Modelling the COVID-19 Pandemic: A Dynamic Systems Approach with MATLAB Simulink

Joan Saurina i Ricós
21783219B

Sergi Tomàs Martínez
39959144W

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Abstract

This paper explores the design, implementation, and analysis of a dynamic system model for the COVID-19 pandemic in Catalunya using MATLAB Simulink. Central themes include the examination of observability, stability, and controllability in the context of pandemic spread and control. We further probe into the design of controllers for dynamic systems that mimic real-world phenomena. The data used is theoretically grounded, although fictional, and is intended purely for academic exercises.

Contents

1 Introduction

The intricate dynamism of infectious diseases poses an immense challenge to global public health. This is acutely felt in the ongoing COVID-19 pandemic. In grappling with these complexities, mathematical modelling has emerged as a critical tool, offering a prism through which we can understand, anticipate and influence the course of the pandemic.

Embarking on this path, our study utilises MATLAB Simulink to explore dynamic systems modelling of the COVID-19 pandemic. This approach allows us to delve into essential control engineering concepts such as observability, stability, and controllability, applied in the unique and demanding context of a pandemic.

Our journey begins with a relatively simple SIR (Susceptible, Infected, Recovered) model, which lays the foundation for our subsequent exploration. This serves as a useful starting point, but, as with all models, it has limitations. As we progress, we introduce additional layers of complexity, refining our model to better reflect the multifaceted reality of a pandemic.

In the SEIRD (Susceptible, Exposed, Infected, Recovered, Deceased) model, we account for an incubation period and introduce a fatal outcome. Then, we factor in the role of healthcare infrastructure, considering how hospital capacity can influence outcomes.

Finally, we incorporate a vaccination programme into our model, reflecting another critical aspect of pandemic response. We also explore how the emergence of a new variant can alter the dynamics of disease spread and control.

With each step, we get closer to a model that captures the essential features of the COVID-19 pandemic. At the same time, we illustrate how dynamic system modelling can illuminate the paths available to us in navigating a complex public health crisis.

2 SIR Model

The SIR model is a simple yet powerful model used to understand the dynamics of infectious diseases in large populations. This model divides the total population, N, into three compartments: susceptible individuals, S, who are capable of contracting the disease; infected individuals, I, who have the disease and can spread it to the susceptible individuals; and recovered individuals, R, who have recovered from the disease and are now immune to it.

2.1 Mathematical Formulation

The SIR model is governed by the following set of ordinary differential equations:

$$\frac{dS}{dt} = -\frac{\beta}{N}SI, \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta}{N}SI - \gamma I, \tag{2}$$

$$\frac{dR}{dt} = \gamma I. \tag{3}$$

In these equations, β is the transmission rate of the disease and γ is the recovery rate. The total population size N is given by the sum of the susceptible, infected, and recovered individuals:

$$N = S + I + R. \tag{4}$$

The standard SIR model assumes that the total population is constant, i.e., no births or deaths are considered outside the disease-caused mortality. This assumption simplifies the understanding of disease spread dynamics, focusing primarily on the transitions between susceptibility, infection, and recovery.

2.2 Initial values

For the variables and ratios exposed in the previous section we have their fictional initial values:

- **Population of Catalonia:** The population of Catalonia is approximately 7.7 million people.

- **S (Susceptible):** In the early stages of a pandemic, we assume that nearly everyone is susceptible. So, let's start with 7,699,000 individuals (approximately 99.99 % of the population).

- **I (Infectious):** We suppose that initially 0 individuals are infectious.

- **R (Recovered):** We suppose that initially 0 individuals are recovered.

- **β** : For COVID-19, early estimates ranged from 0.1 to 0.5, but it would depend on many factors including social behaviors and preventive measures. We suppose it's 0.3 .

- **γ** : is defined as the reciprocal of the mean infectious period. If, for example, the infectious period of COVID-19 is approximately 7-14 days. Therefore, we consider the range of 0.07 to 0.14. Particularly, we suppose it's 0.1.

2.3   Simulink Modeling

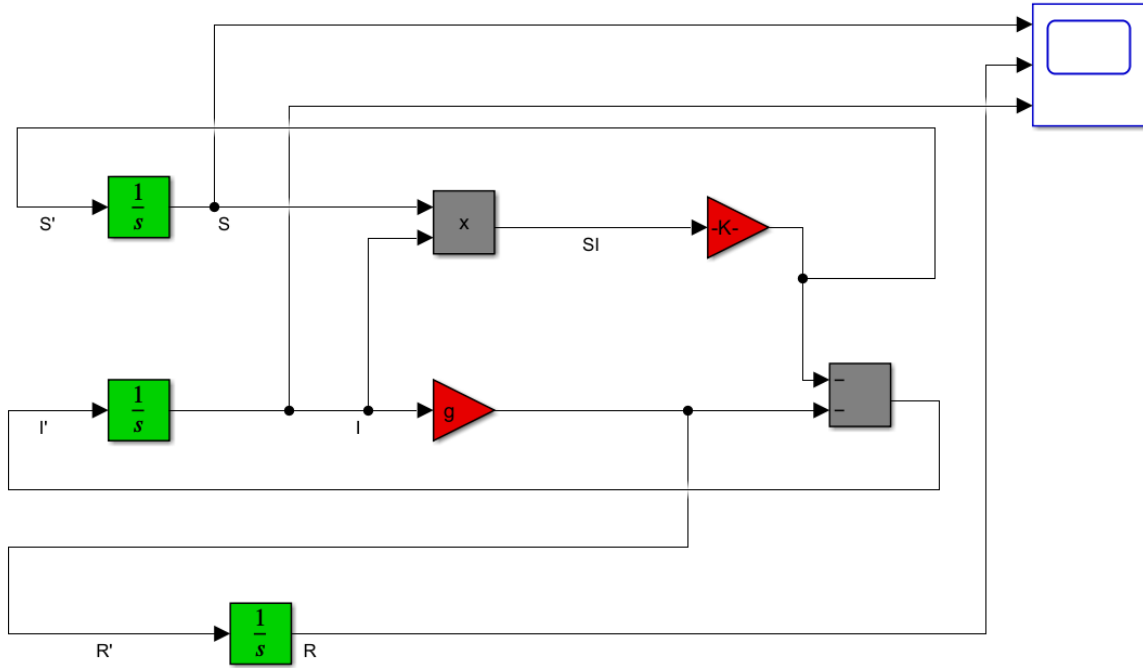The implementation in Simulink of the SIR model is the following:

Figure 1: SEIRD Model in Simulink

2.4   Experimentation

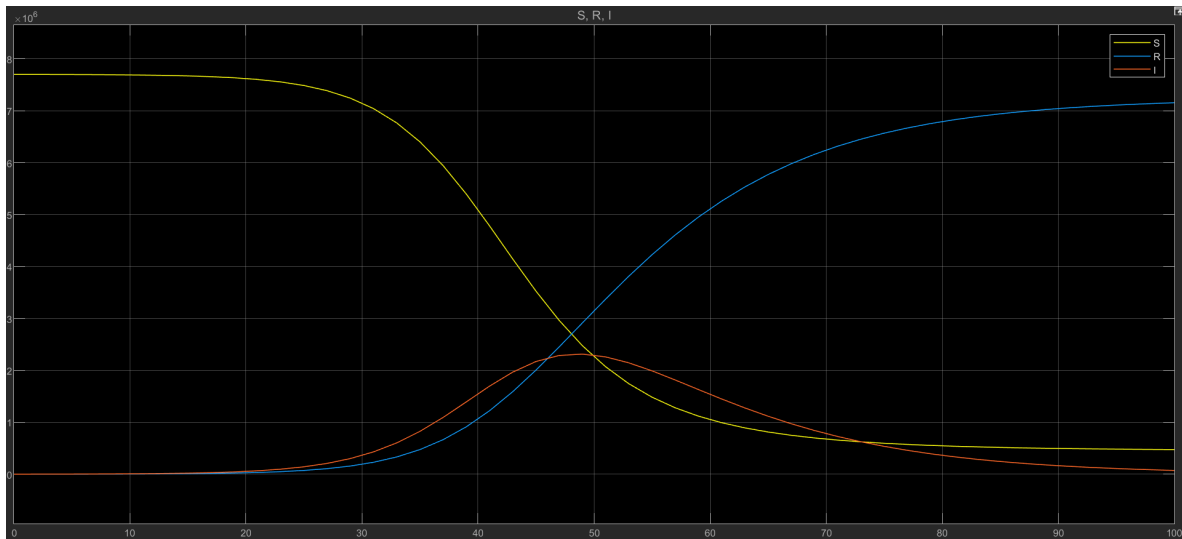The SIR Simulink model working with proposed initial conditions, shows the following curves:

Figure 2: SIR curves model

In order to understand the impacts of the parameters on the model, we experiment by setting them to different values and observing how this changes the outputs of your model. For instance:

Increasing β (while keeping γ constant), it is thought that the disease spreads more quickly because

more people get infected in a given period of time. The peak of the infection curve (I) will be higher and will be reached more quickly:
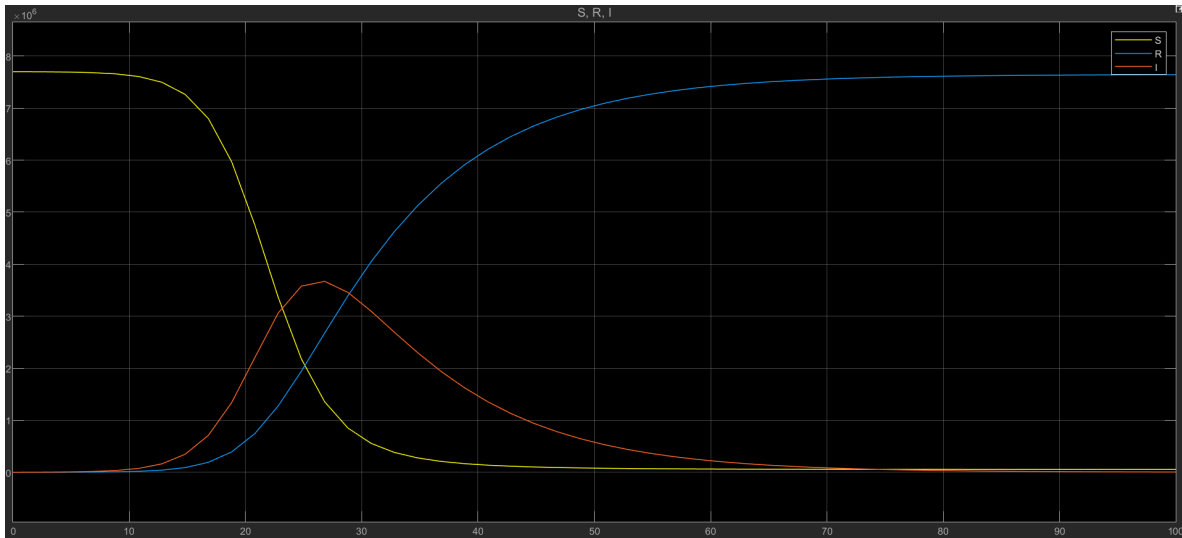
β : 0.5

Figure 3: SIR curves model (β 0.5)

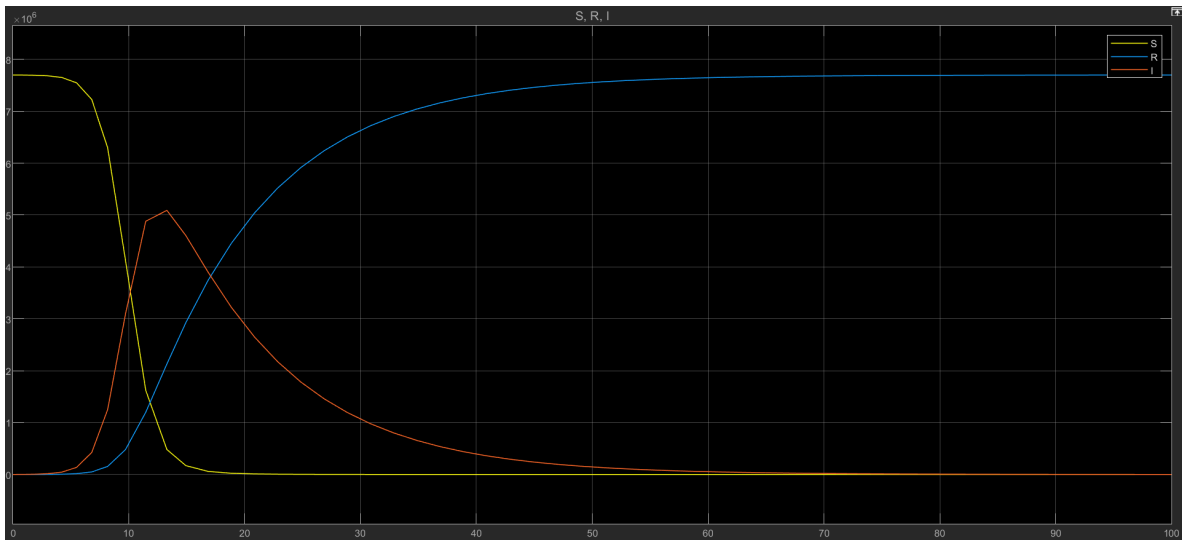β : 1

Figure 4: SIR curves model (β 1)

Increasing γ (while keeping β constant), it is thought that the disease spreads more slowly because people recover more quickly. The peak of the infection curve (I) will be lower and will be reached more slowly.
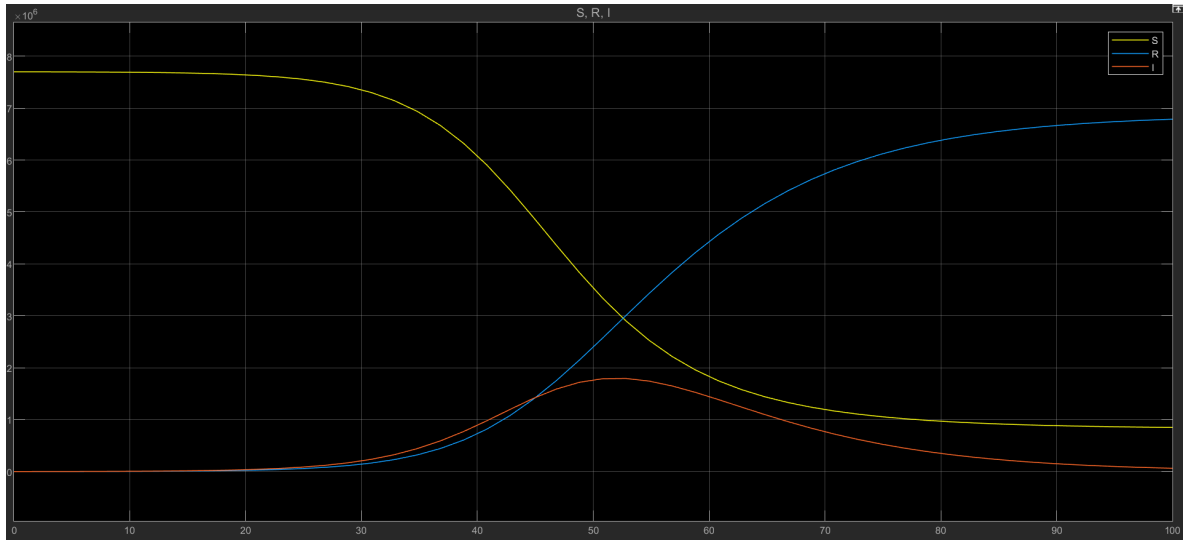
γ : 0.12

Figure 5: SIR curves model (γ 0.12)
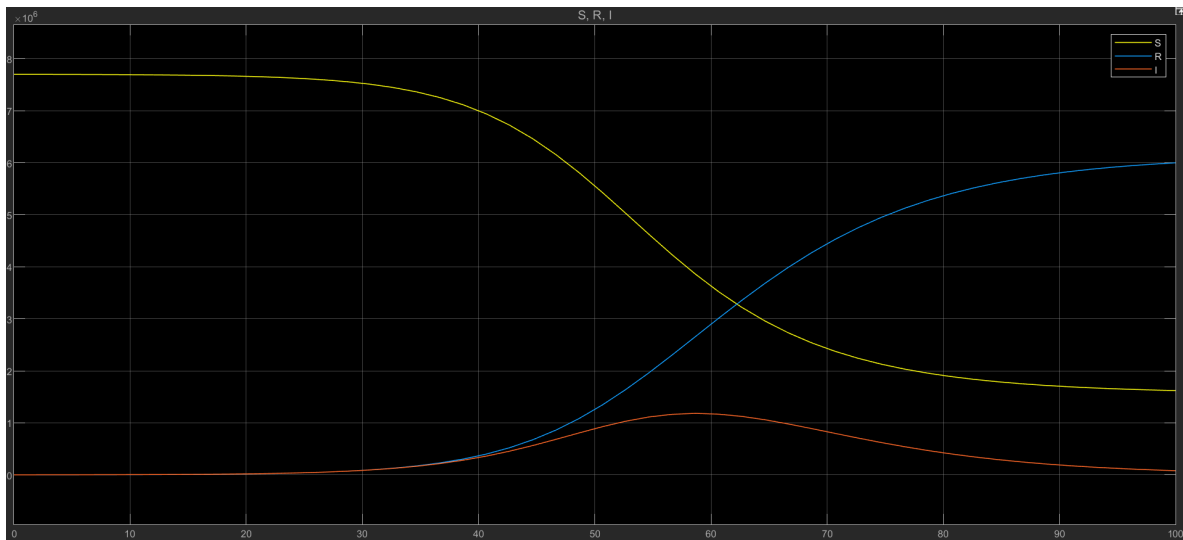
γ : 0.15

Figure 6: SIR curves model (γ 0.15)

3   SEIRD Model

The SIR model, while useful, lacks the ability to account for exposed individuals who are infected but yet to be confirmed as such. Furthermore, it does not provide information on the cases involving infectious individuals who have passed away. To address these shortcomings, we can extend the SIR model by introducing an exposed variable, leading to the SEIR model, and a death variable, leading to the SIRD model. By incorporating both these variables, we arrive at the more general SEIRD model, which is the focus of this section.

3.1   Mathematical Formulation

The SEIRD model can be expressed as a set of differential equations. Let S denote the number of susceptible individuals, E the number of exposed individuals, I the number of infected individuals, R the number of recovered individuals, and D the number of deaths. We introduce the new parameters λ (rate from exposure to infection) and δ (death rate).

The system of differential equations is as follows:

$$\frac{dS}{dt} = -\frac{\beta}{N}SI, \tag{5}$$

$$\frac{dE}{dt} = \frac{\beta}{N}SI - \lambda E, \tag{6}$$

$$\frac{dI}{dt} = \lambda E - \gamma I - \delta I, \tag{7}$$

$$\frac{dR}{dt} = \gamma I, \tag{8}$$

$$\frac{dD}{dt} = \delta I. \tag{9}$$

Adding equations 5 through 9 yields zero, confirming that the total population remains constant:

$$N = S + E + I + R + D. \tag{10}$$

This formulation enables us to account for the progression of the disease through different stages, from susceptibility and exposure to infection, recovery, and death.

3.2 Simulink Modeling

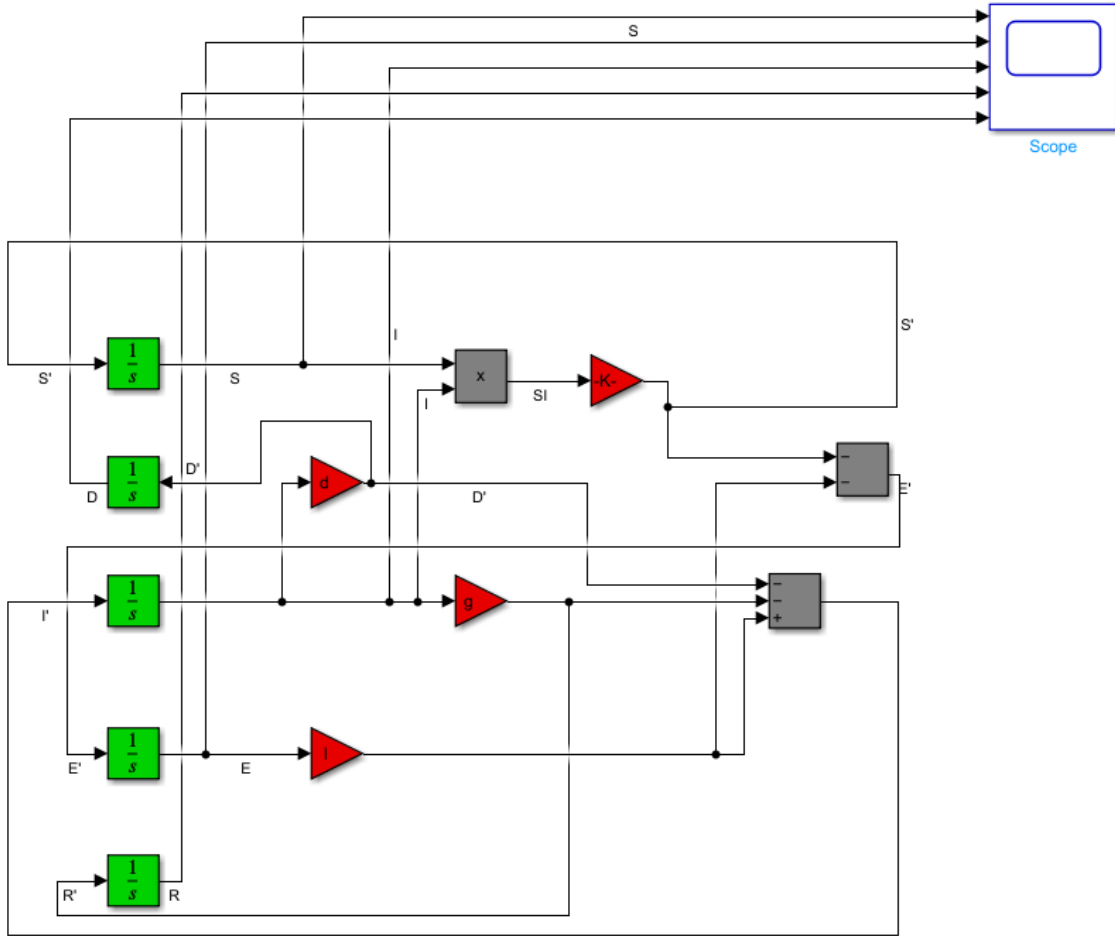The implementation in Simulink of the SEIRD model is the following:

Figure 7: SEIRD Model in Simulink

3.3 New variables values

The new variables take the following values:

- **D (Deceased):** We suppose that initially 0 individuals are deceased.

- **E (Exposed):** We suppose that initially 0 individuals are exposed.

- λ : Given the incubation period of COVID-19 is approximately 2-14 days, with an average of about 5 days, so it's typically set in the range of 1/5 to 1/14 per day, which means 0.07 to 0.2. We suppose it's 0.2.

- δ A value of 0.02 may be reasonable under certain circumstances, but it can range broadly depending on the situation, say between 0.01 and 0.05. We suppose it's 0.02.

3.4 Experimentation

The SEIRD Simulink model working with proposed initial conditions, shows the following curves:
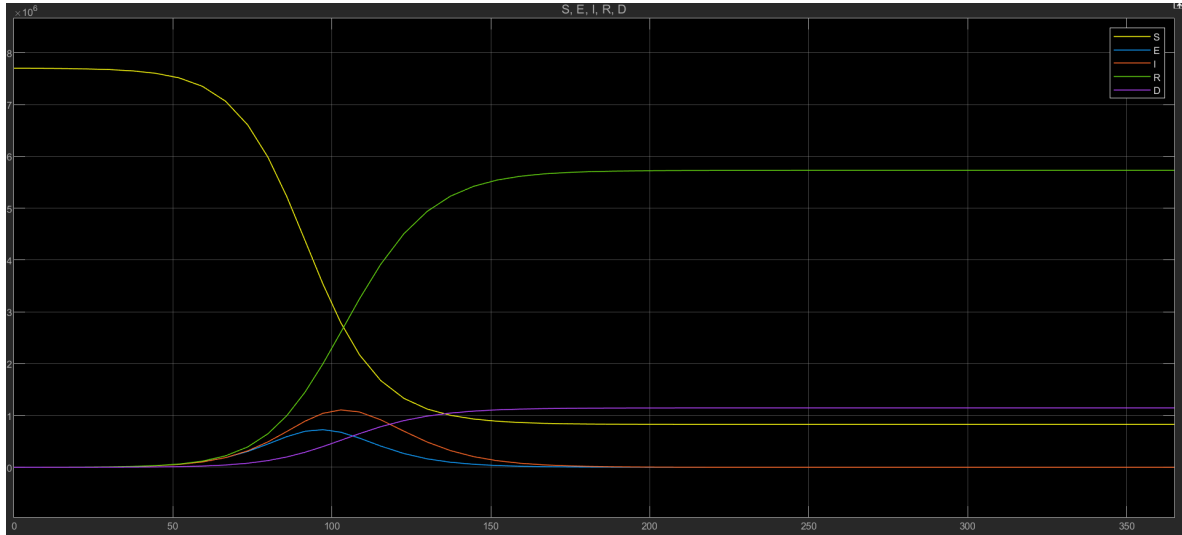

Figure 8: SEIRD Model curves

In order to understand the impacts of the parameters on the model, we experiment by setting them to different values and observing how this changes the outputs of your model. For instance:

Increasing λ (while keeping others constant): This leads to a faster transition from the exposed (E) to the infectious (I) category, meaning that the exposed individuals become infectious more quickly. Consequently, we should expect an earlier peak in the number of infections. On the flip side, if we lower λ, we should expect a delay in the onset of the infectious phase, hence the peak in infections would be reached later than usual:
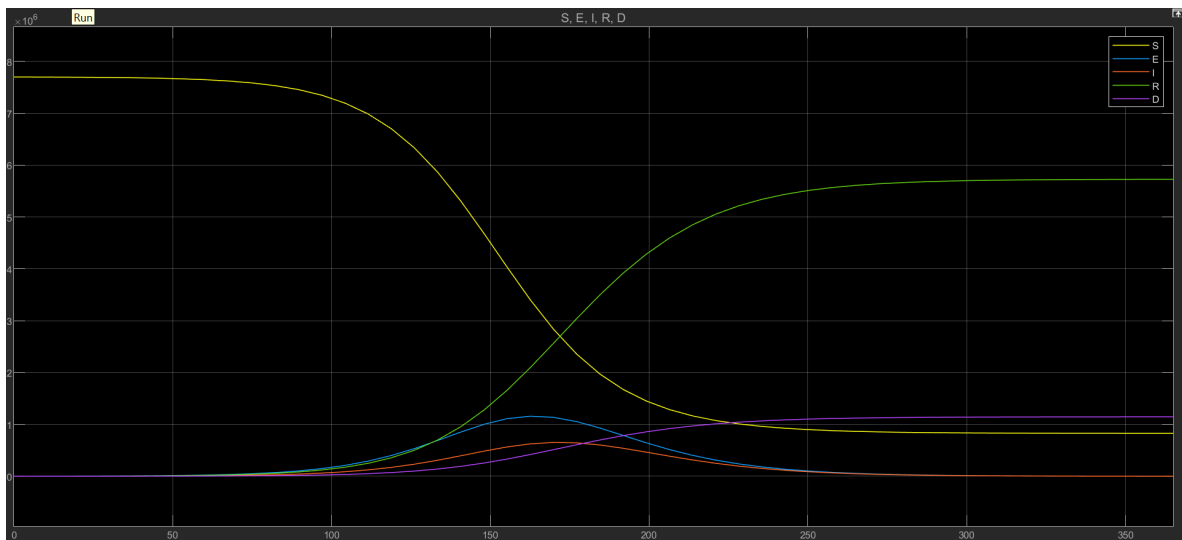
λ: 0.07

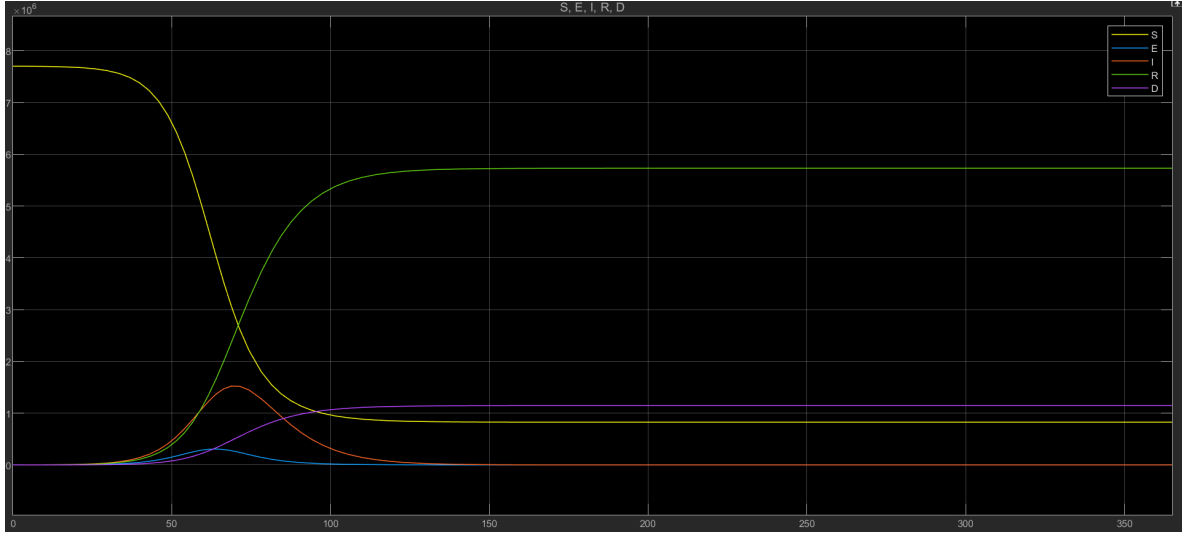Figure 9: SEIRD Model curves (λ : 0.07)

λ: 0.7

Figure 10: SEIRD Model curves (λ : 0.7)

Increasing **δ** (while keeping others constant): This leads to a higher death rate amongst infectious individuals, which would result in a steeper increase in the death curve (D). It also implies a quicker decrease in the infectious curve (I), since more infectious individuals are moving to the death category. If we lower **δ** , we should expect a slower increase in the death curve (D), a slower decrease in the infectious curve (I), and a corresponding faster increase in the recovered curve (R), assuming all other parameters are held constant. This is because a lower **δ** means fewer deaths among the infected population, hence more people are surviving and moving into the recovered (R) category.
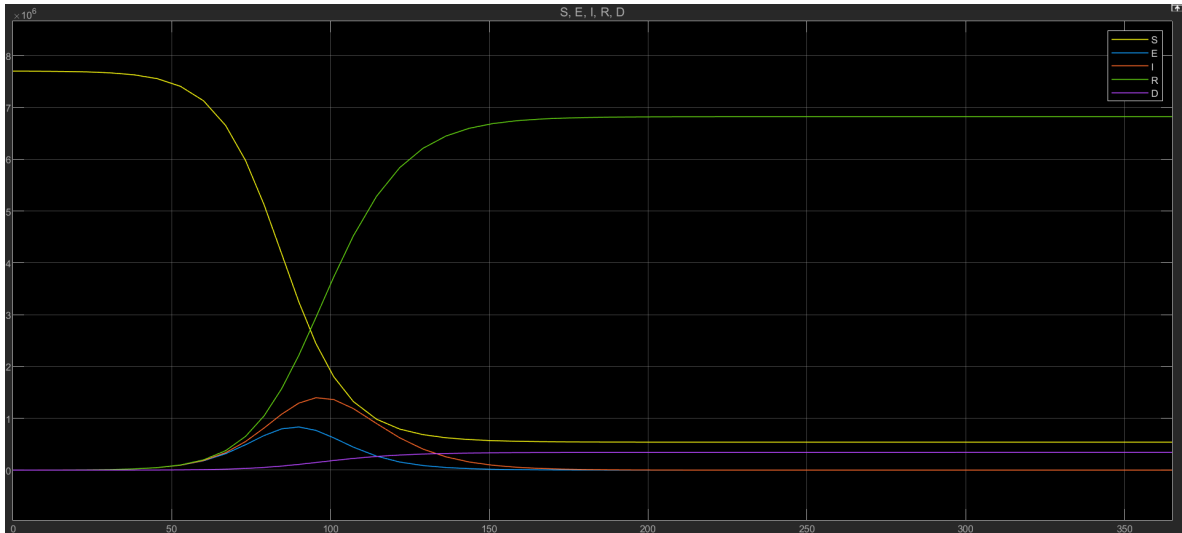
δ: 0.005

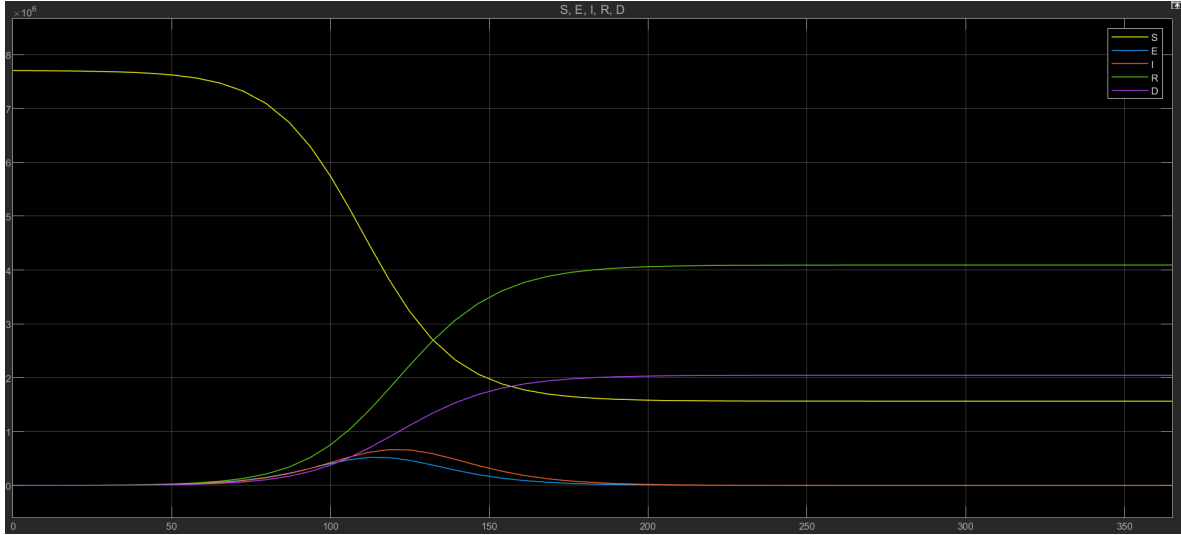Figure 11: SEIRD Model curves (δ : 0.005)

δ: 0.05

Figure 12: SEIRD Model curves (δ : 0.05)

The conducted experimentation on the SEIRD model, involving the manipulation of the transition rate parameter (λ) and the death rate parameter (δ), has yielded valuable insights into the dynamics of disease progression in a population.

When the transition rate parameter (λ) is increased, while keeping all other parameters constant, the model reflects a quicker progression from the exposed state to the infectious state. This manifests in the model as an earlier peak in the number of infections, a reflection of the fact that individuals in the population are becoming infectious at a faster rate. Conversely, a decrease in the value of λ delays the onset of the infectious phase, resulting in a delayed peak in infections.

An increase in the death rate parameter (δ), while other variables are held constant, results in a higher death rate among infected individuals, leading to a steeper rise in the death curve. This simultaneously causes a more rapid decrease in the infectious curve, as more infectious individuals transition into the death category. A decrease in the death rate parameter (δ) results in a slower rise in the death curve and a slower fall in the infectious curve, with a corresponding more rapid increase in the recovered curve. This is attributable to fewer deaths among the infected population, leading to a larger number of individuals transitioning into the recovered category.

These experiments underscore the sensitivity of the SEIRD model to the parameters, and the profound effect that minor changes can have on the resulting dynamics. The findings provide an opportunity to more comprehensively understand the progression of the disease, which in turn can guide the development of effective strategies for managing its spread. The manipulation of the parameters allows us to explore a variety of scenarios and possibilities, underscoring the need for accurate parameter estimation in real-world situations. Furthermore, it demonstrates the role of public health measures in potentially influencing these parameters and, by extension, the course of the epidemic.

4 Hospital

In this modification of the SEIRD model for the COVID-19 pandemic, a vital variable that accounts for hospital capacity has been introduced, thereby adding a layer of realism to the model. This added dimension incorporates the constraint that healthcare systems have a limited capacity, represented here by the number of hospital beds available in the region being modeled, in this case, Catalunya, which has a total of 35,952 hospital beds.

The model now distinguishes between scenarios where the healthcare system is not overwhelmed (i.e., the number of hospitalized cases, given by the ratio of the infected to the total population (0.05 * I), does not exceed the total number of available hospital beds), and scenarios where the healthcare system is overwhelmed (i.e., the number of hospitalized cases exceeds the total number of available hospital beds).

In scenarios where the healthcare system is not overwhelmed, the death rate δ remains at its initial value of 0.02. However, when the healthcare system becomes overwhelmed, the death rate δ doubles to 0.04. This augmentation represents the increased risk of mortality due to lack of sufficient medical care when healthcare systems are stretched beyond their capacity.

Consequently, we anticipate that the incorporation of this hospital capacity constraint into the SEIRD model will yield more pronounced 'peaks' and 'valleys' in the resulting graphs of the number of susceptible, exposed, infected, recovered, and dead individuals over time. In particular, we expect to observe a sharp increase in the death rate (D) once the healthcare system becomes overwhelmed, reflecting the increased mortality risk under such circumstances.

This modification can lead to significant changes in the system's dynamics, especially if the disease spreads rapidly and the number of infected individuals surpasses the healthcare system's capacity. If preventive measures are not enforced to slow down the spread and prevent healthcare systems from being overwhelmed, the model could predict a potentially tragic outcome with a high death toll.

These predictions can be used to inform public health policy decisions, such as implementing social distancing measures, or increasing healthcare capacity in anticipation of an impending wave of infections. They underline the importance of not overloading the healthcare system, and of controlling the spread of the virus to ensure that healthcare resources are not stretched beyond their limits.

4.1 Mathematical Model

The resulting model takes the folowing equations:

$$\frac{dS}{dt} = -\frac{\beta}{N}SI, \tag{11}$$

$$\frac{dE}{dt} = \frac{\beta}{N}SI - \lambda E, \tag{12}$$

$$\frac{dI}{dt} = \lambda E - \gamma I - \delta' I, \tag{13}$$

$$\frac{dR}{dt} = \gamma I, \tag{14}$$

$$\frac{dD}{dt} = \delta' I. \tag{15}$$

$$\delta' = \delta k. \tag{16}$$

where:

$$k = \begin{cases} 1, & \text{if } 0.05I <= 35952 \\ 2, & \text{otherwise} \end{cases} \tag{17}$$

35952 is the oficial number of total hospitalization places in Cataliona whenas Covid-19 pandemic started.

4.2 Simulink Modeling

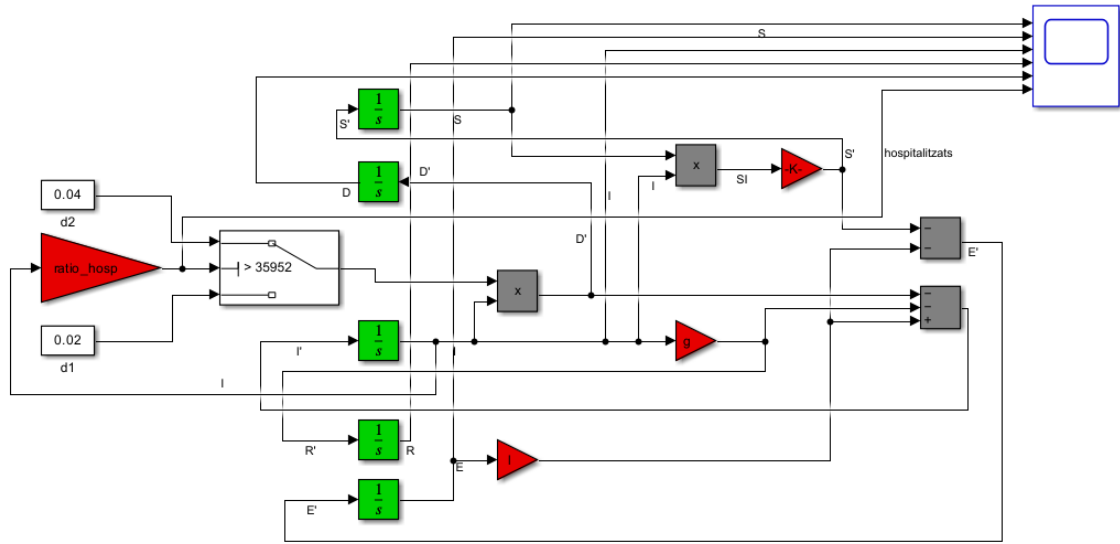The implementation in Simulink of the SEIRD + hospital model is the following:

Figure 13: SEIRD + hospital Model

4.3 Experimentation

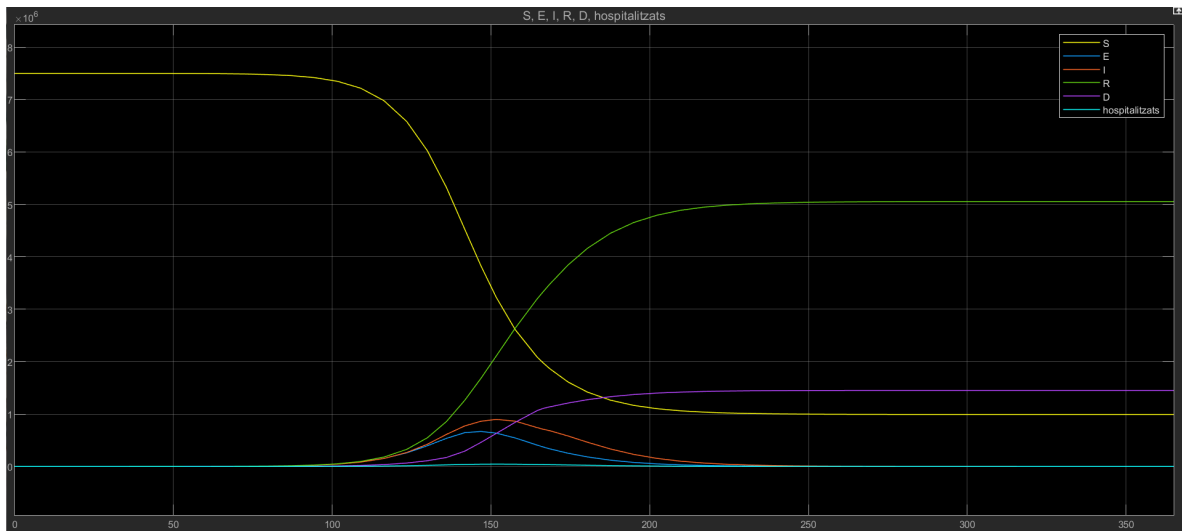The SEIRD + hospital Simulink model working with proposed initial conditions, shows the following curves:

Figure 14: SEIRD + hospital Model curves

4.3.1 Parameter Variations

The parameters to be modified are β and δ. This choice stems from their direct impact on disease spread and healthcare system capacity, respectively. These parameters significantly influence the dynamics of the pandemic, making them critical variables to study for informed public health decision-making.

Hypothesis for Changing Infection Rate (β):

The infection rate in the model represents the average number of contacts per person per time that could lead to transmission of the disease. If it is increased, this indicates that each infected person is transmitting the disease to more individuals within the same time period. Hence, we would expect the number of infected individuals (I) to rise more rapidly, potentially leading to a faster escalation in the number of severe cases requiring hospitalization.

If this surge in hospitalizations exceeds the available healthcare capacity (number of hospital beds), it would mean that the healthcare system is overwhelmed. As a consequence, not only COVID-19 patients but also patients with other severe illnesses might not receive the necessary care, leading to an overall increase in mortality.

Furthermore, an overwhelmed healthcare system could also indirectly increase the death rate (δ) from the disease, as patients may not receive adequate or timely care. Hence, higher values of β, if not accompanied by effective containment measures, could lead to a significant strain on the healthcare system and a higher death toll.
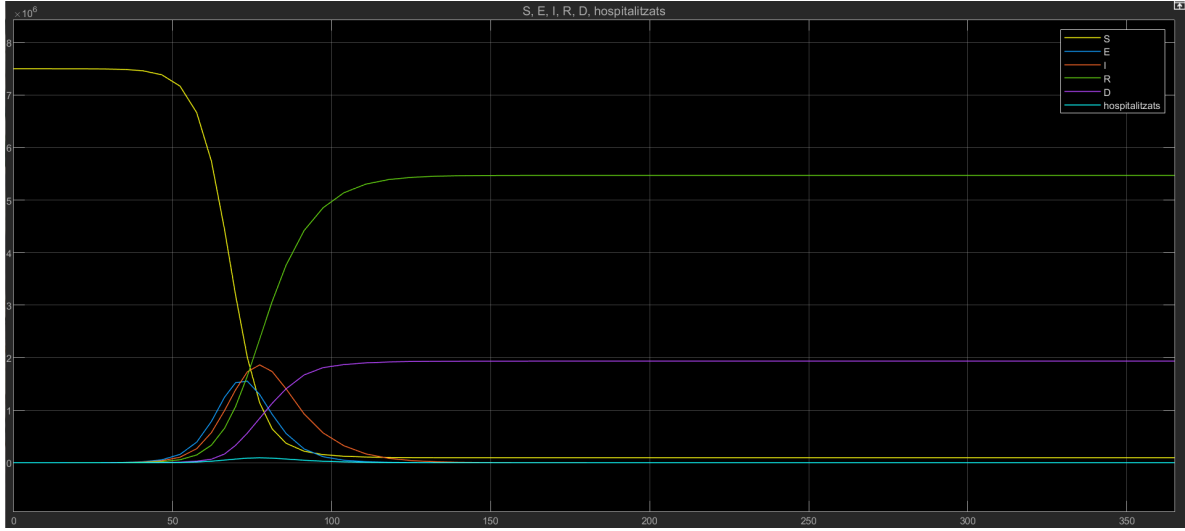
β: 0.6

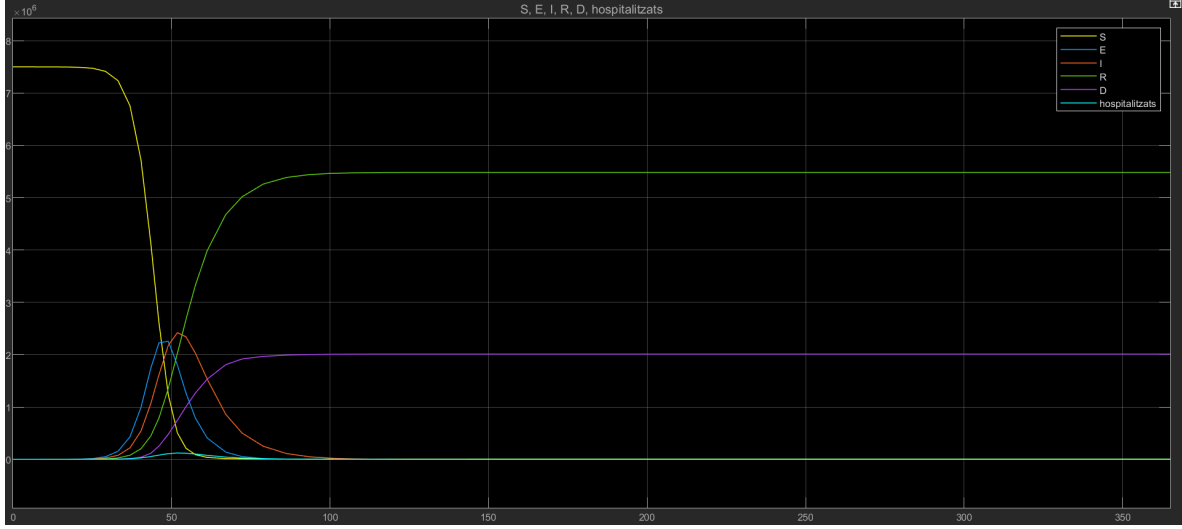Figure 15: SEIRD + hospital β: 0.6

β: 1

Figure 16: SEIRD + hospital β: 1

From this curves we learn that the higher is the death rate the faster the system converges. While the Infection curve pick is higher, the Deceased curve does not pass the 2.000.000, despite it does grow when he have changed β from 0.3 to 0.6.

Hypothesis for Changing Death Rate (δ):

The death rate represents the proportion of infected individuals who die from the disease. If it increases, it implies that the disease is becoming more lethal. This could be due to several reasons, such as the emergence of a more virulent strain of the virus, a decrease in the effectiveness of treatments, or the healthcare system becoming overwhelmed, preventing patients from receiving adequate care.

In this context, a higher δ consequence to healthcare system collapse would lead to an increase in the number of deaths (D), depleting the number of infected (I) at a faster rate, when the system does collapse. Additionally, if the rise is a consequence of an overwhelmed healthcare system, this may create a positive feedback loop where increased deaths further strain the healthcare system, leading to a further increase. Therefore, increased death rates, especially those resulting from an overwhelmed healthcare system, can have severe consequences, further emphasizing the importance of effective disease containment measures to protect healthcare capacity.
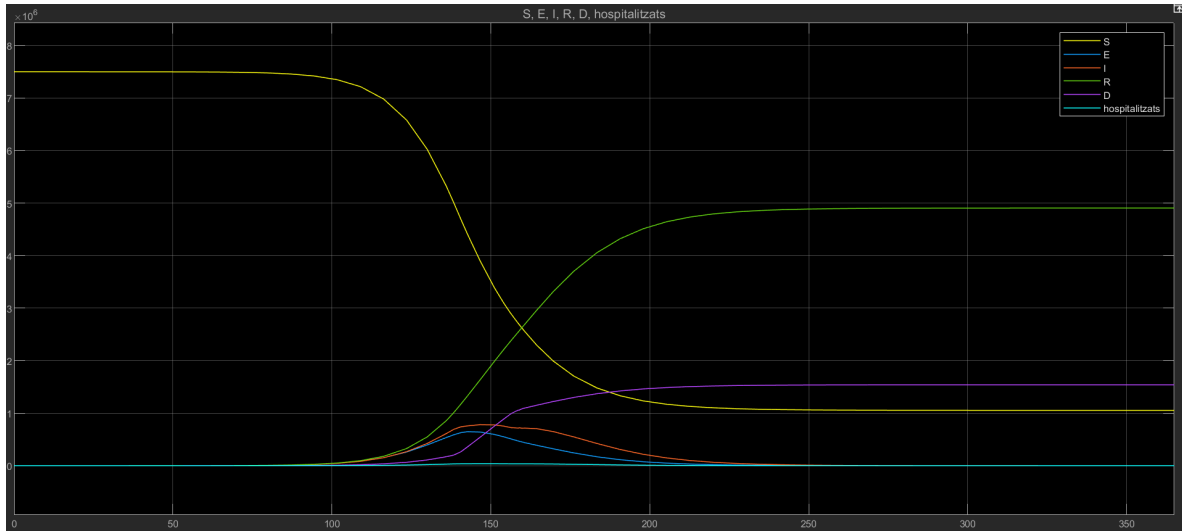
Consequence : δ k=3

Figure 17: SEIRD + hospital k: 3
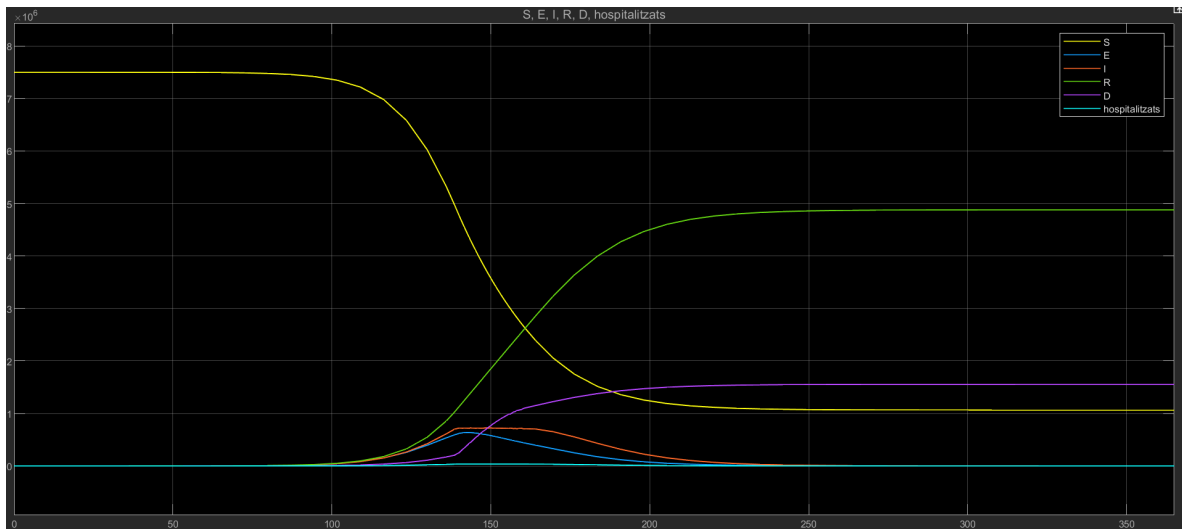
Consequence : δ k=4

Figure 18: SEIRD + hospital k: 4

From this curves we learn that the higher δ consequence to healthcare system collapse the faster the system converges. Consequently, if a virus with more lethal conditions and lower survival rates in case the patient does not receive hospital treatment is received breaks, the people would die quicker.

4.3.2 Hospital Capacity Changes

Hypothesis for Increasing Hospital Capacity:

If the hospital capacity increases, meaning more beds are available for patients, the healthcare system has a higher threshold before becoming overwhelmed. As such, the number of infected individuals requiring hospitalization (ratio_hosp * I) can increase without exceeding the available resources.

As a result, even if the infection rate or the death rate increases, the impact on the overall mortality might be less severe, as more patients are able to receive the necessary medical care. Therefore, an increase in hospital capacity can act as a buffer, protecting against surges in infections and potentially reducing the overall death toll.

If the establish this hospital capacity to 50000 the model shows the following curves:
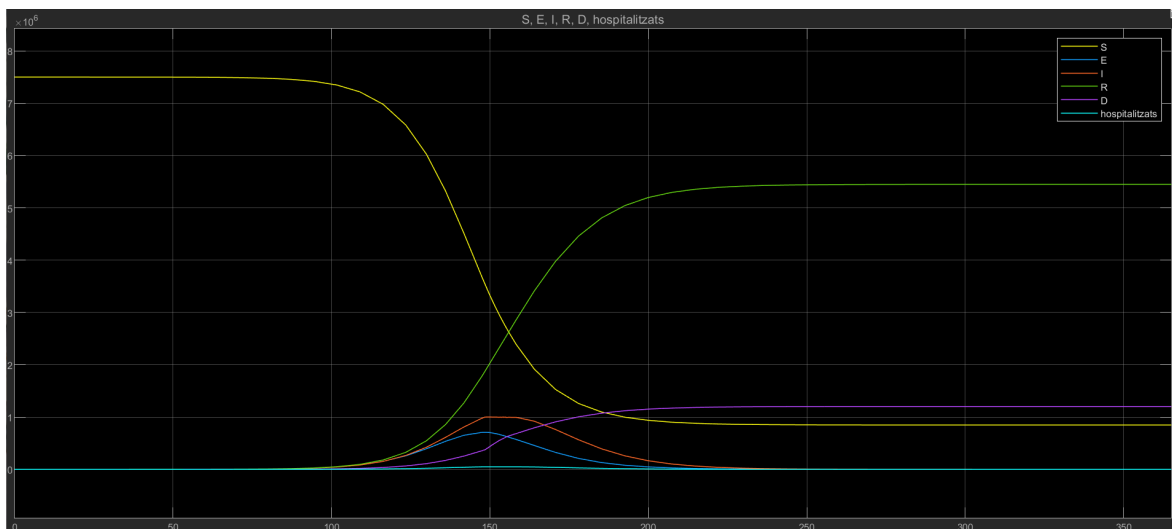

Figure 19: SEIRD + hospital capacity 50000

At the end the Deceased curve is lower since the system has collapsed for less time.

Hypothesis for Decreasing Hospital Capacity:

Conversely, if the hospital capacity decreases, the system becomes more sensitive to changes in the number of infected individuals. The threshold at which the healthcare system becomes overwhelmed is lower, meaning even a small surge in infections could push the healthcare system beyond its capacity.

In such scenarios, the death rate would increase earlier as the hospital capacity is reached faster, leading to more patients being unable to receive the necessary care. The situation could quickly escalate if the infection rate increases simultaneously, leading to a rapidly overwhelmed healthcare system and a sharp increase in the number of deaths. Therefore, a decrease in hospital capacity could have grave consequences, making the system more vulnerable to increases in infection rates and potentially leading to higher mortality.

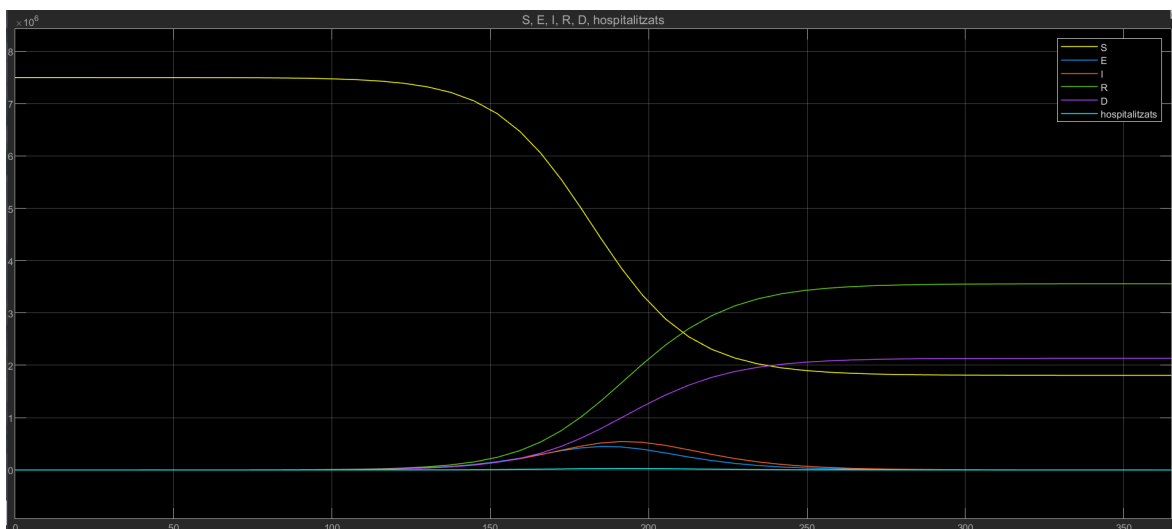If the establish this hospital capacity to 1000 the model shows the following curves:

Figure 20: SEIRD + hospital capacity 1000

5 Vaccination

One of the main worries during the Covid 19 pandemic was to find an effective vaccine that helped to build a herd inmunity on the populaiton to erradicate the disease. Finally, different medical companies such as Pfizer, AstraZeneca or Moderna came up with a working formula leading to a huge descrease on both deceased and infected people and in the general viral propagation leading to a near erradication of the disease at all.

We tried to implement this phenomenon on our model by increasing the γ parameter starting from a certain moment of time representing all the vaccinated individuals which contracted the virus but either not developed the disease or reduced their sick time.

There were several other proposes to implement this scenario such as implementing the vaccinated population as a environment variable or using some less linear approximations which would have been more verisimilar. We finally chose this one in order to prime simplicity and simple implementation and optimization.

5.1 Mathematical Model

$$\frac{dS}{dt} = -\frac{\beta}{N}SI, \tag{18}$$

$$\frac{dE}{dt} = \frac{\beta}{N}SI - \lambda E, \tag{19}$$

$$\frac{dI}{dt} = \lambda E - \gamma'I - \delta'I, \tag{20}$$

$$\frac{dR}{dt} = \gamma'I, \tag{21}$$

$$\frac{dD}{dt} = \delta'I. \tag{22}$$

$$\delta' = \delta k. \tag{23}$$

$$\gamma' = \gamma k_2. \tag{24}$$

where:

$$k = \begin{cases} 1, & \text{if } 0.05I <= 35952 \\ 2, & \text{otherwise} \end{cases} \tag{25}$$

$$k_2 = \begin{cases} 1, & \text{if } t < 75 \\ 1 + 0.3t, & \text{if } t > 75 \text{ and } 1 + 0.3t < 5 \\ 5, & \text{otherwise} \end{cases} \tag{26}$$

Here, t represents the step the model is in, the 75 conditioning the k_2 parameter represents the instant where the vaccination phase starts giving results and the number 5 is it's upper bound. This values will be changed during the experimentation.
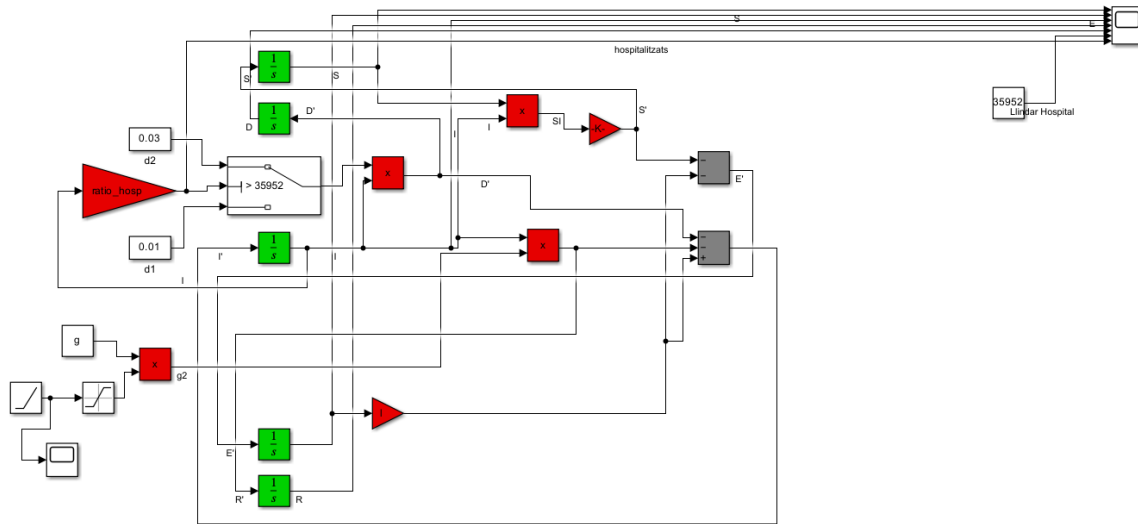
5.2 Simulink Model

Figure 21: SEIRD + hospital Model

This was implemented using a ramp block that kept on value =1 until t=75, where it started growing with a pendent =.3. This value, is multiplied by the γ constant to give it's final value. There is also a saturation block which prevents γ of growing over 5.

5.3 Experimentation

Note: All the plots made in this experimentation follow the following legend:

Figure 22: Legend for the plots of this experimentation

Baseline

For baseline to this model we chose a parameter configuration that, eventhough erradicates the virus, it takes too long, and results i a number of deceased population higher which we will try to decrease.
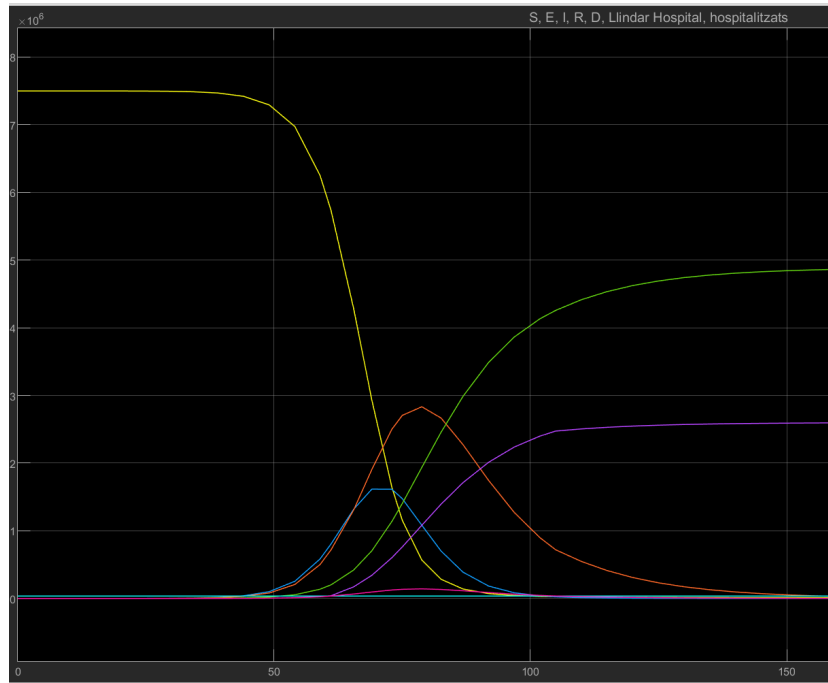

Figure 23: SEIRD + hospital capacity 1000

It is visible that around t=100 the deceased are over 2M, reaching and getting stability around 2.7M at the end of the simulation.

vac_t = 75, vac_slope = 0.3, vac_top = 3

In this phase, we set the time when the vaccination proceudre begins at t=75, the maximum impact that it can have on γ to 3 ($k_2 <= 3$) ans the pendent of $k_2 = 0.3$. This was the result:
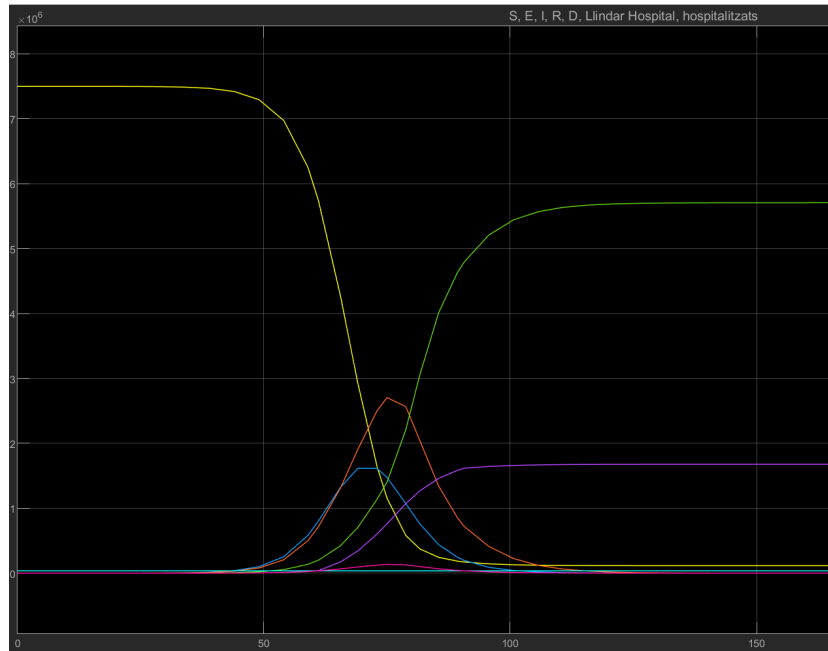
Figure 24: SEIRD + hospital capacity 1000

The vaccine was a success on both the infected curve, which reduced it's area and the total number of deceased people, mantaining it around 1.7M at the end of the simulation.

vac_t = 50, vac_slope = 0.1, vac_top = 1.5

In this experiment, we wanterd to check how well would work a vaccine that has worse efectiveness but can be implemented before that the last experiment, to check if it was worth enough to use a worse vaccine in order to take action in advance.
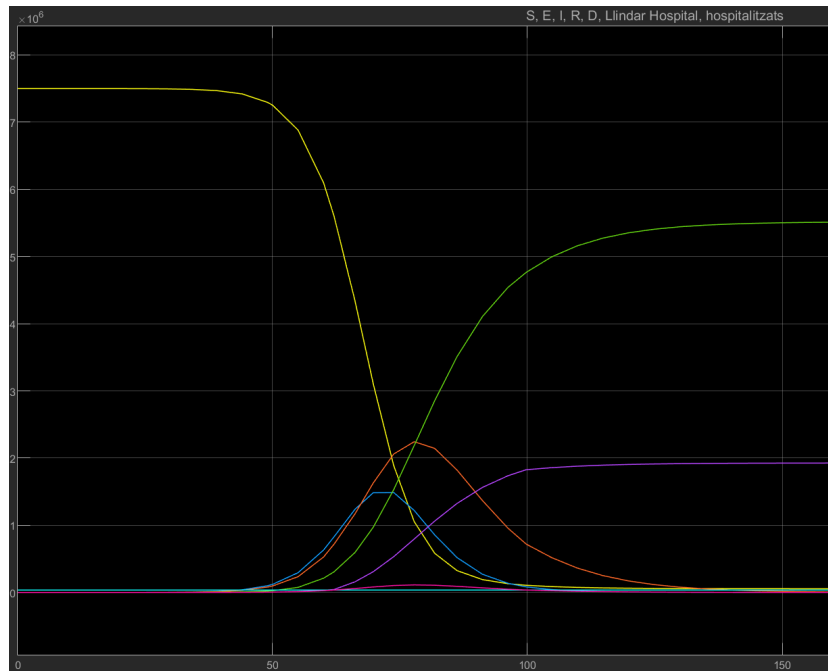

Figure 25: SEIRD + hospital capacity 1000

The number of deceased people here is slighlty bigger than in the previous experimentation. The

decicison here would be tough if there you can be certain of the effect of the actual vaccine or to a possible future better one.

vac_t = 50, vac_slope = 0.3, vac_top = 3

To try the best of both worlds, we wanted to see which would be the impact of the vaccine of the first vaccine but with the timing of the second one. These are the results:
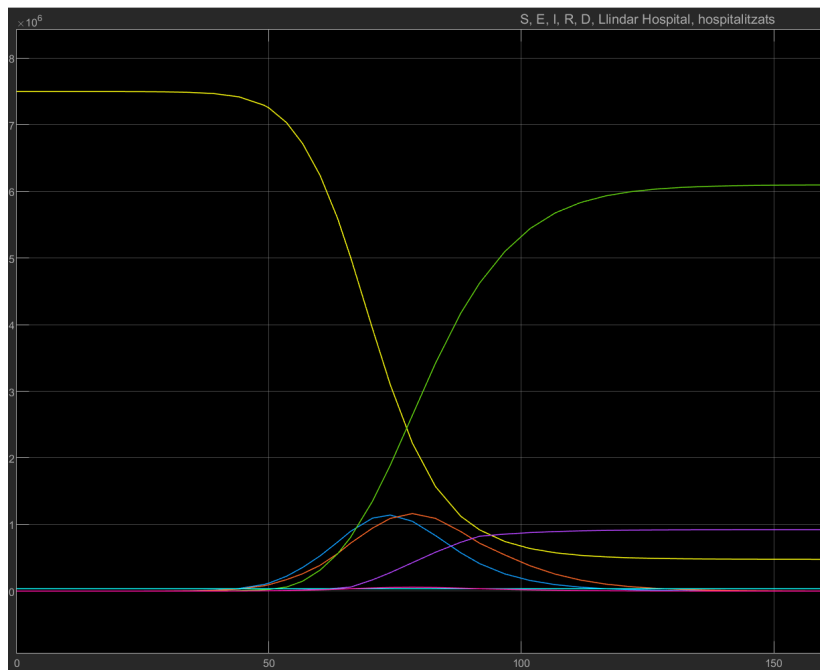

Figure 26: SEIRD + hospital capacity 1000

The results here demolish the prevoius ones. Applying thefirst vaccine in a moment where the virus is in a less mature phase has provided great results reducing by around 60%.

6 New variant

During the pandemic, and specially few months after the general vaccination process, new variants of the virus started appearing since those were more resistant against the improved imnume systems of the vaccinated people. The number of deceased and ill people which had been slowing down their progress started growing faster again and the sensation of and endless pandemic started appearing. The vaccination dosage had to be augmented as the virus continued spreading.

As a final part of this project, we tried to model the appearence of a new variant which made part the recovered be susceptible again, since their inmune system was not ready for that variant. We also implemented an increase on the Infection parameter making ø affect on λ.

6.1 Mathematical model

$$\frac{dS}{dt} = -\frac{\beta}{N}SI + øR, \tag{27}$$

$$\frac{dE}{dt} = \frac{\beta}{N}SI - \lambda'E, \tag{28}$$

$$\frac{dI}{dt} = \lambda'E - \gamma'I - \delta'I, \tag{29}$$

$$\frac{dR}{dt} = \gamma'I - øR \tag{30}$$

$$\frac{dD}{dt} = \delta'I. \tag{31}$$

$$\delta' = \delta k. \tag{32}$$

$$\gamma' = \gamma k_2. \tag{33}$$

$$\lambda' = \lambda + 2ø \tag{34}$$

where:

$$k = \begin{cases} 1, & \text{if } 0.05I <= 35952 \\ 2, & \text{otherwise} \end{cases} \tag{35}$$

$$k_2 = \begin{cases} 1, & \text{if } t < 75 \\ 1 + 0.3t, & \text{if } t > 75 \text{ and } 1 + 0.3t < 5 \\ 5, & \text{otherwise} \end{cases} \tag{36}$$

$$ø = \begin{cases} 0, & \text{if } t < 100 \\ 0.1, & \text{otherwise} \end{cases} \tag{37}$$

We consider the step 100 as the moment when the new variant appears.
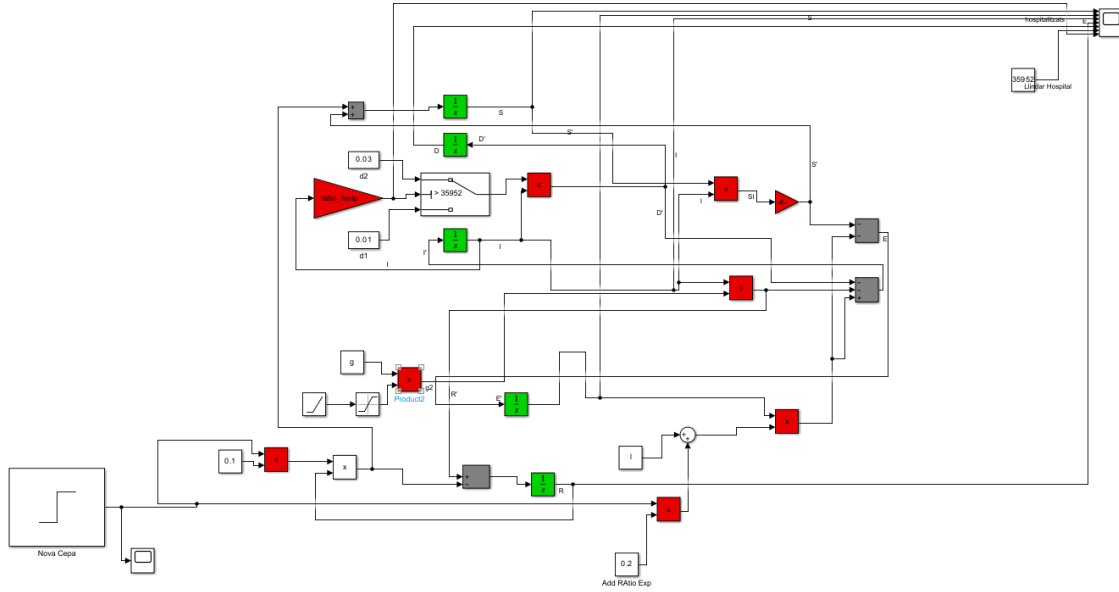
6.2 Simulink Model

Figure 27: SEIRD + hospital Model

Here, we implemented the variant with a step block, which indicates if the new virus has appeared yet or not. It is =0 until t=100, when it becomes 1. This is used for both the ø and λ constants by multiplication and addition blocks, respectively.

6.3 Experimentation

Note: All the plots made in this experimentation follow the following legend:

Figure 28: Legend for the plots of this experimentation

It is important to punctuate that the variant that we implemented is resistent to both the vaccine we implemented on section 5 and to the defenses that the population has been developing or can develop. For this reason, the simulations we will provide here will always finish with all the population deceased. The model keeps making people going from infected to deceased and from recovered to susceptible, so, eventually, all the population will go to the deceased group (from which there is no escape...)

The main point of the experimentation of this section is to analyise the impact and the response time that there is avaliable in relation with the infectiveness of this new variant of the virus, in the case that there is no direct inmunity avaliable, to, for example, develop a new vaccine which is resistant it.

Baseline

As baseline form this experimentation, we will take a "good" case, where the virus gets exterminated. The resulting scope is this:
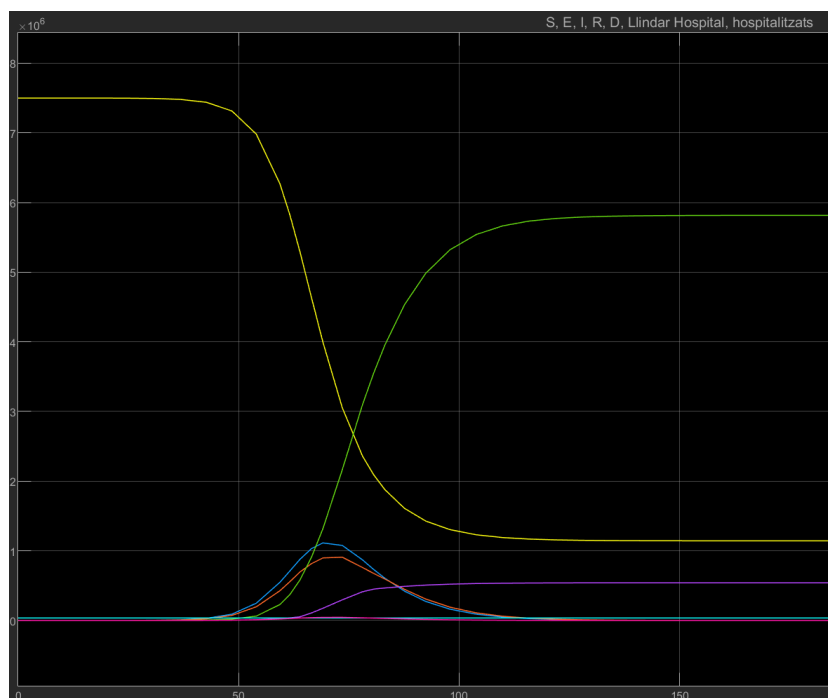
Figure 29: Baseline model

As it is visible, there is still plenty of deceased people (around 600K) at the end of the pandemic but the measures taken were enough to erradicate the virus and build a herd inmunity.

ø= 0.05
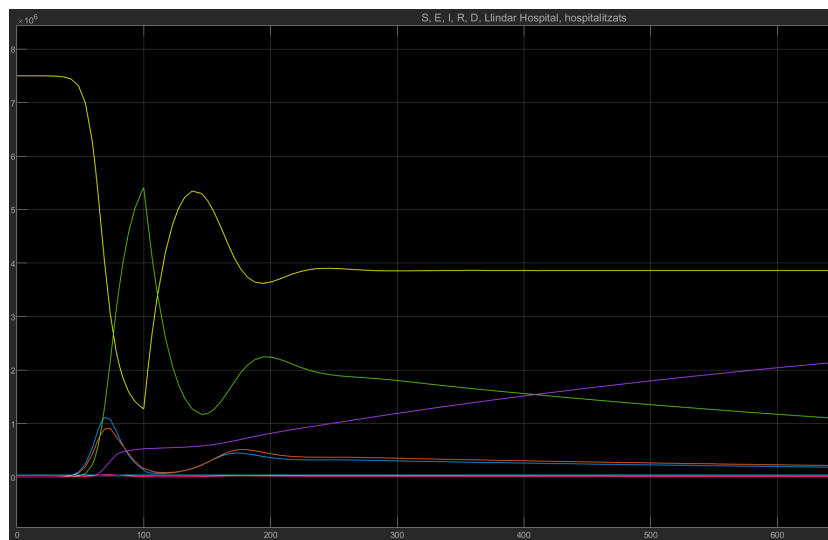

Figure 30: Baseline model

The lowest value for omicron that was tried was 0.05.

There is a clear change of schemes on t=100 due to the new variant, the recovered curve starts dropping inmidiately with a short recovery around t = 150 and then a softener downfall to 0 (although it will not get to 0 until t = 600, more or less).

Although the impact of the variant is immediate, there is some time of reaction to develop a new vaccine or to to take measures to prevent new infections, the bound of the 1M deceased is not reached

until t $\approx$ 230. Anyway, if there is no measure taken, the virus will end killing approximately half of the population.
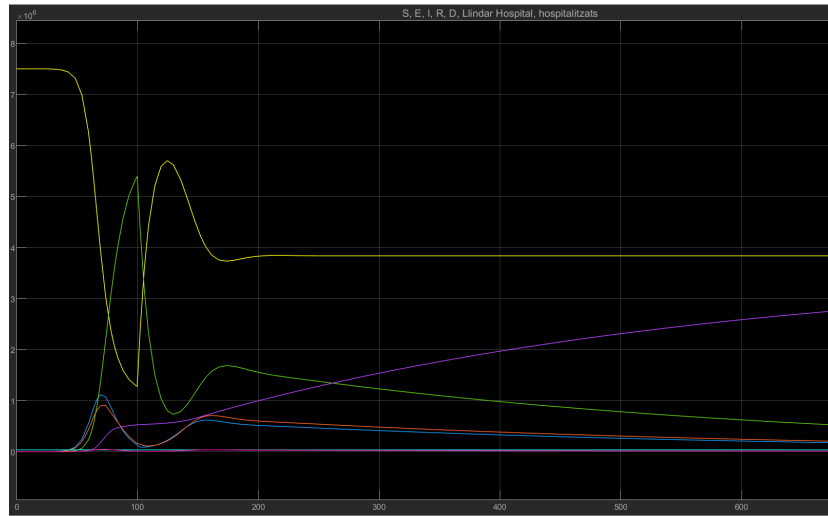
ø= 0.1

Figure 31: Baseline model

In comparison to the previous model, the recovered curve dropped down way faster this time, as the deceased one grew, reaching the 1M befote t=200. Here the time of reaction provided is much less and the situation can become from stable to critical in a very fast pace.

Conclusions

New variants of the virus are a dangerous factor to keep in mind. While the situation might steady, the disease can come back in a few moths with the same or even more power than the initial one, similar to what happened with the øvariant of COVID-19. The model can be expanded for new vaccination procedures to endure the defenses against the desease of to considerate standard recovery for this new variant.

7   Conclusion

In the face of an ongoing global health crisis, our study has used MATLAB Simulink to dynamically model the progression of the COVID-19 pandemic. We have embraced this pursuit not only as a scientific exploration but also as a tool to understand and provide solutions to a complex problem. The ever-evolving nature of this disease has presented us with challenges that have inspired us to delve deeper and innovate in our modeling strategies.

We began our exploration with the SIR (Susceptible, Infected, Recovered) model, a simple yet potent representation of disease transmission dynamics. The SIR model offered us an understanding of the fundamental principles at play in a pandemic, providing a framework from which we could build more complex models. However, we faced the inherent limitation of the SIR model - its inability to capture the intricate real-world aspects of a pandemic.

To address this, we introduced more complexity with the SEIRD (Susceptible, Exposed, Infected, Recovered, Deceased) model, allowing us to account for the incubation period and mortality rate. Yet, implementing the SEIRD model also presented challenges. Establishing accurate initial values for each variable was a meticulous task, demanding an understanding of the disease beyond mathematical equations.

The role of healthcare infrastructure was another significant factor we incorporated into our models. Simulating the effects of different hospital capacities on disease outcomes was a task fraught with uncertainties. As we learned, the healthcare system's resilience directly impacts the severity of a pandemic, but quantifying this in a model introduced a high degree of variability.

Our study then took a proactive turn as we incorporated a vaccination program into our model. Here, we encountered the difficulty of capturing the effects of varying vaccination rates and the problem of vaccine hesitancy. Creating a model that accurately reflects real-world vaccination programs required us to make assumptions and estimations, each with its own potential to distort our findings.

The introduction of a new COVID-19 variant in our modeling marked a significant step towards the reality of this evolving pandemic. This addition, while crucial, proved to be a challenge, as the potential impact of new variants is, by nature, uncertain and unpredictable.

Despite these challenges, our work has provided valuable insights into the dynamics of a pandemic and the factors that influence its course.

Our journey in modeling the pandemic has been a mixture of challenges, learning, and discovery. It has taught us to appreciate the nuanced complexity of real-world situations and the immense potential of mathematical modeling to navigate these complexities. We have grappled with unknowns, tested our assumptions, and continuously refined our models in response to an ever-evolving situation.

Ultimately, the problems we have encountered have underscored the complex and dynamic nature of pandemics. They have revealed the limitations of mathematical models but also their profound value. We have learned that models are not definitive answers, but invaluable tools in our quest to understand and respond to a public health crisis. Moving forward, we hope our work inspires further innovation and refinement in the field of dynamic system modeling, contributing to global efforts to navigate the challenges of the COVID-19 pandemic and beyond.