Stochastic virus machines

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Summary. Virus machines are an abstract computing device capturing viral reproduction and transmission as a computation. Virus machines feature hosts containing viruses, whose evolution is governed by the associated instruction graph, and which migrate via the channels connecting the hosts. In this paper, we propose using virus machines as a modelling device to represent real-world virus propagation. We start with the widely used SIR model, numerically accounting for susceptible (S), infected (I), and recovered (R) individuals, and propose two virus machines representing two simple situations with respectively two and three possible locations for the agents.

Key words: Virus machines, pandemics modelling, SIR model.

1 Introduction

This work can be considered as a contribution to the area of *Natural Computing*, which is a field of research that investigates both human-designed computing inspired by nature and computing that occurs in nature.

In virology, a virus is an infectious agent of small size and simple composition that can only reproduce after infecting a host cell. All animal, plant and protist species on the planet can be and have been infected by viruses. Indeed, biologists estimate that we have about 350 trillion viruses living in our bodies [1], which is

10 times the number of bacteria and cells in the human body. This leads us to believe that it would be very interesting to study this biological structure from a computational point of view. For more details on viruses, see [3].

This study focuses on a new computing paradigm, introduced in [2], based on the transmissions and replications of viruses. This innovative paradigm provides non-deterministic computing devices that consist of several biological *hosts* connected with each another by *directed channels*. The viruses are contained in these hosts and will be able to both transmit and replicate themselves passing through these channels. This processes are controlled by several instructions, which are attached to the channels. These systems can be considered as a heterogeneous network that consists of:

- A *virus transmission network*: a weighted directed graph, wherein each node represents a *host* and each arc represents a *transmission channel* through which viruses can transmit between hosts or exit to the environment. In addition, each arc has an associated weight (a natural number $w > 0$) , which indicates the number of viruses that will be replicated in each transmission.
- An *instruction transfer network*: a weighted directed graph, wherein each node represents a *control instruction unit* and each edge represents an optional *instruction transfer path* with a positive integral weight.
- An *instruction-channel control network*: an undirected graph, wherein each node represents either a control instruction or a transmission channel and each edge represents a relationship between an instruction and a channel.

The computing models of this paradigm are universal (equivalent in power to Turing machines), demonstrated by generating Diophantine sets [4], by computing partial recursive functions [5] and by simulating register machines [2].

2 Stochastic Virus Machines

In order to fit an extension of the Virus Machines (VM for short) with exciting instructions for modelling SIR model, we propose that "excitation" of the hosts can be stochastic, *i.e.*, the weight of the channels between hosts can be a tuple (a, p) where a is the capacity of replication if the channel is opened (as basic VM paradigm) and p is the probability of opening that channel in case the origin host is excited[1].

3 Modelling

The basic idea of this extension is that, from now on, viruses will represent the population and hosts will represent not only a place but also a status, so the num-

[1] Notice that only one of the channels could be opened, in order to avoid further complexity with the number of viruses and the meaning of the probability.

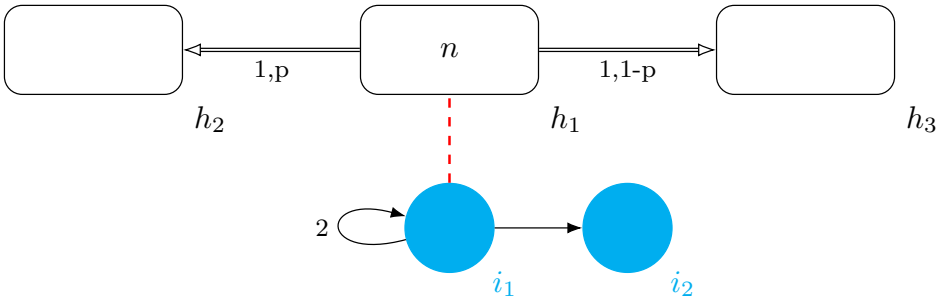

Fig. 1. Initial configuration of a SVM.

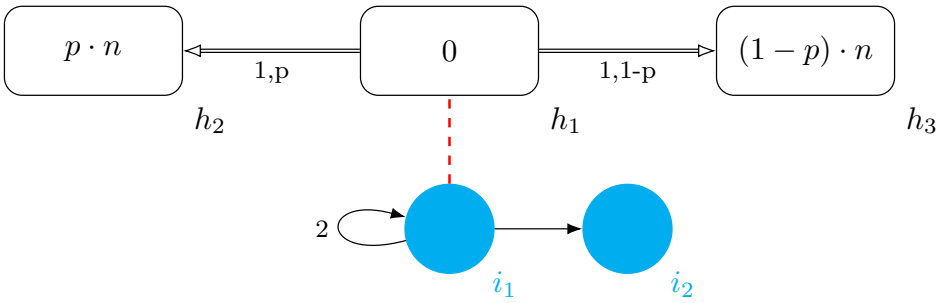

Fig. 2. Average halting configuration of a SVM.

ber of viruses a host is containing at some instant t, $h_{Place_{Status}}$, is the population located at *Place* in compartment *Status* at instant t.

Specifically, for the classical SIR model (susceptible-infected-removed) we will have two kind of hosts:

i) the hosts which contain the people who are susceptible of being infected (**S**),
ii) the infected population (**I**).

In addition, by considering that the recovered people (**R**) in the SIR model is "passive" (if and only if recovered people cannot be re-infected), we can take advantage of the passive behavior of the environment, so that the number of viruses sent to environment represents the number of recovered people.

4 A case of study: Pandemics

A *pandemic* is an epidemic that occurs over a wide geographical area, affecting a significant proportion of the population. It is characterized by the rapid spread of an infectious disease, often caused by a novel pathogen, which has the potential to cause severe illness or death.

In this section, we present a SIR computational model based on Stochastic Virus Machines. SIR in an acronym: **S** stands for the *susceptible population*, those who are not yet infected, but may become infected; **I** stands for the infected population, those who are ill and can transmit the disease, and **R** stands for the dead or recovered individuals that are removed from the infected population and cannot transmit the disease.

The SIR mathematical model for pandemics is an ODEs based model that has been used to understand the temporal transmission dynamics of the infection:

$$\frac{\partial S}{\partial t} = -p \cdot S \cdot I, \quad \frac{\partial I}{\partial t} = p \cdot S \cdot I - r \cdot I, \quad \frac{\partial R}{\partial t} = r \cdot I.$$

where S, I and R represent the number of individuals in the susceptible, infected and recovered compartments respectively, p is the transmission rate, which determines the rate at which susceptible individuals become infected, and r is the recovery rate, which determines the rate at which infected individuals recover and become immune to the disease. The parameter $(\frac{p}{r})$ is known as the basic reproduction number (R_0), which represents the average number of secondary infections produced by a single infected individual in a susceptible population. The SIR model assumes that the population is well-mixed and that the disease spreads through direct contact between individuals. It also assumes that individuals do not acquire natural immunity, and that there is no vaccination or treatment available for the disease.

Our case of study will be restricted to two physically separated places (e.g. home and supermarket). A susceptible person can be infected either in their way to the supermarket, or on their way back. The figure displays a global view of the case stated above.

4.1 Design of a SVM Modelling Pandemics

In this section, the model for the exposed case of study by using SVM is presented.

A first step in the approach of a bigger example, is to start with a simple one, let us suppose a SIR model of a population $N = S_0 + I_0$, where S_0 and I_0 are the initial population of susceptible and infected people resp. and two locations are defined: i) Home (H) and ii) Supermarket (J(amón)). Let us also suppose that the probability of being infected is p with $0 < p \leq 1$ and the probability of being recovered for an infected individual is $0 < r \leq 1$. We propose the SVM shown in Figure 3.

The idea behind this machine is as follows. The population is constantly moving back and forth from home to the supermarket. If there is an infected individual in a place A, then there would be a probability p that a susceptible person will be infected while going to the other place; and similarly, there would be a probability $1 - p$ that they will not be infected. If there are no infected people in that place, then the process is repeated for the other place, and if the other place also ran out of infected people, it leads to a halting configuration. Meanwhile, the infected

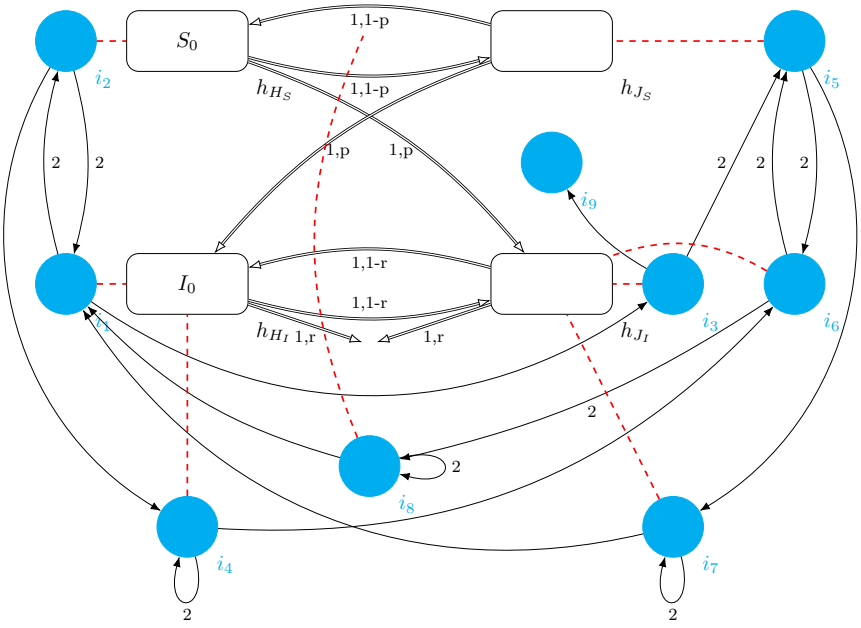

Fig. 3. A SVM modelling the SIR model with two locations

population can be recovered (sent to the environment) with probability r or can go to the other place infected with probability $(1 - p)$.

From now on, let us study a more complex example. Suppose the existence of an extra location D(isco) where the probability of being infected is even higher than in the supermarket. The global idea for this model is presented in Figure 4, and we will use the following notation:

- $0 \leq p_H, p_J, p_D \leq 1$: the probability of travelling form home to each location such that $p_H + p_J + p_D = 1$,
- $0 \leq p_{IH}, p_{IJ}, p_{ID} \leq 1$: the probability of being infected at each location,
- $0 \leq r_H, r_J, r_D \leq 1$: the probability of being recovered at each location.

The SVM modelling the SIR model is presented in two parts, the host graph in Figure 5, and the instruction graph in Figure 6 with a legend of the hosts/channels attached to each instruction.

4.2 Model Analysis

Now we will execute a thorough analysis of the above presented model, in order to provide as much insight as possible, starting with the expected behavior of the model and following with the limitations of the model, as it presents a certain bias, a fact which will be exposed shortly.

Fig. 4. Modules corresponding to the SIR model

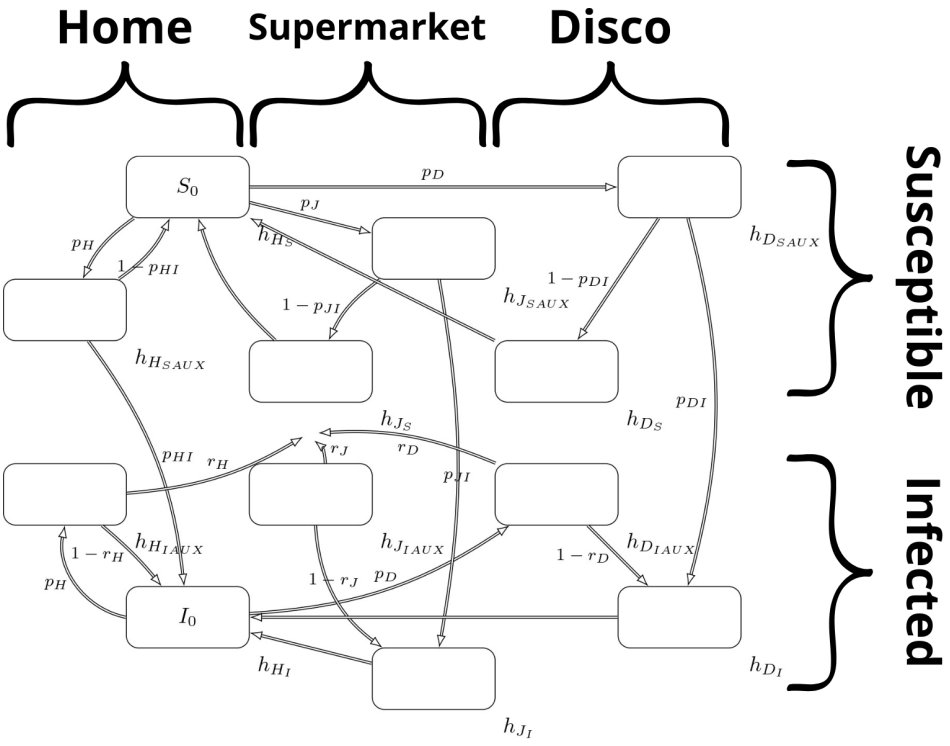

Fig. 5. A SVM modelling the SIR model (Hosts)

To begin with, as this is a really small model, some of its properties can be directly obtained, as exposed above. However, one which could be to a certain degree intuitive but not completely clear is the bias it has for the complete removal of the infected people in a large enough amount of time. Recall that the SIR model, in its most basic configuration, tends to reach a balance situation when only infected and recovered (which can not be infected again) interact, equivalent to a halting configuration in which infected become recovered and the virus finally disappears. This behavior is replicated by our model, as the halting configuration is, as we have already mentioned, one in which there are no infected people.

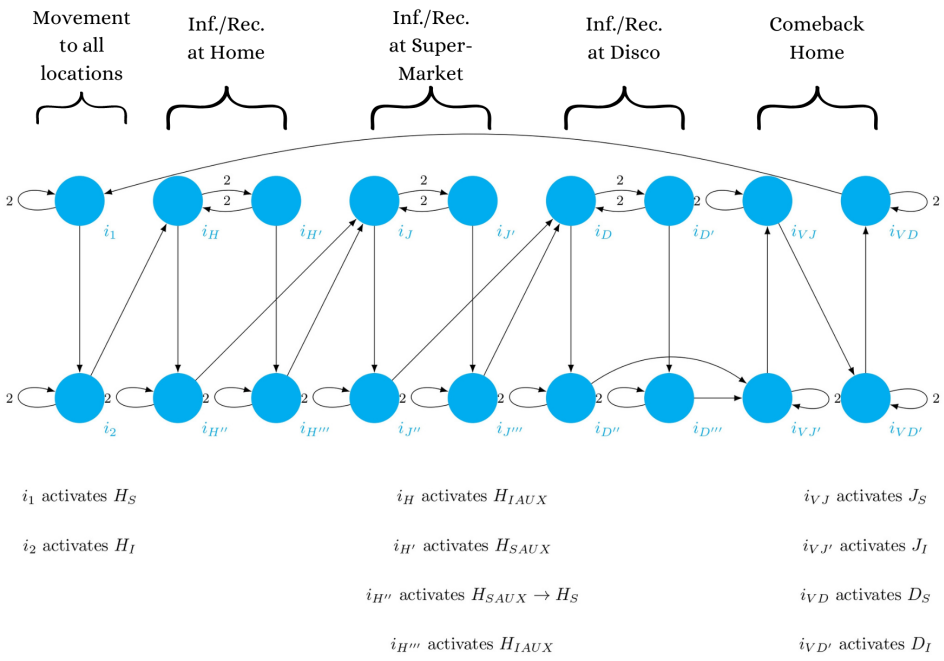

Fig. 6. A SVM modelling the SIR model (Instructions)

Lastly, a fact we must point out for its relevance is that, even if it is the first known modelling of the SIR model in a SVM, expected to be used as a minimal, educational example, and not suitable for real data analysis, an obvious problem of the presented model is its complexity. Generally, VM are not known for their simplicity, but when working with the stochastic variant, specially regarding the graphical representation used in Figure 3, we can assert that another representation is needed, in particular for more complex models.

5 Conclusion

With the aid of the Virus Machines (VM) several phenomena can be modelled, but the reach of these models is limited, especially for the modelling of more complex situations. With that in mind, in this article the Stochastic Virus Machines (SVM) are presented as a non-deterministic extension for the VM, providing more tools for modelling certain events, such as pandemics. To explore this fact, an example of SVM following the classical SIR model is shown and analyzed, pointing out both its suitability as an alternative for the traditional differential model and its complexity, an issue which is yet to be addressed. More precisely, two simple cases have been studied with interesting results, the second one can be easily extended for more locations or kind of populations (young, elder people, etc.).

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