

State the disease you selected to model as well as the region and time period you are considering.

I will do a SIRVD —susceptible/infected/recovered/vaccinated/deceased— model to simulate COVID-19 in Brazil during 2021.

Variables of the model, numerical values, and units for the initial values of the variables.

- $S(t)$: The Susceptible population at time t , representing individuals at risk of COVID-19 infection but not yet infected. Initially, this is the total population of Brazil in 2021, approximately 214.3 million, as vaccinations had not yet begun, and everyone was susceptible.
- $I(t)$: The Infected population at time t , indicating the number of people currently infectious. Initially, this includes 359,593 cases from the first week of January 2021 and an additional 40,432 cases from the last week of 2020. For simplification, we assume an infectious period of 14 days, totaling 400,025 initial infections.
- $R(t)$: The Recovered population at time t , consisting of individuals who have recovered from COVID-19 and have temporary immunity. At the start, 8,075,998 people have recovered.
- $V(t)$: The Vaccinated population at time t , which includes individuals who have gained immunity through vaccination. Initially, this count was 0 as vaccination campaigns had not started. It is different from the recovered population because here we are counting individuals with ACTIVE vaccination.
- $D(t)$: The number of deceased individuals at time t , with an initial count of 202,631 due to COVID-19.

Parameters (b and k).

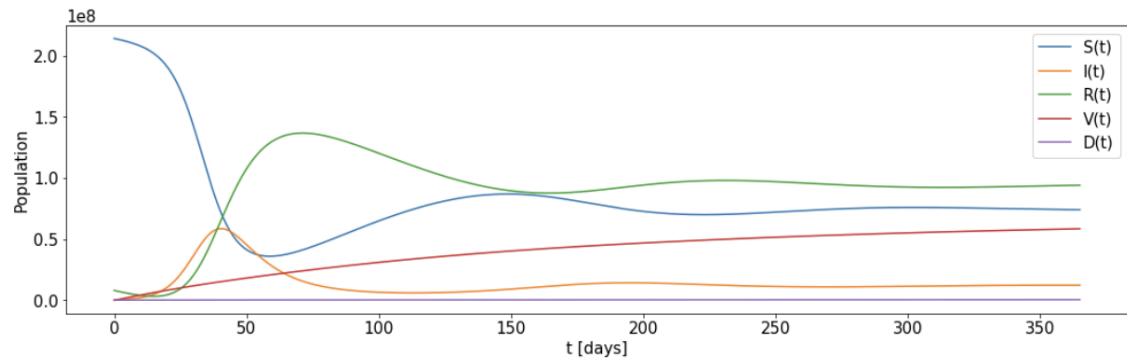
- b (Infection rate): This is the rate at which infectious individuals successfully transmit the virus to susceptible people, resulting in new infections. It reflects how contagious the disease is. With a population of 214,000,000 and 14,611,548 reported cases, the infection rate b can be calculated using the basic reproduction number R_0 and the recovery rate k . Given $R_0 = 3$ and $k = 0.1$, the

infection rate b is determined as $b = R_0 * k = 3 * 0.1 = 0.3$. The unit would be rate per day (day^{-1}).

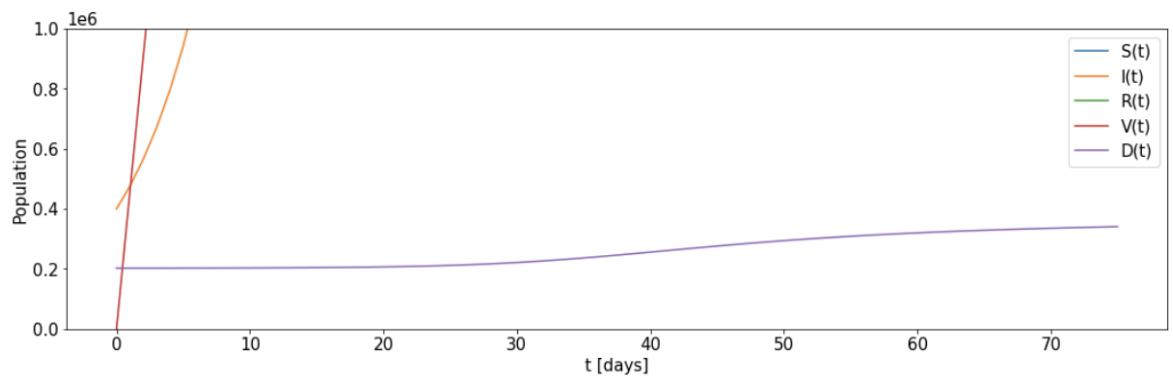
- I set the R_0 as 3 because with my research, I discovered that a person infects 2 to 5 others, so I took 3 as the middle ground.
- k (Recovery rate): This measures the frequency at which infected individuals recover and transition into the recovered category. Typically, it's the inverse of the average duration an individual is infectious, where a higher rate indicates faster recovery. For COVID-19, with an average infectious period of 10 days. Because of this, $k = 1/10 = 0.1$. The unit would be rate per day (day^{-1}).
- v (Vaccination rate): The pace at which susceptible individuals receive vaccinations over time (Higher rate means faster vaccination). Calculated as (percentage of the vaccinated population per 100 = 0.74) divided by 365 days, for a vaccination rate of 0.002. The unit would be rate per day (day^{-1}).
- ω (loss_of_vaccine_immunity_rate): The rate at which the immunity from vaccination decreases, making vaccinated individuals susceptible once more (Higher rate means vaccine immunity for a longer period). Assuming immunity wanes after 6 months, ω is set at $1/180$. The unit would be rate per day (day^{-1}).
- σ (loss_of_natural_immunity_rate): Represents the rate at which individuals who have recovered from the infection naturally lose their immunity and become susceptible again, estimated over a 3-month period as $1/90$. The unit would be rate per day (day^{-1}).
- d (Mortality rate): The likelihood of death among the infected population. Calculated based on the total deaths (416,425) and total cases (14,611,548) in 365 days, leading to a daily mortality rate of approximately 0.00007. The unit would be rate per day (day^{-1}), indicating the daily probability of death for an infected individual.

Results and Interpretation.

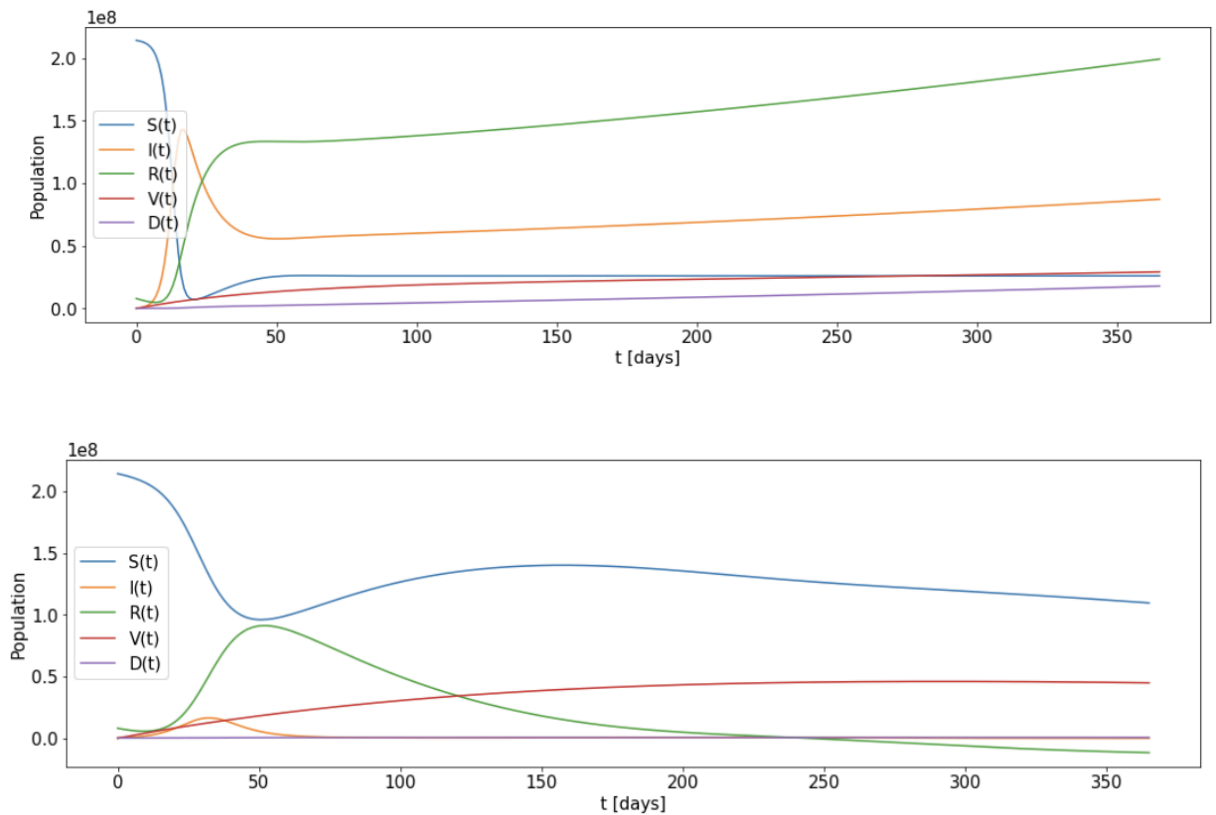
- **Image 1:** SIRVD (Susceptible, Infected, Recovered, Vaccinated, Deceased) visualization of the 365 days



- **Image 2:** SIRVD visualization zoom in on the Y axis, to understand the deceased number and make sure it is not 0.



- **Image 3 and 4: Other values**



With the visualizations, we see that the susceptible population (S) initially strongly decreases as individuals become infected (I). Over time, as people recover (R) or get vaccinated (V), the number of susceptible individuals levels off or even increases slightly due to loss of immunity. The number of infected individuals rises initially but then decreases as the disease runs its course through the susceptible population and people either recover, die, or get vaccinated.

We also notice that adjusting the parameters can greatly affect the dynamics of the model. A higher infection rate results in a faster spread of the disease, with a higher initial peak in the infected population, while a higher recovery rate would increase the speed at which infected individuals move into the recovered class. Faster loss of immunity leads to more individuals moving back into the susceptible class after recovery or vaccination, potentially leading to subsequent waves of infection.

Overall, the behavior observed in the simulations aligns with expectations based on the descriptions of the parameters. For instance, an increase in the infection rate or a decrease in the recovery rate leads to a more significant outbreak, with more individuals infected at the peak. Similarly, an increase in the vaccination rate or the introduction of a vaccine that provides longer-lasting immunity would be expected to reduce the size of the outbreak and the total number of deaths. The simulations demonstrate these dynamics effectively, offering insights into how different public health interventions could impact the course of an infectious disease outbreak.

How useful is this model?

This SIRVD COVID-19 model is useful for understanding the spread dynamics, the effects of vaccination and immunity waning. It can offer insights into potential epidemic trajectories under various public health strategies, aiding in planning and response efforts. The model's results match expected outcomes, such as infections peaking and then declining with recovery and vaccination.

Furthermore, notable assumptions include constant rates of transmission, recovery, and immunity loss, and a closed population without births or non-disease-related deaths. These assumptions, while simplifying the model, can limit its accuracy in reflecting complex real-world interactions and behavioral changes over time, which impacts its predictive usefulness. The model also assumes a homogeneous mixing of populations, which doesn't account for the structured contact patterns seen in reality, and that vaccines are 100% efficient, which is also not true. Lastly, the model does not account for factors like social distancing or quarantine, which could significantly affect the spread of the disease.

Despite these limitations, the model serves as a valuable tool for hypothesis generation and preliminary scenario analysis.

Multidimensional phase space plot

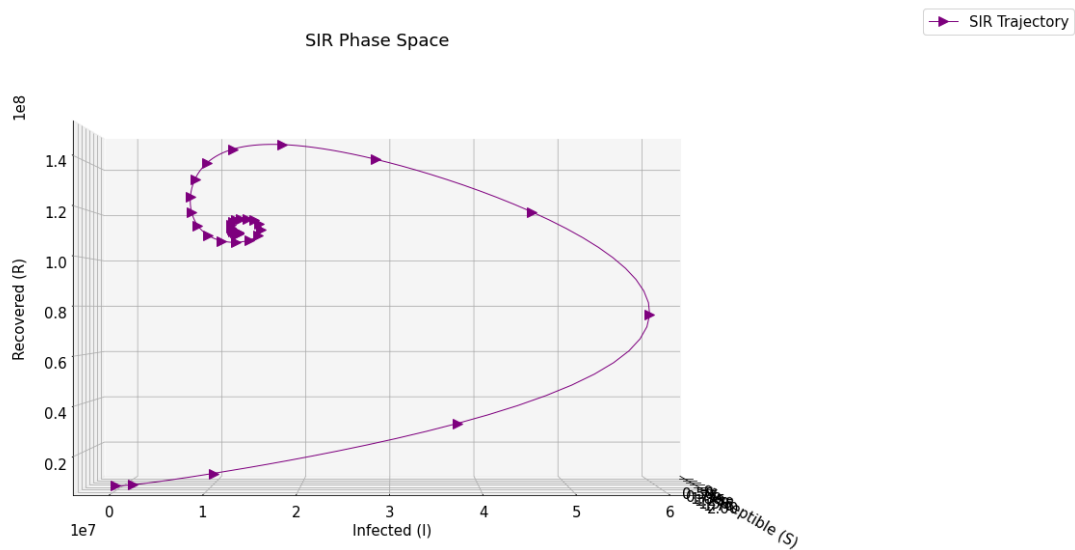
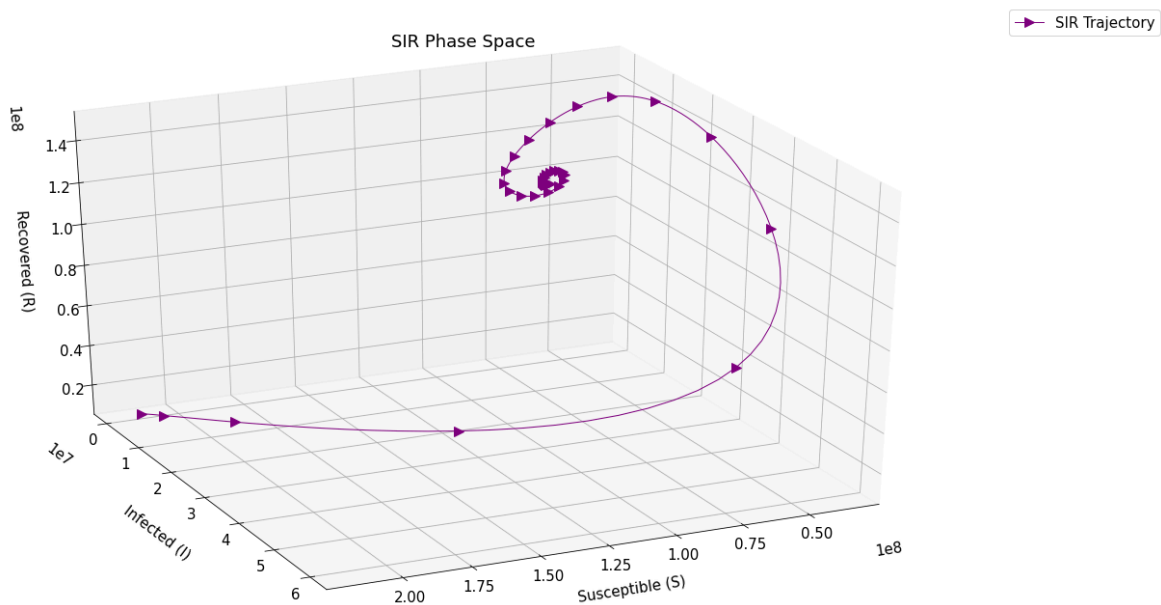
I first made a 2D plot for this code using the classes' version to ensure it gave the correct results and then developed the 3D version.

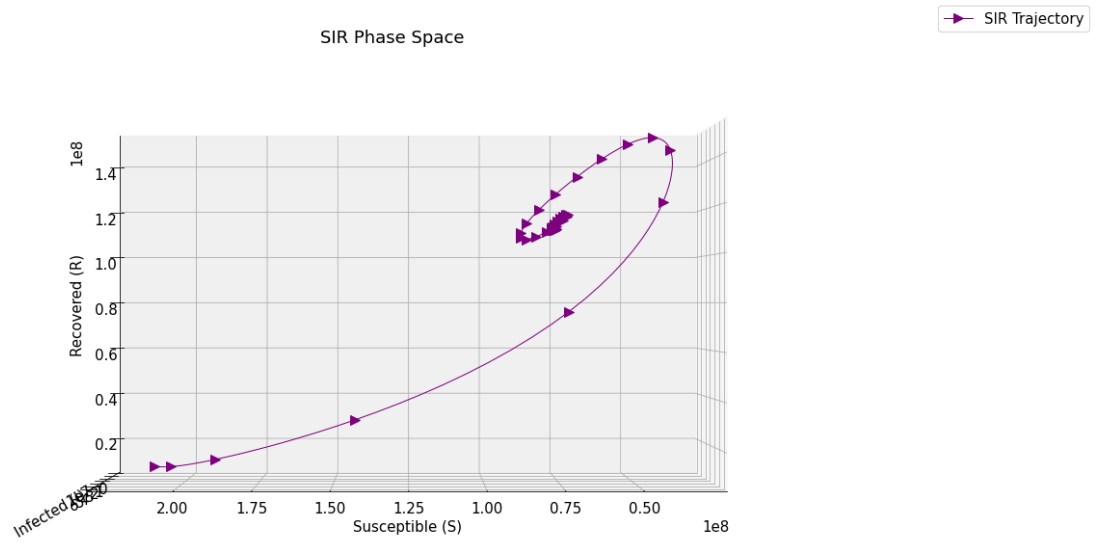
The plots show the population going through an infectious disease spread, represented by the SIR model. These trajectories represent the evolution of the disease over time in a three-dimensional state space where each axis corresponds to one compartment of the model.

The plots show that the disease starts with many susceptible individuals (high S value), which then decreases as the infection spreads (increase in I). Over time, the number of susceptible and infected individuals decreases as the population recovers (increase in R). The trajectory demonstrates a typical epidemic curve where an initial outbreak is followed by a decline in infections due to the depletion of susceptible individuals and the increase of recovered individuals. The loops in the phase space may indicate recurring outbreaks, likely due to the loss of immunity or the introduction of new susceptible individuals into the population.

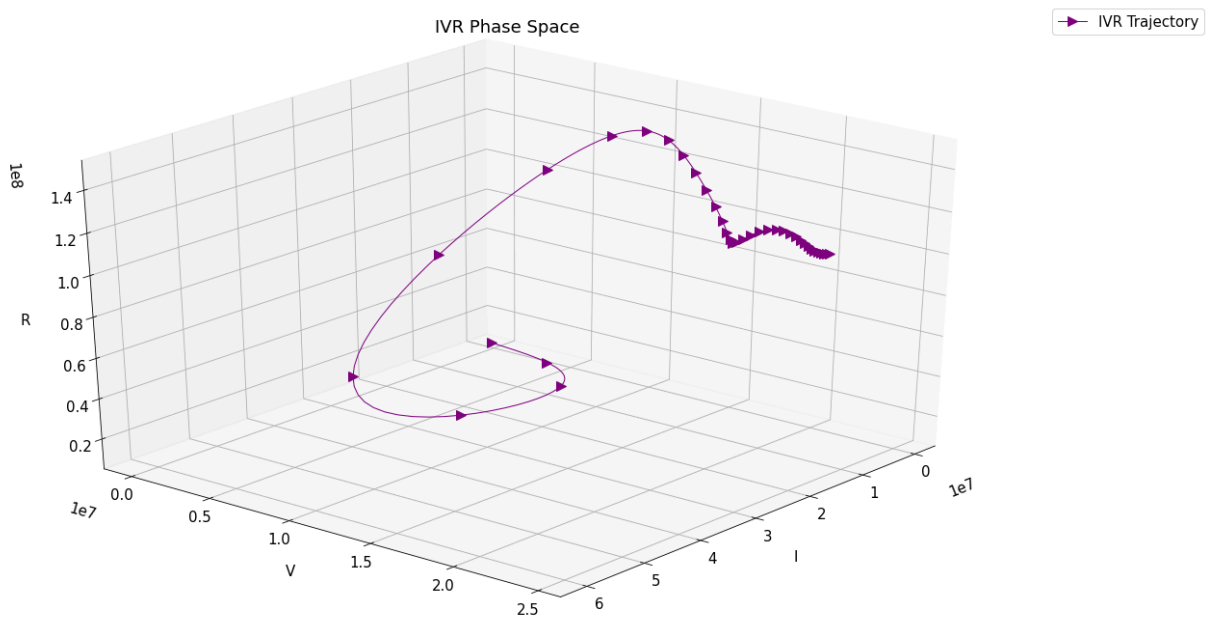
The three-dimensional view lets us understand the connection between different states and how interventions like vaccination can alter the trajectory. The parameters chosen for the simulation will affect the shape of the trajectory, with the rate of infection (β) and recovery (γ) being particularly influential. The model has the same limitations as the SIRVD model.

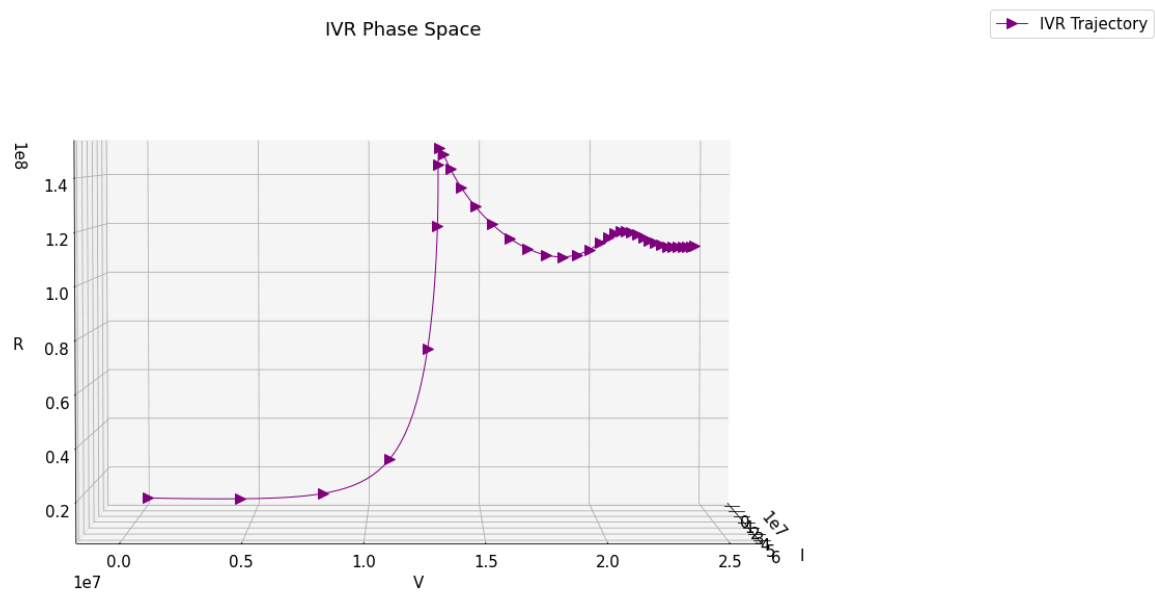
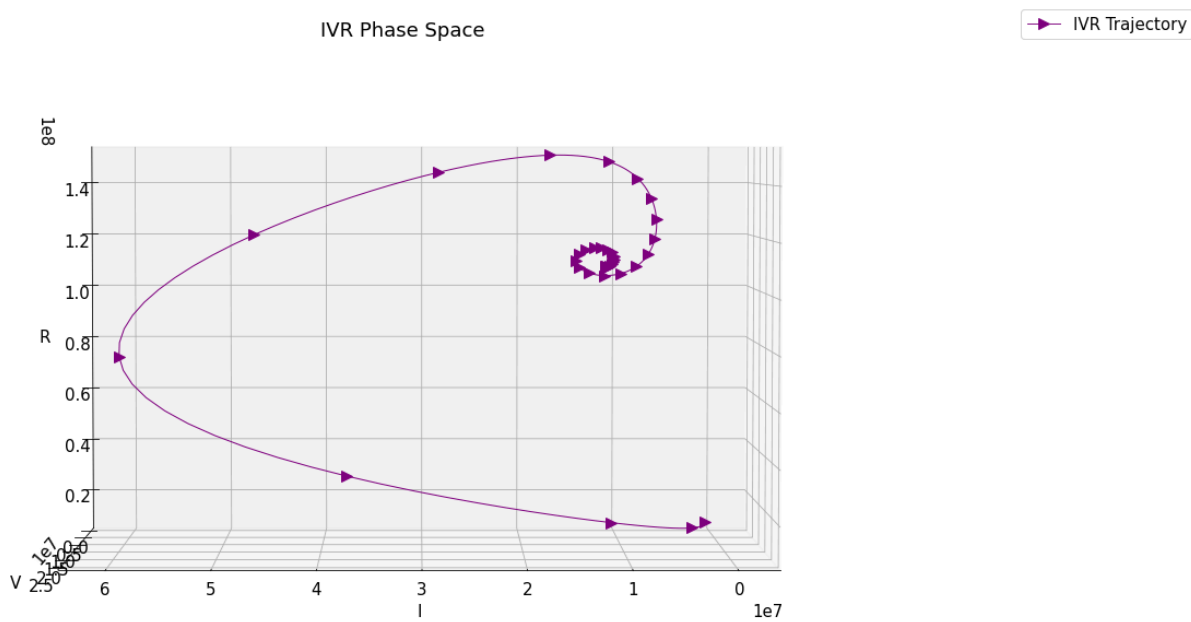
I tried making the arrows in the lines as apparent as possible. The direction from the visualizations in images 5, 6, and 7 is from left to right. In images 8, 9, and 10, we have the first and second visualizations going from right to left, and the third going from left to right.

Imagens 5, 6 e 7: SIR Model



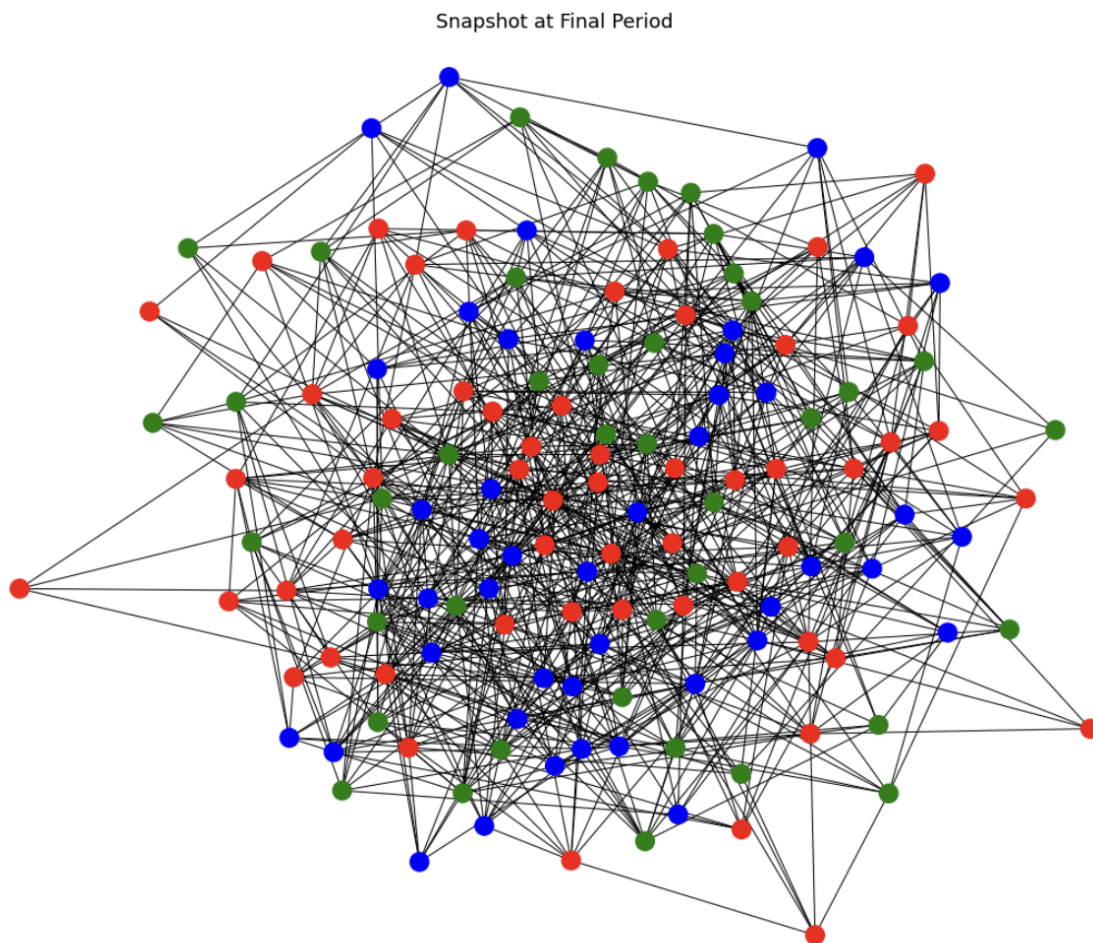
Images 8, 9, and 10: IVR Model





Agent-based simulation

I decided to do a model simulation of the spread of an infectious disease through a population using a network-based approach, considering individual interactions. Each node in the network represents an individual, color-coded by their disease status: susceptible (blue), infected (red), or recovered (green). The model includes vaccination, with a certain percentage of the population initially vaccinated. Infections spread as infected individuals interact with susceptible ones, who may then become infected themselves. Recovery is assumed after 14 days, with a small chance of reinfection. The model runs for a set number of days, taking snapshots of the disease spread at regular intervals. The final snapshot depicts the end state of the outbreak within the network.



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