementing a web service for pandemic viruses that affected or can affect the Romania territory.

1.1 The SIR model

SIR model is an epidemiological model that computes the theoretical number of people infected with a contagious illness in a closed population over time. The name of this class of models derives from the fact that they involve coupled equations relating the number of susceptible people $S(t)$, number of people infected $I(t)$, and number of people removed from the system $R(t)$. Vittoria Colizza et al. (2007), T.Tassier et al. (2005), R. Durrett et al. (1994), A. Pop et al. (2008), A. Morariu et al. (2009), D. S. Jones(1983), H. Valean et al. (2007), H.Valea et al. (2008).

SIR equations:

$$t + 1 : \begin{cases} S_{t+1} = S_t - \beta S_t I_t \\ R_{t+1} = R_t + k I_t \\ I_{t+1} = I_t + \beta S_t I_t - k I_t = I_t (1 + \beta S_t - k) \end{cases} \quad (1)$$

S_t - Number of susceptible individuals

R_t -Number of removed individuals (number of recovered individuals + number of dead individuals)

I_t -Number of infected individuals

β – Coefficient of infected persons during a time interval

k – Recovering coefficient during a time interval

Using population fractions system equation (1) became system equation (5).

$$s_t = \frac{S_t}{N} \quad (2)$$

$$i_t = \frac{I_t}{N} \quad (3)$$

$$r_t = \frac{R_t}{N} \quad (4)$$

N- Population size

$$t+1: \begin{cases} s_{t+1} = s_t - \beta s_t i_t \\ r_{t+1} = r_t + k i_t \\ i_{t+1} = i_t + \beta s_t i_t - k i_t = i_t (1 + \beta s_t - k) \end{cases} \quad (5)$$

$$s_{t+1} + I_{t+1} + r_{t+1} = s_t + i_t + r_t = 1 \quad (6)$$

1.2 H1N1 influenza on Romania territory

The first cases of illness (case 0), in Romania, was reported in May 28, 2009. The infected person was a 30 age woman, arrived in country with a flight from New York, on May 23. (<http://www.ms.ro/>)

The pandemic evolution beginning with 28.05.2009 since 09.04.2010 (when was reported the last case of infection) is presented in Table 1.

Table 1. Pandemic evolution

Data	Infected	Dead
28.05.2009	1	0
29.05.2009	3	0
1.06.2009	5	0
...
29.06.2009	24	0
30.06.2009	25	0
1.07.2009	28	0
2.07.2009	36	0
...
29.07.2009	116	0
30.07.2009	125	0
31.07.2009	143	0
1.08.2009	164	0
...
31.08.2009	305	0
01.09.2009	305	0
02.09.2009	305	0
03.09.2009	305	0
...

27.10.2009	386	0
28.10.2009	414	0
29.10.2009	419	0
30.10.2009	427	0
...
29.11.2009	2975	3
30.11.2009	3259	3
2.12.2009	3427	5
...
11.12.2009	4374	18
12.12.2009	4548	18
13.12.2009	4625	18
14.12.2009	4668	18
27.12.2009	5434	42
28.12.2009	5512	49
29.12.2009	5568	52
30.12.2009	5626	53
31.12.2009	5680	58
...
29.01.2010	6938	119
30.01.2010	6951	119
31.01.2010	6953	119
...
25.03.2010	7007	122
9.04.2010	7008	122

A map representation of the affected areas is presented in next figure (Fig.1), where the color intensity is proportional with the number of infected people.

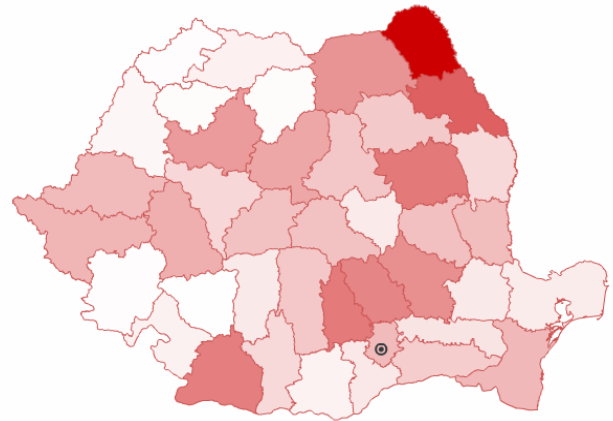


Fig. 1. Map of Romania

2. SIR MODEL CALIBRATION AND SIMULATION FOR H1N1 VIRUS

2.1 Virus evolution analysis

This paragraph will present the H1N1 evolution in time, on the Romania territory. The infected people are represented with red color, and the dead people are represented with green color.

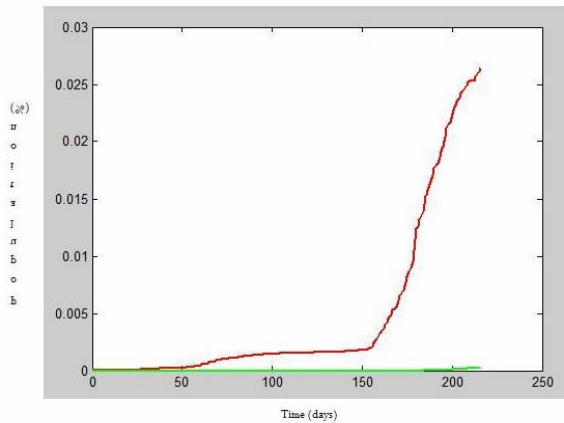


Fig. 2. H1N1 evolution - year 2009

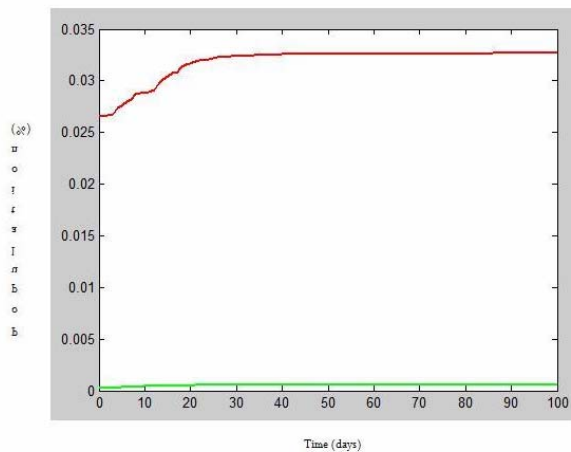


Fig. 3. H1N1 evolution - year 2010

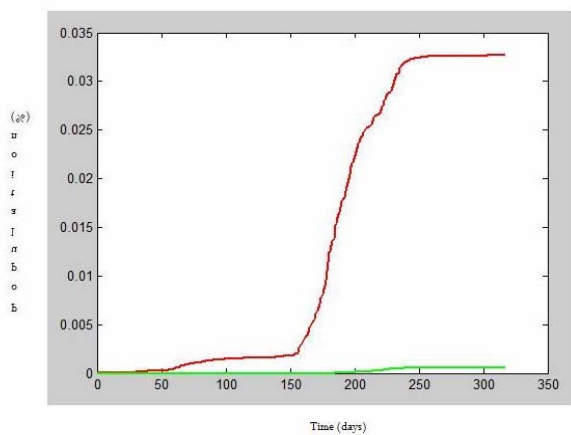


Fig. 4. H1N1 evolution - 28.05.2009-09.04.2010

2.2 SIR model calibration

For fitting SIR model parameters, a computational analysis was done. A simple algorithm for generating values for “beta” and “k” parameters was applied. The best result is presented in figure (Fig. 5), where the red color represents real data, for the infected people in the year 2009, and blue color represent simulation data.

$N = 21462974$ – Population of Romania

$St_0 = N-1$ – Initial number of susceptible people

$It_0 = 1$ – Initial number of infected people

$Rt_0 = 0$ – Initial number of recovered people

$\beta = 0.1755$ – Infection coefficient

$k = 0.1347$ – Recovering coefficient

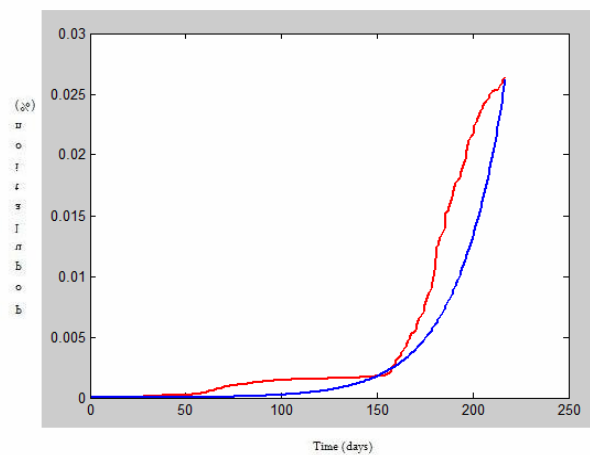


Fig.5. Comparison between real data and simulation data

2.3 SIR simulation results

Using the best fitting values of parameters, presented in paragraph 2.2, a simulation was done. The simulation purpose is to analyze the evolution in time, of the infected populations, without any prevention measurements.

The simulation result is presented in figure (Fig.6).

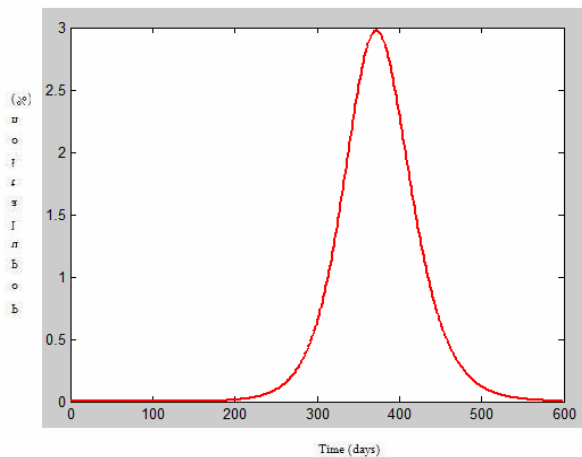


Fig.6. Simulation results for the infected people

Comparing simulation results with real data, we can see that without any prevention measurements, the infection period were almost double than the real period, and the number of infected people were increase from 0.03 % to 3%.

3. SYSTEM ARCHITECTURE

In this paragraph, the architecture for the pandemic system is presented (Fig.7). The system will be implemented as a distributed application, based on web services. Each county or relevant region can be served by a different "County Server".

The system will have several important modules:

- Database – will contain data related to different viruses behaviors, demographic data and simulation results
- Persistence layer – is an Object-relational mapping layer that will simplify and optimize the database access.
- Business layer – will implement the business logic that will contain all the algorithms used for monitoring, analysis and simulations and will provide as well relevant statistics

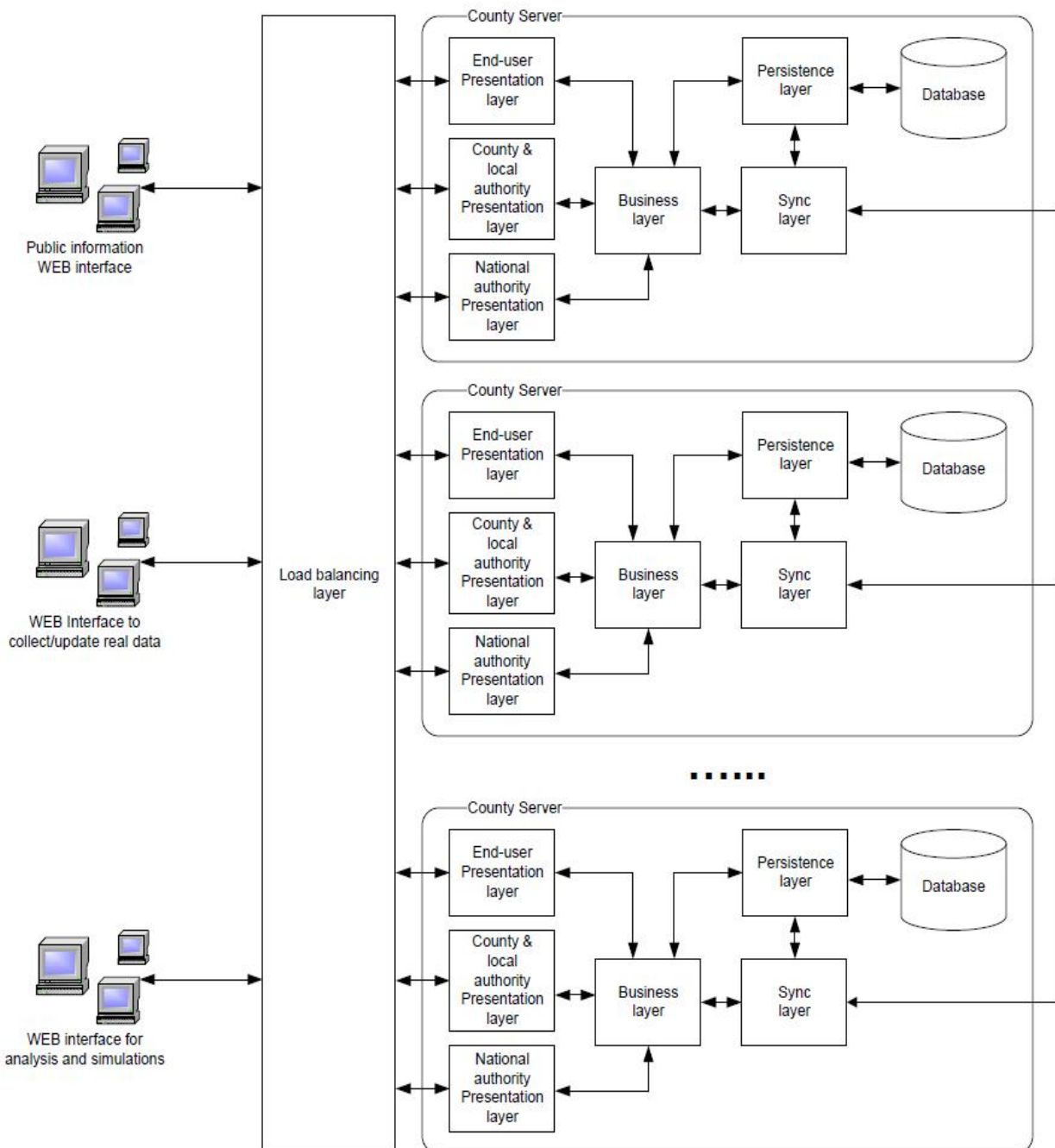


Fig. 7. System architecture

- End-user presentation layer – will be a web service that will provide to updates on the current pandemic situation and estimates for pandemic evolution.
- County & local authority presentation layer – will be a web service that will provide update capabilities for local authorities responsible for public health.
- National authority presentation layer – will be a web service that will provide local and national level statistics. It will enable as well the national authorities to simulate the pandemic evolution and generate reports based on simulations.
- Load balancing layer – will provide load balancing capabilities to enable an scalable and distributed deploy
- Sync layer – will assure that a certain County Server database is in sync with other County Server databases.
- Public information WEB interface – will enable end-users to visualize in a graphical way the current pandemic situation and estimates for pandemic evolution.
- WEB interface to collect/update real data – will enable local authorities responsible for public health to update the system database with relevant data from the field in a visual manner.
- WEB interface for analysis and simulations – will enable local and national authorities responsible for public health to visualize in a graphical way statistics, do simulations and generate reports.

4. CONCLUSIONS

As a conclusion this paper presented an analysis of H1N1 virus, on Romanian territory and a spreading model of the disease. The model was tuned based on real data reported by the National Public Health Department.

Another goal of this paper was to present an application that can be scaled and distributed to national level and will enable the Public Health authorities to record statistical data, decide and manage pandemic situations and forecast pandemic evolutions. The presented applications will enable as well ordinary citizens to monitor the current and predicted situation. The global benefit of the system will be to reduce the illnesses and improve Romanian economy.

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