SIR Models

The original SIR model was proposed in "Contribution to the Mathematical Theory of Epidemics" William Kermack and Anderson McKendrick, 1927. The population (N) is divided into 3 pools: S, I, and R.

$$S \to I \to R$$

$$S(t) = \text{number that are susceptible at time } t \qquad s(t) = S(t)/N$$
$$I(t) = \text{number that are infected} \qquad i(t) = I(t)/N$$
$$R(t) = \text{number that are recovered or dead} \qquad r(t) = R(t)/N$$

At each timestep, individuals move between the 3 pools. Most papers tend to list the change in s, i and r functions, shown below on the left. To actually calculate the next s, i, r numbers for the next time step $(t+1)$ use the functions on the right.

$$\frac{ds}{dt} = -\beta si \qquad s(t+1) = s(t) - \beta s(t) i(t)$$
$$\frac{di}{dt} = \beta si - \gamma i \qquad i(t+1) = i(t) + \beta s(t) i(t) - \gamma i(t)$$
$$\frac{dr}{dt} = \gamma i \qquad r(t+1) = r(t) + \gamma i(t)$$

where:

$$\beta = \text{rate of infection} \qquad \gamma = \text{rate of recovery}$$

```
library(ggplot2)
library(reshape2)
library(latex2exp)
```

To Run the SIR simulation

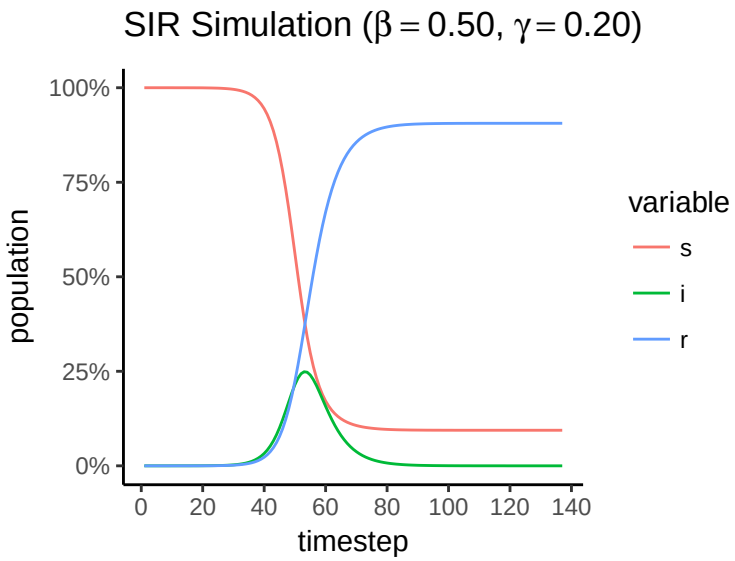
```
# ===== SIR Model Parameters
beta=0.50     # rate of infection, infecting contact per day
gamma=0.2    # rate of recovery, so period of infection is 1/gamma days

# Initial populations of S, I, and R
init_S=7900000    # Everyone susceptible
init_I=10         # Some infected
init_R=0          # No one recovered
N=init_S+init_I+init_R
timesteps=137

# ===== Run Simulation
sim01<-data.frame(t=c(1:timesteps))
sim01$s[1]=init_S/N
sim01$i[1]=init_I/N
sim01$r[1]=init_R/N

for(ii in c(2:timesteps)){
  sim01$s[ii]=sim01$s[ii-1]-beta*sim01$s[ii-1]*sim01$i[ii-1]
  sim01$i[ii]=sim01$i[ii-1]+beta*sim01$s[ii-1]*sim01$i[ii-1]-gamma*sim01$i[ii-1]
  sim01$r[ii]=sim01$r[ii-1]+gamma*sim01$i[ii-1]
}

# ===== Visualize Result
msim<-melt(sim01,id.vars=c("t"))
ggplot(data=msim,aes(x=t,y=value,group=variable,color=variable))+
  geom_line()+
  theme_classic()+
  labs(x="timestep",y="population",title=TeX(sprintf("SIR Simulation ($\\beta = %.2f$, $\\gamma = %.2f$)", beta, gamma)))+
  scale_y_continuous(breaks=c(0,0.25,0.5,0.75,1),labels=c("0%","25%","50%","75%","100%"))+
  scale_x_continuous(breaks=c(0:10*20))
```



An epidemic occurs if the number of infected individuals increases, i.e., $di/dt > 0$

$$\begin{aligned} \frac{di}{dt} &> 0 \\ \beta si - \gamma i &> 0 \\ \beta si &> \gamma i \\ \frac{\beta si}{\gamma} &> i \\ \frac{\beta s}{\gamma} &> 1 \end{aligned}$$

Since at the onset of an epidemic, nearly everyone (except the index case) is susceptible, $s \approx 1$

$$\frac{\beta}{\gamma} = R_0 > 1$$

Assumptions of the SIR Model

- Number of infected increases proportional to both number of infected and susceptible
- rate of recovery proportional to number of infected
- incubation time is negligible
- assume constant population (no births/deaths (outside of recovery))
- once an individual is recovered, the person is no longer susceptible and is immune
- no inherited immunity
- people of the population mix homogeneously (age, gender, race, social status does not affect the probability of a person being affected)

Prior to SIR, two of the reasons commonly put forward as accounting for the termination of an epidemic were:

- susceptible individuals have all been removed
- during the course of the epidemic the virulence of the causative organism has gradually decreased

The Kermack and McKendrick SIR Model were refuting those two reasons showing that susceptible indivudals did not have to be removed before an epidemic died out, and the virulence could be held constant.