Modeling and Analysis of COVID-19 and Dynamical Systems in Biology and Physics

Vladimir Grbić

University of Central Florida - Department of Physics

Abstract

COVID-19 has posed a great threat to public health after the first cases in the U.S. were reported back in January 2020. Since then, the United States has become the country with the most reported cases. A year later, that number is over 30 million as of March 26, 2021. The purpose of this research is to analyze various dynamical systems found in nature and conclude some of the common patterns that tie them. Once we know how to approach modeling such dynamical systems, we will apply those techniques to understand and mathematically describe the propagation of the novel coronavirus known as COVID-19. Hence, this research aims to contribute to a better understanding of the properties of COVID-19 propagation as well as the main factors that initiate its acceleration.
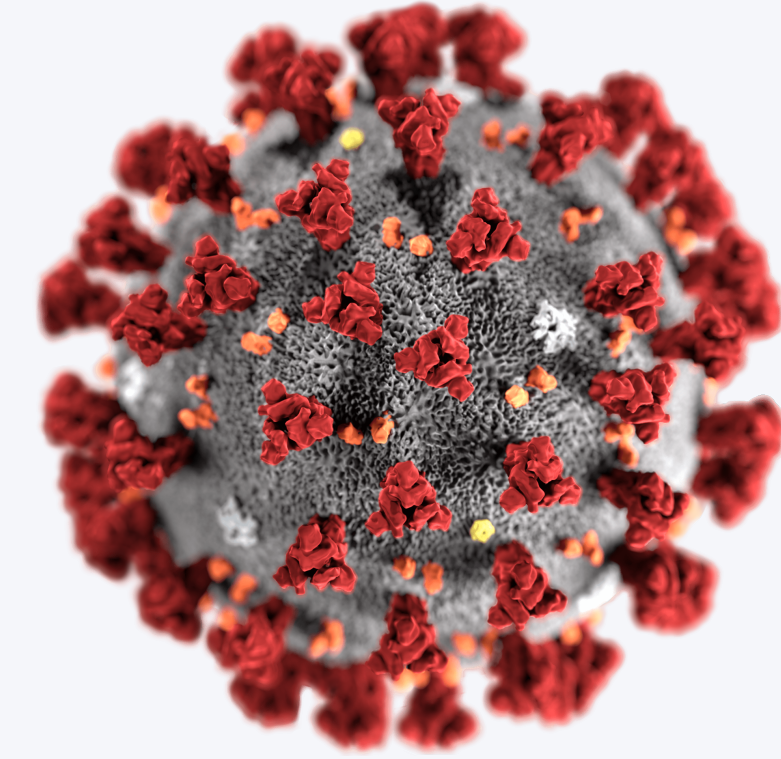
We propose the SIHQARD model to simulate the dynamics of the spread of COVID-19 in some regions of the United States. We use reported data from the CDC and WHO to identify parameters needed to properly represent the dynamics of this contagious agent, and hope to investigate the changes that our model poses through parameter variations. We have also developed an expression for the basic reproductive number $\mathcal{R}_0$ using the Next Generation Matrix method.

Assumptions

- The total number of people N is constant, and always equals the sum of all of the populations of groups.
$$N = S(t) + I(t) + H(t) + Q(t) + A(t) + D(t) + R(t) = \text{constant}$$
- Immunity after recovery is implied. This means that once recovered, an individual is no longer susceptible to getting COVID-19 again.
- Incubation period, the period during which an individual is infective but is not showing any symptoms is 6 days.
- The total number of people (N) is always much greater than the number of people an average person is in contact with.
- Mortality rate due to causes other than COVID-19 is set to zero.
- Population density is uniform (homogeneous).
- Quarantined and Asymptomatic groups always recover.
- Transmission rate is the rate at which different infected groups can transmit the disease at a given time. It depends on
  - the population of an infected group ($I(t)$, $H(t)$, $Q(t)$, or $A(t)$) at a given time,
  - and the effectiveness of transmission.
- Effectiveness of transmission is a constant, intrinsic property of each infected group ($I(t)$, $H(t)$, $Q(t)$, or $A(t)$) and it shows how effective an individual of that group is at transmitting the disease.

Mathematical Model

Groups

- $S(t)$ - *Susceptible*: individuals who can get infected if exposed to the infectious agent
- $I(t)$ - *Infective*: individuals who are infected but not yet showing the symptoms
- $H(t)$ - *Hospitalized*: infected individuals who are showing severe symptoms, and are hospitalized because of their critical state (mostly affected due to the preexisting conditions)
- $Q(t)$ - *Quarantined*: infected individuals who are showing the symptoms and are self-quarantined because they are not in a critical state
- $A(t)$ - *Asymptomatic*: infected individuals who are who will never develop any symptoms and can spread the virus
- $R(t)$ - *Recovered*: individuals who have recovered from the virus and can never get infected again
- $D(t)$ - *Deceased*: individuals who passed away due to the complications caused by the virus

Parameters

- α - transmission rate (same as infection rate)
$$\alpha_j = \varepsilon_j \cdot j \quad \text{where } j = I, \ H, \ Q, \ \text{or } A$$
- γ - recovery rate (constant)
- $\mathcal{R}_0$ - basic reproductive number (constant)
- ε - effectiveness of transmission COVID-19 for a particular group (constant)
- η - harmfulness of COVID-19 to the infected groups (constant)
- μ - mortality rate due to COVID-19 (constant)
- τ - average time taken for a particular event

Methods

The Logic

The SIHQARD model is a deterministic, compartmental model that describes the flow of the virus through an initially susceptible population. After individuals are in contact with the virus, they become infected and will inevitably migrate to either of three different compartments based on the severity of their symptoms. More vulnerable (predisposed) individuals are hospitalized, those presenting mild symptoms are quarantined, and the rest are asymptomatic. Individuals who are infected can ultimately recover, or in the case of more severe cases, pass away.

Solving Methods

The inflow and outflow through the compartments are represented mathematically using a system of nonlinear ordinary differential equations that are solved numerically using Python 3 programming language with the help of Scipy, Sympy, Numpy, and Matplotlib libraries. A linearized subsystem describing infectious compartments about the disease-free equilibrium (DFE) is used to determine an expression for $\mathcal{R}_0$ by the Next Generation Matrix method.

Flowchart

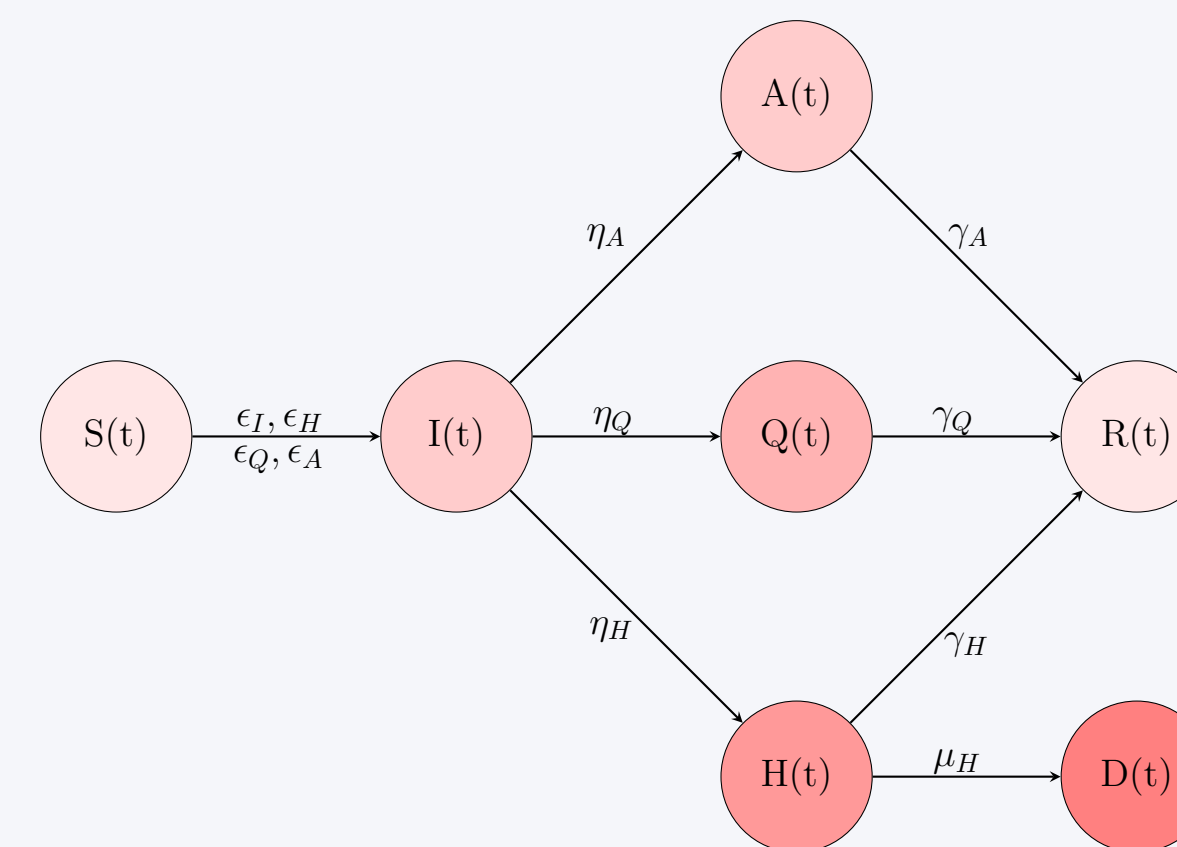The classification and promotion of individuals into different groups are depicted in Figure 1.

Figure 1: The SIHQARD Model Flowchart

SIHQARD Model

The following system of nonlinear differential equations represents the SIHQARD model and tries to explain the dynamics of COVID-19.

$$\frac{dS}{dt} = -(\alpha_I + \alpha_H + \alpha_Q + \alpha_A)S$$
$$= -(\varepsilon_I I + \varepsilon_H H + \varepsilon_Q Q + \varepsilon_A A)S \tag{1}$$

$$\frac{dI}{dt} = +(\alpha_I + \alpha_H + \alpha_Q + \alpha_A)\frac{S}{N} - (\eta_H + \eta_Q + \eta_A)I$$
$$= +(\varepsilon_I I + \varepsilon_H H + \varepsilon_Q Q + \varepsilon_A A)\frac{S}{N} - (\eta_H + \eta_Q + \eta_A)I \tag{2}$$

$$\frac{dH}{dt} = +\eta_H I - (\mu_H + \gamma_H H) \tag{3}$$

$$\frac{dQ}{dt} = +\eta_Q I - \gamma_Q Q \tag{4}$$

$$\frac{dA}{dt} = +\eta_A I - \gamma_A A \tag{5}$$

$$\frac{dR}{dt} = +\gamma_H H + \gamma_Q Q + \gamma_A A \tag{6}$$

$$\frac{dD}{dt} = +\mu H \tag{7}$$

Acknowledgements

Preliminary Results

The following graph in Figure 2 represents the solution of the SIHQARD model based on the current data on COVID-19. The proportions of the groups are portrayed are graphed as functions of time from day 30 to day 450.
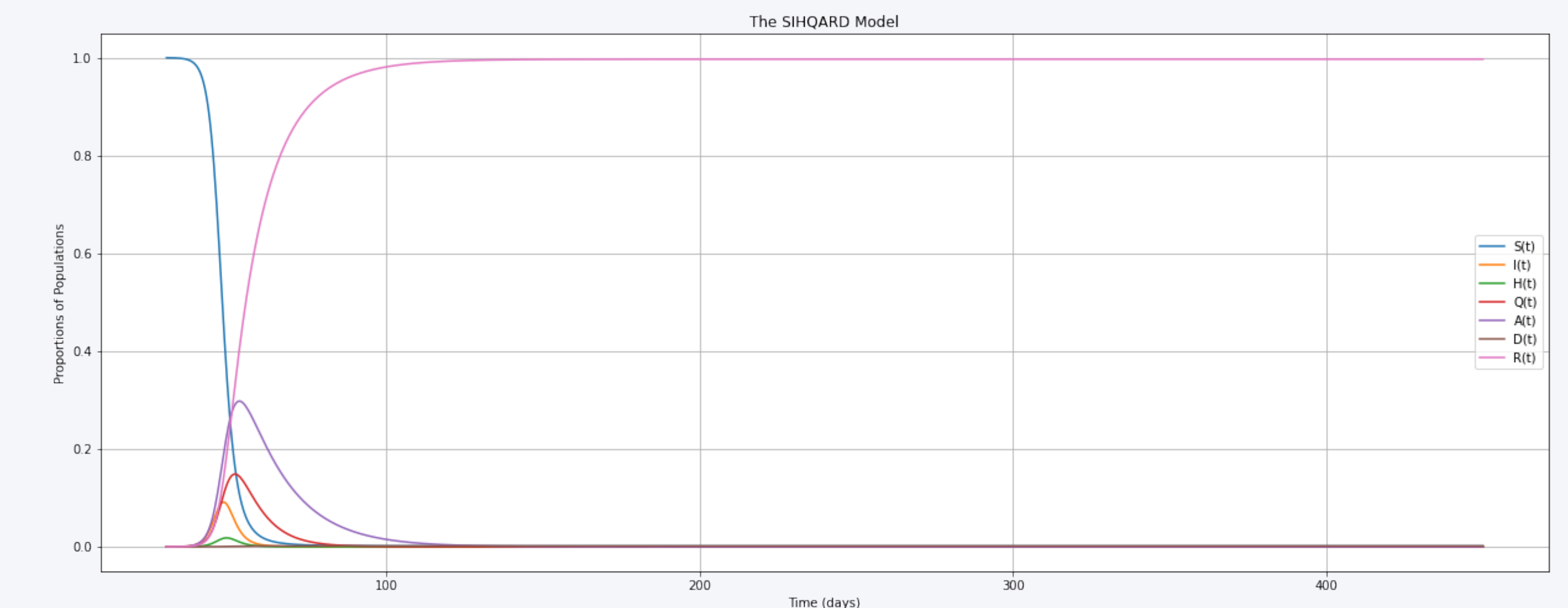

Figure 2: The SIHQARD Model Solution

After analyzing our results, we can conclude that after 450 days, 0.001734% of the population will die. This translates to the death toll of about 577,000.

Basic Reproductive Number

The basic reproductive number $\mathcal{R}_0$, or reproductive ratio, is the number of average cases an infected individual generates during their infectious period in a completely uncontrolled environment with a susceptible or disease-free population. It is, therefore, an important indicator of the contagiousness of an infectious agent. If $\mathcal{R}_0 < 1$ the disease will fail to spread, and if $\mathcal{R}_0 > 1$ the number of infections produced by the next generation will increase and the disease will spread. In our model,

$$\mathcal{R}_0 = \rho(G) \tag{8}$$

where ρ is the spectral radius function and the next generation matrix is

$$G = \begin{bmatrix} \frac{\gamma_Q\gamma_A(\epsilon_I(\mu+\gamma_H)+\epsilon_H\eta_H)+(\mu+\gamma_H)(\epsilon_Q\eta_Q\gamma_A+\epsilon_A\eta_A\gamma_Q)}{(\eta_H+\eta_Q+\eta_A)(\mu+\gamma_H)\gamma_Q\gamma_A} & \frac{\epsilon_H}{(\mu+\gamma_H)} & \frac{\epsilon_Q}{\gamma_Q} & \frac{\epsilon_Q}{\gamma_A} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}. \tag{9}$$

Therefore,

$$\mathcal{R}_0 = \frac{\gamma_Q\gamma_A(\epsilon_I(\mu+\gamma_H)+\epsilon_H\eta_H)+(\mu+\gamma_H)(\epsilon_Q\eta_Q\gamma_A+\epsilon_A\eta_A\gamma_Q)}{\gamma_Q\gamma_A(\eta_H+\eta_Q+\eta_A)(\mu+\gamma_H)} = 6.6208. \tag{10}$$

Future Work

As we believe that our work will be of interest to public health, we plan to improve our model and publish our work in scientific journals such as the American Journal of Physics and the European Journal of Physics. We are already in process of writing a paper. In it, we draw connections to other models, explain our techniques, and reference many useful sources, in hope that this research serves as an excellent starting point for other undergraduate researchers and their mentors in understanding how modeling dynamical systems can be applied to their fields. We hope that we can also get a chance to present our work through various academic events and reach audiences of various disciplines.

References

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