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# AGENT-BASED MODEL SIMULATION OF COVID-19 IN NETLOGO

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REPORT FOR THE FINAL EXAM

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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.

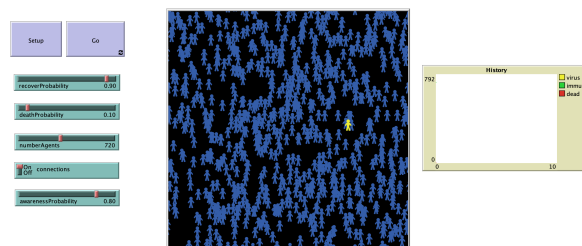


Figure 1: Interface of the instantiated model

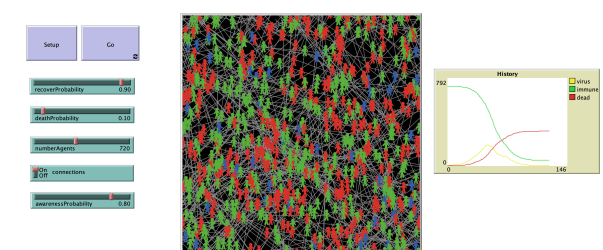


Figure 2: Interface of the executed model

### 2.1 How it works

The model is initialized with 720 people, of which only 1 is infected. People move randomly about the world in one of the following states: not infected (blue), infected (yellow), immune (green). People may die (red) of infection. Upon setup, population is assigned a random age. Elders (those older than 60 years old) have a different risk to die from the disease. 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 `awarenessProbability` slider controls the likelihood that an agent knows its own state. 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. 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. 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:

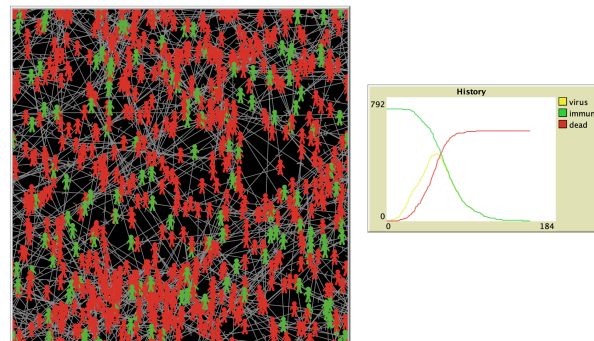
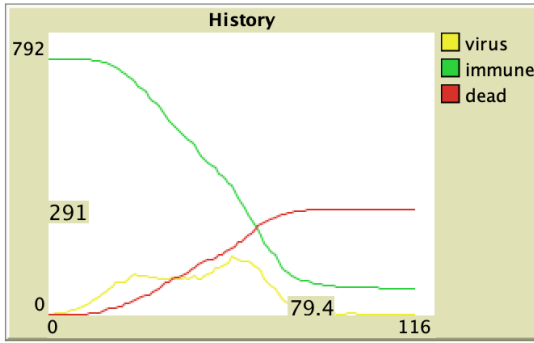
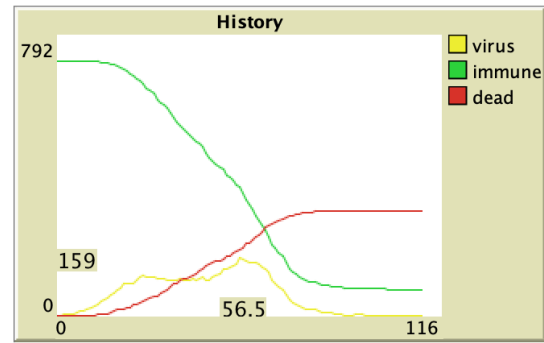


Figure 3: Curve with `recoverProbability` equal to 0.05

However, trying to keep the values of `recoverProbability` and `deathProbability` as similar as possible to the real ones of COVID-19, I think that one interesting simulation is playing with the `awarenessProbability`. The `awarenessProbability` slider controls the likelihood that an agent knows its own state, so basically if it is infected or not. I want that if an agent is sick, there will be 2 cases: it knows that is infected, and it will follow self-quarantine (basically agent does not move); the other case is that it does not know that he is infected, so he will continue to move, spreading the virus. Notice that, also in the first case, when the agent knows that is sick, it will be stopped, but other turtles can touch him anyway (think for example case of a family in a single room and one sick). The `awarenessProbability` is, for each tick, compared with a random float number between 0 and 1. So, the higher is this `awarenessProbability`, less chance will have the agents to know their own state, so less chance to quarantine (stop moving). If this `awarenessProbability` is equal to 1, basically it is like a button that turn off the possibility of quarantine.

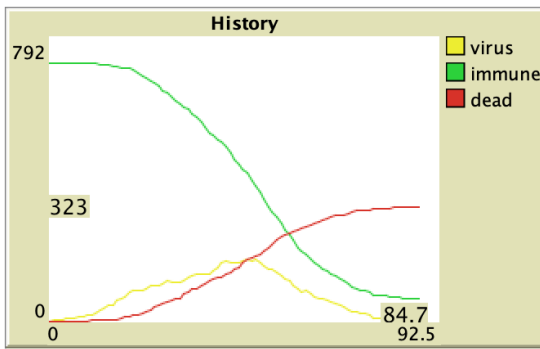


(a) Peak values of dead

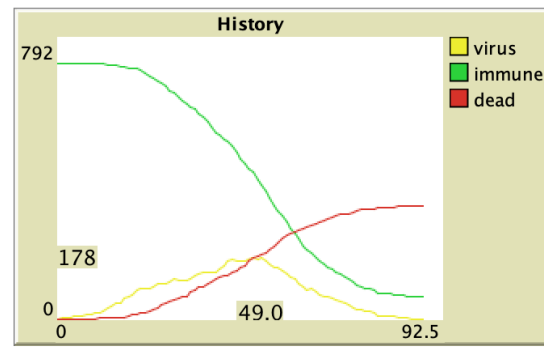


(b) Peak values of virus

Figure 4: A figure showing number of dead and virus when awarenessProbability equal to 0.01



(a) Peak values of dead



(b) Peak values of virus

Figure 5: A figure showing number of dead and virus when awarenessProbability equal to 0.90

It is possible to see that in the first case, with an awarenessProbability very low, of only 0.01, the values of dead and virus are lower than those of the case of 0.90. Moreover, also the x-axis has relevance, indeed, the peaks of the curves, in the case of 0.01, are reached later than the ones of 0.90. In a real scenario, this is important, because it is reflected on the hospital pressure, that will be lower when the curve is more flattened, and consequently it can mean fewer deaths.

For further works, this mechanism of quarantine can be improved. Indeed, at the moment the awarenessProbability is compared to a random float number for each tick. It could be useful to implement a fixed period of quarantine to simulate more real scenarios.

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>

## 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.