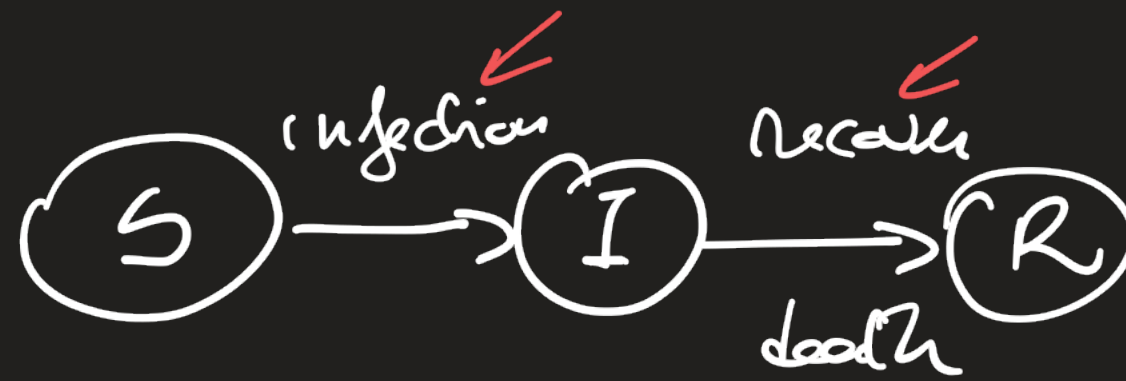


# EPIDEMIC MODELS - SIR

SUSCEPTIBLE

INFECTED

REMOVED



COLLECTIVE LEVEL:

$S(t), I(t), R(t)$

or population variables at time  $t$ .

- ① TIME SCALE of EPIDEMICS is small  $\Rightarrow$  POPULATION IS "CONSTANT"  
(NO BIRTHS OR NORMAL DEATHS)
- ② Infectives leave the infected state at a rate  $d$  per individual  $\Rightarrow dI$  at pop. level
- ③ An infected makes on average  $\beta \cdot N$  contacts (infective) per unit of time ( $N$  is the total population)

$\beta \cdot N \cdot \frac{S}{N} = \beta \cdot S$  rate of infection per infected individual

$$\left[ \dot{S} = \frac{dS}{dt} \text{ Newton notation} \right]$$

$$\begin{cases} \dot{S} = - \underbrace{\beta \cdot S \cdot I}_{\text{infection rate}} \\ \dot{I} = \beta \cdot S \cdot I - \underbrace{\alpha I}_{\text{recovery rate}} \\ \dot{R} = \alpha I \\ \dot{N} = 0 \end{cases}$$

$$\dot{R} = \alpha \cdot f \cdot I$$

$$\dot{N} = -\alpha(1-f)I \quad (< 0)$$

$$N = S + I + R$$

$$f \in [0, 1]$$

$f$  = fraction of removed individuals that recover

$(1-f)$  = fraction of individuals that die

$$\begin{cases} \dot{S} = -\beta \cdot S \cdot I \\ \dot{I} = (\beta S - \alpha) I \end{cases}$$

$$S(t), I(t) \geq 0$$

$$\dot{S} < 0$$

what about  $\dot{I}$

$$\dot{I} > 0 \iff (\beta S - \alpha > 0) \iff S > \frac{\alpha}{\beta}$$

$$\dot{I} = 0 \iff (\beta S = \alpha)$$

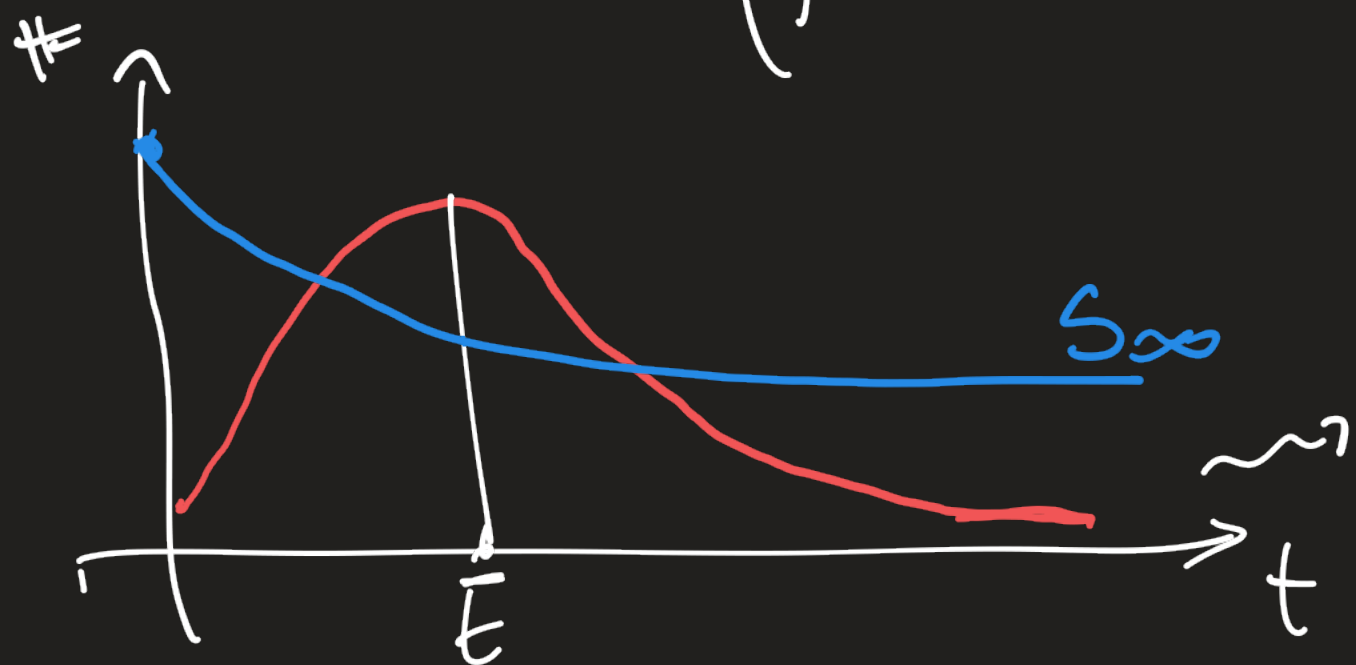
$$\dot{I} < 0 \iff (\beta S < \alpha)$$

$$I(0) = I_0$$

$$S(0) = S_0$$

$\Rightarrow \forall \boxed{S_0 > \frac{\alpha}{\beta}}$ , then  $\dot{I}(0) > 0$

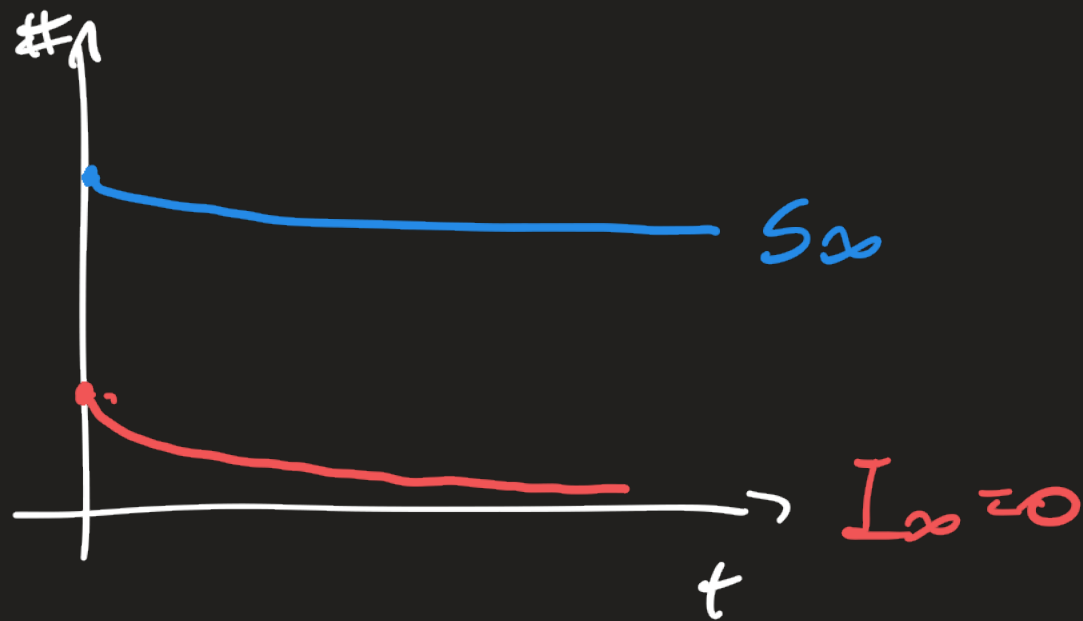
when  $S(t) = \frac{\alpha}{\beta}$ , then  $\dot{I} = 0$ , then for  $t > \bar{t}$ , then  $\dot{I} < 0$



$$\underline{I(t) \xrightarrow{t \rightarrow \infty} I_\infty = 0}$$

$$\text{If } S_0 < \frac{\alpha}{\beta}$$

Then  $I \rightarrow 0$



① We have a total population of  $K$  individuals

$$S_0 \approx K \quad I_0 \approx 0$$

$$\beta K \cdot \frac{1}{\alpha} = R_0$$

$\beta$ 
contact rate
 $\frac{1}{\alpha}$ 
average time to recovery

average number of secondary cases of infection per infected individual

BASIC REPRODUCTION NUMBER.

$$R_0 = \frac{\beta K}{\alpha} \approx \frac{\beta S_0}{\alpha}$$

$$S_0 > \frac{\alpha}{\beta}$$

$$\Leftrightarrow \frac{\beta S_0}{\alpha} > 1 \Leftrightarrow R_0 > 1$$

$$\boxed{R_0 > 1}$$

$$S_{\infty} \begin{cases} \dot{S} = -\beta SI \\ \dot{I} = (\beta S - \alpha)I \end{cases}$$

$$\frac{\dot{I}}{\dot{S}} = \frac{dI/dt}{dS/dt} = \frac{dI}{dS} = -1 + \frac{\alpha}{\beta S}$$

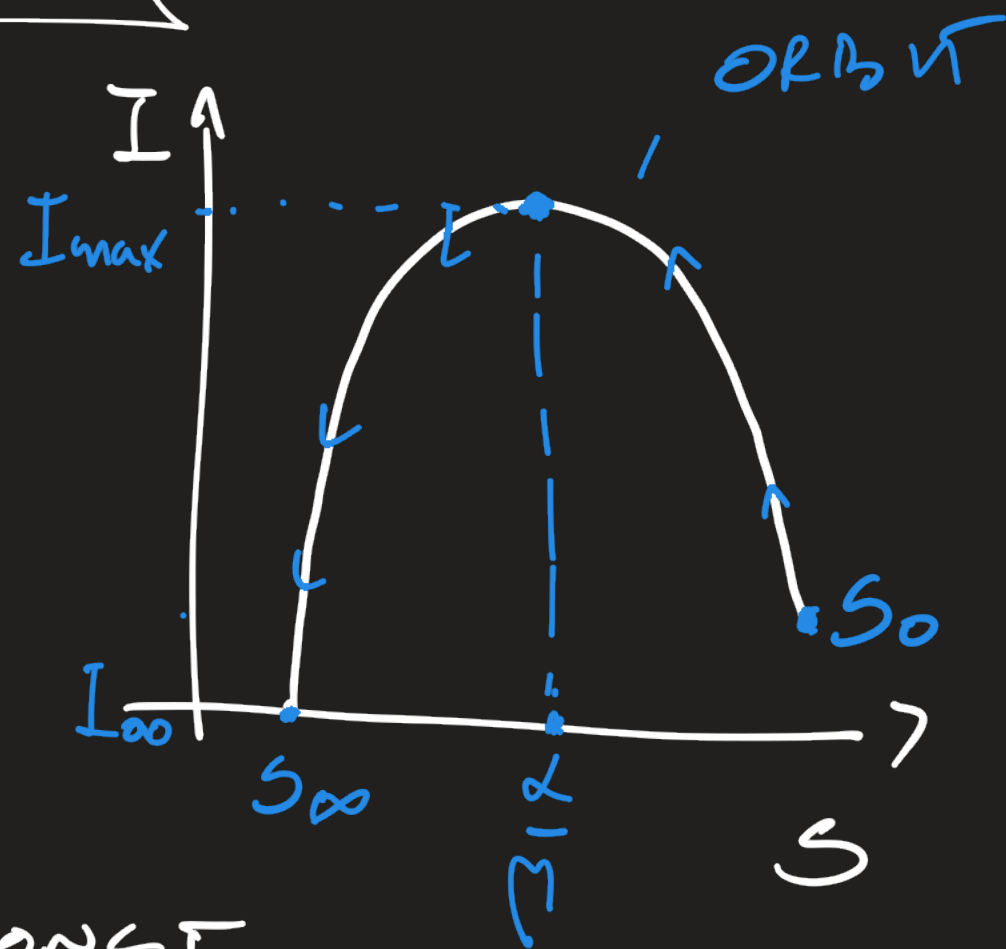
$$\int dI = \int \left(-1 + \frac{\alpha}{\beta S}\right) dS \Rightarrow$$

$$V(S, I) = I + S - \frac{\alpha}{\beta} \log S = \text{CONSTANT}$$

$$V(S_0, I_0) = S_0 + I_0 - \frac{\alpha}{\beta} \log S_0 = \text{CONST}$$

$$V\left(\frac{2}{\beta}, I_{\max}\right) = V(S_0, I_0) \text{ solve for } I_{\max}$$

$$S_0, I_0 \approx K_1, 0$$





$$V(S_\infty, 0) = V(S_0, I_0) \quad S_0, I_0 \sim K, 0$$

$$K - \frac{2}{\beta} \log K = S_\infty - \frac{2}{\beta} \log S_\infty$$

$$\frac{\beta}{2} = \frac{\log K - \log S_\infty}{K - S_\infty}$$

$$\log K - \log S_\infty = \underbrace{\beta \left[ 1 - \frac{S_\infty}{K} \right]}_{\text{FINITE } < \infty} \leftarrow S_\infty > 0$$

What is  $\begin{cases} K & \text{total population} \\ \alpha & \text{no easy to observe from cases.} \\ \beta & \text{HARD.} \end{cases}$

INITIAL PHASE OF EPIDEMICS. (EXPONENTIAL PHASE)

$S \approx K$ ,  $K$  is large, so  $S \approx K$

$\dot{I} = (\beta K - \alpha) I$  in initial phase

$$I(t) = I(0) \cdot e^{\lambda t}, \quad \lambda = (\beta K - \alpha) = \alpha (R_0 - 1)$$

$$\Downarrow \left\{ (t_i, \underline{I(t_i)}) \right\}_{i=1 \rightarrow K} \rightsquigarrow \left\{ (t_i, \log \underline{I(t_i)}) \right\}$$

LINEAR REGRESSION  
TO FIT  $\lambda$

$$\rightarrow \left[ t, \log I(0) + \lambda \cdot t \right]$$

$$\beta = (\lambda + \alpha) / K; \quad R_0 = \frac{\lambda}{\alpha} + 1$$

## CUMULATIVE INFECTED CASES

$C_0 \dots C_K$  observed data

$$\underbrace{L(\beta)} = \sum_{i=0}^K \left( C_i - (K - S(t_i)) \right)^2$$

least squares fit: the smaller  $L$ ,  
The best the fit of model to  
data

(FIX  $\beta$ , SOLVE THE ODE numerically,  
compute  $S(t_i)$  and then  $L(\beta)$ ,  
MINIMIZE  $L(\beta)$  w.r.t.  $\beta$ )

FOR CORONAVIRUS, note:

1)  $\approx 14^{-1}$  days (e.g. recovery takes about 14 days)

2)  $K$  can be determined easily: we are all susceptible  
(FOCUS ON: CHINA, ITALY, LOMBARDIA, BERGAMO PROVINCE)



## FUNDAMENTAL HYPOTHESIS OF SIR

- ① we are concerning a deterministic behaviour of the system  
 $S, I$ , are relatively large ( $\gg 1$ )
  - ② For low  $I$ , the behaviour will be stochastic
  - ③ IT ASSUMES WELL-MIXING
- 

WHAT IF WE VACCINATE

$$R_0 = \frac{\beta}{\alpha} \cdot K \quad q \in [0, 1] \text{ fraction of population we vaccinate}$$

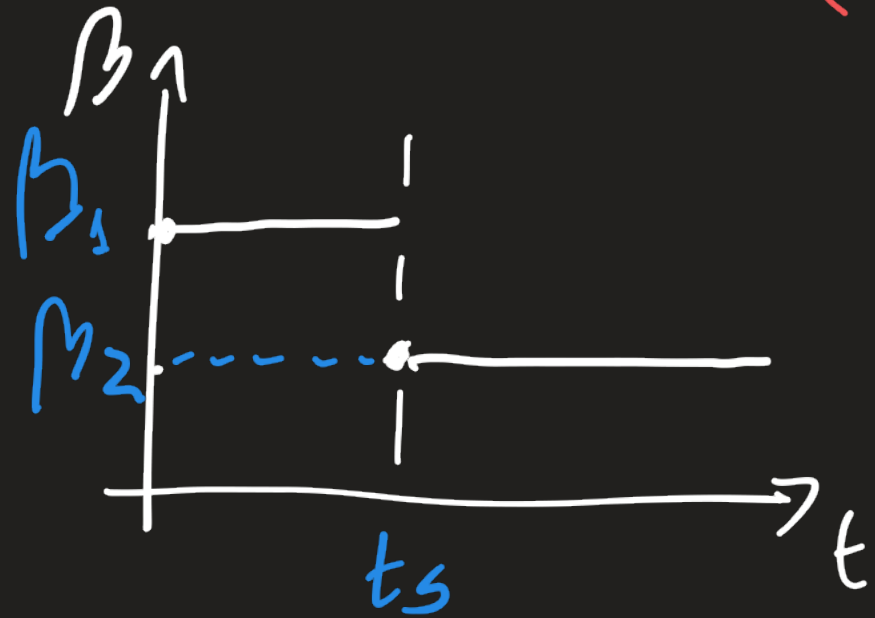
↑  
vaccinating, we influence  $K$

$$R_0^q = \frac{\beta}{\alpha} \cdot K(1-q)$$

$$R_0^q \leq 1 \Rightarrow$$

$$q = 1 - \frac{\alpha}{\beta K} = 1 - \frac{1}{R_0}$$

# MORE COMPLEX (TIME DEPENDENT) INFECTION RATE

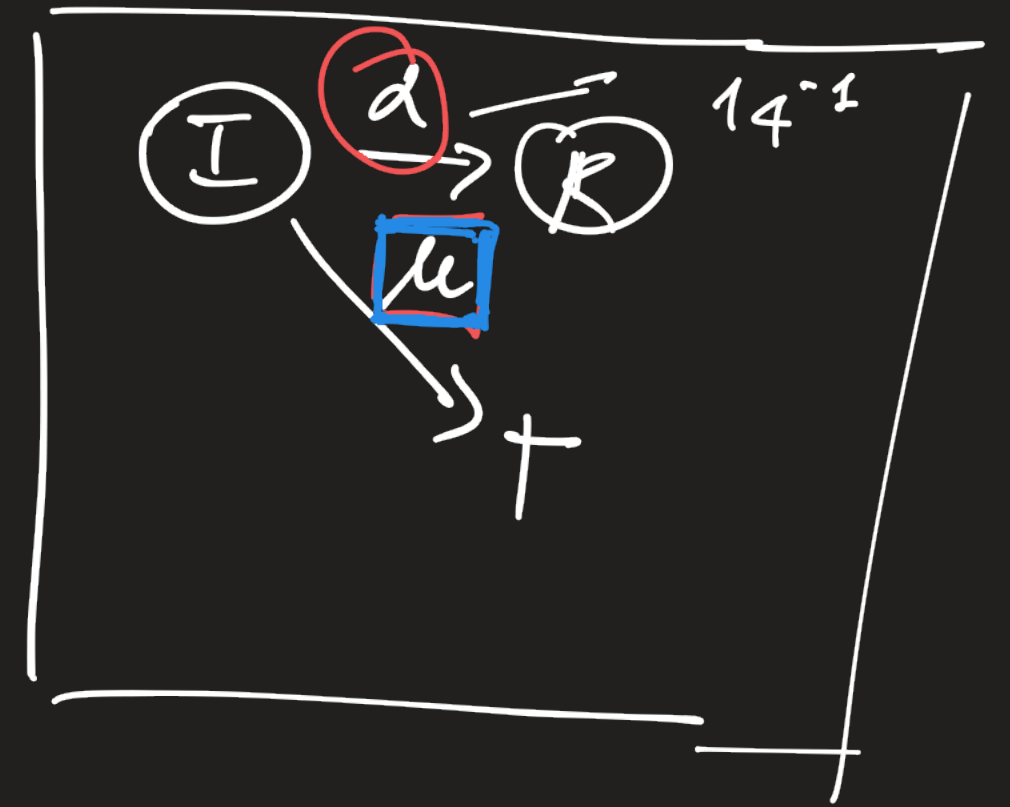
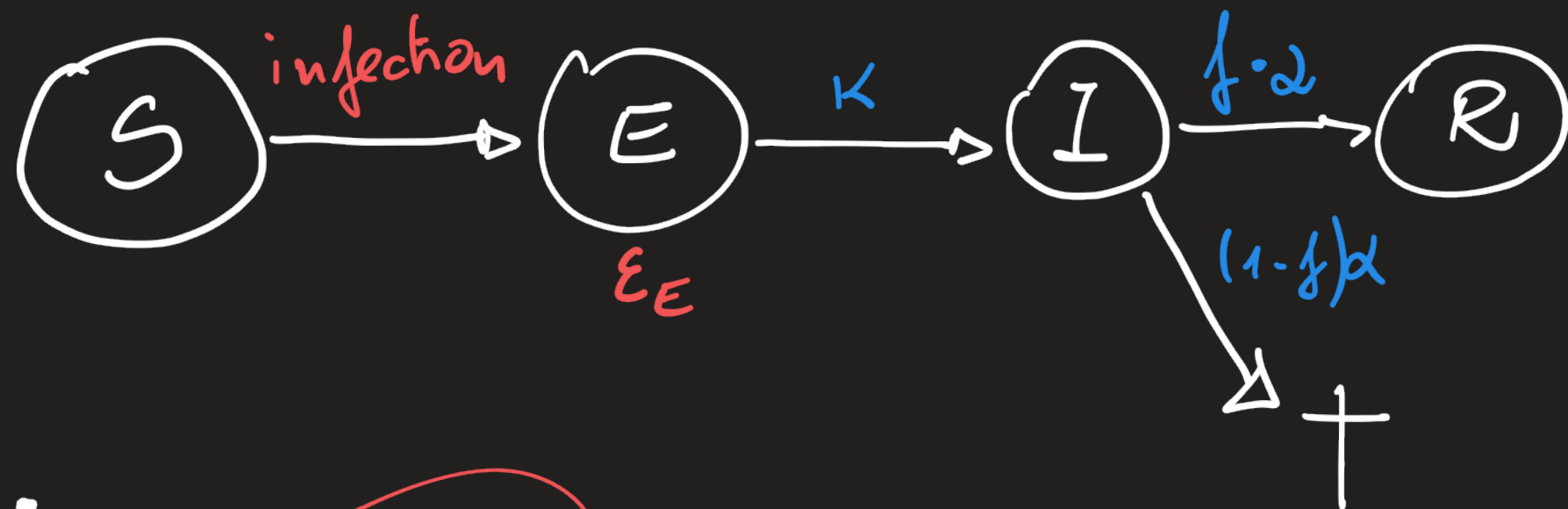


$$\dot{S} = \begin{cases} -\beta_1 S I & , 0 \leq t \leq t_s \\ -\beta_2 S I & , t > t_s \end{cases}$$

↑ This models a change in spreading, e.g. due to a change in quarantine policy.

EXERCISE: write down the loss for this model (SIR with time dep. infection rate)

# SEIR model



$$\begin{cases} \dot{S} = \text{infection} \\ \dot{E} = \text{infection} - k \cdot E \\ \dot{I} = kE - \alpha I \\ \dot{R} = \alpha f I \\ \dot{N} = - (1-f) \alpha I \end{cases}$$

infection only from I  
 infection =  $\beta \cdot S \cdot I$

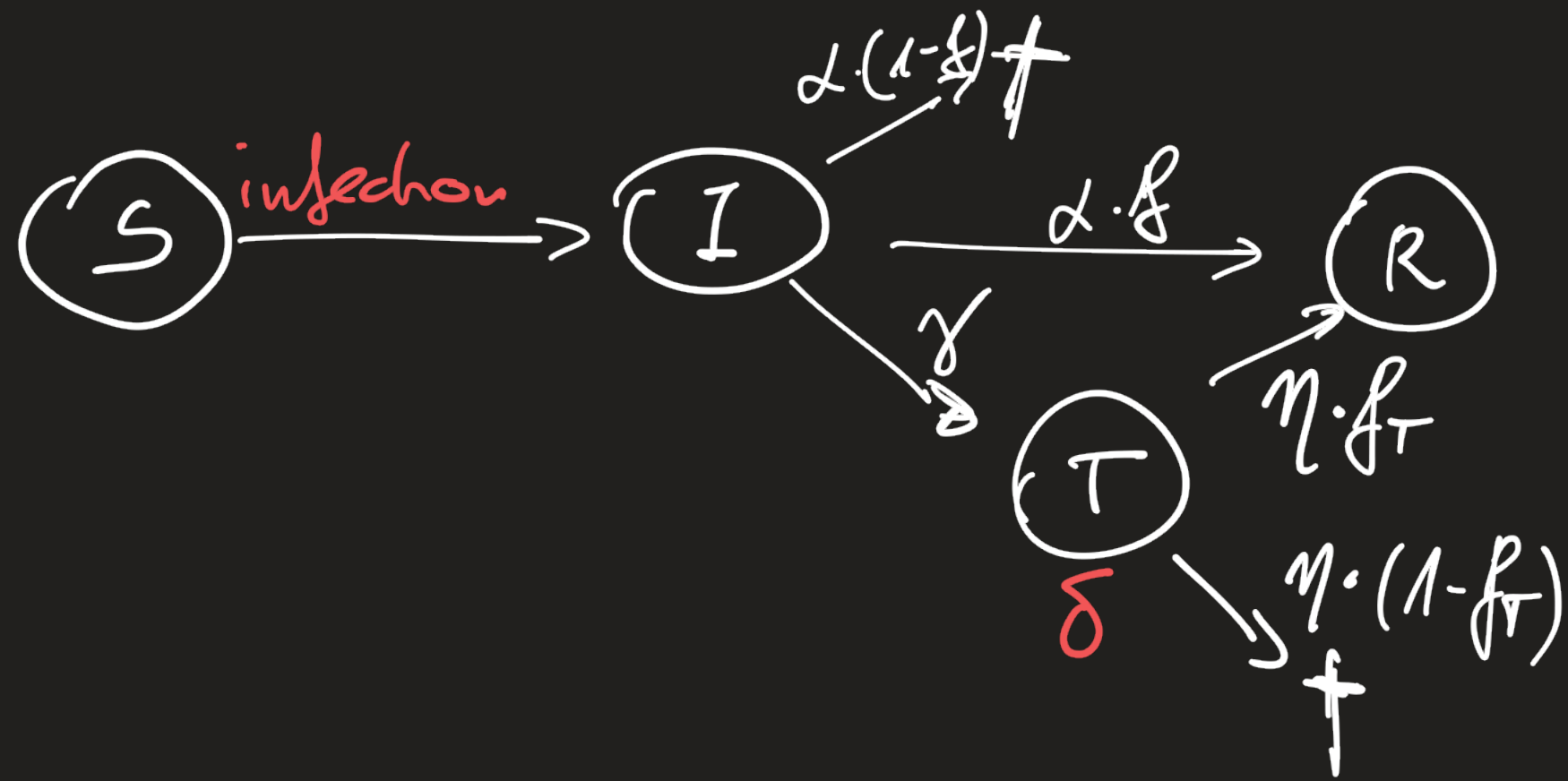
infection from I and E  
 $\epsilon_E \in [0, 1]$   $\beta$  in I  
 $\epsilon_E \beta$  in E

$$R_0 = \frac{k \cdot \beta}{\alpha} + \epsilon_E \frac{k \beta}{\alpha}$$

$$\text{infection} = \beta S \cdot (\epsilon_E \cdot E + I)$$

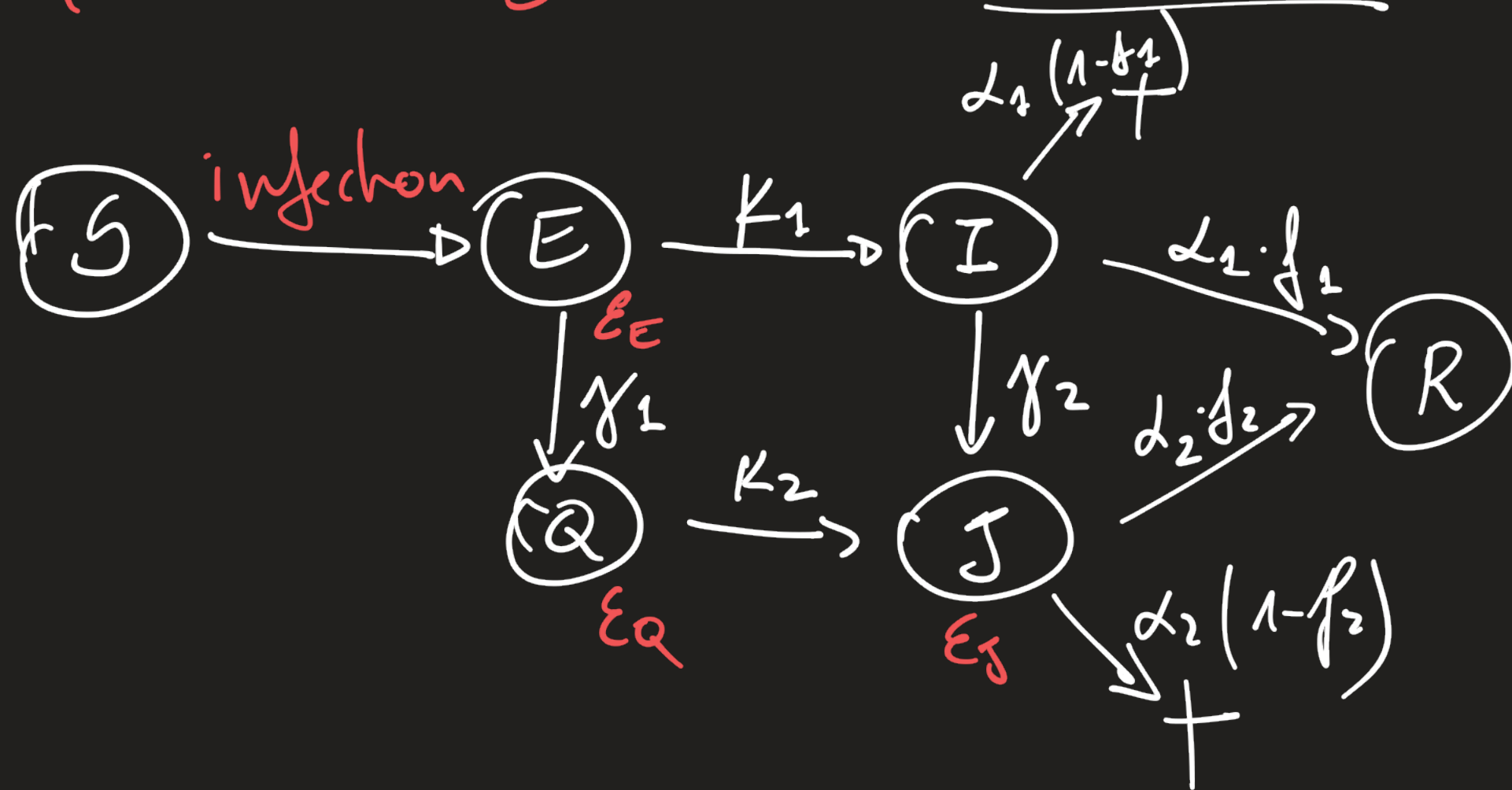
TREATMENT.

SITR



QUARANTINE - ISOLATION  
Q

SEQIR - model

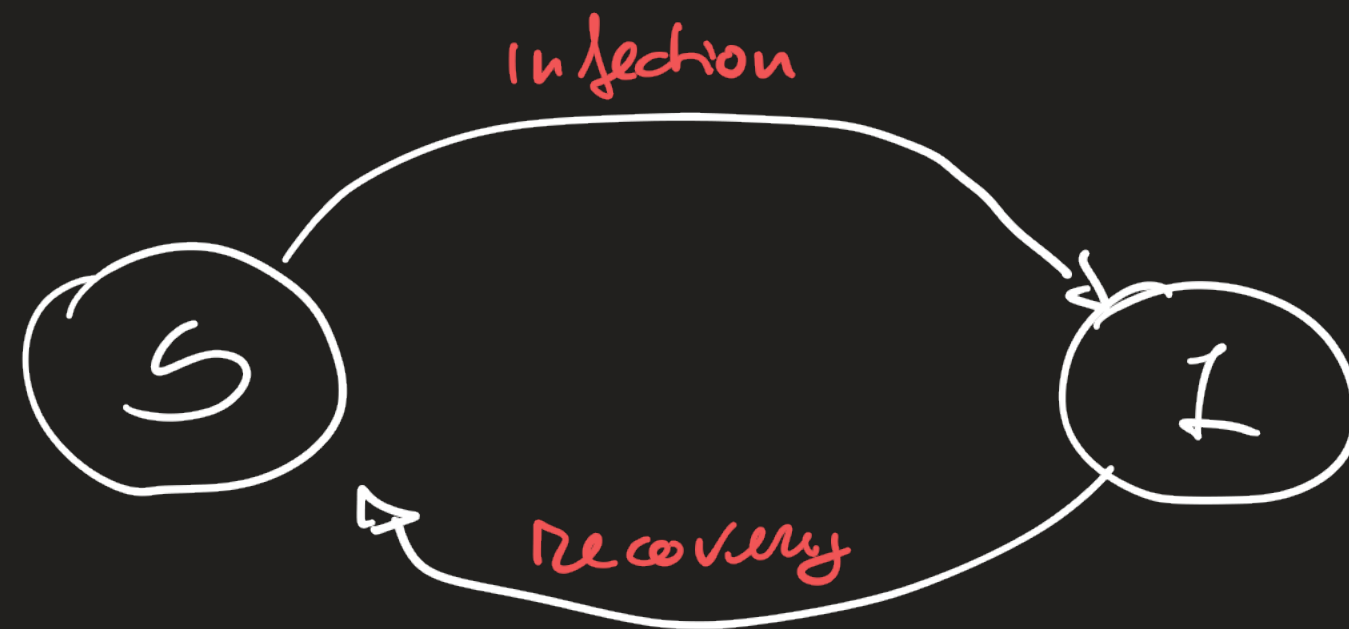


$R_c = \dots$

CONTROL REPRODUCTION NUMBER

## OTHER EPIDEMIC MODELS

SIS - Susceptible, Infected, Susceptible



- NO IMMUNITY (e.g. Bacterial diseases like bronchitis)

For SIS models, if  $R_0 > 1$ , then we have an ENDEMIC equilibrium: the disease is endemic.