

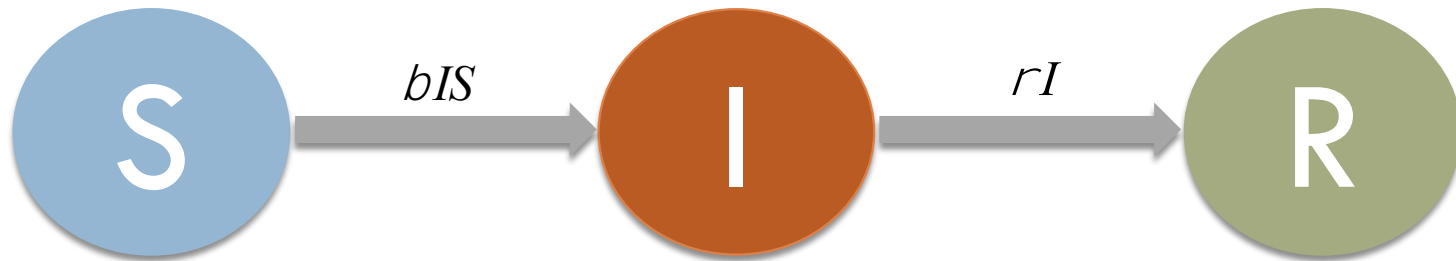
# ON RATES, STATES, AND THE SIR MODEL

Modelling Biological Systems, BIOS13  
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# The SIR model

- The SIR model is a classic model from epidemiology (it actually is a class of models)
- The model describes the spread of a disease in a population
- It has three state variables:  $S$ ,  $I$  and  $R$ 
  - ▣  **$S$  : Susceptibles** – the number of susceptible individuals
  - ▣  **$I$  : Infected** – the number of infected individuals
  - ▣  **$R$  : Recovered** – the number of recovered (immune) individuals

# The basic SIR Model



$$\begin{cases} \frac{dS}{dt} = -bIS \\ \frac{dI}{dt} = bIS - rI \\ \frac{dR}{dt} = rI \end{cases}$$

S : Susceptibles

I : Infected

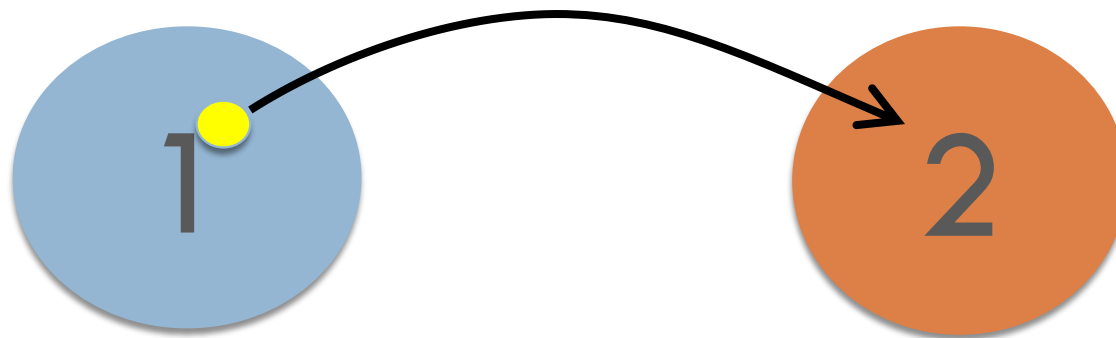
R : Recovered

$\beta$  : contact rate

$\rho$  : recovery rate

# Transition rates

- A *rate* is a 'speed of change'. It is often a direct rate of change, such as a growth rate,  $dn/dt$ , but can also be a *transition rate*.
- *Transition rates* describe how frequently the transition from one state to another occurs.  
Examples: death rate (alive  $\rightarrow$  dead), dispersal rate (here  $\rightarrow$  there), or rate of a chemical reaction (compound 1  $\rightarrow$  compound 2).



# Transition rates, interpretation



# Transition probability

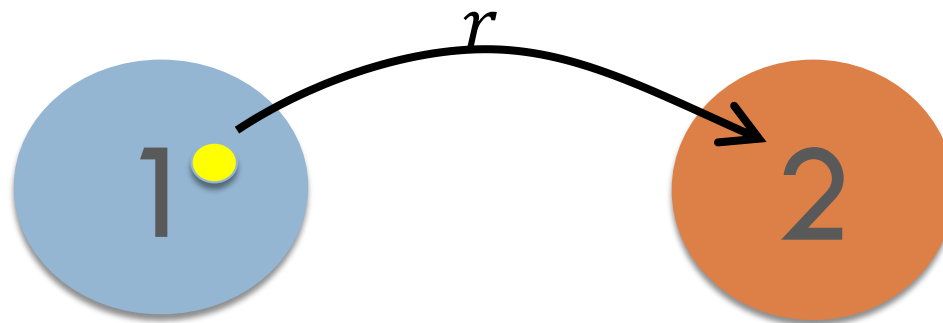
- Transition rates are (most often) probabilistic.

The probability that a transition from state 1 to state 2 at rate  $r$  will occur in a time interval  $\Delta t$  is  $r\Delta t$  (if  $\Delta t$  is small).

Example: The probability that an individual with death rate  $2/y$  (two per year) will die in a time interval  $\Delta t = 0.01y$  is  $2 \cdot 0.01 = 0.02$ .

- An alternative, equivalent, interpretation: On average  $r\Delta t$  transitions occur in the time interval  $\Delta t$ .

Example: The individual above will die on average 0.02 times during that time interval.



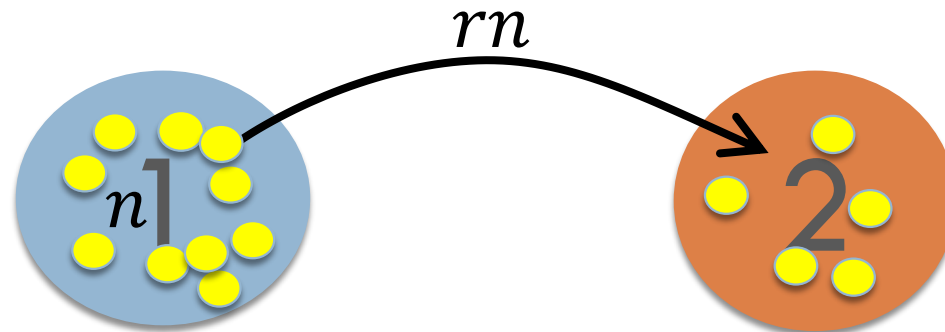
# Total transition rate

- Rates are often given *per item* (individual, or other object) or *per unit* (per mass unit, volume unit, or other).

Examples: death rate per individual, decay rate per kg.

- The total rate at which a transition occurs is thus the per item rate multiplied by the number of items (e.g. individuals).

Example: The total death rate of a population of size 1000 with a *per capita* death rate of  $2/\gamma$  is  $2000/\gamma$ . The average number of deaths in a time interval of  $0.01\gamma$  is thus  $2000 \cdot 0.01 = 20$ . (the probability interpretation fails here)

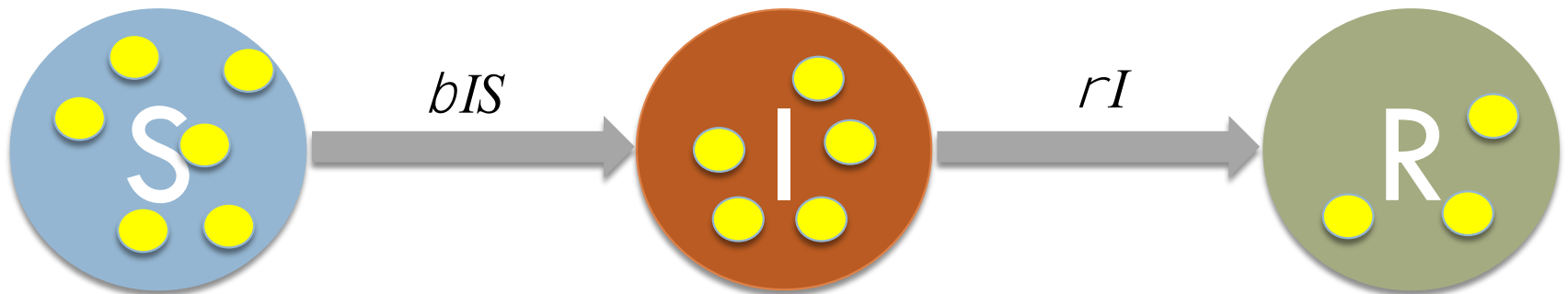


# Average dynamics

- Even though the outcome is stochastic, it can be approximated by its average for large populations.

For example, the group of infected in an SIR model decrease at a rate  $-\rho I$ .

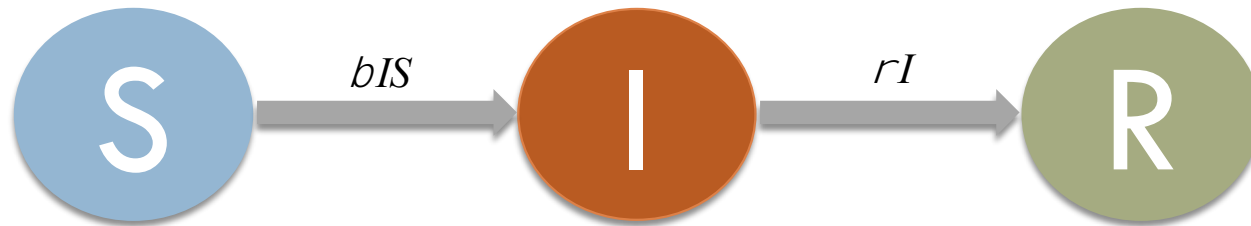
$$\begin{cases} \frac{dS}{dt} = -bIS \\ \frac{dI}{dt} = bIS - rI \\ \frac{dR}{dt} = rI \end{cases}$$





# Average time to transition and $R_0$

- The average time an individual (or mass unit, or whatever) will stay in a state is  $1/r$  if  $r$  is the transition rate *from* that state.  
Example: The SIR model



$$\begin{cases} \frac{dS}{dt} = -bIS \\ \frac{dI}{dt} = bIS - rI \\ \frac{dR}{dt} = rI \end{cases}$$

The average time to recovery is  $1/\rho$ , i.e. the average time in illness. The higher the recovery rate, the shorter is the time an individual remains infected.

Additionally, each infected individual infects  $\beta S$  new individuals per time unit (the total infection rate is  $\beta IS$ ). The total number of new infected per infected individual is then  $\frac{1}{\rho} \cdot \beta S = R_0$ .

$R_0$  is a central concept in epidemiology. A disease will not spread as long as  $R_0 < 1$ .

# Some Covid-19 data

- $R_0$  has been estimated to between 1.5 and 3.5
- Incubation period (from exposure to symptoms): 1 - 14 days (average 5.2)
- Recovery in 2 weeks (mild cases)

$$R_0 = \frac{1}{\rho} \cdot \beta S \quad \Rightarrow \quad \rho R_0 / S = \beta$$

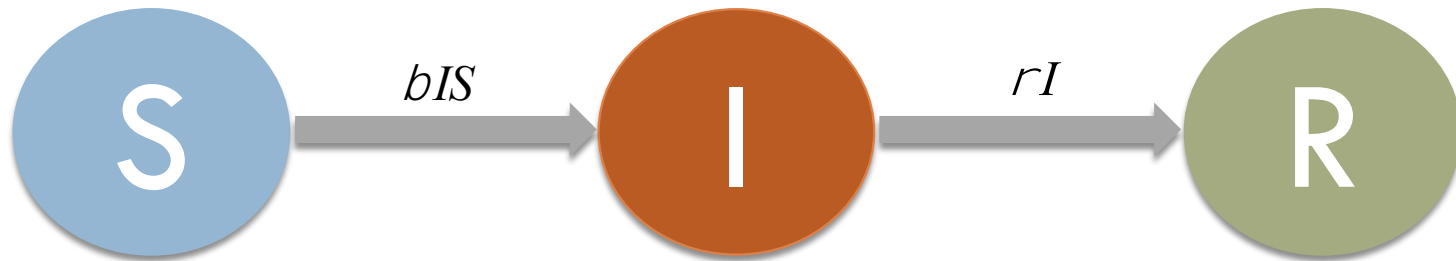
Sources:

<https://www.worldometers.info/coronavirus/>

<https://www.ecdc.europa.eu/en/covid-19/facts/questions-answers-basic-facts>

<https://ourworldindata.org/coronavirus>

# The basic SIR Model



$$\begin{cases} \frac{dS}{dt} = -bIS \\ \frac{dI}{dt} = bIS - rI \\ \frac{dR}{dt} = rI \end{cases}$$

S : Susceptibles

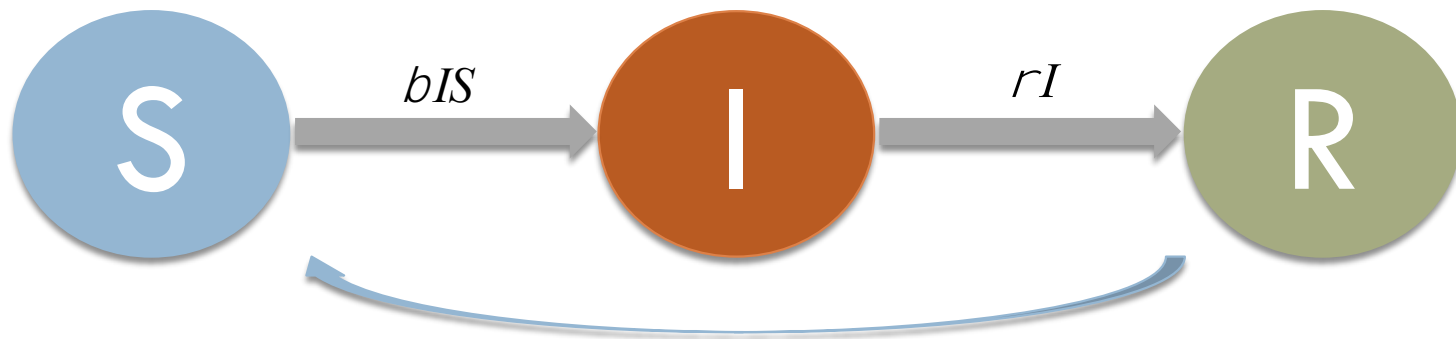
I : Infected

R : Recovered

$\beta$  : contact rate

$\rho$  : recovery rate

# The basic SIR Model (limited resistance)



$$\frac{ds}{dt} = \beta IS + \gamma R$$

$$\frac{dI}{dt} = \beta IS - \rho I$$

$$\frac{dR}{dt} = \rho I - \gamma R$$

S : Susceptibles

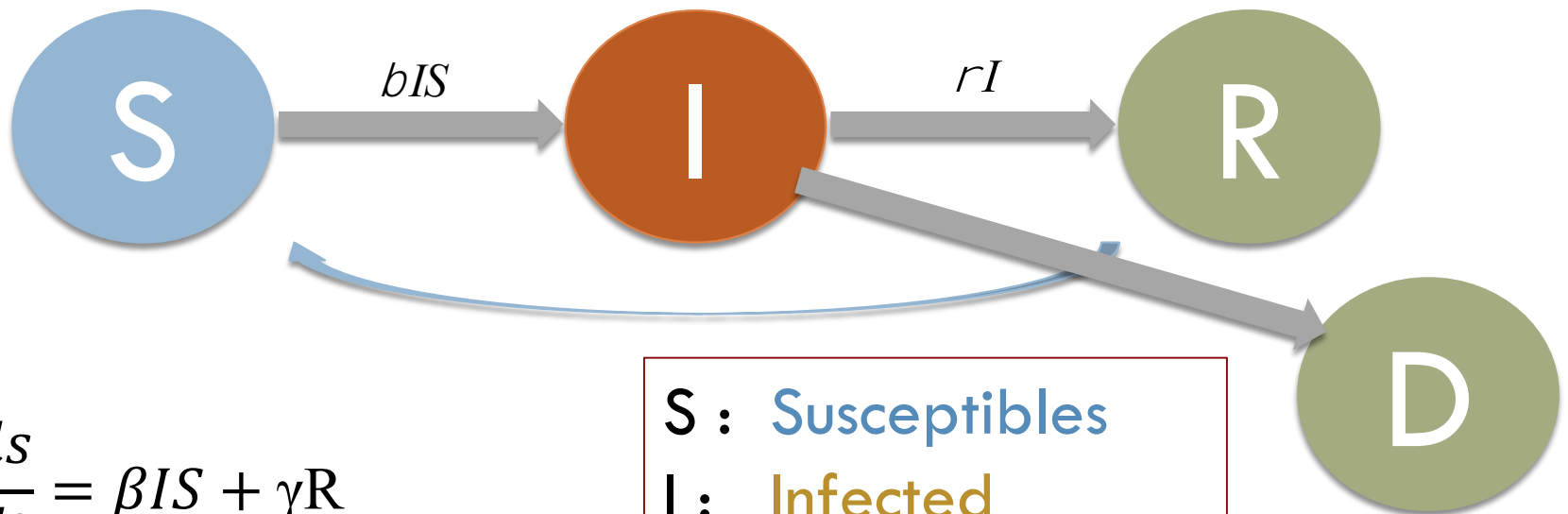
I : Infected

R : Recovered

$\beta$  : contact rate

$\rho$  : recovery rate

# The basic SIR Model (death)



$$\frac{ds}{dt} = \beta IS + \gamma R$$

$$\frac{dI}{dt} = \beta IS - \rho I - \mu I$$

$$\frac{dR}{dt} = \rho I - \gamma R$$

S : Susceptibles

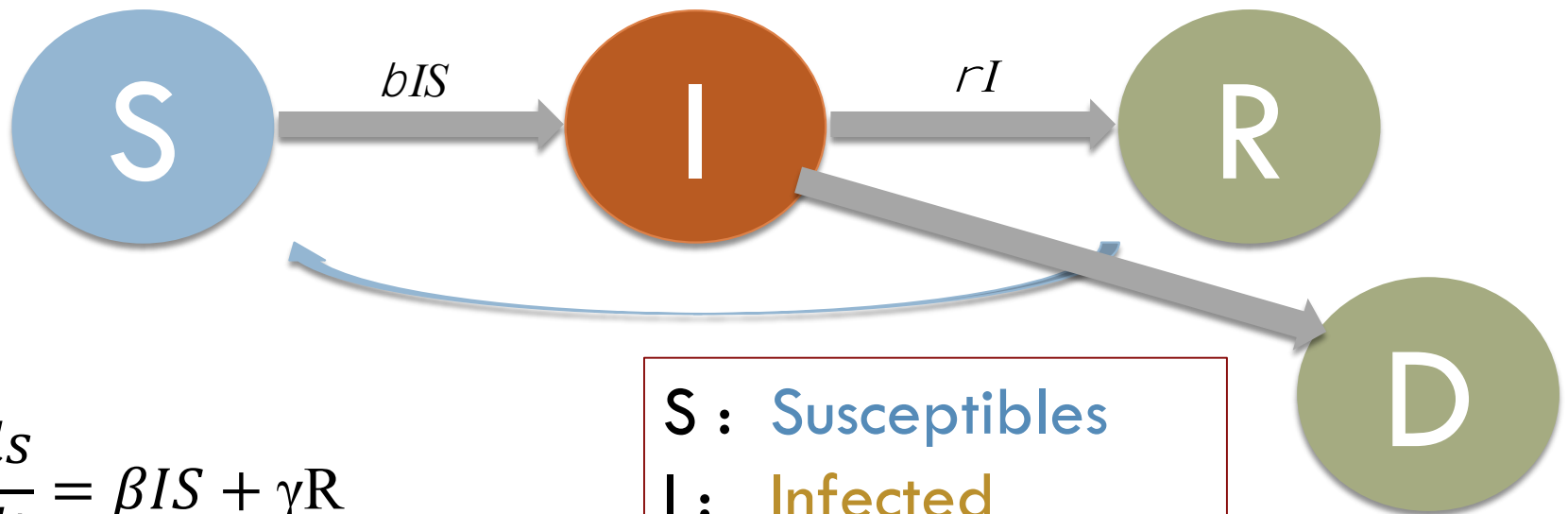
I : Infected

R : Recovered

$\beta$  : contact rate

$\rho$  : recovery rate

# The basic SIR Model (death)



$$\frac{ds}{dt} = \beta IS + \gamma R$$

$$\frac{dI}{dt} = \beta IS - \rho I - \mu I$$

$$\frac{dR}{dt} = \rho I - \gamma R$$

S : Susceptibles

I : Infected

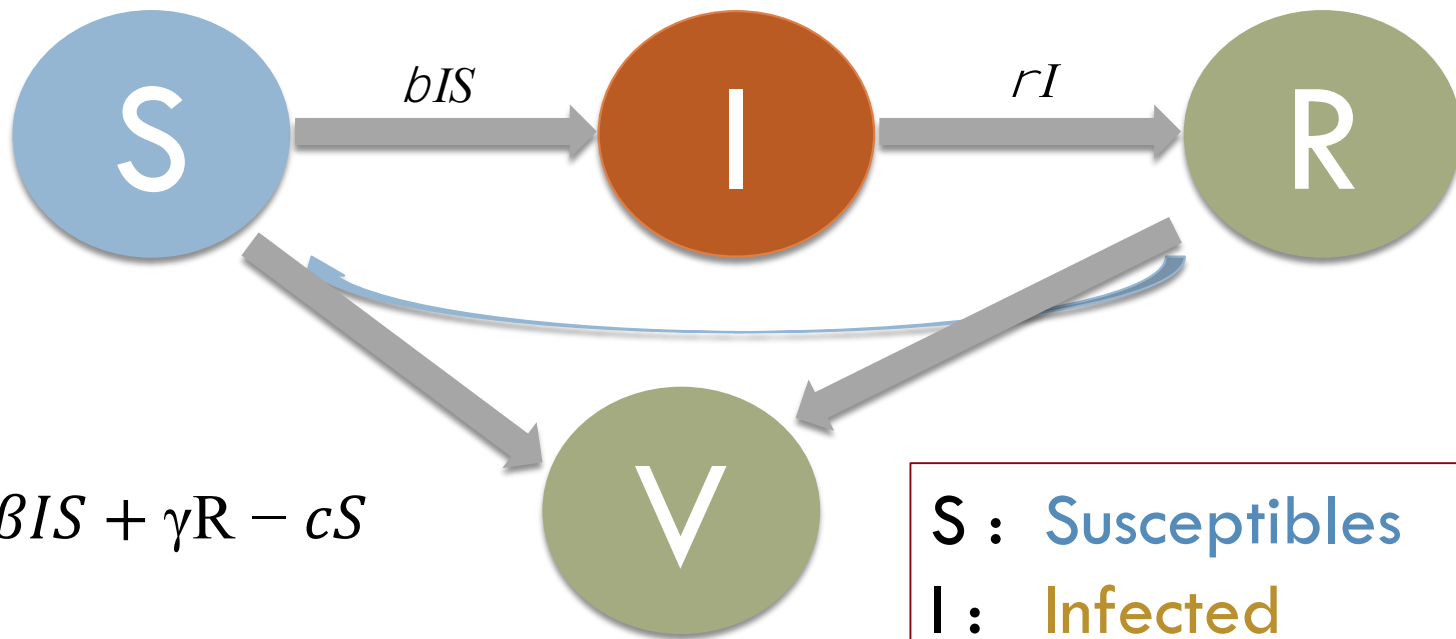
R : Recovered

$\beta$  : contact rate

$\rho$  : recovery rate

... human birth, non-infected deaths, ect, ect

# The basic SIR Model (vaccination)



$$\frac{ds}{dt} = \beta IS + \gamma R - cS$$

$$\frac{dI}{dt} = \beta IS - \rho I$$

$$\frac{dR}{dt} = \rho I + \gamma R - cR$$

$$\frac{dV}{dt} = c(S + R)$$

S : Susceptibles

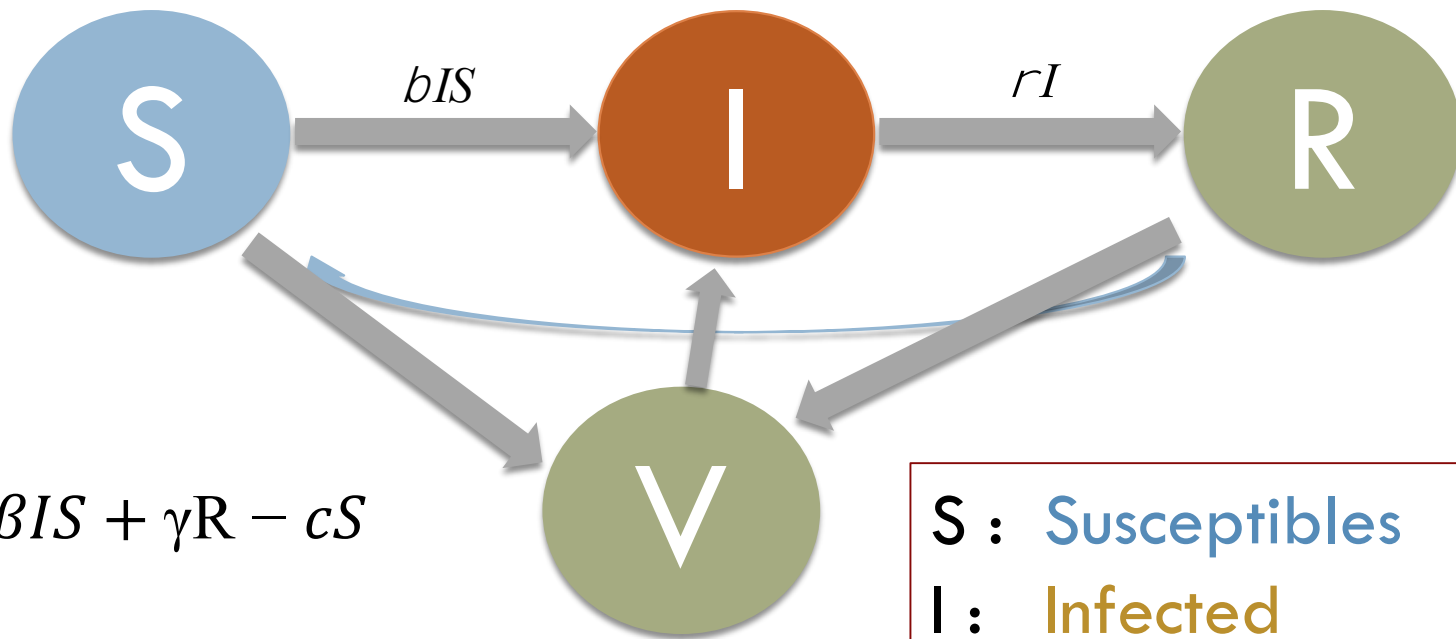
I : Infected

R : Recovered

$\beta$  : contact rate

$\rho$  : recovery rate

# The basic SIR Model (vaccination)



$$\begin{aligned}\frac{ds}{dt} &= \beta IS + \gamma R - cS \\ \frac{dI}{dt} &= \beta IS - \rho I + e\beta IV \\ \frac{dR}{dt} &= \rho I + \gamma R - cR \\ \frac{dV}{dt} &= c(S + R) - e\beta IV\end{aligned}$$

S : Susceptibles  
I : Infected  
R : Recovered  
 $\beta$  : contact rate  
 $\rho$  : recovery rate