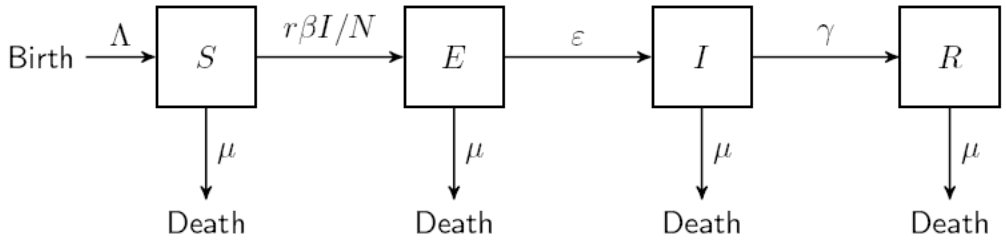
II. Analysis of Covid-19 data of UK using SEIR Model

1.0 Introduction to SEIR Model

Susceptible-Exposed-Infectious-Recovered Model: applicable to COVID19, measles, mumps, rubella,etc [1=3].



E: Exposed (latent) humans

ε: Per-capita rate of progression to infectious state

$$\frac{\mathrm{d}S}{\mathrm{d}t} = \Lambda - r\beta S\frac{I}{N} - \mu S$$
$$\frac{\mathrm{d}E}{\mathrm{d}t} = r\beta S\frac{I}{N} - \varepsilon E$$
$$\frac{\mathrm{d}I}{\mathrm{d}t} = \varepsilon E - \gamma I - \mu I$$
$$\frac{\mathrm{d}R}{\mathrm{d}t} = \gamma I - \mu R$$

with

$$N = S + E + I + R.$$

$$R_0 = \left(\begin{array}{c}\text{Number of}\\ \text{contacts}\\ \text{per unit time}\end{array}\right)\left(\begin{array}{c}\text{Probability of}\\ \text{transmission}\\ \text{per contact}\end{array}\right)\left(\begin{array}{c}\text{Duration of}\\ \text{infection}\end{array}\right)$$
$$\times\left(\begin{array}{c}\text{Probabililty of}\\ \text{surviving}\\ \text{exposed stage}\end{array}\right)$$

$$R_0 = r \times \beta \times \frac{1}{\gamma+\mu} \times \frac{\varepsilon}{\varepsilon+\mu}$$
$$= \frac{r\beta\varepsilon}{(\gamma+\mu)(\varepsilon+\mu)}$$

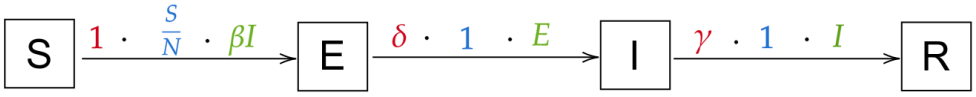
- If R0 < 1, the disease-free equilibrium point is globally asymptotically stable and there is no endemic equilibrium point (the disease dies out).

1.1 R0 for the Endemic SEIR Model

- If R0 > 1, the disease-free equilibrium point is unstable and a globally asymptotically stable endemic equilibrium point exists.
- Basic compartmental models assume a homogeneous population.
- Divide the population into di_erent groups based on infection status:
  M: Humans with maternal immunity
  S: Susceptible humans
  E: Exposed (infected but not yet infectious) humans
  I: Infectious humans
  R: Recovered humans.
- Can include time-dependent parameters to include the effects of seasonality.
- Can include additional compartments to model vaccinated and asymptomatic individuals, and di_erent stages of disease progression.
- Can include multiple groups to model heterogeneity, age, spatial structure or host species.[3]

2.0 Derivation of the Exposed-Compartment

- Many infectious diseases have an incubation period before being infectious during which the host cannot yet spread the disease. We'll call such individuals — and the whole compartment — ***Exposed***.
- Intuitively, we'll have transitions of the form S → E → I → R: Susceptible people can contract the virus and thus become exposed, then infected, then recovered. The new transition S → E will have the same arrow as the current S → I transition, as the probability is the same (all susceptibles can be exposed), the rate is the same ("exposition" happens immediately) and the population is the same (the infectious individuals can spread the disease and each exposes β new individuals per day). There's also no reason for the transition from I to R to change. The only new transition is the one from E to I: the probability is 1 (everyone that's exposed becomes infected), the population is E (all exposed will become infected), and the rate gets a new variable, δ (delta). We arrive at these transitions:



From these transitions, the following equations are obtained.

$$\frac{dS}{dt} = -\beta \cdot I \cdot \frac{S}{N}$$
$$\frac{dE}{dt} = \beta \cdot I \cdot \frac{S}{N} - \delta \cdot E$$
$$\frac{dI}{dt} = \delta \cdot E - \gamma \cdot I$$
$$\frac{dR}{dt} = \gamma \cdot I$$

2.1 Programming the Exposed-Compartment

- We are modeling a highly infectious (R_0 =5.0) disease in a population of 1 million, with an incubation period of 5 days and a recovery taking 7 days.

Imports needed:

```
from scipy.integrate import odeint
import numpy as np
import matplotlib.pyplot as plt
%matplotlib inline
```

The equations and initial values now look like this:

```
n [0]:
def deriv(y, t, N, beta, gamma, delta):
    S, E, I, R = y
    dSdt = -beta * S * I / N
    dEdt = beta * S * I / N - delta * E
    dIdt = delta * E - gamma * I
    dRdt = gamma * I
return dSdt, dEdt, dIdt, dRdt
    In [0]:
    N = 1000
    beta = 1.0  # infected person infects 1 other person per day
    D = 4.0 # infections lasts four days
    gamma = 1.0 / D
    delta = 1.0 / 3.0  # incubation period of three days

S0, E0, I0, R0 = 999, 1, 0, 0  # initial conditions: one exposed, rest susceptible
```

We calculate S, E, I, and R over time:

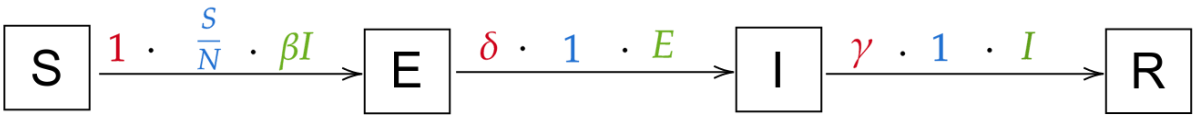
```
In [0]:
t = np.linspace(0, 100, 100) # Grid of time points (in days)
y0 = S0, E0, I0, R0 # Initial conditions vector

 # Integrate the SIR equations over the time grid, t.
 ret = odeint(deriv, y0, t, args=(N, beta, gamma, delta))
 S, E, I, R = ret.T
```

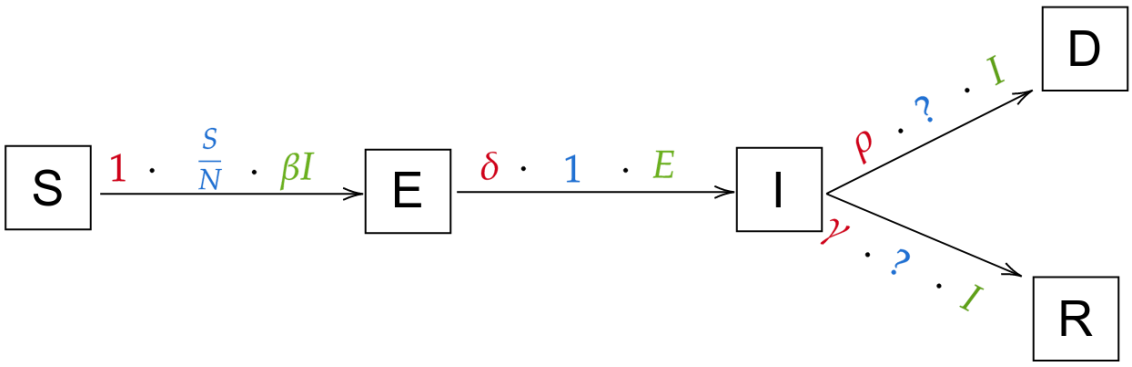
2.2 Deriving the Dead-Compartment

For very deadly diseases, this compartment is very important. For some other situations, you might want to add completely different compartments and dynamics (such as births

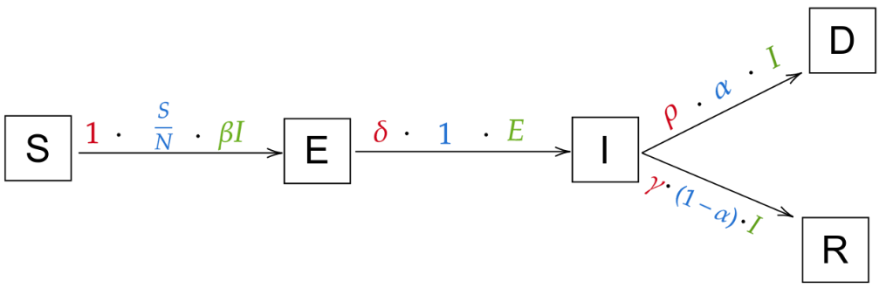
and non-disease-related deaths when studying a disease over a long time); these models can get as complex as you want!



Let's think about how we can take our current transitions and add a ***Dead*** state. When can people die from the disease? Only while they are infected! That means that we'll have to add a transition I → D. Of course, people don't die immediately; We define a new variable *ρ (rho) for the rate at which people die* (e.g. when it takes 6 days to die, ρ will be 1/6). There's no reason for the rate of recovery, γ, to change. So our new model will look somehow like this:



The only thing that's missing are the probabilities of going from infected to recovered and from infected to dead. That'll be one more variable (the last one for now!), the *death rate α.* For example, if α=5%, ρ = 1 and γ = 1 (so people die or recover in 1 day, that makes for an easier example) and 100 people are infected, then 5% · 100 = 5 people will die. That leaves 95% · 100 = 95 people recovering. So all in all, the probability for I → D is α and thus the probability for I → R is 1-α. We finally arrive at this model:



Which naturally translates to these equations:

$$\frac{dS}{dt} = -\beta \cdot I \cdot \frac{S}{N}$$
$$\frac{dE}{dt} = \beta \cdot I \cdot \frac{S}{N} - \delta \cdot E$$
$$\frac{dI}{dt} = \delta \cdot E - (1-\alpha) \cdot \gamma \cdot I - \alpha \cdot \rho \cdot I$$
$$\frac{dR}{dt} = (1-\alpha) \cdot \gamma \cdot I$$
$$\frac{dD}{dt} = \alpha \cdot \rho \cdot I$$

2.3 Programming the Dead-Compartment

We only need to make some slight changes to the code (and we'll set α to 20% and ρ to 1/9).

Time-Dependent Variables

Here's an updated list of the variables we currently use:

- **N:** total population
- **S(t):** number of people susceptible on day t
- **E(t):** number of people exposed on day t
- **I(t):** number of people infected on day t
- **R(t):** number of people recovered on day t
- **D(t):** number of people dead on day t
- **β:** expected amount of people an infected person infects per day
- **D:** number of days an infected person has and can spread the disease
- **γ:** the proportion of infected recovering per day ($\gamma = 1/D$)
- **R_0:** the total number of people an infected person infects ($R_0 = \beta / \gamma$)
- **δ:** length of incubation period
- **α:** fatality rate
- **ρ:** rate at which people die (= 1/days from infected until death)

3.0 Results and Discussion

The SEIR Model is used to analyse the Covid10 data of UK to obtain the exposed people to the Covid19 and the following plot is obtained shown in Fig.1. It clear shows that the exposed cases increases initially and reaches a maximum at 50 days and subsequently follows a decreasing trend.

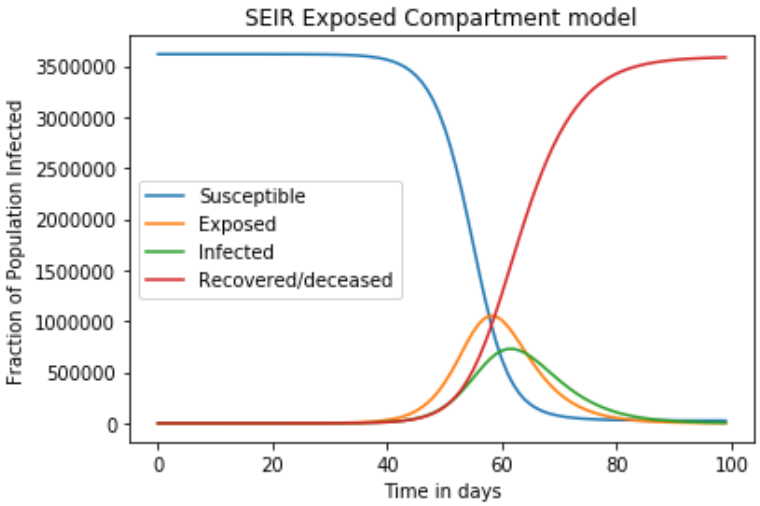


Fig.1 SEIR analysis of Covid19 data for the Exposed Category

Similarly, the dead cases are anaysed using SEIR and the following plot is obtained as shown in Fig.2. It is observed the dead cases attains the plateau after 60 days of infections.

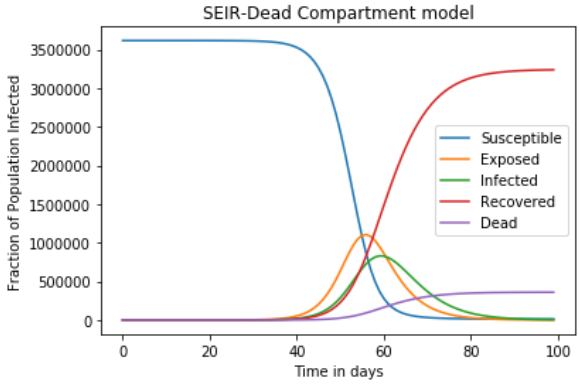


Fig.2 SEIR analysis of Covid19 data for the Dead Category

4.0 Conclusions

The SEIR Model has been used to analyse the Covid-19 data of north eastern UK. It is observed that exposed people who don’t transmit the disease ought to be taken in to account to provide an insight in to rate of infection. The dead category shows a similar qualitative trend as of recovered cases.

References

1 Diekmann, H. Heesterbeek, and T. Britton, Mathematical Tools for Understanding Infectious Disease Dynamics. Princeton Series in Theoretical and Computational Biology. Princeton University Press, Princeton, (2013).

2 H. W. Hethcote, \The mathematics of infectious diseases", SIAM Review 42, 599{653 (2000).

3 M. J. Keeling and P. Rohani, Modeling Infectious Diseases in Humans and Animals. Princeton University Press, Princeton, (2007).