MDM1 REP0 Part B: Compartmental (SIR) Models

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Abstract

The second part of the assignment tries to deeper models compared to logistic and exponential ones discussed in the first part. Here, the so called "SIR" (Susceptible-Infectious-Recovered) containment model is going to be discussed and results will be shown correspondingly.

1 Introduction

In the previous assignment we discussed that the discrete growth of infectives is not quite true, and it would be more realistic if we use a non-discrete version of a geometrical progression function. However, in reality, a way more accurate model is the SIR model[1] which became quite popular during the pandemic in 2020

The basis of a model is dividing a constant group of individuals (i.e. a number of people in group stays generically constant) into 3 subgroups: susceptibles (who have a potential of catching a virus: $s(t)$), Infectives (who already have a virus: $n(t)$) and, recovered ones respectively (who either healed from the virus or died: $r(t)$).

2 Methods and Results

We assume that the increase rate of infected people is directly proportional to the communications between infected and susceptibles which gives a lowering number of susceptibles:

$$\frac{ds}{dt} = -\rho s n$$

where ρ is the so called infectiousness parameter (we set up it as 0.0005).

We also assume that recoveries are happening with a constant rate as well, hence:

$$\frac{dr}{dt} = \alpha n$$

with α being a recovery coefficent (used value: 0.1), which means the whole model looks like the following:

$$\frac{dn}{dt} = \rho s n - \alpha n$$

Below presented plot shows the number of infectious individuals for all above mentioned 3 differential functions' solutions (i.e. functions) considering the case that the initially there are 700 people in an experiment 15 of which are considered as "zero patients".
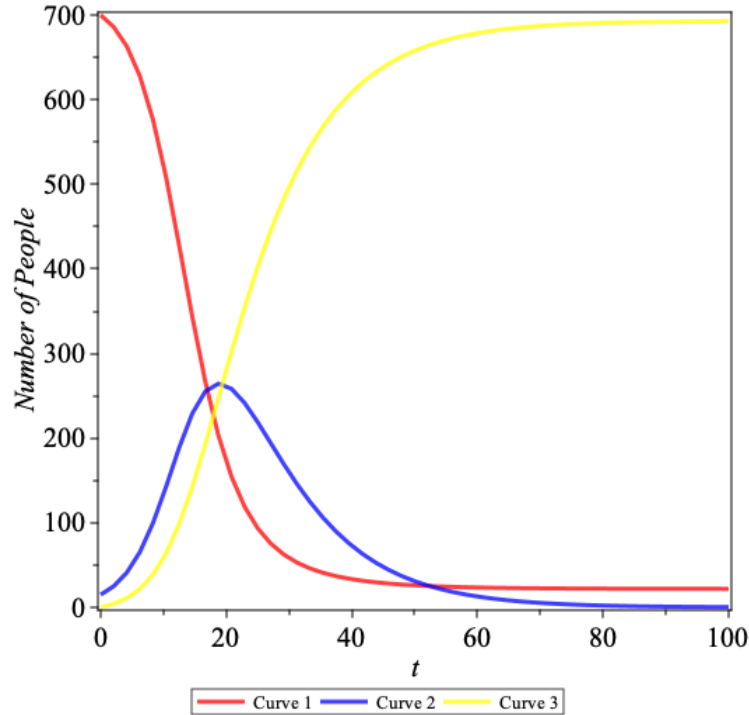
3 Discussion and Conclusion

We can notice that if we try to make α smaller or ρ bigger, as it is vivid, the yellow curve (which represents the 3rd model) is changing rapidly in the beginning period by reaching the possible peak.

Because we have 2 parameters: α and ρ, we can comprise them into one parameter: $R_0 = \frac{\alpha}{\rho}$[1], which, in case of being greater than 0, will tell us that the infection will spread, otherwise: the reverse.

The model is generically acceptable if the ratio of all humans experimented and zero patients is not very big; otherwise the change of models is not visible.

The model could be improved if we start considering a fluctuating number of individuals experimented during a time (i.e. account cases that someone dies from a virus and, meanwhile, some new individuals are being born). Also, basing on that, new parameters can be added (e.g. the problem could be divided into several age groups and then some approximation can be found for them).

References

[1] T. Crawford. *Tom Rocks Maths: Oxford Mathematician explains SIR Disease Model for COVID-19 (Coronavirus)*. 2020. URL: https://youtu.be/NKMHhm2Zbkw?si=yF7pOqLOOZJTKzft.