The SIR Model for Spread of Disease

1) SIR differential equation

S = S(t): # susceptible, healthy individuals that can be infected

I = I(t): # infected indiviuals

R = R(t): # recovered/deceased individuals

N: # population

To avoid the computational expense, let's only deal with the fraction of the population

$$s(t) = \frac{S(t)}{N}, i(t) = \frac{I(t)}{N}, r(t) = \frac{R(t)}{N}$$

 β : # contacts of susceptible individuals that are sufficient to spread the diseases

 γ : Fraction of population recover each day

Assumption:

- Recovered individuals gain the immunity (it can be lost over time but the pandemic is still at the early stage)
- · The population is a constant, ignore death/birth/immigration and other factors

Since susceptible depends on the number of infected it is decreasing over time

(1) Susceptible equation:

$$\frac{ds}{dt} = -\beta s(t)i(t)$$

(2) Recovery equation:

$$\frac{dr}{dt} = \gamma i(t)$$

Since

$$\frac{ds}{dt} + \frac{di}{dt} + \frac{dr}{dt} = 0$$

(3) Infected Equation:

$$\frac{di}{dt} = \beta s(t)i(t) - \gamma i(t)$$

Note that we know $s(t_0)$, $i(t_0)$, $r(t_0)$, N

We also do not have the constants β and γ , we will find it with the real data in section 4

2) Runge-Kutta

It is hard to solve the differential equations (1), (2), and (3) for s(t), r(t), and s(t) but there is a method that can approximate these values at time t with high accuracy. The method is called the 4th Order Runge-Kutta. (The higher the order, the more accurate result)

Consider the differential Equation

$$\frac{dy}{dx} = f(x, y), y(x_0) = y_0$$

Calculate successively

$$k_1 = hf(x_0, y_0)$$

$$k_2 = hf\left(x_0 + \frac{h}{2}, y_0 + \frac{k_1}{2}\right)$$

$$k_3 = hf\left(x_0 + \frac{h}{2}, y_0 + \frac{k_2}{2}\right)$$

$$k_4 = hf(x_0 + h, y_0 + k_3)$$

$$k = \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

Since,

$$y_1 = y_0 + k$$
 and $x_1 = x_0 + h$

Therefore,

$$y_{n+1} = y_n + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4) + o(h^5)$$

3) Calculation

```
In [10]:
```

```
import matplotlib.pyplot as plt
```

```
In [250]:
```

```
# Susceptible equation
def dsdt(s, i, beta):
    return -beta*s*i

# Infected equation
def didt(s, i, beta, gamma):
    return beta*s*i - gamma*i

# Recovered/deceased equation
def drdt(i, gamma):
    return gamma*i
```

In [276]:

```
#4th order Runge-Kutta for 1 time step
def rk_4th(s, i, r, dsdt, didt, drdt, beta, gamma, h):
    s1 = h*dsdt(s, i, beta)
    i1 = h*didt(s, i, beta, gamma)
    r1 = h*drdt(i, gamma)
    s2 = h*dsdt(s + s1*0.5, i + i1*0.5, beta)
    i2 = h*didt(s + s1*0.5, i + i1*0.5, beta, gamma)
    r2 = h*drdt(i + i1*0.5, gamma)
    s3 = h*dsdt(s + s2*0.5, i + i2*0.5, beta)
    i3 = h*didt(s + s2*0.5, i + i2*0.5, beta, gamma)
    r3 = h*drdt(i + i2*0.5, gamma)
    s4 = h*dsdt(s + s3, i + i3, beta)
    i4 = h*didt(s + s3, i + i3, beta, gamma)
    r4 = h*drdt(i + i3, gamma)
    s = s + (s1 + 2*(s2 + s3) + s4)/6
    i = i + (i1 + 2*(i2 + i3) + i4)/6
    r = r + (r1 + 2*(r2 + r3) + r4)/6
    return s, i, r
```

In [307]:

```
#Initialize s,i,r and iterate 1000 days

def SIR(N, i0, beta, gamma, h):

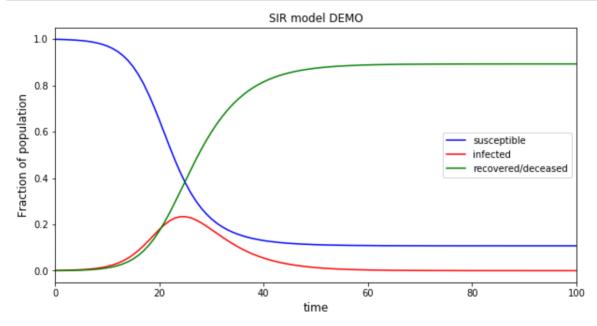
    # Initial condition
    s = float(N-1)/N -i0
    i = float(1)/N +i0
    r = 0

sus, inf, rec= [],[],[]
for j in range(1000):
    sus.append(s)
    inf.append(i)
    rec.append(r)
    s,i,r = rk_4th(s, i, r, dsdt, didt, drdt, beta, gamma, h)

return sus, inf, rec
```

In [337]:

```
N = 327.2*(10**6)
i0 = 311357/N #fraction of infected
beta = 0.5
qamma = 0.2
h = 1
sus, inf, rec = SIR(N, i0, beta, gamma, h)
f = plt.figure(figsize=(10,5))
plt.plot(sus, 'b', label='Susceptible');
plt.plot(inf, 'r', label='Infected');
plt.plot(rec, 'g', label='Recovered/Deceased');
plt.title("SIR model DEMO")
plt.xlabel("Day", fontsize=12);
plt.ylabel("Fraction of population", fontsize=12);
plt.legend(loc='best')
plt.xlim(0,100)
plt.show()
```



4) Why is social distance important?

The γ constant is the recovery rate. It also indicates the effectiveness of medical treatment. Assume it takes on average 14 days to treat a patient so $\gamma = \frac{1}{14}$. Since there is no major medical advancement yet, we are only in control of the β , which is the rate of transmitting the disease.

Decreasing β is the same as flattening the infected curve. There are two main reasons we want to flatten it:

- · Reducing the number of deceased
- · Preventing hospital overload

Let's take a look at different values of β

In [340]:

```
N = 327.2*(10**6)
i0 = 311357/N #fraction of infected
gamma = 1/14
h = 1
beta 1 = 1
beta 2 = 0.6
beta 3 = 0.4
beta 4 = 0.2
sus, inf 1, rec = SIR(N, i0, beta 1, gamma, h)
sus, inf 2, rec = SIR(N, i0, beta 2, gamma, h)
sus, inf 3, rec = SIR(N, i0, beta 3, gamma, h)
sus, inf 4, rec = SIR(N, i0, beta 4, gamma, h)
f = plt.figure(figsize=(10,5))
plt.plot(inf_1, 'b', label='beta={}'.format(beta_1));
plt.plot(inf 2, 'r', label='beta={}'.format(beta 2));
plt.plot(inf_3, 'g', label='beta={}'.format(beta_3))
plt.plot(inf_4, 'black', label='beta={}'.format(beta_4))
plt.title("SIR model Compare Different Betas")
plt.xlabel("Day", fontsize=12);
plt.ylabel("Fraction of population", fontsize=12);
plt.legend(loc='best')
plt.xlim(0,150)
plt.show()
```

