# Study of Human Influenza's Spreading Phenomenon

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**Abstract.** The paper starts from the human influenza's spreading phenomenon, as a complex of observable occurrences, and develops a stochastic process, defined as a set of procedures that convert its initial state into a sequence of different states during the phenomenon's lifespan. The Monte Carlo simulation method for a stochastic discrete event system is used. This system is completely described in terms of: entities, sequential states, transition tables of states, sets of input/output events, internal/external transition function, events/time advance function, input/output parameters. The simulation can encompass several contagion schema and health policy responses. Finally, some information about the software in the field is given.

**Keywords:** Spreading Diseases, RNA Viruses, Stochastic Discrete Event Systems, Monte Carlo Simulation, Analysis and Prognosis.

## 1 Introduction

Human influenza's spreading phenomenon concerns, on the one hand, the symptoms of a specific group of individuals caused by a set of viruses (RNA viruses of the Orthomyxoviridae family: types A, B C, Isa, Thogoto, etc.) in precise climate conditions, in a given time period, and on the other hand, the response of medical organizations [5,6]. The symptoms include chills, fever, nasal secretions, watering eyes, sore throat, muscle pain, severe headache, coughing, nausea, vomiting, diarrhea, abdominal pain, weakness/fatigue and general discomfort, sometimes leading to death. The group of individuals is defined by number, age, sex, general state of health, vaccinations, topological placement in subgroups, distance between the subgroups, interacting coefficient, and shedding. The climate conditions combine sunlight, air-temperature, humidity, wind, and aerosols. This paper attempts to provide information that would aid with the second aspect of human influenza's spreading phenomenon, the response of the medical organizations.

There are several contagion schema, such as direct (from person to person) or indirect (airborne or through contact with a contaminated surface), leading from

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limited spreading to epidemics or even to pandemics. Obviously, the health policy response implies several direct and indirect costs. A study of the phenomenon and its consequences using mathematics and information technology techniques has merit and is the purpose of this paper. Modeling the human influenza's spreading phenomenon can be a valuable tool in analysis and prognosis.

The paper is organized as follows: the next section proposes a contagion scheme for human influenza's spreading phenomenon that may be utilized in the numerical simulation. One presents afterwards a general methodology for describing the stochastic discrete event system and its application for the proposed contagion scheme. The corresponding algorithm to solve this problem given in the next section. A general presentation of the software in the field is made in the conclusions' section. Some suitable references are also present.

## 2 Numerical Simulation of Contagion Schema

Contagion schemes can be modeled using the framework of chains with complete connections [10] or stochastic discrete-event systems [4,9,1]. In this paper we use the last approach.

First, a simple human influenza's spreading problem is stated, then an algorithm for numerical simulation of the contagion scheme is developed, and then some improvements of this algorithm are presented.

The analysis and prognosis of the spreading phenomenon of the virus is performed using computer simulation and based on a mathematical and logical model describing the behavior of real systems.

Let $\mathcal{O}$ be a human population of cardinality $No$ distributed on a region of $K$ communities and let $\mathcal{V}$ be a set of virus types of cardinality $Nv$. Suppose that for every virus type $v \in \mathcal{V}$ there is an incubation period ($v = 0$ means no virus), represented by an uniform random variable on $[l_v, u_v]$. For the sake of simplicity, suppose that an individual contaminated with a virus type cannot be contaminated with another virus type. Every community is characterized by following attributes: the number of healthy individuals ($Nh_i$), the number of contaminated individuals for every virus type ($N_{v,i}$), its Cartesian coordinates $(x_i, y_i)$, the proportion of commuters ($F_i = (pc_i)$, $i = \overline{1, K}$) and the radius of its area ($r_i$). Denote with $\mathcal{S}$ the set of states characterizing an individual $o \in \mathcal{O}$, i.e. $\mathcal{S} = \{H$ – healthy; $Hi$ – healthy and immune; $Ck$ – contaminated, aware of it; $Ct$ – contaminated, under treatment; $Cknt$ – contaminated, aware but not under treatment; $D$ – dead$\}$, and with $\mathcal{O}c$ the set of contagious individuals ($\mathcal{O}c = \{Ck, Ct, Cknt\}$).

Suppose that:

- all previous input data are known at time $t_0$;
- at time $t_1$, an commuter from $L_i$ can meet $\eta_M$ individuals from $L_i$. If the commuter is infected with virus type $v$, $\xi_c$ among the individuals met will be contaminated. Here $\eta_M$ is a realization of a Poisson random variable with parameter $\alpha_i$ ($Po(\alpha_i)$), and $\xi_c$ is a realization of a binomial random variable with parameters $(\eta_M, q_v)$ ($Bi(\eta_M, q_v)$);

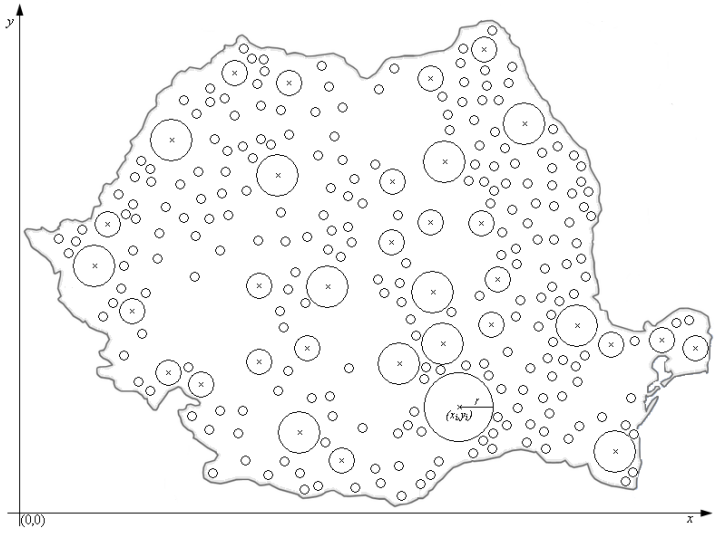


**Fig. 1.** Communities in the system built for the study on human influenza spreading

- the $\xi_c$ contaminated individuals are distributed as follows: $\xi_k \in Ck$, where $\xi_k$ is a realization of a binomial random variable $Bi(\xi_c, q_k)$; $\xi_t \in Ct$, where $\xi_t$ is a realization of a binomial random variable $Bi(\xi_c, q_t)$; $\xi_h \in Hi$, where $\xi_h$ is a realization of a binomial random variable $Bi(\xi_c, q_h)$; $\xi_{knt} \in Cknt$, where $\xi_{knt}$ is a realization of a binomial random variable $Bi(\xi_c, q_{knt})$; and $\xi_D = \xi_c - \xi_t - \xi_h - \xi_{knt}$.

The purpose is to determine the average cardinality of the subsets of $\mathcal{S}$ and the average treatment costs for each virus type $v$ and for every community. The corresponding algorithm needs to be executed multiple times in order to obtain these output data. The parameters of the random variable distributions involved are provided by a specialized company.

## 3 Stochastic Discrete-Event System

The formal framework for modeling and simulating discrete-event systems, DEVS, and stochastic discrete-event system specifications, STDEVS, is presented in [2,7,11,12,8].

A STDEVS model $\mathcal{M}$ representing the proposed contagion scheme has the following components:

- $X$: set of events of type "an individual infected with a certain virus type has contact with non-contaminated individuals";
- $Y$: the set of averages of the random variables giving the cardinalities of the sets of individual states and of the average costs at the end of the simulation;

- $ta$: a random variable indicating the contamination time for a virus type;
- $\delta_{ext} : Q \times X \to \mathcal{S}$: the function giving the number of individuals that switch into state $s \in \mathcal{S}$ (note that $\delta_{ext}$ is a random variable);
- $\delta_{int} : \mathcal{S} \to \mathcal{S}$: the function giving the number of individuals that switch from one state to another (e.g., $H \to Ck$, $Ckt \to Hi$, $Cknt \to D$, etc.), characterized by the distribution table $\mathcal{H}_{v,i}$;
- $Q = \{(s, ta)\}$;
- $\lambda : S \to Y$: the exit function, which calculates the averages of the cardinalities of the sets of states and the average costs.

## 4 Simulation Algorithm

In order to analyze this contagion scheme with some type of distribution for the involved input random variables, a simulation model needs to be constructed. An algorithm produces artificial experiments via computer runs. These experiments (in fact realizations of output variables) are processed and analyzed, yielding solutions for the management of actual contagion scheme described by the simulation model. The instruments used to construct the simulation model (i.e. algorithm) are the clock time and the agenda. The clock time has a dual purpose: to record the time elapsed in the system and to track the correct order of the events produced by the simulation model. The agenda is a concept related to recording the events produced by the simulation. The clock time increases by a finite number. After each increment of the clock, the simulation algorithm processes the events occurred at that moment in time (these events define the agenda of current events, $ACE$). When the $ACE$ is empty, the clock is incremented with some value and the process is repeated for the new events from $ACE$. When an event is processed, it can produce another event (at a future moment, in which case the set of these events is the agenda of future events, $AFE$) or can cancel some events from $ACE$ (this is the set of canceled events, $CE$). Therefore the agenda $A$ has a dynamic evolution in the form

$$A = ACE + AFE - CE$$

The clock time can be incremented in two ways: with variable increments (called variable increment clock time) or with constant increments (called constant increment clock time). Initially the clock is zero. In the case of variable increments, the clock time is increased up to the time of occurrence of the first event in $AFE$. In the case of constant increments, the clock is increased by a constant $c$. After incrementing the clock, the main cycle of the simulation algorithm selects the events from $AFE$ with time of occurrence equal to the current clock time and places them in $ACE$. Then, the events from $ACE$ are processed; when $ACE$ is empty, the clock time is advanced again and the process is repeated until the clock time takes the value $TS$, where $TS$ is the input value for the end time of the simulation. As an alternative, the simulation ends when the number of

simulated events of a specific type takes a given value $Nmax$. Sometimes, this equivalent rule (the next-event rule) is used instead of the variable clock time; in this case, the end of the simulation is determined by $Nmax$.

**Algorithm 1.** Main algorithm

Input: $K$, $Nv$, $N_{v,i}$, $l_v$, $u_v$, $pc_{v,i}$, $x_i$, $y_i$, $d_i$, $\alpha_i$, $q_{v,i}$, $qk_i$, $qt_i$, $qh_i$, $qknt_i$, $i = \overline{1,k}$, $v = \overline{1,Nv}$, $Dist \in \mathcal{M}_{K,K}(R)$, $Nmax$, $Ts$
Initialize: $N = 0$; {count of current iteration} $n = 1$; {index in agenda} $Clock = 0$;
**repeat**
Generate $i \sim \mathcal{U}(1, K)$; {a community}
Step 1: Generate $u \sim \mathcal{U}(0, 1)$; {determine if the current individual is commuter}
**if** $u < pc_i$ **then**
**begin**
Generate $d \sim \mathcal{U}(0, d_{max})$ {$d_{max} = \max_{1 \le i \le K} d_i$}
**if** $d < r_i$ **then**
$I = i$ {the individual remains in his community}
**else**
**begin**
Determine $\mathcal{L} = \{L_k | Dist_{i,k} \le d_i, k = \overline{1,K}\}$, $|\mathcal{L}| = L$
Generate $I \sim \mathcal{U}(1, L)$ {determine the destination community}
Generate $v \sim F_i$ {a virus type}
**if** $v = 0$ **then**
go to Step 1 {$v = 0$ means no virus}
Generate $\eta_M \sim Po(\alpha_I)$ {a value of the random variable representing the number of individuals met by an individual contaminated with virus type $v$}
Generate $\xi_c \sim Bi(\eta_M, q_{v,I})$ {a value of the random variable representing the number of individuals from $\eta_M$ contaminated after the contact with the individual contaminated with virus type $v$}
**for** $i = 1$ **to** $\xi_c$ **do**
**begin**
Generate $T_{v,i} \sim \mathcal{U}([l_v, u_v])$ {a value of the random variable representing the contamination period of individual $o$, contaminated with virus type $v$}
$n = n + 1$
$T_n = Clock + T_{v,i}$
**end**
$N_{v,I} = N_{v,I} + \xi_c$
$|C_{v,I}| = |C_{v,I}| + \xi_c$
$Clock = T_o$ {time of the last processed event/individual}
{determine the state of the current individual at time $T$ according to the probability distribution $\mathcal{H}$}
**if** $o_n \in Ck$ **then**
Compute $|Ck_{v,I}| = |Ck_{v,I}| + 1$
**if** $o_n \in Ct$ **then**
Compute $|Ct_{v,I}| = |Ct_{v,I}| + 1$ and the Cost;
**if** $o_n \in Cknt$ **then**
Compute $|Ckknt_{v,I}| = |Cknt_{v,I}| + 1$;

**Algorithm 1.** *(Continued)*

```
            if o_n ∈ Hi then
                Compute |Hi_{v,I}| = |Hi_{v,I}| + 1;
            if o_n ∈ D then
                Compute |D_{v,I}| = |D_{v,I}| + 1;
            N = N + 1    {next event; the first event/individual having T_n > Clock}
            end
        end
until N = Nmax or Clock > Ts
                                                        {Outputs of simulation}
for i = 1 to K do
    for v = 1 to Nv do
        begin
        Calculate E[|Hi_{v,i}|] = |Hi_{v,i}|/N, E[|Ci_{v,i}|] = |Ci_{v,i}|/N, E[|Ck_{v,i}|] = |Ck_{v,i}|/N,
E[|Ct_{v,i}|] = |Ct_{v,i}|/N, E[|Cknt_{v,i}|] = |Cknt_{v,i}|/N, E[|D_{v,i}|] = |D_{v,i}|/N, Cost_{v,i}
        end
```

Classical algorithms can be used to generate samples of the different types of random variables involved in this algorithm, such as the Poisson, Binomial and discrete distributions [3].

It is assumed that the transition of a contaminated individual from one state to another, for each community, is according to the distribution table $\mathcal{H}$:

$$\tau_i : \begin{pmatrix} Hi & Ckt & Cknt & D \\ p_{1,i} & p_{2,i} & p_{3,i} & p_{D,i} \end{pmatrix}$$

and that the virus types have the distribution table

$$\zeta_i : \begin{pmatrix} 1 & 2 & \cdots & Nv \\ p'_{1,i} & p'_{2,i} & \cdots & p'_{Nv,i} \end{pmatrix}$$

The proposed contagion scheme would be closer to reality if contaminated individuals with virus type $v$ do not become immune to that virus type after healing, but rather can be contaminated with any virus type. Also, individuals contaminated with one virus type could be contaminated with another virus type during their contamination period. In this case, the exact cause of death is not known if the individual dies. In the situation when there are sufficient data to determine suitable distribution functions for the random variables involved in this model, the corresponding algorithms can be used to generate samples for these variables.

## 5 Conclusions

The human influenza phenomenon is still studied by scientists in various disciplines. The medical field regularly faces new variants of the virus, such as bird influenza or H4N1, and has to find new treatments. The mathematics or

computer science fields try to improve the systems that mimic the behavior of viruses in its spreading phenomenon. This paper is an example of an attempt to simulate the spreading of a virus as close to reality as possible. The chosen framework-model is STDEVS, which is very complex and can represent the entire phenomenon. The technique chosen for simulations is Monte Carlo, which produces good results for a sufficiently large number of iterations.

The experience of the authors in this area shows that the carefully made simulations with the HIS software (Human Influenza Spreading software) yield useful results for analysis and forecast. There are several programs used to model and solve stochastic discrete event systems, such as SimEvents, DevSim++, adevs, PowerDES etc, but it seems more appropriate to consider software especially built for this particular problem. The proposed algorithm would provide such a specialized software. The software designers could allow the users to change certain parameters, such as the target region or the distribution function of commuters and of infected individuals for every community in the system.

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