AGENT-BASED MODEL SIMULATION OF COVID-19 IN NETLOGO

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ABSTRACT

This is a report made for the final exam of the course *Behavioral Economics and Complexity*, taught by Prof. A. E. Biondo, at University of Catania, about the roots of complexity in human behaviors, with reference to their consequences on dynamic perspectives of economic relations. The purpose of this paper is to show a case study related to an agent-based model simulation of COVID-19, using *NetLogo*.

Introduction

The case study of this report is the simulation of the spread of COVID-19 using agent-based modeling in NetLogo. The report is organized as follows. In Chapter 1, it will be illustrated the reasons why stop travelling fails to stop the virus spreading around the world, showing real data of COVID-19. In Chapter 2, the proposed model will be shown, and conclusions will be drawn. In appendix, the implemented software code will be reported.

1 How the Virus got out(1)

The proposed model of this report was thought for COVID-19, but can be generalized to other viruses. Let's see some real data about COVID-19, to understand the context, and why stop travelling does not work to fight the spread of the virus. Here are analyzed the movements of hundreds of millions of people to show why travel restrictions, even the most rigid, to stop an outbreak are not enough. About COVID-19, the first known cases clustered around a seafood market in Wuhan, China, a city of 11 million and a transportation hub. Four cases grew to dozens by the end of December. This disease belong to the family of Coronavirus, an already existent family of viruses, but doctors discovered that sick people had viral pneumonia that did not respond to the usual treatments. Probably, the true size of the outbreak was much larger — an invisible network of nearly 1,000 cases, or perhaps several times more. So, even a perfect response may not have contained the spread, because each sick was infecting two or three others on average, However, chinese officials underestimated the risks, and did not alert the public. It wasn't until Dec. 31 that they alerted the World Health Organization and released a statement — and a reassurance, saying that the disease is preventable and controllable. But it was too late, the timing of the outbreak could not have been worse. For the Lunar New Year, hundreds of millions of people were about to travel back to their hometowns. Here's the data about movements of people on Jan. 1. More than 175,000 people left Wuhan just on that day. The departures from Wuhan accelerated over the next three weeks. In January, before travel restrictions, about 7 million people left. Thousands of travelers were infected. Local outbreaks were already seeded in Beijing, Shanghai and other major cities. On Jan. 23, the authorities locked down Wuhan, and many cities followed in the next few weeks. Travel across China nearly stopped, but local outbreaks were already growing quickly, and moreover, international travel continued as normal. Thousands of people flew out of Wuhan to cities around the world. Over 900 people went to New York every month on average, based on recent trends, over 2,200 to Sydney, and over 15,000 people went to Bangkok, the most popular destination. That's where the first known overseas case appeared in mid-January, a 61-year-old woman who traveled from Wuhan to Bangkok despite having

a fever, headache and a sore throat. The U.S. confirmed its first case near Seattle. Researchers believe that about 85 percent of infected travelers went undetected. It was only at the end of January that Wuhan was placed under a lockdown and airlines started canceling flights. By Jan. 31, when the United States announced it would shut down entry from China for non-Americans, travel out of Wuhan had basically stopped. It was too late. Outbreaks were already growing in over 30 cities across 26 countries, most seeded by travelers from Wuhan. The virus started spreading locally, moving easily in confined spaces like churches and restaurants, and infecting people who had not traveled to China — the start of a pandemic. By March 1, thousands of cases were reported in Italy, Iran and South Korea. China was no longer the main driver of the outbreak. In fact, as China started systematically testing, tracing and isolating patients, new cases there declined dramatically, showing that it was possible to slow the virus. Similar measures slowed the spread in Singapore, Hong Kong and South Korea. In the United States, where testing has lagged, President Trump suspended most travel from Europe. "The virus will not have a chance against us," he said. But by then, the virus had a secure foothold. It continued to spread locally throughout parts of Seattle, New York City and across the country, once again outpacing efforts to stop it.

2 The proposed model

Inspired in the COVID-19 pandemic, this simplified model simulates the transmission and perpetuation of a virus in a human population.
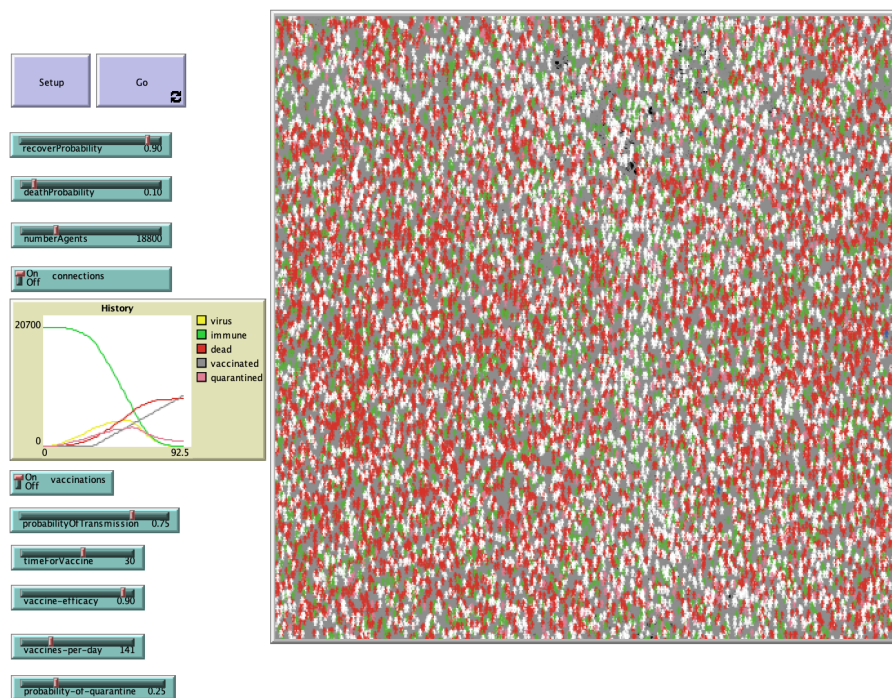

Figure 1: Interface of the model

2.1 How it works

The model is initialized with 18800 people, of which only 1 is infected. I have chosen 18800 simply because is the number of people of the comune where I live, Aci Castello, in Catania. People move randomly about the world in one of the following states: not infected (blue), infected (yellow), immune (green), quarantined (pink), vaccinated (white). People may die (red) of infection.

Some of these factors are summarized below with an explanation of how each one is treated in this model.
The density of the population Population density affects how often infected, immune and susceptible individuals come into contact with each other. You can change the size of the initial population through the numberAgents slider.
Population decrease People may die from the virus, the chances of which are determined by the slider deathProbability and the duration of the infection in the agent.
Infectiousness (or transmissibility) How easily does the virus spread? Some viruses with which we are familiar spread

very easily. Some viruses spread from the smallest contact every time. Others (the HIV virus, which is responsible for AIDS, for example) require significant contact, perhaps many times, before the virus is transmitted. In this model, infectiousness is determined by the "turtles-here" command patch.

Duration of infectiousness How long is a person infected before they either recover or die? This length of time is essentially the virus's window of opportunity for transmission to new hosts. In this model, duration of infectiousness is fixed to 10, and matched with a probability of recover, to recover, otherwise is fixed to 5 and matched with a probability of death, to die.

2.2 How to use it

Each "tick" represents a day in the time scale of this model.
The recoverProbability slider controls the likelihood that an infection will end in recovery/immunity.
The deathProbability slider controls the likelihood that an infection will end in death.
The numberAgents slider controls the number of agents involved in the simulation.
The connections switch controls the possibility of drawing links among the infected.
The Setup button resets the graphics and plots and randomly distributes numberAgents in the view. The GO button starts the simulation and the plotting function.
The vaccinations switch controls the possibility of vaccinate people or not. The timeForVaccine slider is basically the number in days after which the vaccine is released. Vaccines-per-day controls the flow of vaccinations per day. And probabilityOfTransmission controls the possibility of infection according with the vaccine-efficacy.
The probability-of-quarantine slider controls the probability of agent to be quarantined (stop moving) when infected. If 1, it always stop the agent.
An output monitor plots the number of agents that are infected, the number of agents that are immune, and the number of agents that are dead.

2.3 Things to notice

The factors controlled by the four sliders interact to influence how likely the virus is to thrive in this population. Notice that in all cases, these factors must create a balance in which an adequate number of potential hosts remain available to the virus and in which the virus can adequately access those hosts. Often there will initially be an explosion of infection since no one in the population is immune. This approximates the initial "outbreak" of a viral infection in a population, one that often has devastating consequences for the humans concerned. Soon, however, the virus becomes less common as the population dynamics change. What ultimately happens to the virus is determined by the factors controlled by the sliders. Notice that viruses that are too successful at first (infecting almost everyone) may not survive in the long term. Since everyone infected generally dies or becomes immune as a result, the potential number of hosts is often limited.

2.4 Simulations

You can play with the sliders and simulate different types of virus.

Let's start seeing some numbers of the simulation in the following simple condition: no vaccines, no quarantine, a recover probability of 90%, and a death probability of 5%.
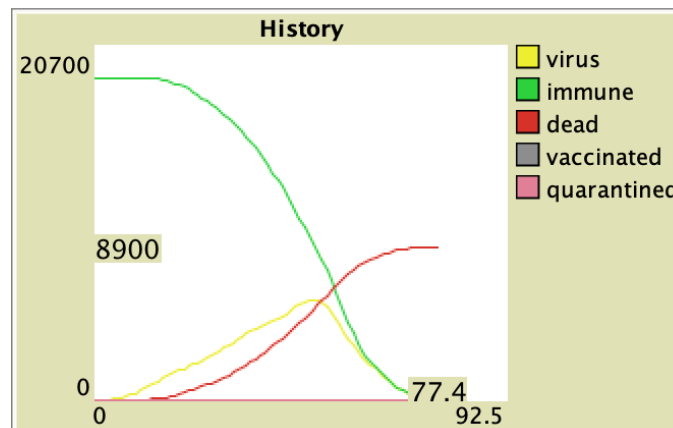

Figure 2: Simplest scenario

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It is possible to see that in this baseline case we reach to a total of about 9000 deaths and a peak of infected little less than 6000. We will use these values as reference points.

If you try to decrease the *recoverProbability* to a low value, like 0.05, you can see a dramatic scenario with an increasing exponential curve (2) for the values of dead and virus:
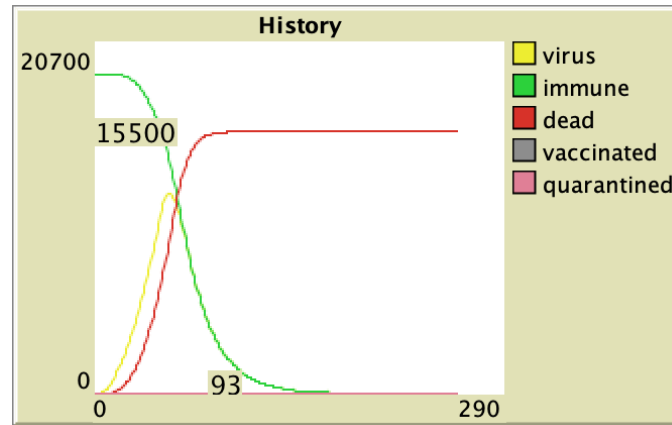

Figure 3: Scenario with recover probability of 0.05

In this situation there are more or less 15500 deaths and a peak of about 12000 infected.

However, trying to keep the values of recoverProbability and deathProbability as similar as possible to the real ones of COVID-19, so considering recoverProbability of 90% and deathProbability of 5%, we can play with the options of vaccinations and quarantine.

So, first of all, let's enable the vaccinations. I start considering these options: 75% of probability of transmission, 30 days to release the vaccine, with an efficacy of 90%, and that the rhythm of vaccination is 140 people per day:
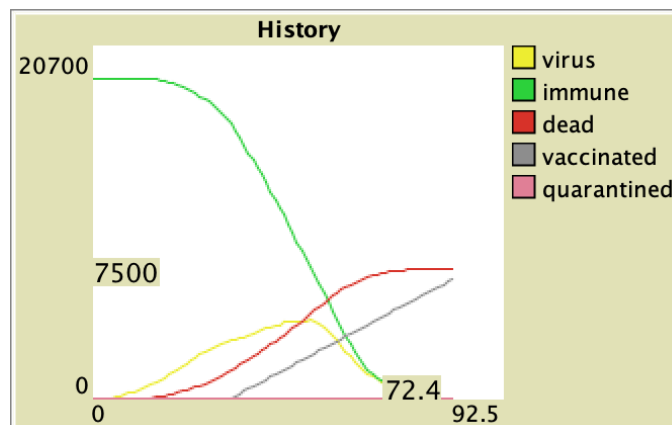

Figure 4: Vaccine scenario

It is possible to see that in this case the total number of deaths decreases of 1000 and the peak of infected of 1500 units, showing the effect of vaccines. Moreover also the number of ticks to finish the simulation decreases, indicating in this way a reduction in time of the pandemic.

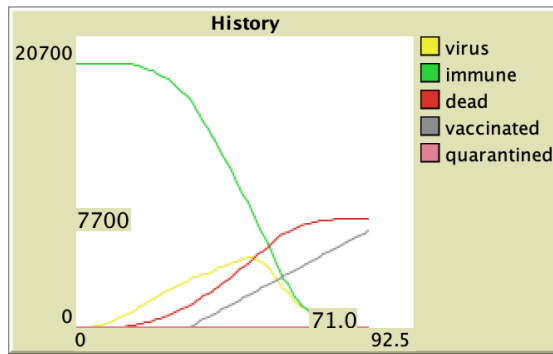Now, I will illustrate several results with different options relative to the vaccines:

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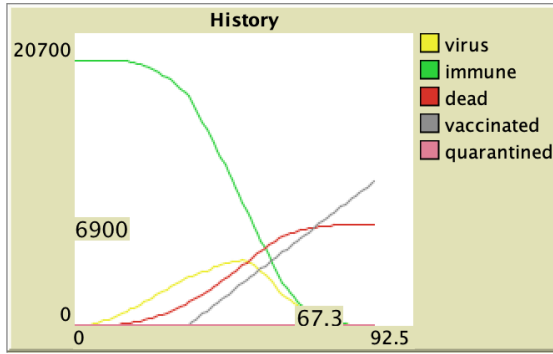
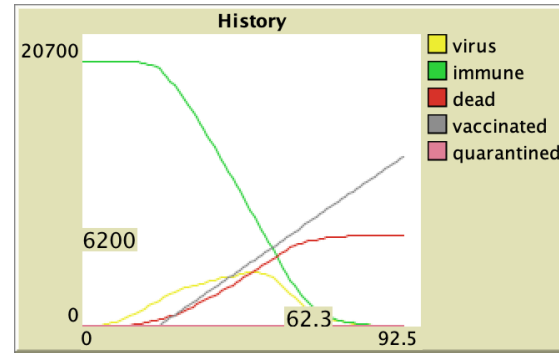(a) A rhythm of 200 vaccinations per day
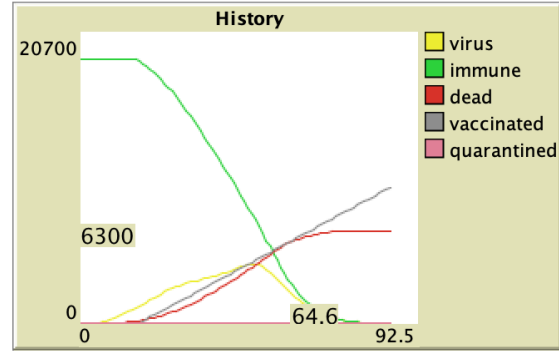
(b) Start vaccinating after 15 days

Figure 5: A figure showing number of dead and virus when vaccinations per day are 200 (a) and when vaccines start after 15 days (b)

(a) Vaccine efficacy of 40%

(b) Case with 180 vaccinations per day, starting after 20 days, with an efficacy of 75%

Figure 6: A figure showing number of dead and virus when efficacy is 40% (a) and when we have 180 vaccinations per day, starting after 20 days, with an efficacy of 75% (b)

Starting from Fig. 5a we can see that an increase in vaccinations-per-day decreases from about 7500 to 6900 deaths wrt the case of 140 vaccinations-per-day. Fig. 5b shows that with 140 vacc. per day, but starting after 15 days, there is a bigger reduction than Fig. 5a; indeed here the deaths is more or less 6300, showing that a quick release of a good vaccine is very important in braking the pandemic. Fig. 6a shows that a reduction in the vaccine-efficacy from 90% to 40% means more deaths wrt Fig. 4. However, also a low value like 40% is useful, because it reduces from 8900 deaths of the simplest scenario to about 7700 deaths.

Finally, increasing from 140 to 180 vaccinations per day, reducing from 30 to 20 days the time needed for developing a vaccine, and considering an efficacy of 75%, it can be seen that deaths are about 6200, so the best value obtained until now. This means that timeliness in releasing a vaccine, and an increase in the rhythm of vaccination (so both production side and organization of vaccination) is very important, also if it done at the cost of a lower efficacy.

Now let's consider the effects of quarantine with and without vaccinations.

First of all, if we set a probability of quarantine of 90%, so preventing the agents from moving when are infected, this is what happens:
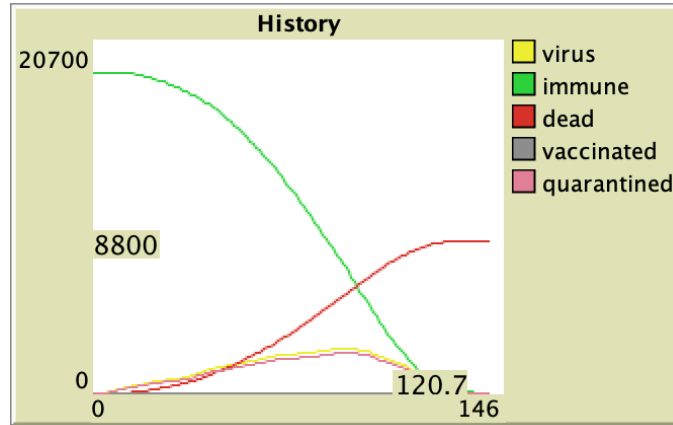
Figure 7: Scenario with quarantine and without vaccines

Basically, comparing this figure with the scenario of Fig. 2 we can see that number of deaths is more or less the same. What it changes is the curve of infected people. Indeed in this case the curve is platykurtic, more flattened, and in consequence of this the simulation is longer. In a real scenario this can be very useful because, this simple model does not consider hospital pressure and other variables. Indeed, in real life the mortality depends also on the hospital pressure, so having a flattened curve of infected people means less hospital pressure, so less deaths.

Now, let's consider the effects of both quarantine and vaccinations:
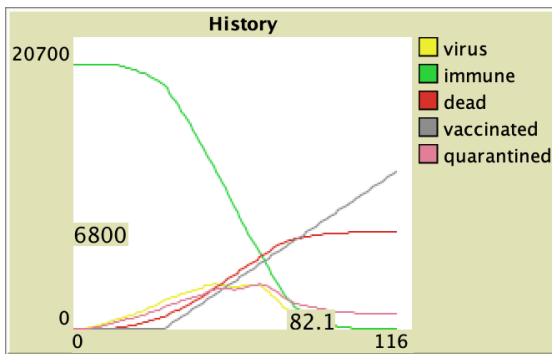
(a) Probability of quarantine of 0.5
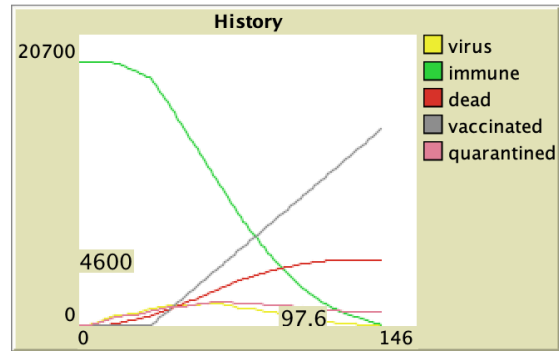
(b) Probability of quarantine of 0.9

Figure 8: Baseline vaccine scenario and probability of quarantine of 0.5 (a) and 0.9 (b)

We can see from Fig. 8b that a 90% change of quarantine combined with vaccinations have a huge impact on the number of deaths, that decreased to about 4600. Also a probability of 50% (Fig. 8a) has a good effect on the deaths, indeed compared with Fig. 4 it decreased from 7500 to 6800.

For further works, a mechanism that can be implemented is assigning a random age to the population, and a different risk to from the disease depending on the age (elders have a higher risk).

These simulations vastly oversimplify the complexity of real life.

Appendix

You can find the script on this Github repository: https://github.com/CasellaJr/AGENT-BASED-MODEL-SIMULATION-OF-COVID-19-IN-NETLOGO

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References

[1] NYTIMES, *https://www.nytimes.com/interactive/2020/03/22/world/coronavirus-spread.html*.

[2] WASHINGTONPOST, *https://www.washingtonpost.com/graphics/2020/world/corona-simulator/*, 2020.