Because 100% of people are not being tested, confirmed cases under-reports the total infected population. $C = \phi\,(N - S)$ or $s = 1 - \frac{c}{\phi}$

Instituting perfect social distancing, decreases $R_o$ to 0. Imperfect social distancing reduces $R_o$. This is visible when the exponential order of growth in infections decreases over time. This change can also be modelled.

**We are not testing everyone**

$$I = \phi(N - S)$$

**There is a lag: Compartment model**

There is no incubation or latent period. An incubation period delays the entire epidemic timeline. There is a delay between new infections and the currently infectious. One way to account for this in the model would be to **decrease $\mu$ or increase $R_o$** as a representation of the time between infection and infectiousness. But the newly infected are not infectious.

We can address this limitation by adding one extra step (compartment) to our epidemic model: The *Exposed*. When a *Susceptible* person comes in contact with an infections person, s/he moves to the *Exposed* population. While in the *Exposed* population the person is said to be "incubating" the disease, but is not yet able to infect other individuals. This results in the following revisions to our differential equations:

- The Exposed Equation: $\frac{de}{dt} = \beta\, s(t)\, i(t) - \epsilon\, e(t)$
- The Infected Equation: $\frac{di}{dt} = \epsilon\, e(t) - \mu\, i(t)$

Compare different i vs. t with various $\epsilon$

**Temporal immunity**

The SIR model assumes that recovered persons are permanently immune from the disease. There have been some reports of C-19 patients being reinfected after their recovery. This would result a modification to our current model

- The Susceptible Equation: $\frac{ds}{dt} = -\beta\, s(t)\, i(t) + \rho\, r(t)$
- The Recovered Equation: $\frac{dr}{dt} = \mu\, i(t) - \rho\, r(t)$

The model doesn't consider asymptomatic cases. This leads to a focus only on severe cases and a delay in detection. Asymptomatic individuals are often less infectious that those displaying symptoms by some fraction $r_b$. We can model their effect by splitting the infections compartments in two. To keep the model simple we will ignore the possibility of reinfections.

- The asymptomatic infected: $\frac{di_a}{dt} = \epsilon \boldsymbol{p_a} e(t) - \mu\, i_a(t)$
- The symptomatic infected: $\frac{di_s}{dt} = \epsilon(1 - \boldsymbol{p_a})e(t) - \mu i_s(t)$
- The Exposed Equation: $\frac{de}{dt} = \beta\, s(t)\, i_s(t) + \beta r_b s(t)\, i_a(t) - \epsilon\, e(t)$
- The Susceptible Equation: $\frac{ds}{dt} = -\beta\, s(t) i_s(t) - \beta r_b s(t) i_a(t)$
- The Recovered Equation: $\frac{dr}{dt} = \mu\, i_s(t) + \mu\, i_a(t)$

Since we have split the original infections compartment in two:

- $\beta = \frac{R_o \mu}{p_a r_b + (1 - p_a)}$ & $R_o = \frac{\beta}{\mu}[p_a r_\beta + (1 - p_a)$

Mortality Rate:

- The symptomatic infected: $\frac{di_s}{dt} = \epsilon(1 - \boldsymbol{p_a})e(t) - \mu p_d i_s(t)$
- Death rate: $\frac{dm}{dt} = \mu p_d i_s(t)$
- The Recovered Equation: $\frac{dr}{dt} = \mu(1 - p_d)\, i_s(t) + \mu\, i_a(t)$

Plot a MATLAB model for at least the infections and deaths in your city. Plot the model on the same graph as your collected data. Calculate and plot residuals regression values. Publish as a *.pdf document. Describe the assumptions you made when modelling the trends. Where does your model perform well? Where does it perform poorly?