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Parameters Analysis Of The Pandemic Curve

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Introduction

Compartmental models are a technique used to simplify the mathematical modelling of infectious diseases. The population is divided into compartments, with the assumption that every individual in giving compartment has the same characteristics. Its origin is in the early 20th century, with an important early work of Kermack and McKendrick in 1927 [1].

The models are usually investigated through ordinary differential equations (which are deterministic). They can also be viewed in a stochastic framework, which is more realistic, but also more complicated to analyze.

Compartmental models may be used to predict properties of how a disease spreads, for example the prevalence (total number of infected) or the duration of an pandemic. Also, the model allows for understanding how different situations may affect the outcome of the epidemic, e.g., what's the most efficient technique for issuing a limited number of vaccines in a given population.

There are several models which are used worldwide with different range of complexity describing the pandemic dynamics and its evolution with time, in this study, we will be using one of these models to study how their parameters change with time, and how this results in achieving a herd immunity .

In this study, we are using a compartmental model made by Giuseppe Gaeta [2] to study and analysis the Padua province pandemic situation and the pandemic curve parameters and comparing different clinical parameters that we have from different studies.

And in order to have deep analysis, we have introduced techniques and algorithms to see more clearly the pandemic situation in Padua province and how these parameters changed with time. At the end, we introduced a parameter to optimise the model for long term predictions .

Model Dynamics

0.1 SIR Model

The Susceptible-Infected-Recovered (SIR) model [3–6] was first used by Kermack and McKendrick in 1927 and has subsequently been applied to a variety of diseases, especially airborne childhood diseases with lifelong immunity upon recovery, such as measles, mumps, rubella, and pertussis, with the total population $N = S(t) + I(t) + R(t)$.

The SIR model is used where individuals infect each other directly (rather than through a disease vector such as a mosquito). An individual who recovers from the illness is also modeled to have perfect immunity to the disease thereafter. Contact between people is also modeled to be random.

The rate of people that become infected is proportional to the number of people who are infected, and the number of people who are susceptible. If there are lots of people infected, the chances of a susceptible coming into contact with someone who is infected is high. Likewise, if there are very few people who are susceptible, the chances of a susceptible coming into contact with an infected is lower (since most of the contact would be among the non-susceptible people—either infected or resistant).

The SIR model of an infectious pandemic, providing permanent immunity to those who have already been infected and recovered is based on the following dynamics:

$$dS/dt = -\alpha SI \tag{1}$$

$$dI/dt = \alpha SI - \beta I \tag{2}$$

$$dR/dt = \beta I \tag{3}$$

Where we have that α is the parameter controlling how often a susceptible-infected contact results in a new infection and β is the rate an infected recovers and moves into the recovered phase; they depend both on the characteristics of pathogen and on social behavior, and we can see easily that for any pandemic to start growing the second equation should have a positive result which means $S > \gamma$ with $\gamma = \beta/\alpha$ known as *pandemic threshold*. If this raised above the level of the total population N the pandemic stops (which means the number of infected individuals starts to decrease, albeit new individuals will be infected).

The SIR model has subsequently been applied to a variety of diseases, but with the COVID-19 we are having an issue that the model is not taking in account the presence of important categories of the infected population, which is the asymptomatic infected population that contains a significant percentage of the total infected population.¹ Therefore it is more convenient for COVID-19 to use a model that takes in account the presence of asymptomatic infected population for example A-SIR [2] which is a modified version of the standard SIR.

¹there are various studies about this percentage, for example, in Li et al contribution [8] was estimated to be almost 86% and in the Italian study made in Vò [7] it has been estimated to be 43%.

0.2 A-SIR Model

It may happen to have a pandemic with a large fraction of infected people are actually asymptomatic, but still fully infective, as it appears to be the case for COVID-19, the infected asymptomatic population can cause a formidable vehicle of contagion, as they have no reason to take special precautions, they get in contact with a number of people which themselves do not take the due precautions (which would be taken in the case of an individual with evident symptoms). Therefore, in this model we still assume permanent immunity of individuals who have been infected and recovered, and constant population. We will have susceptible $S(t)$ in a unique class, but two classes of infected and infective people: symptomatic $I(t)$ and asymptomatic $J(t)$; and similarly two classes of recovered people: registered recovered $R(t)$ and unregistered recovered (those who were passing unnoticed through the infection) $U(t)$. Symptomatic infects are removed from the pandemic dynamics through isolation (in the hospital or at home) at a removal rate β (thus with typical delay β^{-1}), while asymptomatic people are removed from the pandemic dynamics through spontaneous recovery, at a recovery rate $\Gamma < \beta$.

Thus after a typical time $\Gamma^{-1} > \beta^{-1}$ we assume that both classes of infected people are infective in the same way, and that an individual who gets infected passes with probability μ to the class I and with probability $(1 - \mu)$ to the class J . Therefore the model is based on the following dynamics :

$$dS/dt = -\alpha S(I + J) \quad (4)$$

$$dI/dt = \mu \alpha S(I + J) - \beta I \quad (5)$$

$$dJ/dt = \alpha(1 - \mu)S(I + J) - \Gamma J \quad (6)$$

$$dR/dt = \beta I \quad (7)$$

$$dU/dt = \Gamma J \quad (8)$$

In the case of COVID-19, it's known that the incubation time β^{-1} is $\approx 5-7$ [9] with a mean value about 5.1 days; And $\Gamma^{-1} \approx 14$ [10] assuming that symptomatic infection is promptly recognized and swiftly treated, epidemiological and clinical data suggest these approximate values (note that asymptomatic removal time includes both the incubation time and the healing time), the value of μ is more controversial and in this study, we will use the hypothesis that $\mu = 0.57$ ².

We note that $I(t)$ will increase as far as the condition $S > \gamma_1$ with $\gamma_1 = \frac{\beta I}{\mu \alpha (I+J)}$. Thus the epidemic threshold (for symptomatic patients) depends both on the fixed parameters β, μ, α and on the variable ratio of known infected over total infected $I(t)/(I(t) + J(t))$. And we have the same idea for the asymptomatic population, $J(t)$ will increase as far as $S > \gamma_2$ with $\gamma_2 = \frac{\Gamma J}{(1-\mu)\alpha(I+J)}$ which depends both on the fixed parameters Γ, μ, α and on the variable ratio of the asymptomatic infection over total infective $J(t)/(I(t) + J(t))$, and calculating the ratio between the two factors we have:

$$\frac{\gamma_1}{\gamma_2} = \left(\frac{1-\mu}{\mu}\right) \left(\frac{\beta}{\Gamma}\right) \left(\frac{I}{J}\right) \quad (9)$$

As we can see we cannot claim there is a definite ordering between γ_1 and γ_2 as we have that $\mu \approx 1/2$, $\beta > \Gamma$ but on the other hand $I > J$ for the early phase of the pandemic and it could be the opposite after, this means that we will have situations where $I(t)$ declines and $J(t)$ is still growing, but the opposite is also possible. We expect that in the very first phase when the different removal times have not yet shown their effects we have.

$$J \approx \frac{1-\mu}{\mu} I \quad (10)$$

Which results in $\gamma_1 = \gamma$ that we can use it for a simulation of early dynamics.

²in the last part of this study we will see the effects of using another value for μ .

0.2.1 Early Dynamics Of A-SIR

It is relevant noticing that in the initial phase of the pandemic the number of susceptible varies very little and can thus be considered as constant, $S(t) \approx S_0$. With this approximation, therefore the A-SIR equations reduce to a linear system of four equations with constant coefficients, or more precisely to a “master” system of two equations as follows:

$$dI/dt = (\mu \alpha S_0 - \beta) I + \mu \alpha S_0 J \tag{11}$$

$$dJ/dt = \alpha(1 - \mu)S_0 I + (\alpha(1 - \mu)S_0 - \Gamma) J \tag{12}$$

Plus two auxiliary equations are amounting to a direct integration, which are :

$$R(t) = R_0 + \int_0^t I(y)dy \tag{13}$$

$$U(t) = U_0 + \int_0^t J(y)dy \tag{14}$$

0.2.2 Fitting the parameters

Due to the fact that we do not have full knowledge about the number of infected people at each time; the best we can have is the number of people who are hospitalized or however registered by the health system. Assuming that infected people are immediately isolated, this provides an estimate of $R(t)$. Thus we should be able to compare the predictions for the removed class with epidemiological data, in order to do this we should focus on $R(t)$, we can use Taylor series to approximate $R(t)$ for small t values as it expected for the early dynamics phase of the pandemic as following:

$$R(t) \approx R_0 + \frac{\partial R(t)}{\partial t} t + \frac{1}{2} \frac{\partial^2 R(t)}{\partial t^2} t^2 + \dots \tag{15}$$

with $\frac{\partial R(t)}{\partial t} = \beta I$, and $\frac{\partial^2 R(t)}{\partial t^2} = \beta \frac{\partial I(t)}{\partial t}$.

On the other hand we notice that using the equations (4) and (7) and the approximation between $J(t)$ and $I(t)$ at early dynamics we have $dS/dR = -\frac{\alpha}{\beta\mu} S_0$ therefore $S(R) = S_0 e^{-\frac{(R-R_0)}{\mu\gamma}}$ which give us a hint to use the $\text{Log}(R(t))$ fit⁴, which is applied as following :

$$\log(R(t)) \approx \log(R_0) + \frac{R'(t)}{R(t)} t + \frac{1}{2} \frac{R''(t)R(t) - R'(t)^2}{R(t)^2} t^2 + \dots \tag{16}$$

with $\frac{R'(t)}{R(t)} = \frac{\beta I_0}{R_0}$ and $\frac{R''(t)R(t) - R'(t)^2}{R(t)^2} = \frac{\beta [\alpha(I_0 + J_0)R_0 S_0 \mu - \beta I_0(I_0 + R_0)]}{R_0^2}$.

Applying one of the two methods with the real data that we have at the early phase of the pandemic we can have:

$$R(t) = A + Bt + \frac{1}{2} Ct^2 \tag{17}$$

we have $R_0 = A, I_0 = \frac{B}{\beta}, \frac{\beta}{\alpha} = \frac{\beta B S_0}{(\beta B + C)}$ for the equation (15), and for the equation (16) we have $R_0 = e^A, I_0 = \frac{Be^A}{\beta}, \frac{\beta}{\alpha} = \frac{\beta S_0 B}{\beta B + B^2 + 2C}$.

³Trying to fit with higher order truncation of the Taylor series is not reliable in the presence of a short time series.

⁴we always write “log” for the natural logarithm.

Model Applying

0.3 Province Of Padua

The province of Padua is one of the first areas in Italy, where the pandemic started to grow and in which the first death case of the COVID-19 have been registered, choosing a Province as a case of study is due to the block between the Provinces (to decrease the spread of the pandemic) during the period of time in which this study has been applied, therefore we can start our study by using the data of the cumulative number of registered infected communicated by the Azienda Zero of Veneto region [11] as reported in Table 1 for the first part of March (1-11) as following:

Table 1: Early Data Of COVID-19 Of Padua Province

DAY	Mar 1	Mar 2	Mar 3	Mar 4	Mar 5	Mar 6	Mar 7	Mar 8	Mar 9	Mar 10	Mar 11
R	12	28	51	74	104	112	138	171	186	241	284

At this point we can use the fitting of our curve of the early phase of Covid-19 as mentioned in the last chapter and by using both methods $R(t)$ and $\text{Log}(R(t))$ of fitting we obtain :

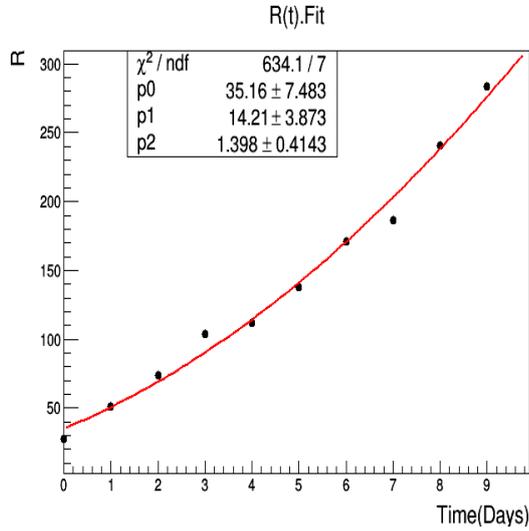


Figure 1: Fit Using $R(t)$

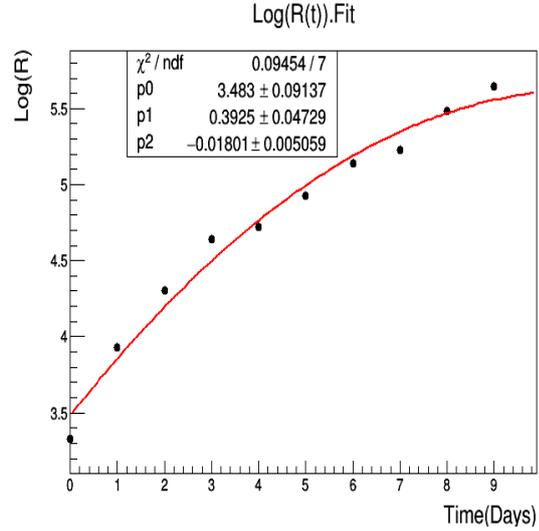


Figure 2: Fit Using $\text{Log}(R(t))$

However, we can rescale the factor $S(t)\alpha$ in our equations by multiplying and dividing by S_0 therefore $\alpha S(t) = \lambda S_p$ with $\lambda = \alpha S_0$ and $S_p = \frac{S(t)}{S_0}$ and using the equations (15)-(16) with $\beta^{-1} = 5.1$, $\Gamma^{-1} = 14$ and $\mu = 0.57$, we can calculate the rest of the parameters which result in the following table :

Table 2: Early Dynamics Parameters Estimation

$R(t) - fit$	$\lambda = 0.297$	$I_o = 180$	$J_0 = 146$
$\text{Log}(R(t)) - fit$	$\lambda = 0.405$	$I_o = 63$	$J_0 = 48$

For our fitting we can note that the $\text{Log}(R(t))$ fit is predicting higher λ value and smaller initial values for both $I(t)$ and $J(t)$. Therefore, in order to see which one is more appropriate, we can run a simulation for both fits and we compare that with the real data as follows:

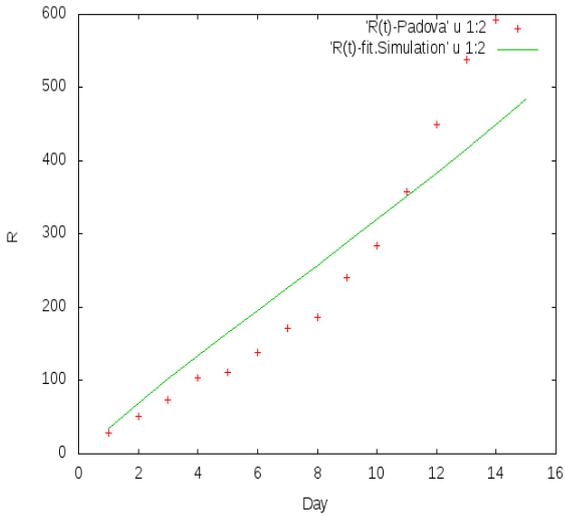


Figure 3: $R(t)$ Fit Simulation

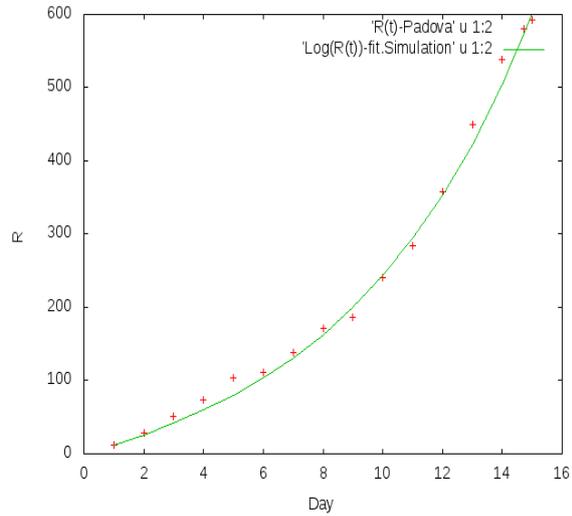


Figure 4: $\text{Log}(R(t))$ Fit Simulation

As we can see that the simulation using the $\text{Log}(R(t))$ fit parameters is more realistic comparing to the real data as the simulation with the $R(t)$ fit parameters is reasonably good just within the beginning of the interval used to estimate the parameters and fails outside of it.

0.4 Simulation For Padua Province

At this point with the parameters that we obtained from the early dynamic fit we can run a simulation for Padua province and compare it with the real data that we have as following:

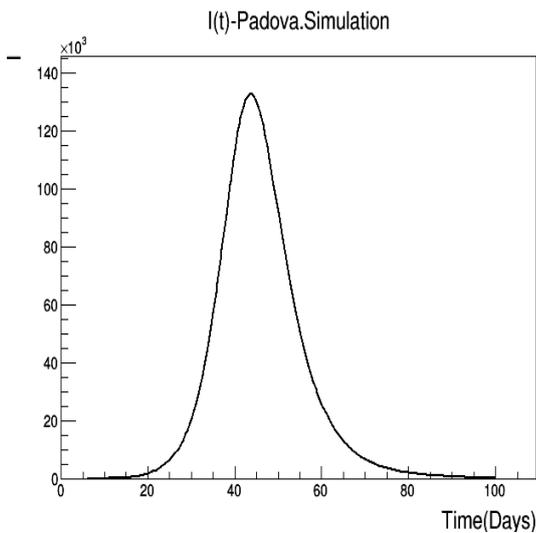


Figure 5: Model Simulation

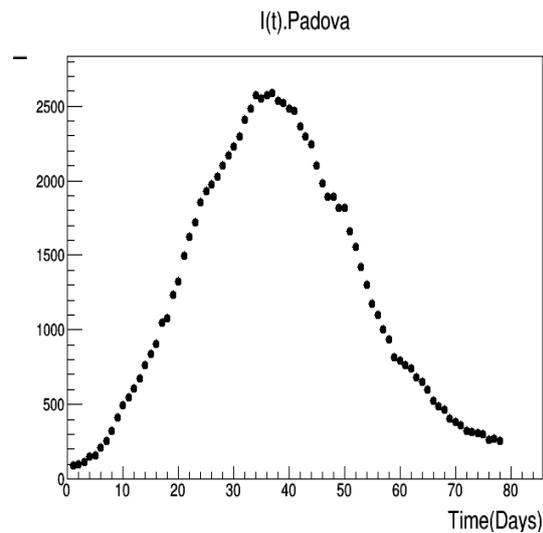


Figure 6: Real Data Of Padua Province

It is quite clear that we have a very different situation between our simulation and how the pandemic really spreads in Padua province, it is due to a lot of factors, mainly the measures that have been applied by the Italian government and the Veneto regional government [12], starting from the last period of February more effective ones on the 8th of March and 18th of the same month followed by other ones that has led to efficient decreasing of the pandemic spreads in the Padua province.

However, we can analyze this mathematically by introducing a new factor in our equations that will estimate the effect of this kind of measures in such way :

$$\lambda(t) = r(t)\lambda_0 \quad (18)$$

With λ_0 is the parameter that we estimated on the early phase of the pandemic as we suppose that the measures were not of significant influence at the early phase, $0 < r < 1$ is a reduction factor that represents the measure's effect with $r = 1$ for the early phase as no measures were applied.

At this point we run a various simulations for $I(t)$ with different r value and using $\beta^{-1} = 5.1$, $\Gamma^{-1} = 14$ and $\mu = 0.57$ as following :

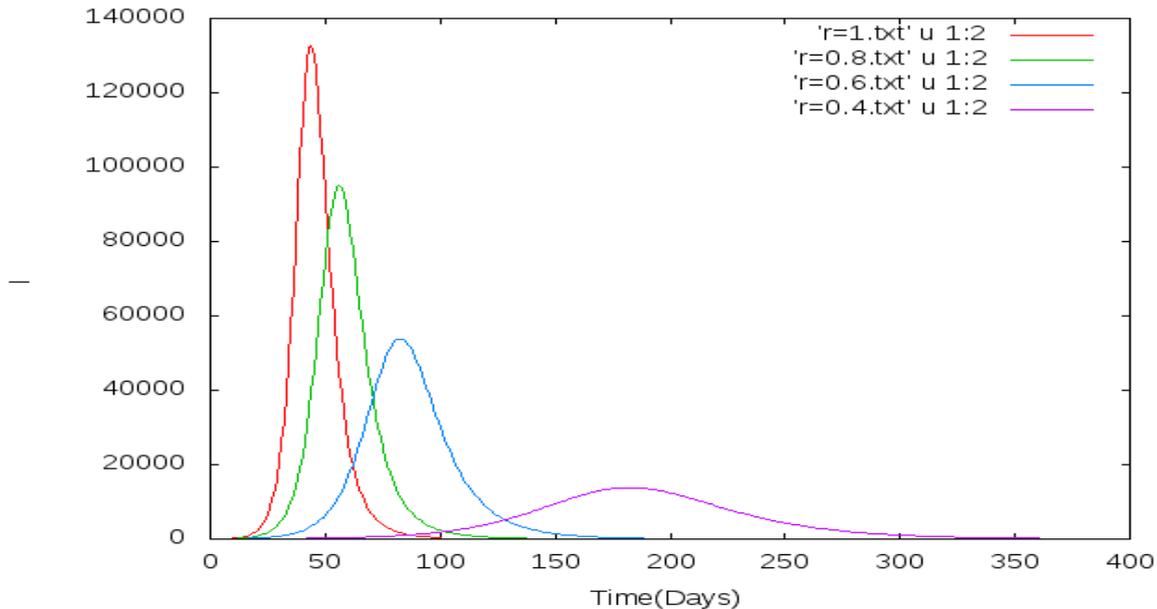


Figure 7: Simulations With Different r Values

Here we can see our simulation of $I(t)$ with t measured in days for $r = 1$, $r = 0.8$, $r = 0.6$ and $r = 0.4$ (the curves for higher r are those with higher peak), and it is quite clear that we can see that the higher the r value we have the higher and faster we arrive to the peak respect to smaller r values.

As we can easily see in the figure 6 that the pandemic situation in Padua province is not following any of these simulations that we made due to the fact that in Padua province the situation we have a earlier peak similar to the one with $r = 1$ and with smaller peak than the one with $r = 0.4$. Therefore, it is evident that we cannot represent the pandemic situation in Padua province with a constant r value due to the changing of the measures that they have been increasing with time.

Therefore, it is more appropriate to study the pandemic situation with variable r value for different time intervals, in this study, we will be using 7 days as a time interval due to the fact that we have the mean value of the incubation period is between 5-6 days, using longer time interval will lead to bigger interference between the measure's effects that have been applied . Therefore, we can run various simulations of the data for 7 days with the model and compare them with the real ones that we have and changing $r(t)$ value for each simulation, at the end we take the best fitting one for our data by using the least-squares method.

Studying a variable r value, respect to the time with 7 days as a time interval starting with the data from 5th of march to 21th of may using the same parameters used in the last simulation will led us to the following $r(t)$ ⁵ graph :

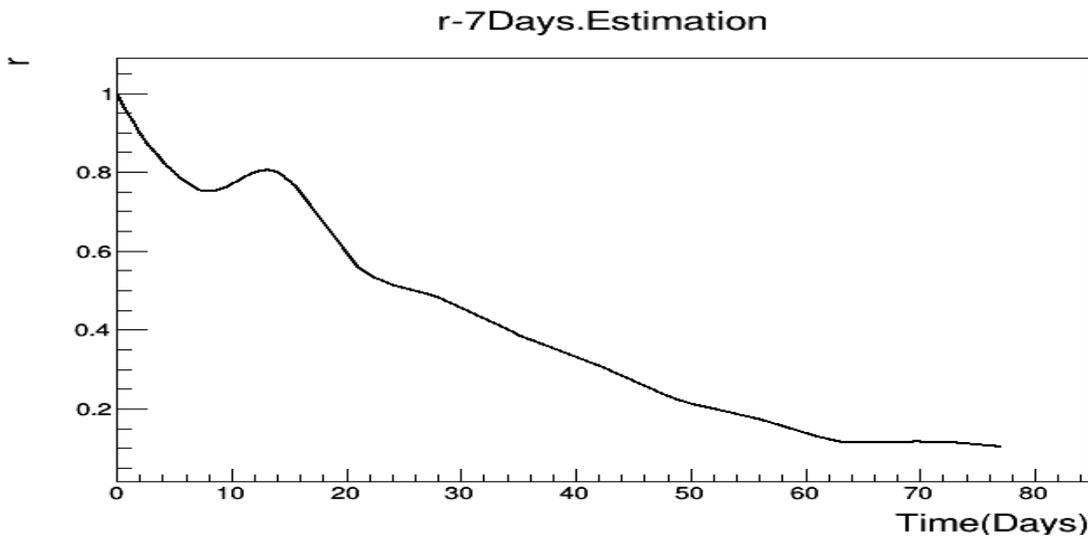


Figure 8: $r(t)$ For Padua Province

At this point with these $r(t)$ values we can run a simulation for the pandemic situation in Padua province and compare it with the data that we have as following:

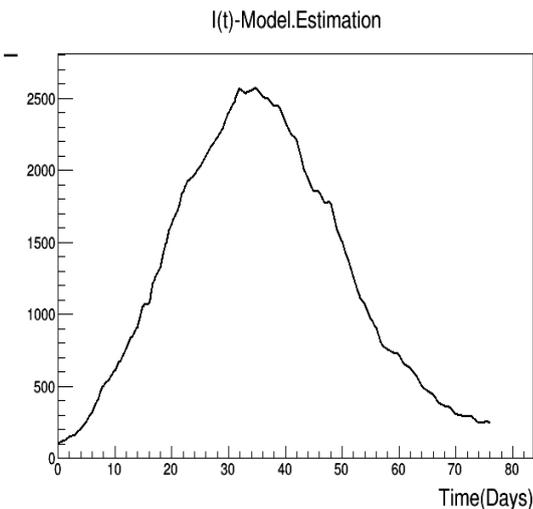


Figure 9: Model Simulation With $r(t)$

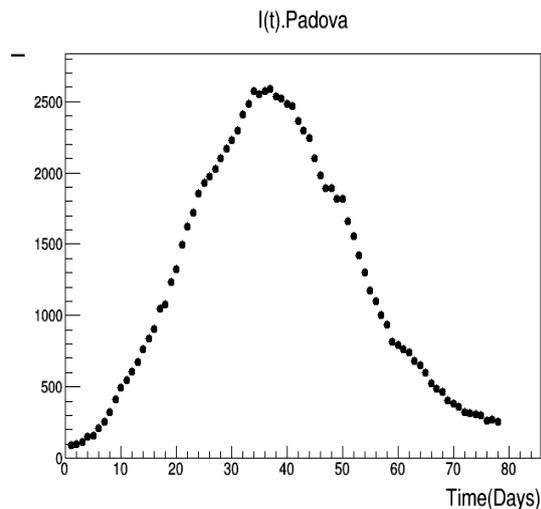


Figure 10: Real Data Of Padua Province

⁵due to the long period of the study, there could be other reasons caused the decrease of the pandemic spreading like the increase of temperature or a mutation of the virus, here we see their effects included in the $r(t)$ parameter.

We can see easily from the figure 8 the effect of the measures applied by the Italian government and Veneto regional government , that the graph is estimating the measures from the 2nd of March until the 18th of May by using the data from the 5th of March until 21th of May due to the fact that we are able to start seeing the measures effect starting from 3-5 [9] days after the measures have been applied as we are using the hypothesis of $\beta = 5.1$.

On the other hand, using any data after 21th of may would not work well with our model due to the fact that the Padua province it is not a closed population anymore due to the significant reopening procedure applied from the 18th of may [12] that led to a total changing of our parameters $\lambda(t)$, $S_p(t)$, $I(t)$, and $J(t)$ therefore we are not able to keep the study of the data after the 21th of may with the same model parameters.

We can however make a 5 days estimation for the reduction factor $r(t)$ to see more clearly this measure's effect as the following figure :

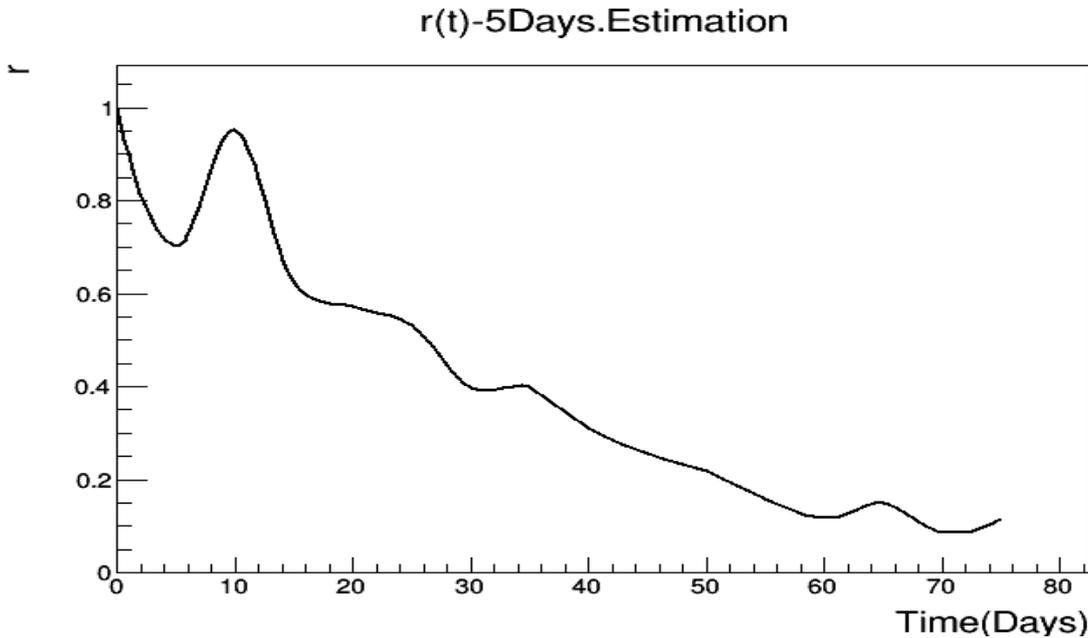


Figure 11: $r(t)$ 5-Days Estimation

With 5 Days interval estimation we can notice clearly the strong effect of the 8th of march measures (the Prime Minister of Italy had declared the total block of Padua Province and declared it as a red zone) We see significant decreasing of the reduction factor from the 10th day of the study which corresponds to the 12th of March (4 days after the measures have been applied). After that, other measures have been applied and we have a smooth decreasing of the reduction factor until the last part in which it has been stable and started to increase due to the reopening procedure that has started from the 4th of May.

On the other hand, we can see that this model is working well describing the pandemic situation in Padua province due to the fact that we have small pandemic situation ($S_p(t) \approx 1$ in all the study period) therefore to describe the pandemic situation on the long term we should introduce a parameter that will optimise this model to describe the situation when $S_p(t) \not\approx 1$ and having $R(t)$ and $U(t)$ become considered as significant quantities respect to $S(t)$ as we will see in the next section.

0.5 Model Optimisation

As we mentioned in the last section that we need to optimise the model to make appropriate predictions about the pandemic situation of Padua province, the first thing that we should take into consideration is that the model is having predictions of very high peaks as we see on the figure 7, it is higher respect to a real pandemic situation, this is due to the fact that the model is not taking into account the decrease of the probability that an infected individual will come in contact with a susceptible individual.

In the early dynamics phase we estimated the probability of infected and susceptible individual to come in contact to be ≈ 1 due to the fact that it was very much probable for an infected individual to come in contact with a susceptible individual rather than with the other mentioned categories.

However, we can optimise the model and analyze this mathematically by introducing a new factor in our equations that will take into account this decrease of probability as following :

$$\lambda(t) = h(t)r(t)\lambda_0 \quad (19)$$

$$h(t) = 1 - \frac{R(t) + U(t) + I(t) + J(t) - D(t)}{S_0 - D(t)} \quad (20)$$

Where $D(t)$ is the mortality caused by the pandemic⁶, As we can easily see that the $h(t)$ parameter (h coming from herd immunity) will decrease the peaks of the simulated curves and will have no significant effect on the early phase of the pandemic as we hypothesised. At this point we can run a different simulations with different r values and compare it with previous simulations as following :

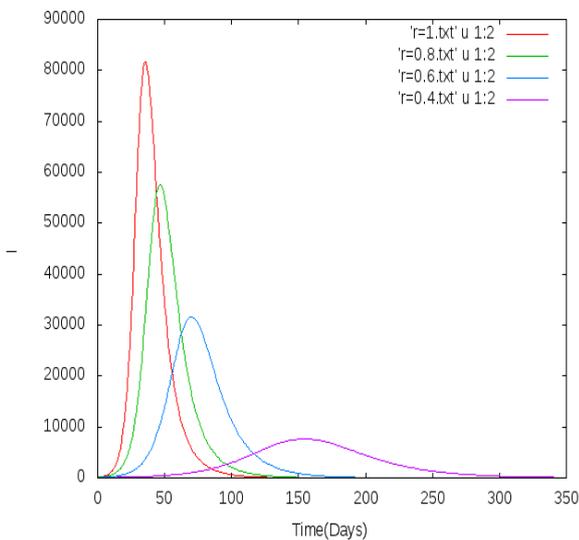


Figure 12: Model Simulations With $h(t)$

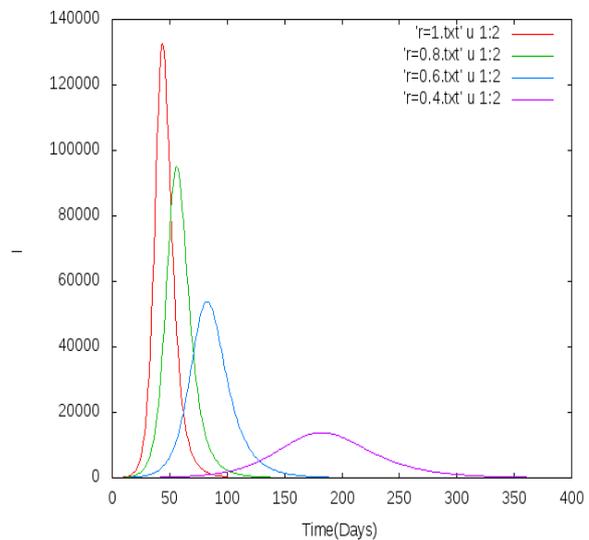


Figure 13: Model Simulations Without $h(t)$

We can see that it is quite clear that adding the $h(t)$ parameter to our equations had made our simulation curves slightly earlier respect to the previous ones (the ones without $h(t)$ parameter) and with smaller peaks leading them to be more similar to a real pandemic situation.

⁶ $D(t)$ parameter was estimated from the real data of Padua province to be $\approx 3.7\%$ of the total infected population.

At this point, we can use our new $\lambda(t)$ that we hypothesized and run a simulation with a $r(t)$ and stimulate the pandemic situation of Pauda province and compare it with the real data as follows :

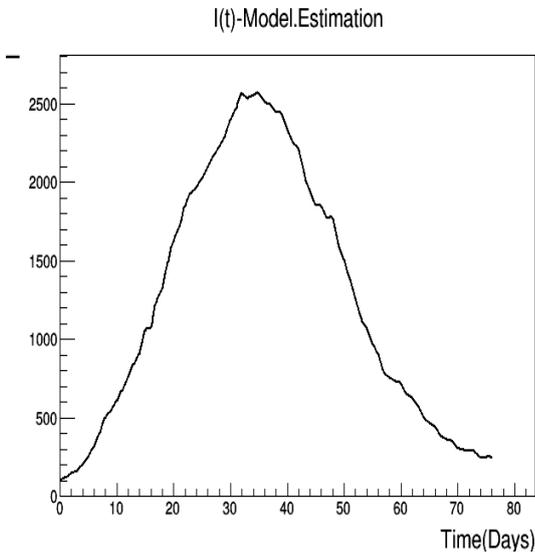


Figure 14: Model Simulation With $h(t)$

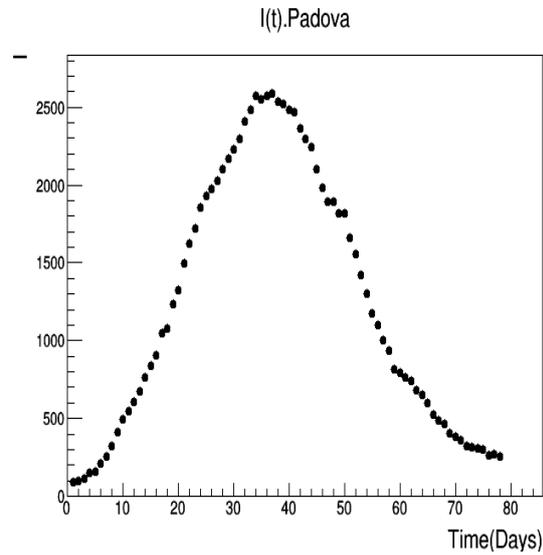


Figure 15: Real Data Of Padua Province

We can see clearly that we do not have any significant difference between the simulation figure 14 and the one that we made in the last section figure 9, this is due to the fact that in the Padua province, we have the numerator $I(t) + J(t) + R(t) + U(t) - D(t)$ that we are estimating from the model is less than 1% of the denominator $S_0 - D(t)$ during all the study that we made .

Therefore, in the Padua province pandemic situation we are still far away from any significant effects of the herd immunity. To see this more clearly we graph $h(t)$ parameter for the Padua province during the period of study mentioned before as follows:

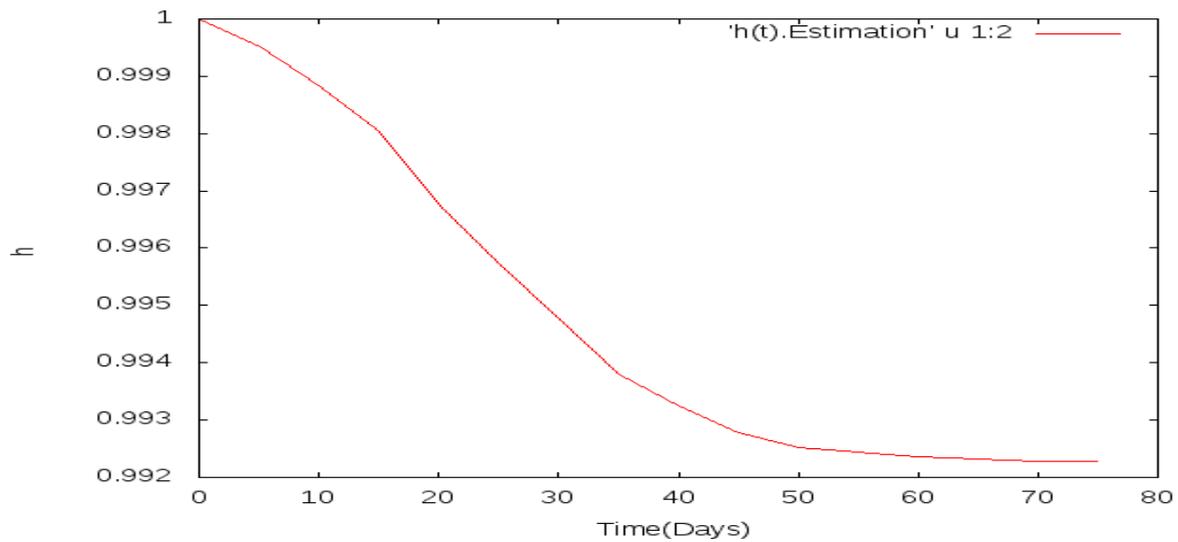


Figure 16: $h(t)$ For Padua Province

On the other hand, the other reason for not having any significant difference between our simulation with $h(t)$ and without it is due to the fact that the model was seeing any effects of the herd immunity as measures were applied . Therefore, we expect a change with our $r(t)$ estimation in case we will have a significant change in $h(t)$ parameter .

We can see that adding $h(t)$ parameter have no significant difference on $r(t)$ in our current pandemic situation (due to the small change of $h(t)$) by graphing both $r(t)$ estimation with and without $h(t)$ parameter as following :

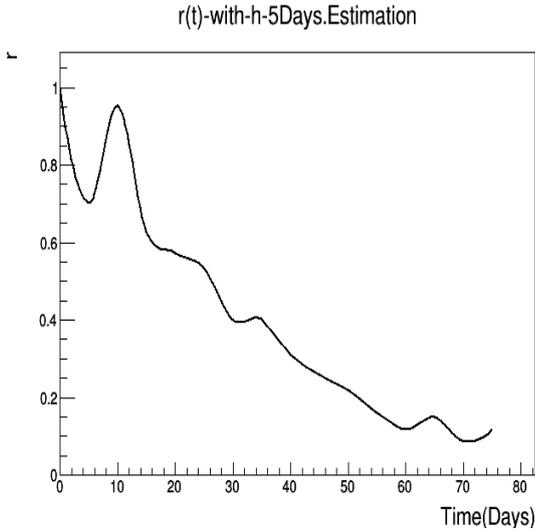


Figure 17: $r(t)$ Estimation with $h(t)$

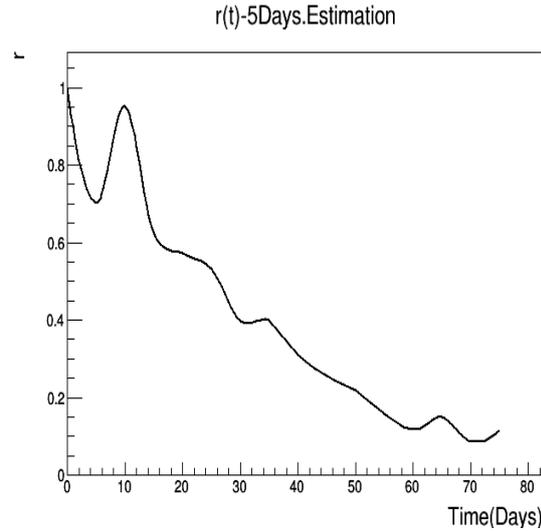


Figure 18: $r(t)$ Estimation without $h(t)$

As we can see there is no significant difference between the two graphs due to the small change of $h(t)$ parameter. However, we can study how we can achieve a herd immunity and stop the spreading of the pandemic. There are two ways to achieve this by using vaccine or gaining an immunity after having been exposed to the virus. For the first one we can use:

$$dI/dt = hr\mu\lambda_0 S_p(I + J) - \beta I \tag{21}$$

$$dJ/dt = hr\lambda_0(1 - \mu)S_p(I + J) - \Gamma J \tag{22}$$

And by using the relation between $I(t)$ and $J(t)$ from the eq (10)⁷we have :

$$dI/dt = (hr\lambda_0 S_p - \beta)I \tag{23}$$

$$dJ/dt = (hr\lambda_0 S_p - \Gamma)J \tag{24}$$

In order to stop the pandemic from spreading we need to have both equations to equal zero or less. Due to the fact that $\Gamma < \beta$ we can focus just on the second equation as the first one will automatically be in the range that we need if the second one ≤ 0 . As we are using a vaccine hypothesis, we can use $r = 1$ (we do not have any measures when we use a vaccine) and for $h(t)$ we can use $h(t) = 1 - \frac{S_0 - S(t)}{S_0} = S_p(t)$.⁸ And using these estimations and replace them in the equation (24) we have :

$$S_h = \pm \sqrt{\frac{\Gamma}{\lambda_0}} \tag{25}$$

⁷after the early phase, we will have $I(t) \leq \frac{\mu}{1-\mu} J(t)$ during the rest of the pandemic due to the fact that $\beta > \Gamma$ and using the max of $I(t)$ for the equation (24) will give us the max of the vaccinated population needed.

⁸for the hypothesis of using the vaccine, we have very small mortality, therefore we can use the difference between initial population and the vaccinated one as a numerator and the initial population as a denominator.

Where S_h is the ratio of the population that do not need to be vaccinated, here we use the positive root of S_h as the negative one dose not have any physical meaning. At this point we can use $\Gamma^{-1} = 14$ as we used for our simulation and we have $S_h = 0.42$. Therefore, we conclude from that in order to have a herd immunity in Padua province by vaccination, we need almost 58% of our initial population S_0 to be vaccinated .

On the other hand, in order to achieve the herd immunity by exposing to the virus the situation is quite different as we can see that having the 58% of the initial population infected correspond to be around the top of the peak of the pandemic curve ($J(t)$ curve) . Therefore, in order to arrive to the bottom of the curve more individuals will be infected, based on that we expect a bigger percentage of individuals to be infected before achieving a herd immunity by exposing to the virus.

By using the same Γ used before and $r = 1$, and $h(t)$ from the equation (20) we can estimate this percentage through the model by calculating the difference between the initial population and remaining susceptible population at the end of the pandemic curve. Therefore, we have that in order to achieve the herd immunity by exposing to the virus we will have the 76% of the initial population will be infected.

In any case we can optimise this percentage of the infected population achieved by exposing to the virus in order to have similar one like the vaccination method we can apply a constant measure with $r \approx 0.6$ during all the pandemic situation or with a variable r (more realistic) to achieve the herd immunity by exposing to the virus with less infected individuals . However, we can see the effect of the $h(t)$ parameter in achieving the herd immunity by exposing to the virus and how this result in reducing the $\lambda(t)$ parameter in a similar way as applying strong measures:

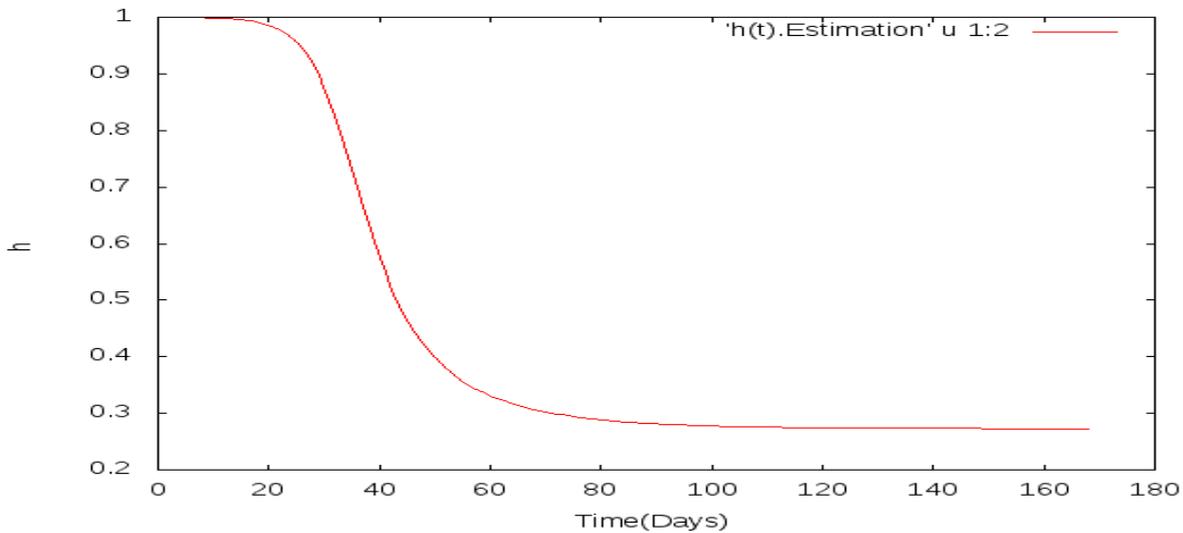


Figure 19: $h(t)$ For Achiving Herd Immuntiy

0.6 Asymptomatic Population

As we mentioned at the beginning of this study, The asymptomatic population is the reason for using the A-SIR model rather than SIR for COVID-19 pandemic, due to the fact that the significant percentage of this population that we estimated to be $1-\mu$ of the total population. In this study, we used this percentage as 43% from a study made in Padua province [7].⁹

⁹it is more appropriate to use this percentage as the study has been made on the same population that we studied.

However if we use higher percentage for example 86% from Li et al contribution [8] we will have totally different situation mainly with our simulations with different r values as we can see from the following graphs:

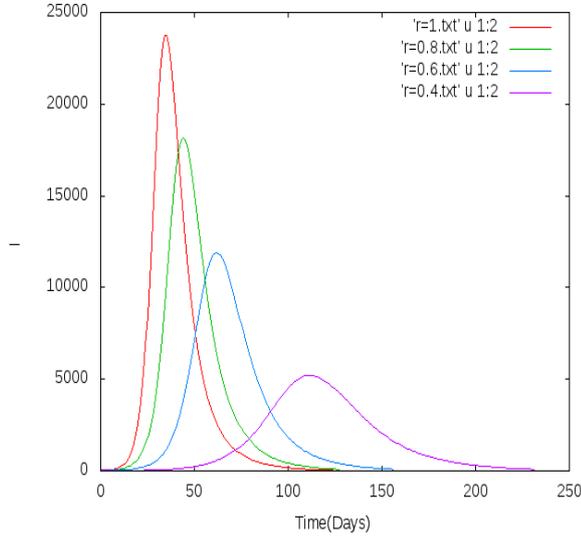


Figure 20: $I(t)$ Simulations With $1 - \mu = 86\%$

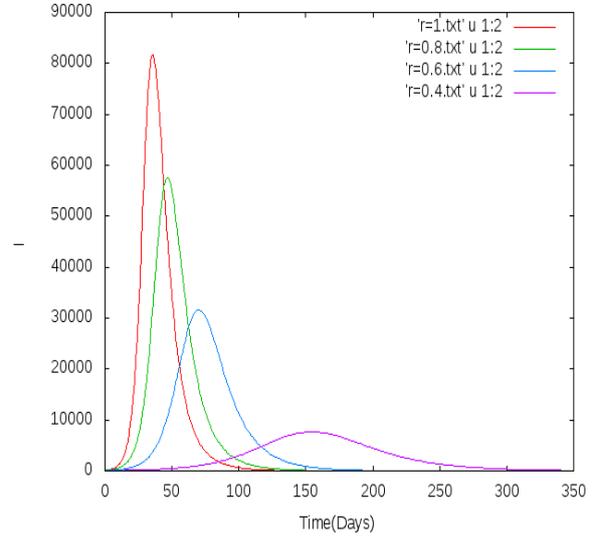


Figure 21: $I(t)$ Simulations With $1 - \mu = 43\%$

We can see easily that the simulated curves are having different peaks due to the significant difference in the $1 - \mu$ parameter used for the simulations. However, for our pandemic situation in Padua province using $1 - \mu = 86\%$ will result in a similar estimation of our $r(t)$ parameter as we can see from the following graphs :

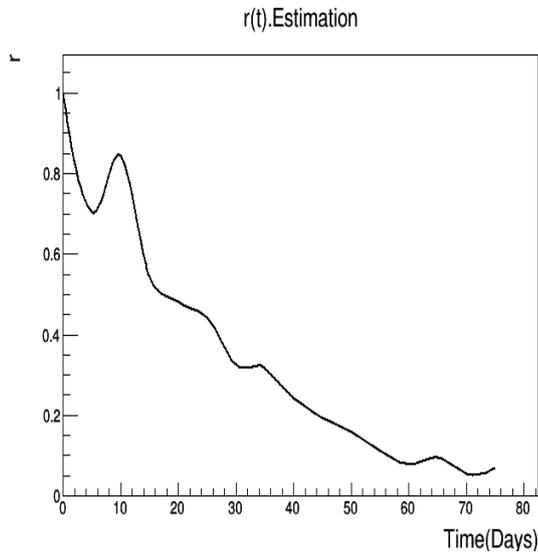


Figure 22: $r(t)$ Estimation With $1 - \mu = 86\%$

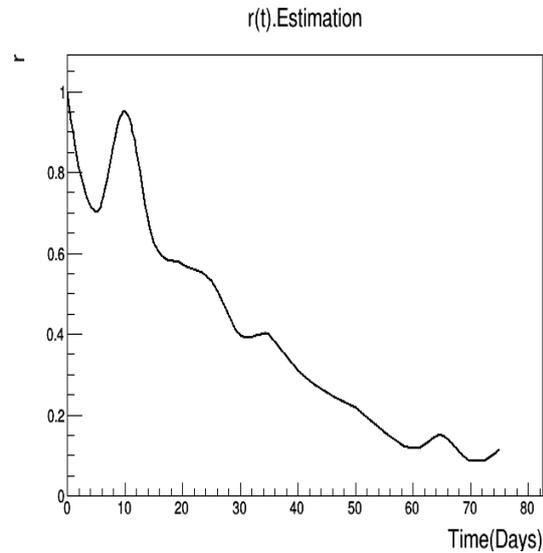


Figure 23: $r(t)$ Estimation With $1 - \mu = 43\%$

We can conclude from the graphs above that using a bigger $1 - \mu$ value will result in the estimation of stronger measures (smaller $r(t)$ values) of our pandemic situation with a similar time evolution .

Conclusion

Studying diseases and pandemics with compartmental models can give us a plenty of information about the diseases and pandemics and their characteristics and translating their evolution and effects on a community into numbers and graphs to give clear idea and understanding more the current health status. And predictions about the diseases and pandemics on long and short term, aiming to take various decisions based on the information that we get from the models to decrease and stopping the spreading of the diseases and pandemics.

For our case study of Padua province, we saw how applying measures reduced the spreading of the pandemic by significant factor and resulted in a small pandemic situation $S_p \approx 1$ during all the study period thanks to these measures that have been applied by the Italian government and Veneto regional government and the collaboration of Padua province's population with the local authorities.

We concluded that in our case study of Padua province, we are still far away from any herd immunity effects due to the small pandemic situation that we have. Therefore, it is very possible to have another pandemic curve in the future unless a vaccine will be available before another pandemic curve start.

We even concluded, based on our model parameters how it is possible to stop the pandemic for the long term by vaccination and how this is significantly different from stopping it by exposing to the virus.

At the end, we saw how the percentage of asymptomatic infected population is effecting our estimations and parameters of the pandemic curve, and we used as examples two different values for this percentage from two different studies and we saw how much our estimations changed and which one was more realistic.

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