The SIS model and its generalisations

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CONTENTS

I. INTRODUCTION

The epidemiological modeling is a developing discipline with a roughly hundred years history. Its main goal is to predict the future to have maximal control on an epidemic by studying the the spreading mechanism of the disease. The models try to give a prediction about how the disesase spreads, how fast can get a group of the population infected, what percentage of it will be infected or die due to the virus and also estimate epidemiological parameters, such as the so-called reproduction rate. Nowadays, the scientific community is highly motivated to investigate this field, due to the serious COVID-19 pandemic.

The modelling of infected diseases is a very useful mathematical toolkit which is constantly evolving to get able to descibe different real-life (or in theory, mathematical) scenarios. As in all models, there are assumptions. One of them could be the stationary population or the undifferentiability characteristics and resistance of arbitrary 2 people of the population, 2 samples of the ensamble that the model works on.

We can chategorize every model in a way that it is Stochastic or Deterministic. In the first occasion, we have random, in other words, stochastically varying variables. If we have such a large population, deterministic or compartmental models are frequently used. [1] The latter is based on a really simple, but important idea by partitioning the society for different subgroups which behave differently (e.g. one gets infected and after that recovered or died). Then we construct differential equations for the time evolution of the population of these subgroups what are changing in time.

II. SINGLE SOCIETY MODELS

Here we refer to single societies as the ones which are small enough to consider only one parameter.

A. Models involving constant populations

Models within a single society with a constant populations often serve as the toy models focusing on the possible interactions between the members of the society, neglecting the possible changes of the parameters of each individual. Here, each individual is considred to be identical, posessing the same immune system, making contact with identical amount of people, etc. This irrealistic assumption can be made more realistic (see III.) when one breaks the society into smaller classes, where each class should posess different parameters and by introducing *coupled* interactions between them, describing how do they interact. But, first we describe the easier, interaction-free cases to learn the methods to use and understand the dynamics.

1. SIS

In the case of SIS model, we have a constant population $\mathcal{P}$ with $\mathrm{card}\,(\mathcal{P}) = N \in \mathbb{N}$ people, while we introduce two subsets $\mathcal{S}, \mathcal{I} \subseteq \mathcal{P}$ of subceptive and infected people. Let $S = \mathrm{card}\,(\mathcal{S}) \in \mathbb{N}$ and $I = \mathrm{card}\,(\mathcal{I}) \in \mathbb{N}$ denote the number of *susceptible* and *infected* people, respectively. (The second S, in the name of the model, indicates the possibility that infected individuals can become susceptible again.) Define $\mathbb{R}_+ = [0, \infty)$. Due to the assumptions made above, it is enough to fix a number $N \in \mathbb{R}_+$, called the population, which is constant. Note that here we have considered N to be a nonnegative real number instead of natural in order to avoid the difficulities arising because of working with integer-valued difference equations, while we make the choice to approximate them with differential equations. Obviously, we will proceed similarly in the case of S and I.

The SIS model stands for describing the time-dependence of the number of susceptive and infected people. Since these numbers are considered to vary continuously, they may become smaller than 0. Now, we have $S, I : \mathbb{R} \to \mathbb{R}$, while the following relationship holds by definitions:

$$S + I = N \tag{1}$$

The differential equation system that defines the model [2]:

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\frac{\beta SI}{N} + \gamma I$$
$$\frac{\mathrm{d}I}{\mathrm{d}t} = +\frac{\beta SI}{N} - \gamma I,$$

where β is the *infection rate* (characterizing the speed of getting infected) and γ is the *recovering rate* (characterizing the speed of becoming susceptible again). An important parameter of the model is the *reproduction number*, defined as: $R = \frac{\beta}{\gamma}$. If $R > 1$, further action are needed to moderate the spread of the pandemic.

There are many possible generalizations of the SIS model which compensates for the obvious simplicity and completes the set of assumptions to a more realistic one. The first and possibly the most obvious one is considering the effects of the changing measures taken to stop the spread of viruses, which can be modeled by letting the infection rate β being a (not necessarily continuous) function of time. It may be useful to follow the effects of some moderating actions (e.g. mask wearing, quarantine) by the study of different functions for β (and testing whether the out-of-time regularizations can effect the pandemic in a long-term manner).

a. Numerical solution

We have considered 4 types of infection rates what we will see in a minute. In the first case, it is worthwhile to consider the case of the constant infection rate to have a reference basis. After that we studied 3 other scenarios, where the infection rates are linearly or exponentially decreasing in time or depending on the number of infected people. These mappings are the followings[1].

1. $\beta_{CONST}(t) = \beta_{max}$ (2)
2. $\beta_{LIN}(t) = -Bt + \beta_{max}$ (3)
3. $\beta_{EXP}(t) = \beta_{max}\mathrm{e}^{-Bt} + \beta_0$ (4)
4. $$\beta_I(t) = \begin{cases} \beta_{max}, & \text{if } I < I_{crit} \\ 0.3\beta_{max}, & \text{otherwise.} \end{cases}$$ (5)

We tried to choose a realistic multiplication factor at the 4th case. (We used the number $I_{crit} = 10^{-4}N$ in every model at this project.) We used Phython 3 for solving the differential equation system numerically with the "scipy.integrate.odeint" function. During the numerical solution we needed the numerical value of the reproduction rate, R, which we get from [3]. The recent R value in Hungary is 1.41. We used Hungary's population (roughly $N = 10.000.000$) to be able to compare the numerical and the experimental results. The last free parameter what we have control on is the timestep. Our choice was the 1 day scale. We update the groups in every day because it can be seen in the international practice and we think it is a representative time interval to characterize the lingering of the virus (with an adequate precision).

After that, one can see what are the derivatives of these functions. It is useful because we can get the number of people who become infected / susceptible in a day-to-day basis.

b. Results

We can see the *relative populations* of the groups normed to the total population on Fig. 1-12.'s left sides. On their right side, we can see the derivatives that give the day-to-day alteration of each epidemiologically different group. Fig. 1-3., 4-6., 7-9., 10-12. consecutively shows the constant, linearly decreasing, exponentially decreasing and the number of infected people depending cases for β with $R = 0.5, 1.41$ and 10 reproduction rate values, one below the current value and one much higher. The higher values can represent the initial period of a pandemic because at that time nor the average people, not the medics know the existence and the treatment for the virus. The lower values obviously indicate the final part where the infection is a highly suppressed process. The used parameter values can see on top of the Figures, the initial conditions were $S_{init} = 0.9N$, $I_{init} = N - S_{init}$ and the sample frequency is $T_{div} = 1$ [day].

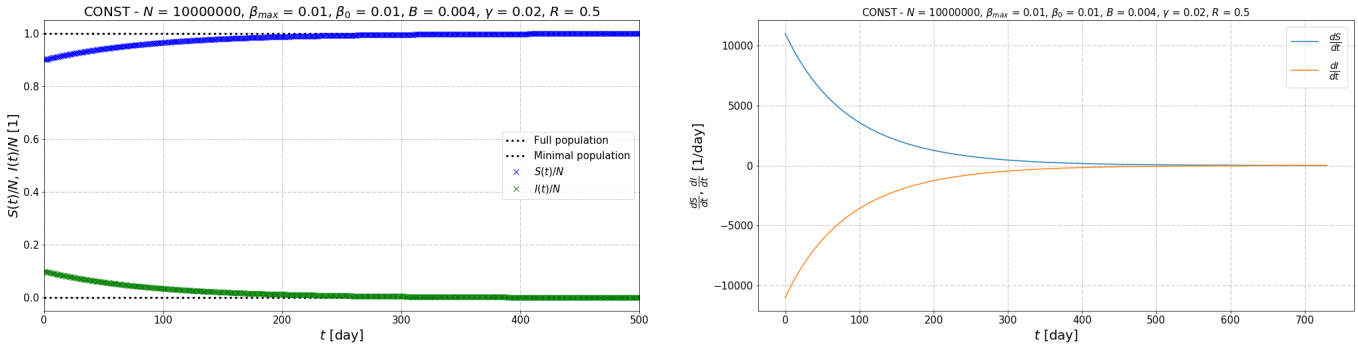

Figure 1: β_{CONST}, $R = 0.5$

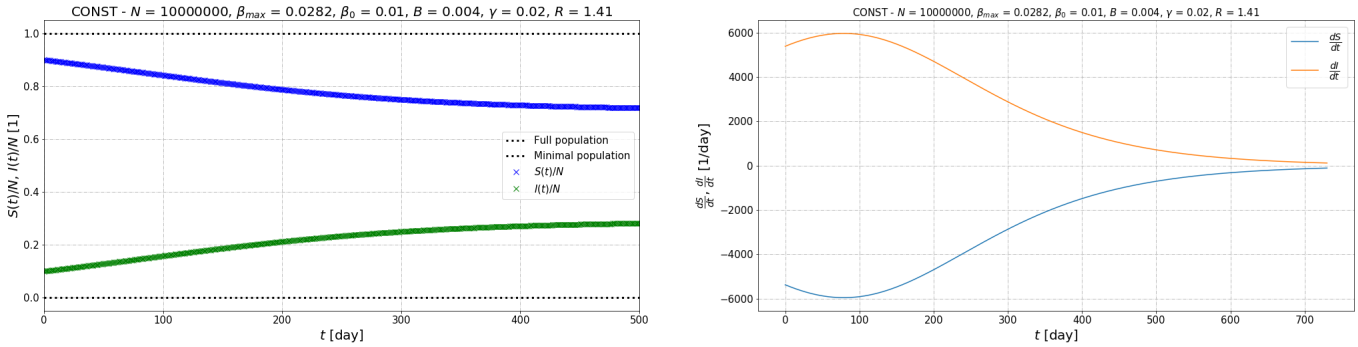

Figure 2: β_{CONST}, $R = 1.41$

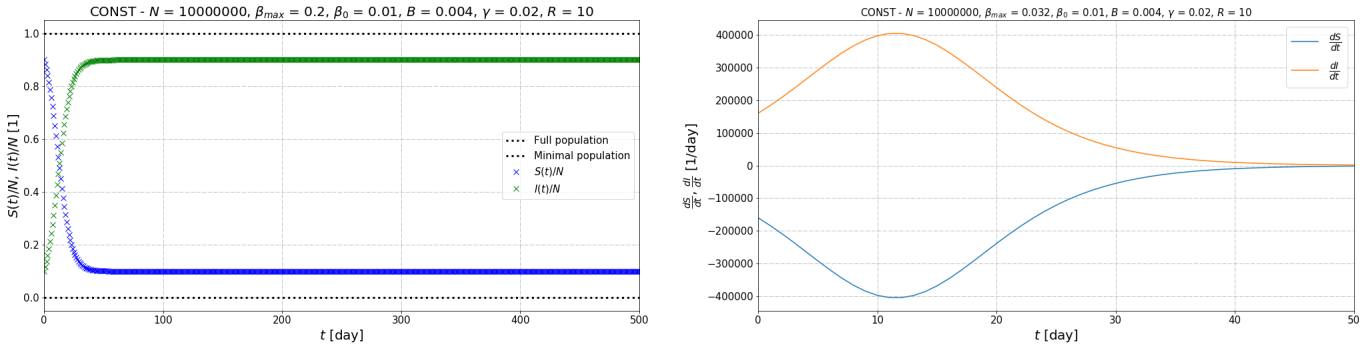

Figure 3: β_{CONST}, $R = 10$

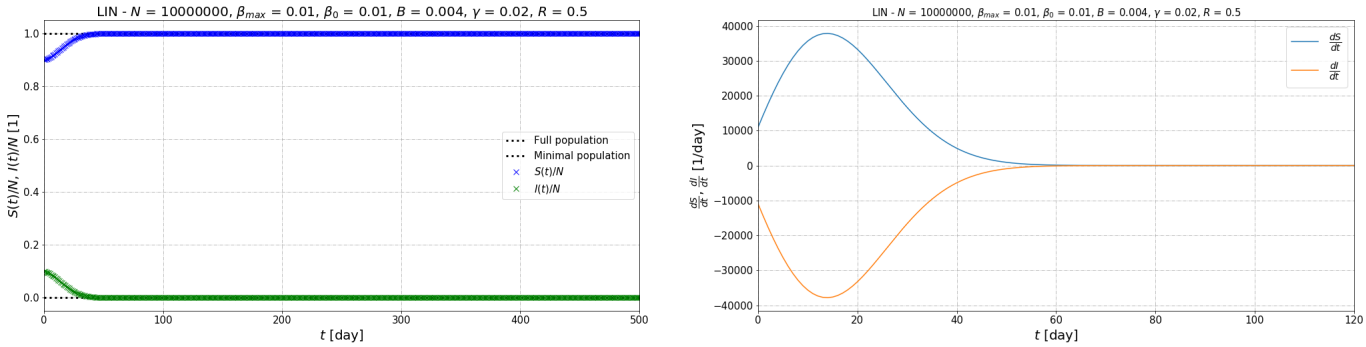

Figure 4: β_{LIN}, $R = 0.5$

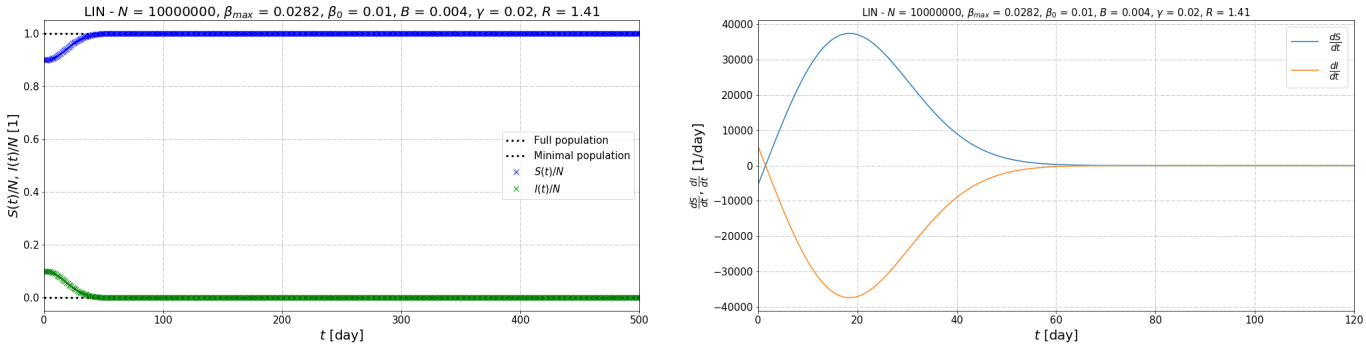

Figure 5: β_{LIN}, $R = 1.41$

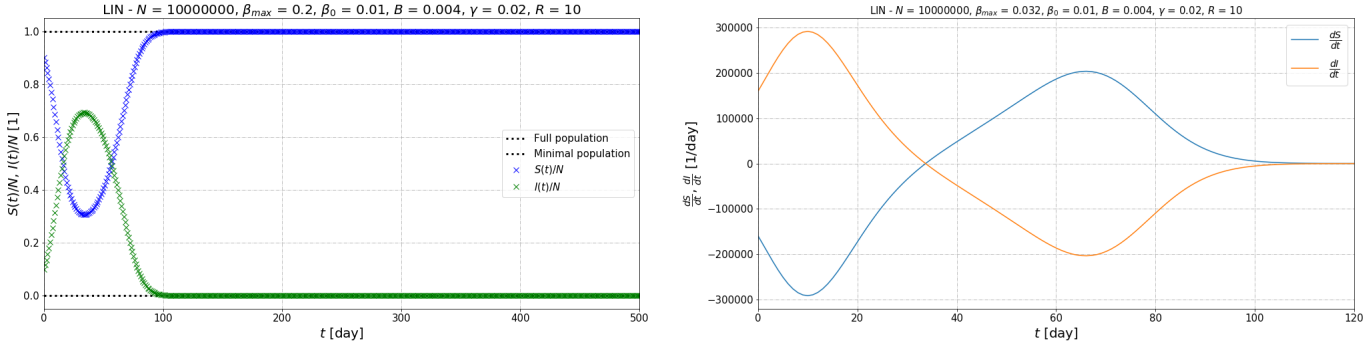

Figure 6: β_{LIN}, $R = 10$

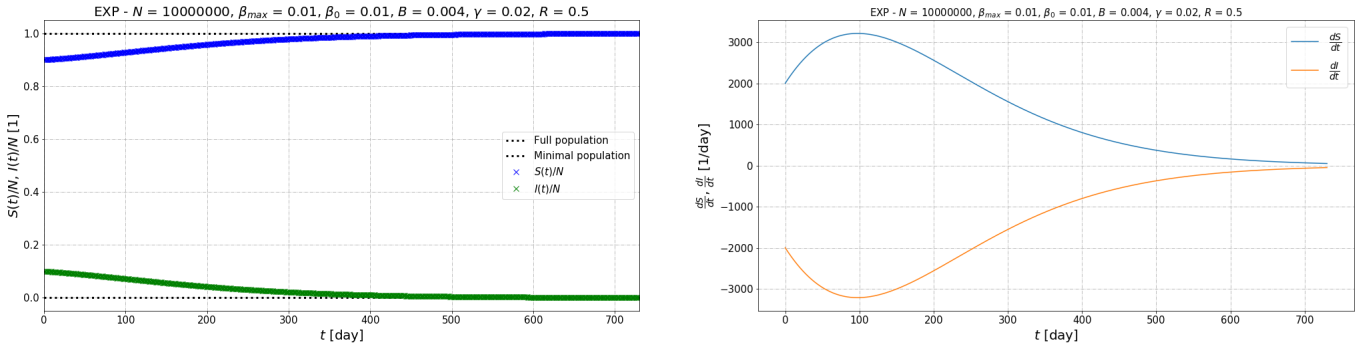

Figure 7: β_{EXP}, $R = 0.5$

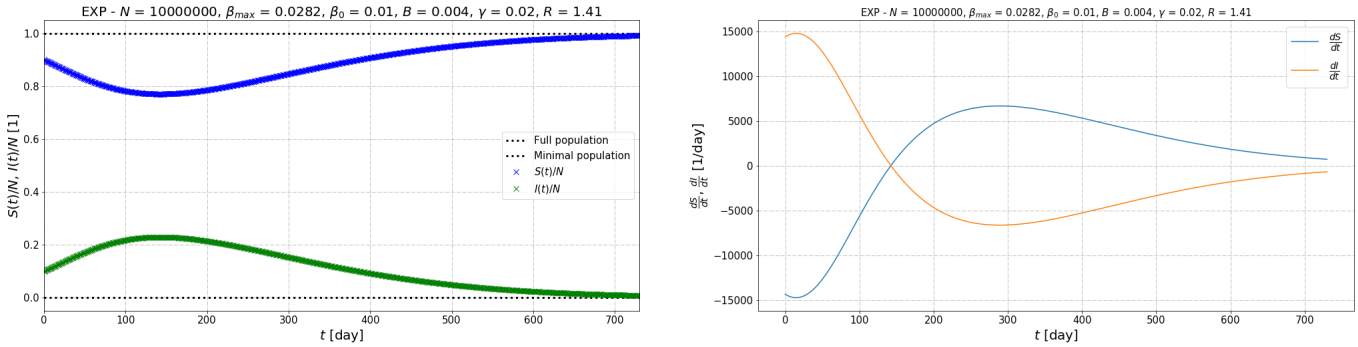

Figure 8: β_{EXP}, $R = 1.41$

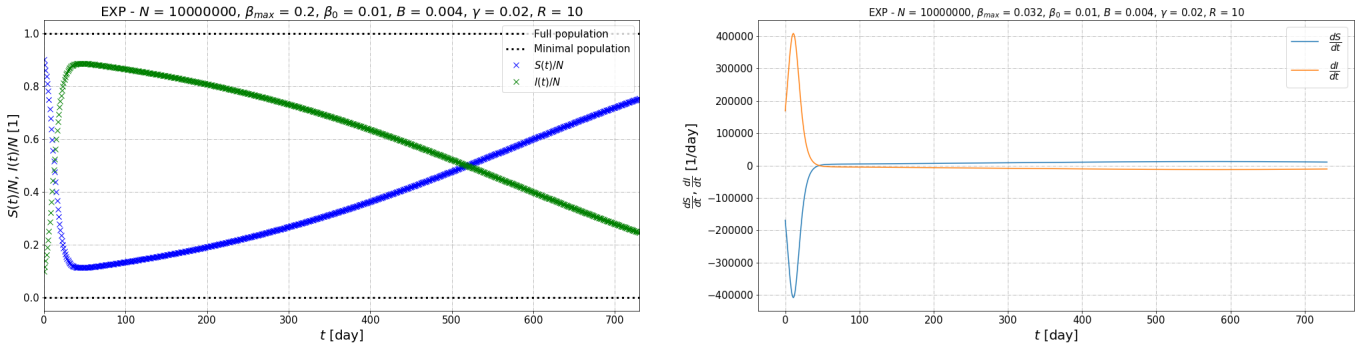

Figure 9: β_{EXP}, $R = 10$

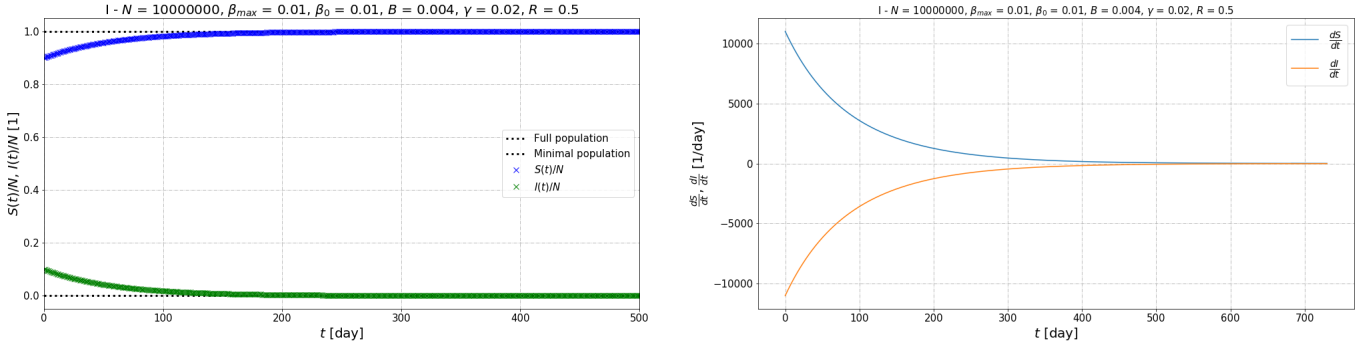

Figure 10: $\beta_I,\ R = 0.5$

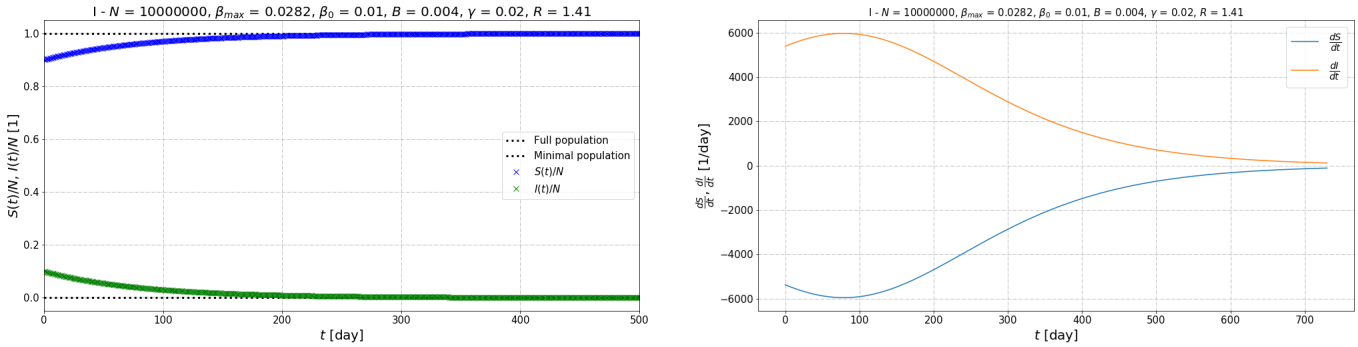

Figure 11: $\beta_I,\ R = 1.41$

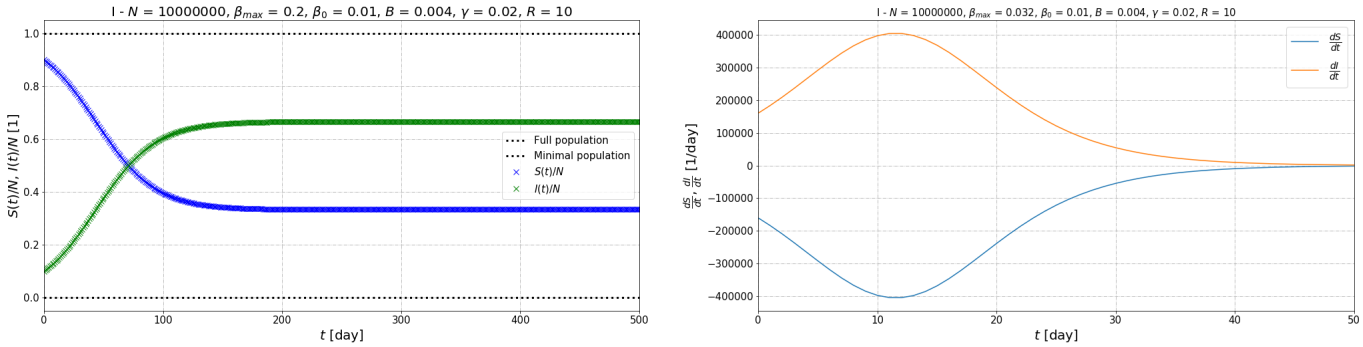

Figure 12: $\beta_I,\ R = 10$

c. Conclusion

From Fig. 1-12. we can came to our conlusion about the single society, constant population SIS model with various infection rate functions.

In every case, we can experience the asymptotic convergence of the time dependent number of susceptible / infected groups. One can see the different directed relation between the derivative functions at $t = 0$. This means that we can find an R_0 value what separates the 2 solution families from each other. If $R > R_0$ the number of infected people will increase at some point and decrease after that, but if $R \leq R_0$ the infected group will be smaller at every timestep. These values are summarized here.

- **Constant** case: $R_0 = 1.1115$
- **Linear**ly decaying case: $R_0 = 1.1111$
- **Exponential**ly decaying case: $R_0 = 0.611$
- **Proportional to I** case: $R_0 = 1.1111$

We can see that the R_0 value of the constant, the linear and the proportional to I case are almost the same, which means that the effect of the slowly changing infection rate has almost no effect. The above mentioned result is not only valid where the order of magnitude of B is smaller than β_{max}'s and γ's. The important difference is the higher the value of B is, the less lingering the virus is.

One of the two most important differences between the cases with $R = 1.41$ is the lingering time of the virus. In the linear case it is ~ 60 days, whilst the other three have about ~ 700 days which is (i) much less realistic that the previous one and (ii) cannot be the real value because of the frequentlier experienced waves of the virus.

The other is that the magnitude of the day-to-day infections. The linear case with the coefficient $R = 1.41$ case is not really give back the experienced values, because the maximum value due to the model is ~ 37000 infections/day, but in reality was 11265 and the run-up was ~ 40 days in reality [4], but in the model it's just ~ 18 days. The exponential case with the coefficient $R = 1.41$, has a better maximal infections/per day value, namely ~ 15000 but the run-up is also too short, approximately ~ 20 days and the lingering is really slow, couple hundred days.

We can conlude that these simply models cannot give back the experienced values in Hungary with a great precision. The reasons or the errors are there were more waves in Hungary, the distribution of the restrictive measures was not uniform, it varied a lot of times, in a lot of different ways. So, if we want to have some improvement, we have to study more complex models (e.g. SIR, SIRD, ...) and possibly taking the beta function based on the sum of couple different types of restrictive actions.

d. Exact solution

Finally, we want to have a few words about the analitical solvabitily of the SIS model. In the constant and the linear cases we can get the exact, analitical solution of the differential equation system[2]. As a remark, we will not do the detailed calculation of the $S(t)$ and $I(t)$ curves with respect to the $S + I = N$ requirement, we just mention the solutions of the model in the analitically solvable cases.

First, let's have a look at the **constant** case, as shown in (2). The analitical solutions are the followings:

$$S(t) = \frac{(N\gamma - c_1\beta_{max})\mathrm{e}^{\frac{c_1\beta_{max}}{N}t + c_2 N\gamma}}{\mathrm{e}^{\gamma t + c_1 c_2 \beta_{max}} + \beta_{max}\mathrm{e}^{\frac{c_1\beta_{max}}{N}t + c_2 N\gamma}} + c_1, \tag{6}$$

$$I(t) = \frac{(-N\gamma + c_1\beta_{max})\mathrm{e}^{\frac{c_1\beta_{max}}{N}t + c_2 N\gamma}}{\mathrm{e}^{\gamma t + c_1 c_2 \beta_{max}} + \beta_{max}\mathrm{e}^{\frac{c_1\beta_{max}}{N}t + c_2 N\gamma}} = c_1 - S(t), \tag{7}$$

where c_1 és c_2 are free parameters determined by the initial conditions. We have to keep an eye on the requirement that these functions are bounded to the $[0, N]$ interval. The constant population, as an initial condition, requires the following identity: $c_1 = N$! We come to the conclusion that $\beta > \gamma \iff R > 1$ must hold in the examined case because of the

domain of the S and I functions.

$$S(t) = \frac{N(\gamma - \beta_{max})\mathrm{e}^{\beta_{max}t + c_2 N\gamma}}{\mathrm{e}^{\gamma t + N c_2 \beta_{max}} + \beta_{max}\mathrm{e}^{\beta_{max}t + c_2 N\gamma}} + N, \tag{8}$$

$$I(t) = -\frac{N(\gamma - \beta_{max})\mathrm{e}^{\beta_{max}t + c_2 N\gamma}}{\mathrm{e}^{\gamma t + N c_2 \beta_{max}} + \beta_{max}\mathrm{e}^{\beta_{max}t + c_2 N\gamma}} = N - S(t), \tag{9}$$

Secondly, the case of **linear**ly decaying rate, as shown in (3).

$$S(t) = c_1 - \left[\frac{1}{c_1} + c_2 e^{x_1(t)} + \frac{e^{x_2^2(t)}\sqrt{N}\sqrt{\frac{\pi}{2}}\gamma \cdot \mathrm{Erf}(x_2(t))}{\sqrt{B}c_1^{3/2}}\right]^{-1} \tag{10}$$

$$x_1(t) = \frac{c_1 B \cdot t^2 + 2N\gamma \cdot t - 2c_1\beta_{max}}{2N} \tag{11}$$

$$x_2(t) = \frac{c_1 B \cdot t + (N\gamma - c_1\beta_{max})}{\sqrt{2c_1 BN}} \tag{12}$$

$$I(t) = c_1 - S(t) \tag{13}$$

2. SIR

We now consider the SIR model [2] where we introduce a new group of individuals (R), those who have *recovered* and possess immunity for a given time, requiring to have $S + I + R = N$ stationary. None the less, this model is widely known, but it's a relevant generalization of the SIS model in some sense. The system of differential equations describing this model is given by the following.

$$\begin{aligned}\frac{\mathrm{d}S}{\mathrm{d}t} &= -\frac{\beta SI}{N}\\ \frac{\mathrm{d}I}{\mathrm{d}t} &= +\frac{\beta SI}{N} - \gamma I\\ \frac{\mathrm{d}R}{\mathrm{d}t} &= +\gamma I\end{aligned}$$

a. Results

We can see the relative populations of the groups normed to the total population on Fig. 13-24.'s left sides. On their right side, we can see the derivatives that give the day-to-day alteration of each epidemiologically different group. Fig. 13-15., 16-18., 19-21., 22-24. consecutively shows the constant, linearly decreasing, exponentially decreasing and the number of infected people depending cases for β with $R = 0.5, 1.41$ and 10 reproduction rate values, one below the current value and one much higher. The higher values can represent the initial period of a pandemic because at that time nor the average people, not the medics know the existence and the treatment for the virus. The lower values obviously indicate the final part where the infection is a highly suppressed process. The used parameter values can see on top of the Figures, the initial conditions were $S_{init} = 0.9N$, $R_{init} = 10000$, $I_{init} = N - S_{init} - R_{init}$ and the sample frequency is $T_{div} = 1$ [day].

b. Conclusion

In my opinion, the best choice from Fig. 13-24. is not a case with $R = 1.41$ because the infection curve can only represent a wave when it has a peak, in a fully suppressed case it is impossible to see. So, the march 2021 wave should be represented as a higher R than now. The best case from the plotted ones is when the day-to-day number of infections shows a well-defined peak and the associated time to is not strongly determined by the rate. This is the linear case where the length is about $\sim$ 60-120 days, depending on R. We should focus on the cases when $\frac{\mathrm{d}I}{\mathrm{d}t}(t = 0) \approx 11200$ and after that is has a minima and fastly converges to 0. Note that the derivative is not a small number because we have an initial condition for I, so we try to study the lingering only and deduce to the optimal parameters. But we can have an R big enough to see the increasing in the day-to-day infections.

The optimal value for the rate is $R = 1.73$, in the linear case. The initial condition was $\frac{\mathrm{d}I}{\mathrm{d}t}(t = 0) = 11200$. This case (see Fig. 25) has a $\sim$ 60 days long wave with $\sim$ 20 days long run-up, which is well enough to correspond to the march 2021 wave. The sad part is the reproduction rate was 1.22 in march 2021 [3], so we could get some characteristics right, but not all of them. This is an indicator that we have to work on more complex models with more compartments, more sophisticated β functions and more effects.

As a remark, we mention that in every case with arbitrary R values the $I(\infty) = 0$, so the virus will disappear as opposed to the SIS model where $I(\infty)$ can be a nonzero constant.

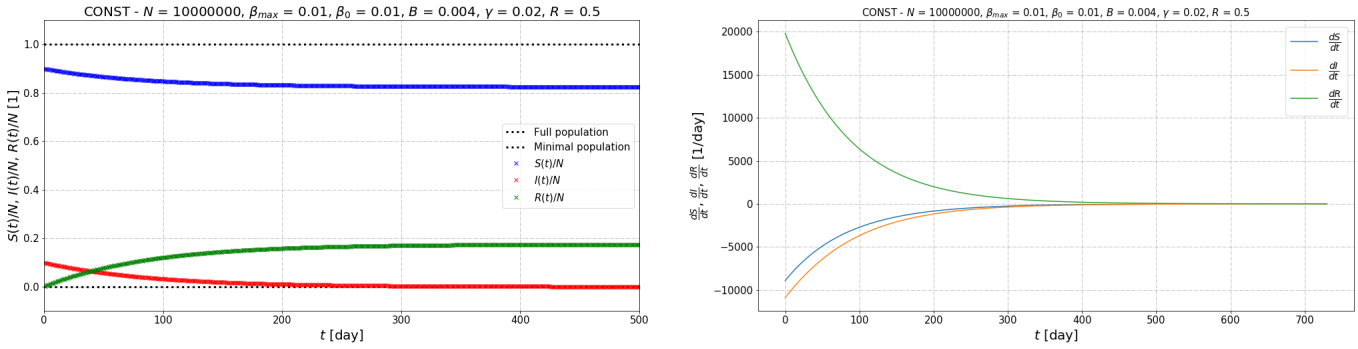

Figure 13: $\beta_{CONST}, R = 0.5$

c. Exact solution

We are not able to solve the differential equation system of the SIR model analitically even in the $\beta = \text{const.}$ case according to Wolfram Mathematica, therefore we do not continue to study the following models analitically.

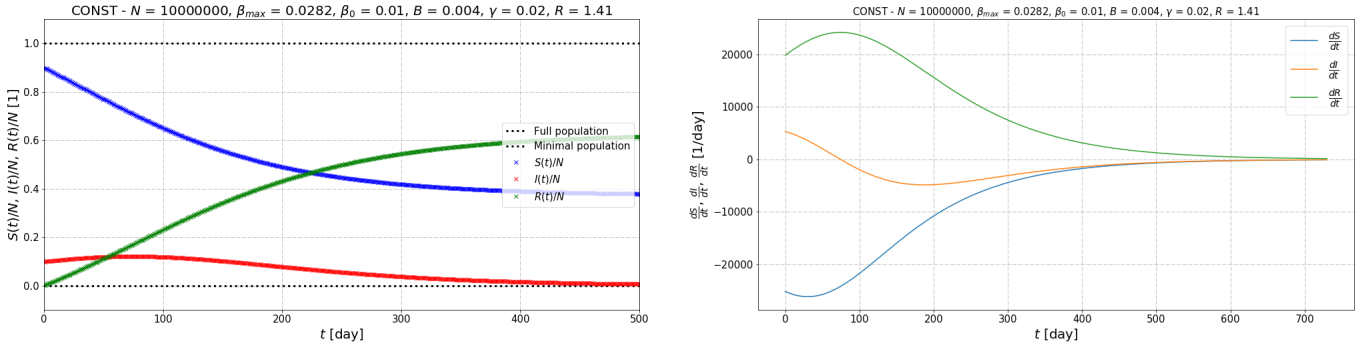

Figure 14: $\beta_{CONST}, R = 1.41$

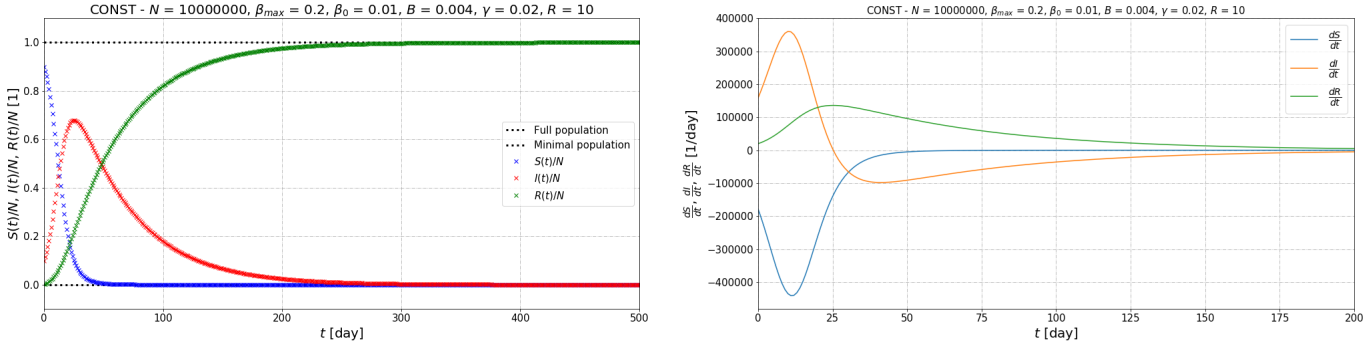

Figure 15: $\beta_{CONST}, R = 10$

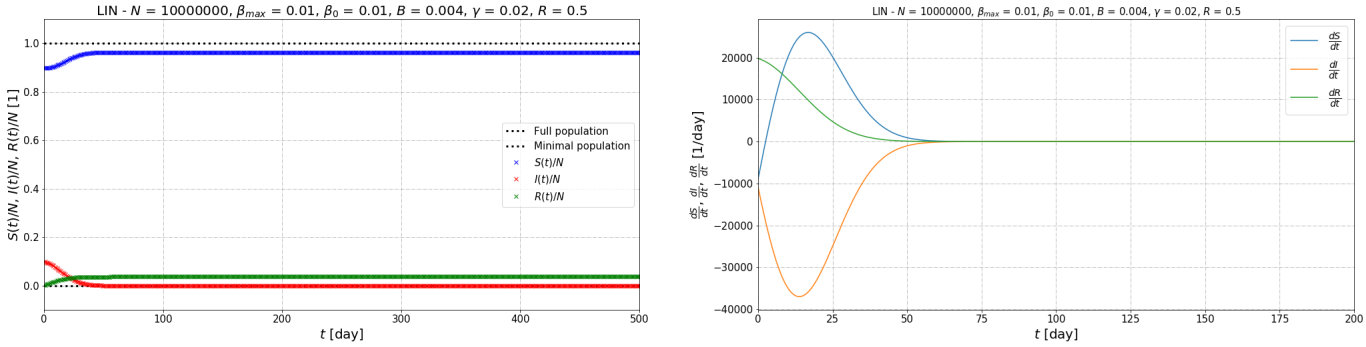

Figure 16: $\beta_{LIN}, R = 0.5$

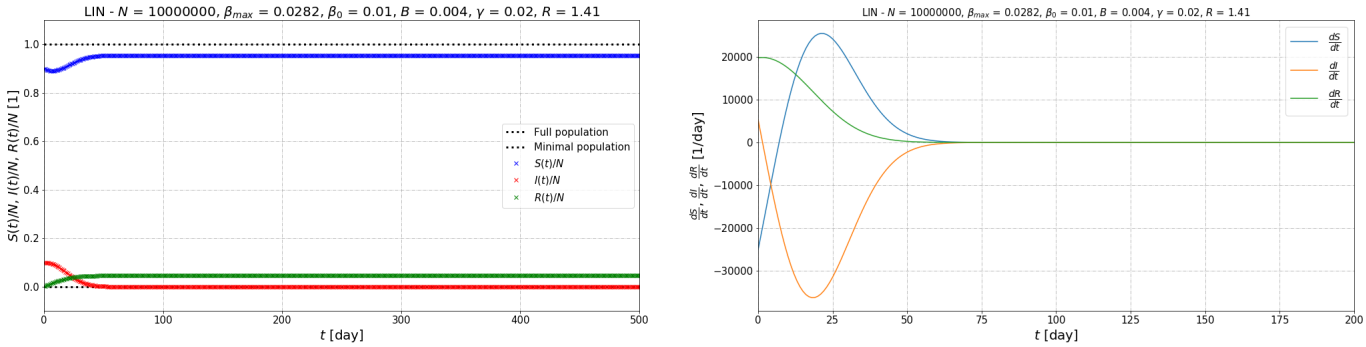

Figure 17: $\beta_{LIN}, R = 1.41$

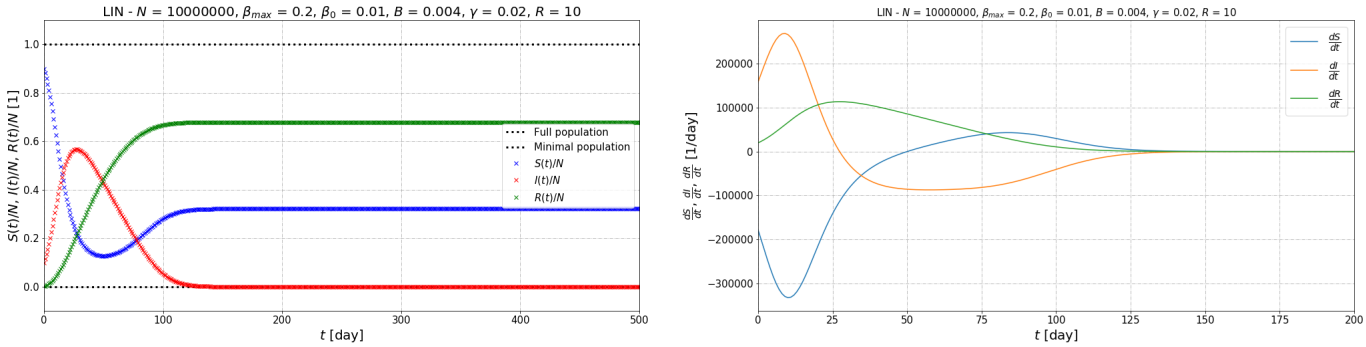

Figure 18: $\beta_{LIN}, R = 10$

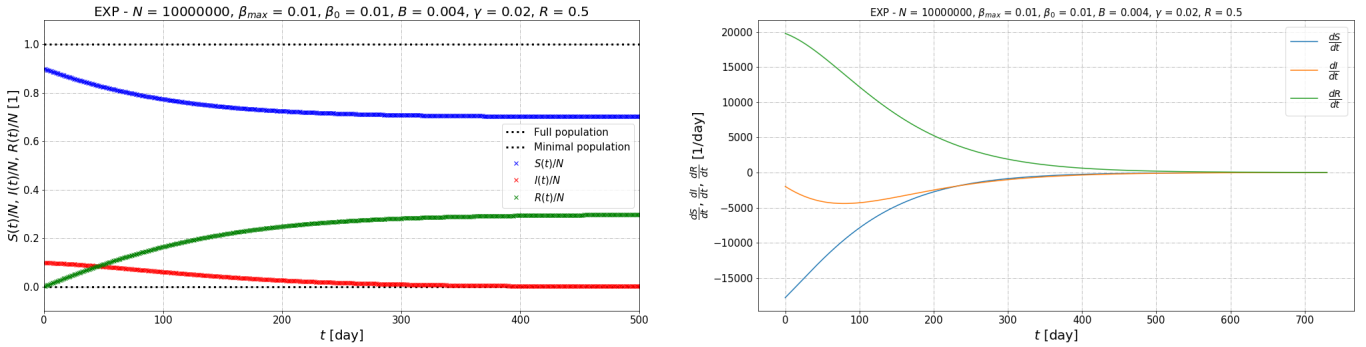

Figure 19: $\beta_{EXP}, R = 0.5$

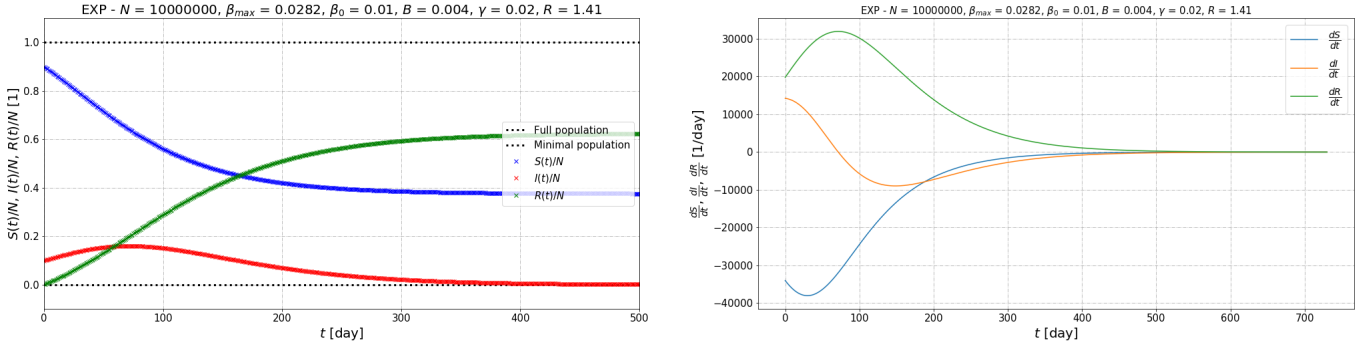

Figure 20: $\beta_{EXP}, R = 1.41$

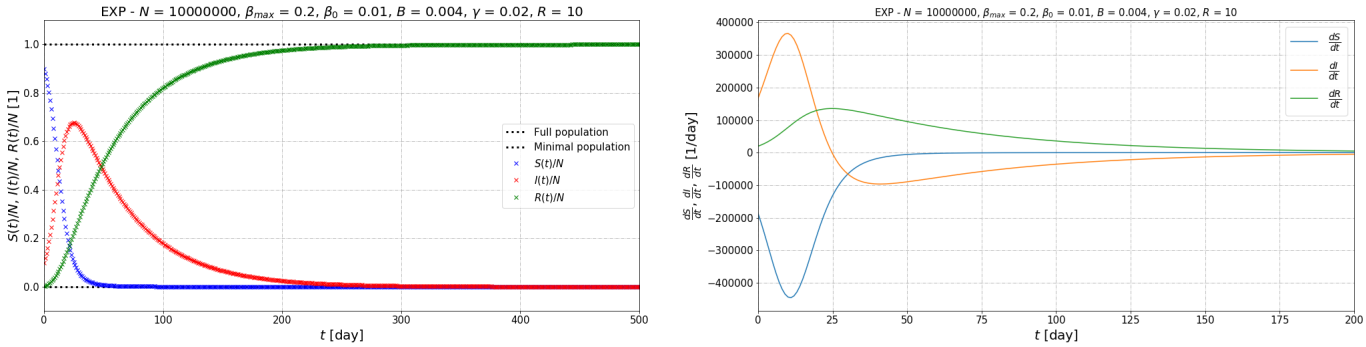

Figure 21: $\beta_{EXP}, R = 10$

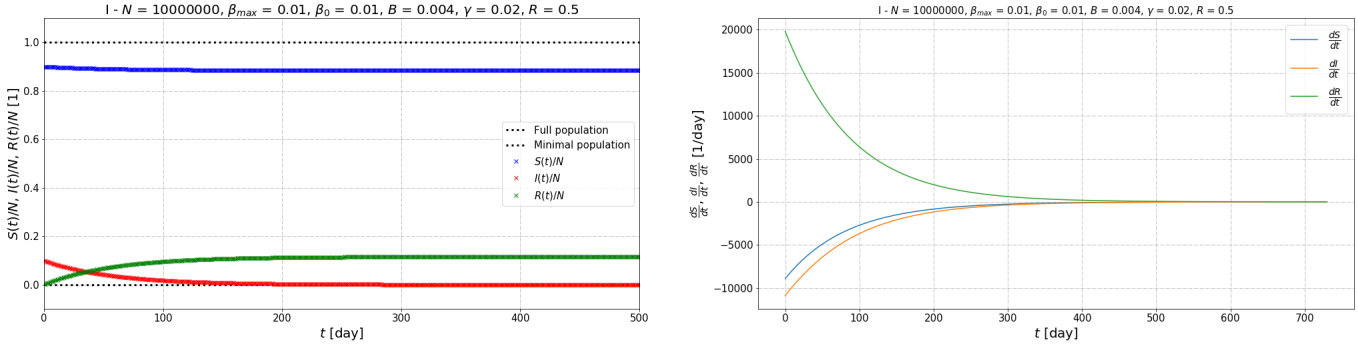

Figure 22: $\beta_I, R = 0.5$

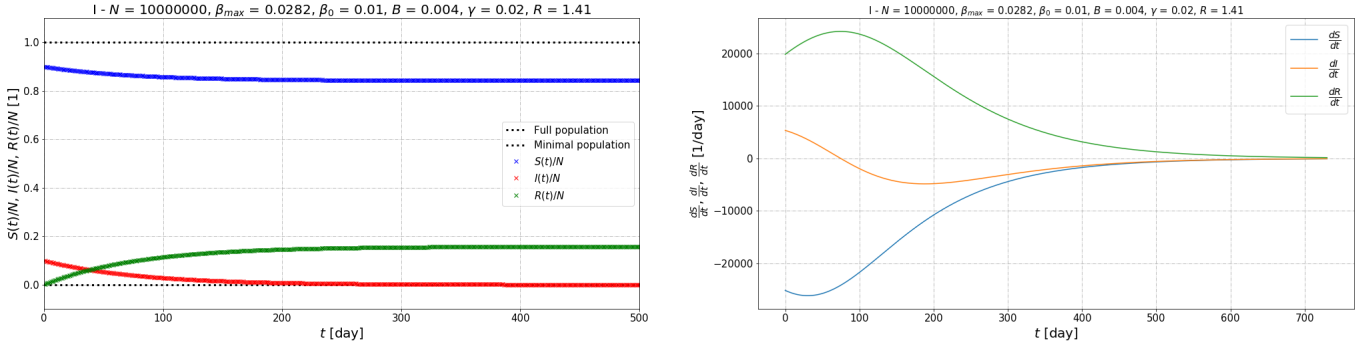

Figure 23: $\beta_I, R = 1.41$

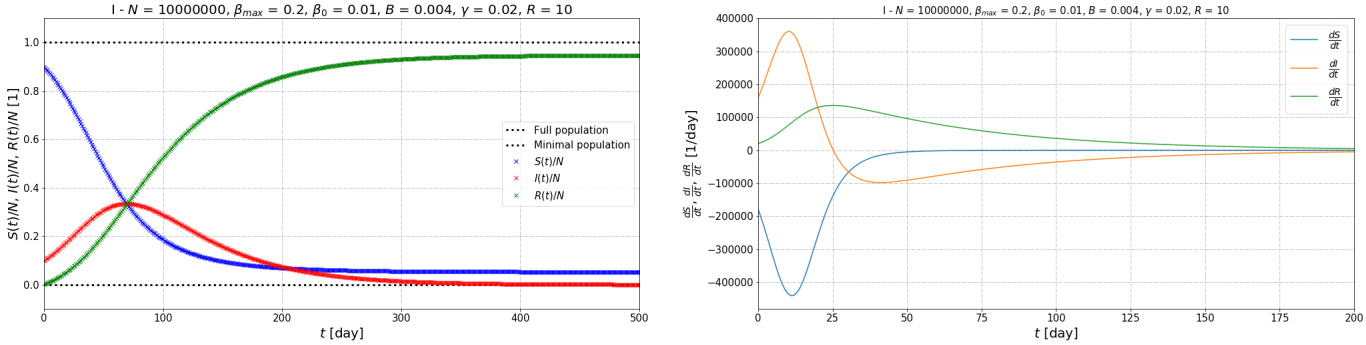

Figure 24: $\beta_I, R = 10$

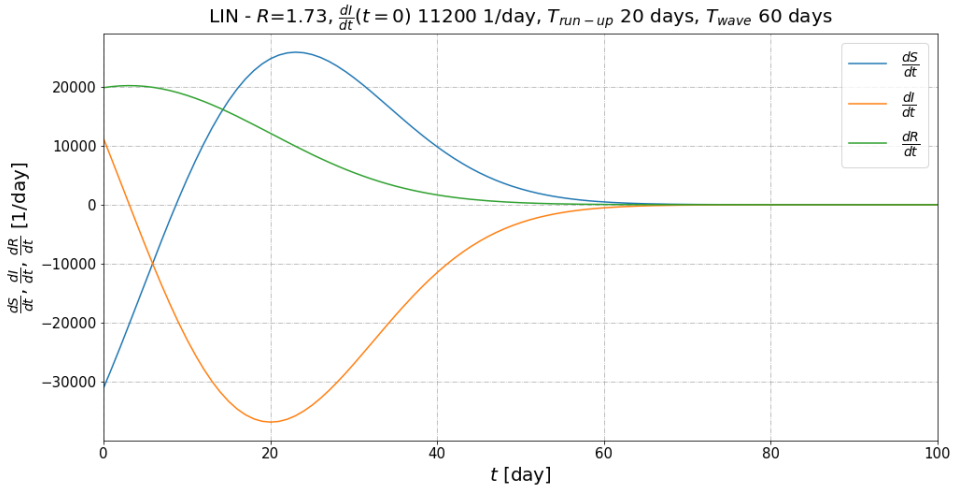

Figure 25: Optimal solution based on our model.

B. Involving changing population - SIRD model

We now consider changes in population due to births and deaths (other effects such like migration are not considered here). The simplest model that can take into account this phenomenon is the SIRD model, which introduces a new part of the population, the Deceased ones (due to the virus). Its number will obviously be proportional to the measure of the Infected group. We look at the full population in such a way that the sum of the number of Susceptible, Infected, Recovered and Deceased people are fixed, in other words, $S+I+R+D=N$,c they form a closed system and inside this, the number of living people varies every day. We can describe the model with the following differential equation system.

$$\begin{aligned}\frac{\mathrm{d}S}{\mathrm{d}t} &= -\frac{\beta SI}{N}\\ \frac{\mathrm{d}I}{\mathrm{d}t} &= +\frac{\beta SI}{N} - \gamma I - \mu I\\ \frac{\mathrm{d}R}{\mathrm{d}t} &= +\gamma I\\ \frac{\mathrm{d}D}{\mathrm{d}t} &= +\mu I\end{aligned}$$

On the long-run, it is possible that the whole population will die, so one needs to take births in account.

a. Results

We can see the relative populations of the groups normed to the total population on Fig. 26-37.'s left sides. On their right side, we can see the derivatives that give the day-to-day alteration of each epidemiologically different group. Fig. 26-28., 29-31., 32-34., 35-37. consecutively shows the constant, linearly decreasing, exponentially decreasing and the number of infected people depending cases for β with $R = 0.5, 1.41$ and 10 reproduction rate values, one below the current value and one much higher. The higher values can represent the initial period of a pandemic because at that time nor the average people, not the medics know the existence and the treatment for the virus. The lower values obviously indicate the final part where the infection is a highly suppressed process. The used parameter values can see on top of the Figures, the initial conditions were $S_{init} = 0.9N$, $R_{init} = 10000$, $D_{init} = 500$, $I_{init} = N - S_{init} - R_{init} - D_{init}$ and the sample frequency is $T_{div} = 1$ [day].

b. Conclusion

From Fig. 26-37. plots the $R = 1.41$ case seems to be the most accurate to describe Hungary's march 2021 wave. The linear case is the only one who has reasonable lingering time by ~ 60 days (with ~ 17 days with increasing daily infections). The number of the infections is not so correct, it is more than 3-times larger than it actually was, but the number of deaths is also not realistic. It has a really simple reason, namely that the derivative of the deceased population is proportional to the infected population. If the initial value of I is high the initial derivative of D will also be high, in some sense. The conclusion about this thoughtprocess is that the $\mu \ll \gamma$ relation should hold for the sake of reality.

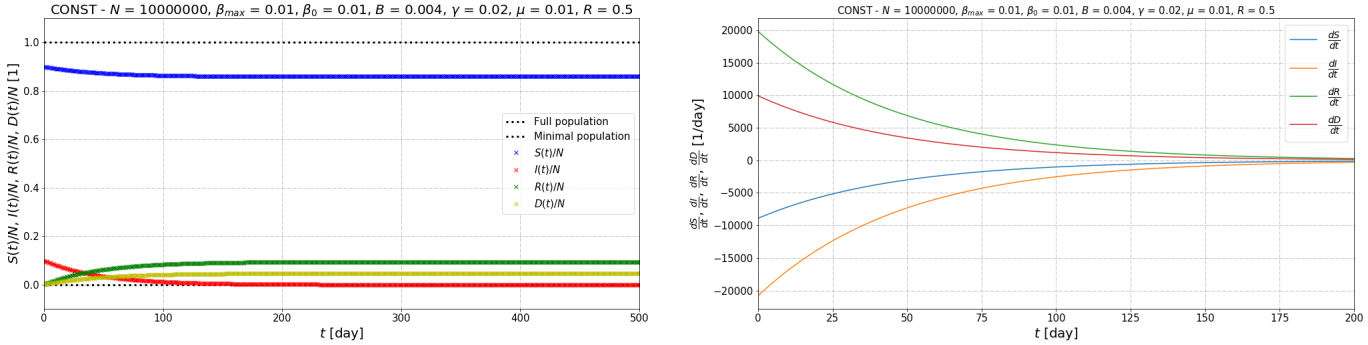

Figure 26: $\beta_{CONST}, R = 0.5$

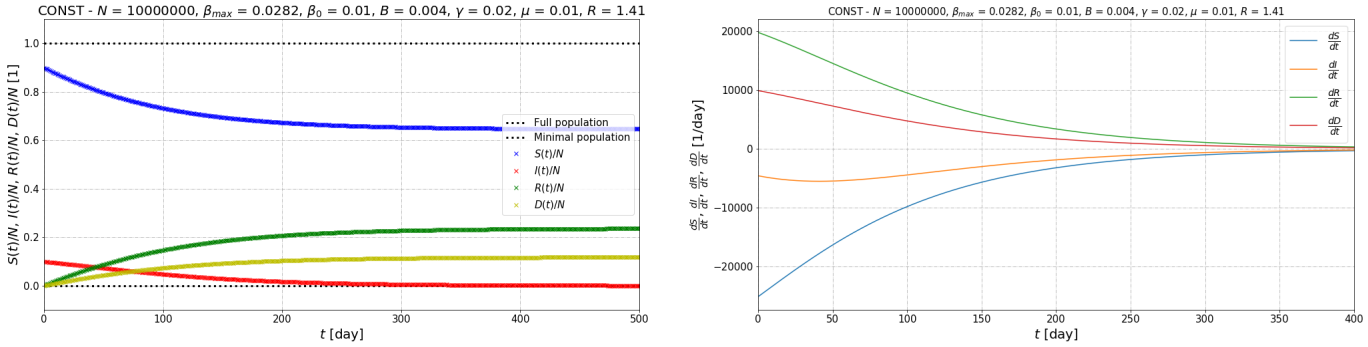

Figure 27: $\beta_{CONST}, R = 1.41$

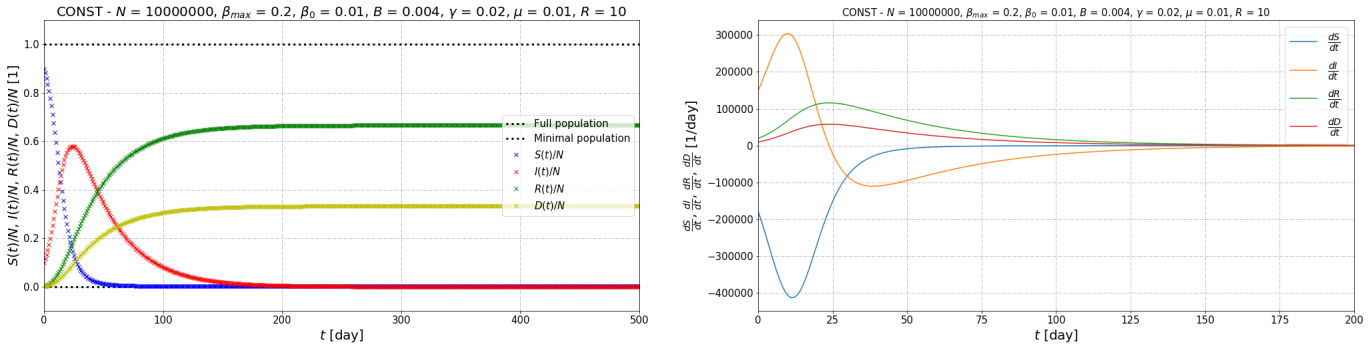

Figure 28: $\beta_{CONST}, R = 10$

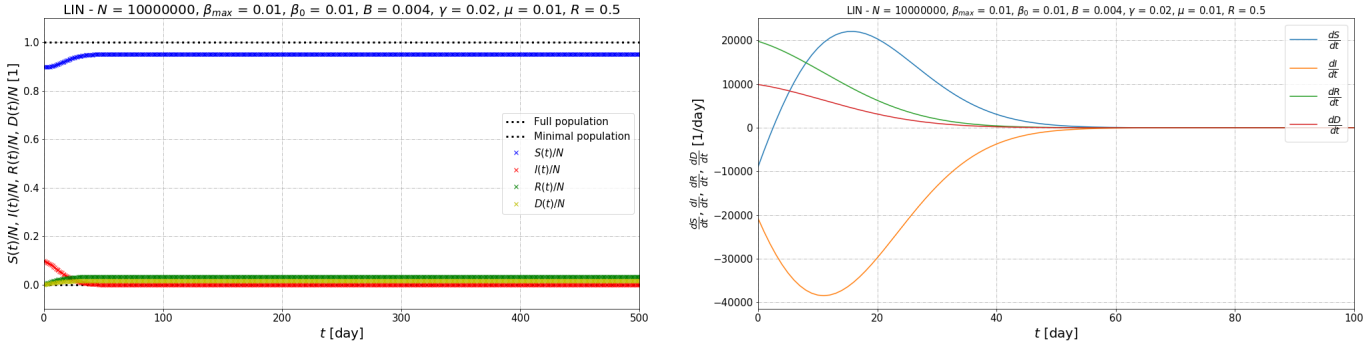

Figure 29: $\beta_{LIN}, R = 0.5$

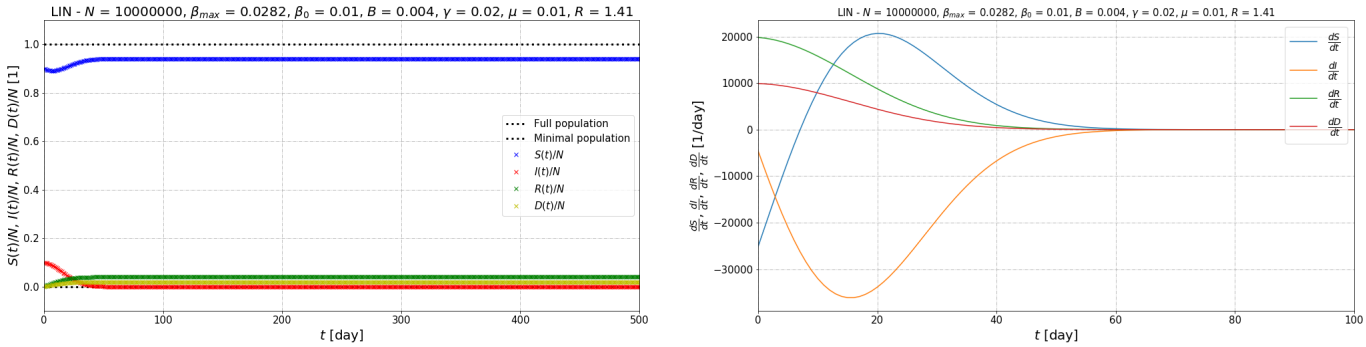

Figure 30: $\beta_{LIN}, R = 1.41$

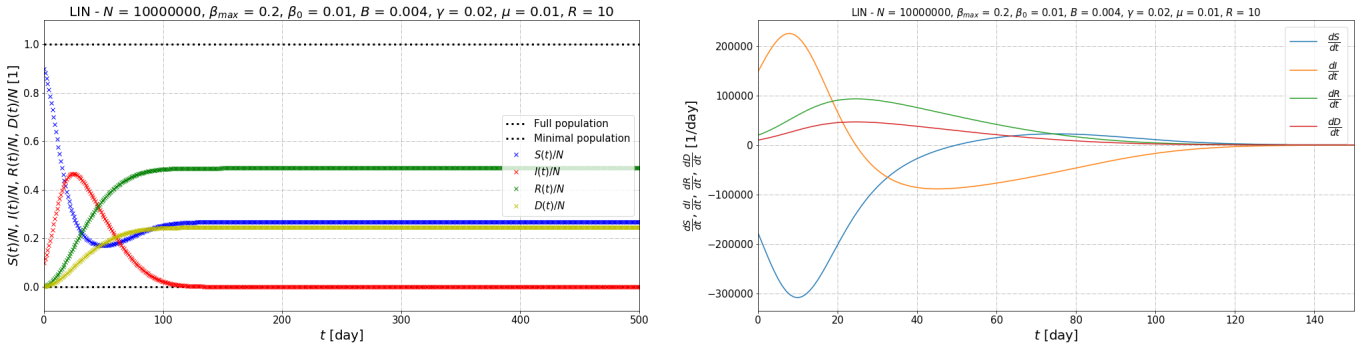

Figure 31: $\beta_{LIN}, R = 10$

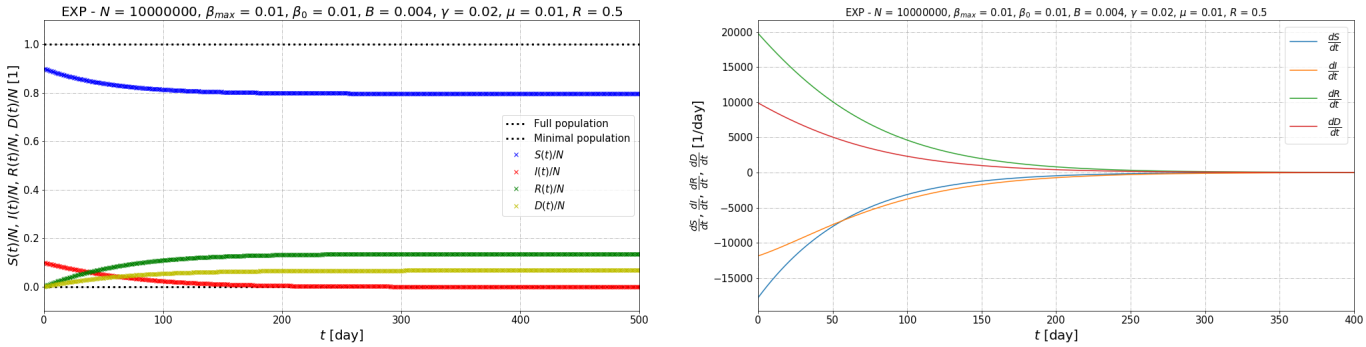

Figure 32: $\beta_{EXP}, R = 0.5$

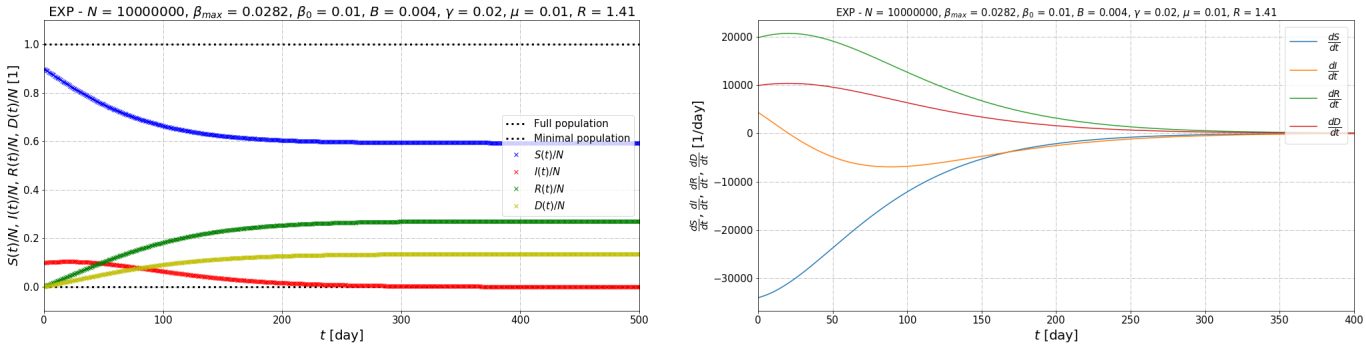

Figure 33: $\beta_{EXP}, R = 1.41$

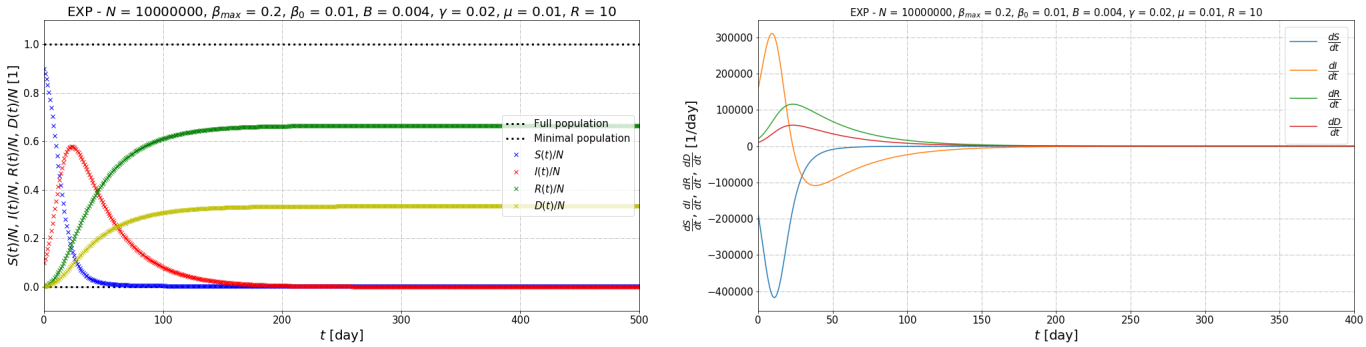

Figure 34: $\beta_{EXP}, R = 10$

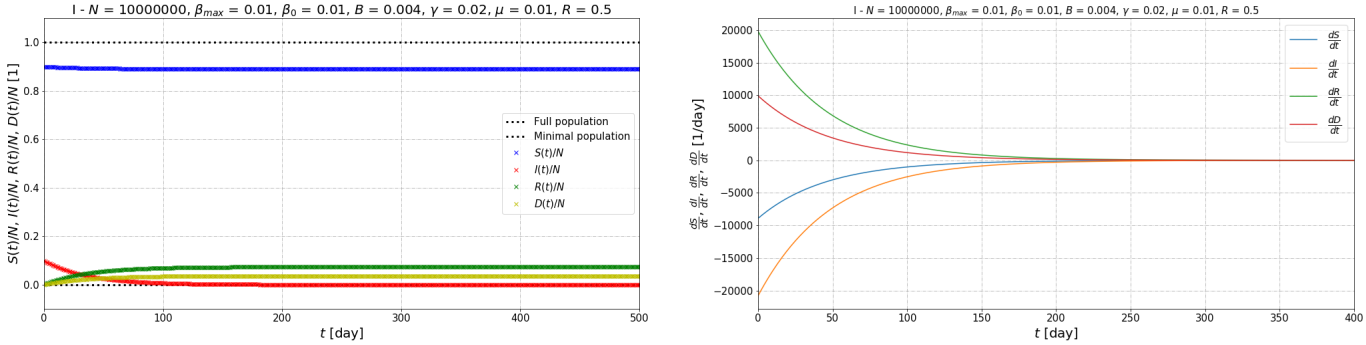

Figure 35: $\beta_I, R = 0.5$

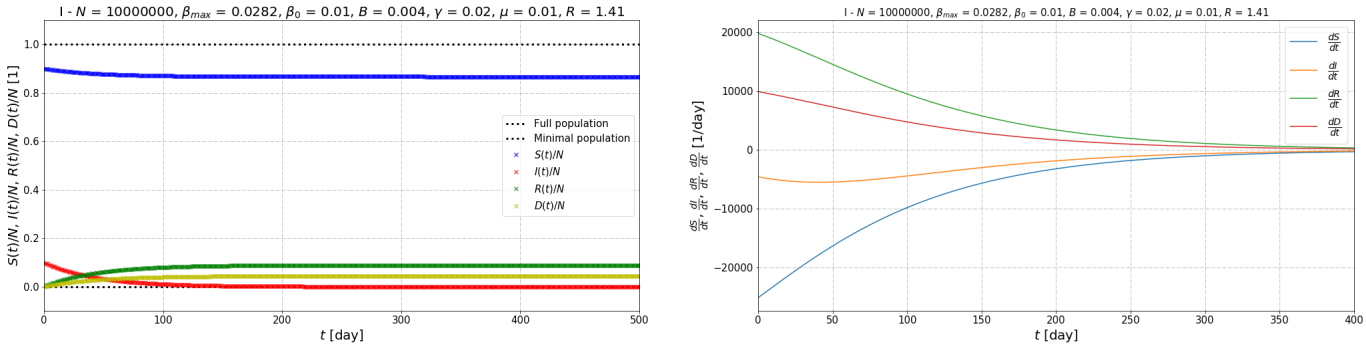

Figure 36: $\beta_I, R = 1.41$

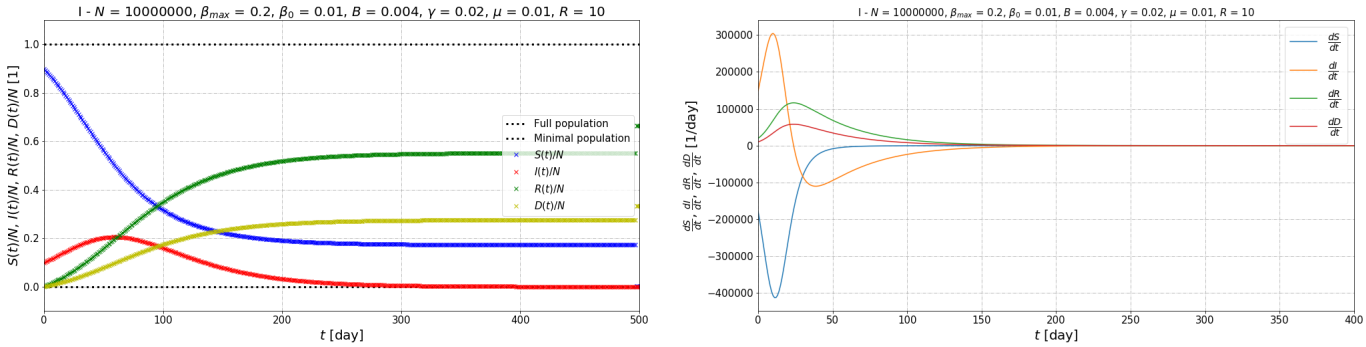

Figure 37: $\beta_I, R = 10$

III. COUPLED SOCIETIES

In a real world situation there are many, more or less isolable and characterizable societies which we can identify as the nations. These subparts of the humanity can have their own time evolution and healthcare system but if we want a more accurate model to describe a pandemic, we have to introduce interactions between them. One of the aspects which provides the motivation for that is the presence of international travellers, agents, who can easily strenghten the spreading of a virus.

First, we want to investigate the properties of the interactions. In order to have a clearer vision, we fix the population of the humanity. In this case, the Coupled SIS model can provide us a great framework for the description. After that, we will allow the humanity's population to change and study the pandemic through the lens of the Coupled SIRD model.

A. Coupled SIS model

In a real-life scenario, due to the globalistic nature of our society, it might be fruitful to consider the partitioning of groups to interacting subgroups which have their own S_k, I_k, β_k and γ_k parameters ($k \in \{1, ..., n\}$), each evolving in time. This way, we might model people coming from countries with different healthcare systems of different ages with different immune systems (different β-s), connecting with a varying number of contacts in a given time period (different γ-s), using empirical probability density functions, then taking the averages:

$$\begin{aligned}
\frac{\mathrm{d}S_k}{\mathrm{d}t} &= -\beta_k \frac{S_k I_k}{S_k + I_k} + \gamma_k I_k + \sum_{j=1,\, j\neq k}^{n} p_{k,j} \left(-\beta_j \frac{S_j I_j}{S_j + I_j} + \gamma_j I_j \right) \\
\frac{\mathrm{d}I_k}{\mathrm{d}t} &= +\beta_k \frac{S_k I_k}{S_k + I_k} - \gamma_k I_k + \sum_{j=1,\, j\neq k}^{n} p_{k,j} \left(+\beta_j \frac{S_j I_j}{S_j + I_j} - \gamma_j I_j \right),
\end{aligned}$$

where $p_{j,k} \in [0, 1]$ describes the connection of society j with society k (in order to make the equation look simpler, we might introduce the values $p_{k,k} = 1$ for every $k \in \{1, ..., n\}$).

$$\begin{aligned}
\frac{\mathrm{d}S_k}{\mathrm{d}t} &= \sum_{j=1}^{n} \left(-p_{k,j}\beta_j \frac{S_j I_j}{S_j + I_j} + p_{k,j}\gamma_j I_j \right) \\
\frac{\mathrm{d}I_k}{\mathrm{d}t} &= \sum_{j=1}^{n} \left(+p_{k,j}\beta_j \frac{S_j I_j}{S_j + I_j} - p_{k,j}\gamma_j I_j \right)
\end{aligned}$$

We now also have constraints:

$$\begin{aligned}
&S_k + I_k = N_k \quad \forall k, \\
&\sum_{k=1}^{n} N_k = N = \text{fixed!}
\end{aligned}$$

Let's define the interaction matrix in the following way:

$$p_{j,k} = \delta_{j,k} + (1 - \delta_{j,k})\varepsilon,$$

where the δ symbol notates the Kronecker delta function. We make the interaction homogenuous amongst 2 countries, independently from their physical localisation on Earth. We can have the calculation for arbitrary $\varepsilon \in [0, 1]$, but it is preferable to choose a small number (e.g. 0.01) to represent the real-life scenario better. There are no separate societies in the $\varepsilon = 1$ case, therefore, we get back the original SIS model.

a. Parameters

During the numerical computation we used the followings:

- $n = 4$
- $N_k = 10.000.000 \equiv N \quad \forall k$
- $S_{k,init}$ is a random, integer valued number from $(0.9N, N) \quad \forall k$.
- $I_{k,init} = N - S_{k,init} \quad \forall k$
- $\varepsilon = 0.01$

b. Results

Unfortunately, we were cannot be able to finish this task. We have almost all the program code that needed to the plots, you can find it too.

B. Coupled SIRD model

We would like to studied the SIRD model, which is more rigorous and robust model than the previous ones, therefore it should describe the real-life situation better. Unfortunately, we did not have more capacity to do its full study.

IV. RESULTS AND CONSEQUENCES

a. Contribution

Our contribution to the topic were the introduction of the time-dependent β functions and the coupled models. Unfortunately, we did not have the capacity to study the coupled SIRD model, too.

b. Results

We examined 4 different scenarios moderated by the β functions. We saw that from these 4, the linear case is the best, this gives back the reality with highest accuracy. We investigate 3 different reproduction rates, as it mentioned above. The most accurate was the $R = 1.41$ which corresponds to the last month's situation. The other 2 could represent rather the starting and the ending phases.

c. Problems and errors

As it is always, there were some points where some problems could have arised and numerical errors came from. One of them was the realistic parameter estimation for the processes. We think that it needs a lot of work and investigation to have such a parameter values that fits well to tha data (which is also needed in detail, if we want to have a correct optimalisation). We saw that most of the cases gave us long-tailed functions for the derivatives, in other words, the asymptotic convergence to the number of the populations. The only source of the numerical errors was solving the differential equation systems numerically.

d. Further generalisations

A possible model describing coupled societies with different aged groups. The couplings can be different (inhomogenous model). The populations of the subgroups (N_k-s) are different. The γ (and μ for SIRD) parameters could also have time-dependence.

V. APPENDIX

As it mentioned above, the SIS model can not be solved fully in the analitical way in the case of **exponential**ly decaying rate, as seen in (4), but we can reach a certain point of analiticality. The formulas that we can not simplify further are

here.

$$
\begin{aligned}
S(t) &= c_1 - \frac{e^{y_1(t)-y_2(t)}}{c_2 + \frac{1}{N}\int_1^t e^{y_3(k)}(\beta_{max} + \beta_0 \cdot e^{Bk})\mathrm{d}k} \\
y_1(t) &= \left(\frac{c_1\beta_0}{N} - \gamma\right)t \\
y_2(t) &= \frac{c_1\beta_{max}}{NB}e^{-Bt} \\
y_3(k) &= -\frac{c_1\beta_{max}}{NB}e^{-Bk} - (B+\gamma)k + \frac{c_1\beta_0}{N}k \\
I(t) &= c_1 - S(t)
\end{aligned}
$$

VI. REFERENCES

[1] https://en.wikipedia.org/wiki/Mathematical_modelling_of_infectious_disease

[2] https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology#The_SIR_model_with_vital_dynamics_and_constant_population

[3] https://www.theglobaleconomy.com/Hungary/covid_reproduction_rate/

[4] https://en.wikipedia.org/wiki/COVID-19_pandemic_in_Hungary

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[1] For a more robust model we have to take into account different kind of functions, for instance a saw-tooth function for modeling the quarantine. But from our point of view, for modeling the e.g. mask wearing, these functions will be adequate.

[2] The analitical results of the exponentially decaying rate can be found in the V Appendix. We compute the analitical formulas with Wolfram Mathematica.