# Lab 1 of models of epidemics



## Subtask 1:

## **Description:**

I chosed a model with two kinds of infected: vaccinated and not vaccinated.  $\Lambda = \mu N$  is our constant recruitment rate; more specifically, in our case, It is our birth rate (recruitment rates can mean something else like a person entering the group of sexually active persons for instance) and newborn babies fell in the susceptible group(the disease is not hereditary i.e. not vertical).  $\mu$  is our mortality rate and It is the same mortality rate for all groups in our model.  $\gamma$  is the rate of the infected getting vaccinated(this parameter comes from the fact that our model was inspired by a S I V model that was itself based upon a S I R model).  $\beta$  is our infection rate.  $I_1$  and  $I_2$  are our infected without and with vaccination groups, R is the recovered group. Our model is based off the (2.23) model in P. 73: BRAUER, FRED - MATHEMATICAL MODELS IN EPIDEMIOLOGY.-SPRINGER (2019).

### Model from the book:

(2.23) 
$$\begin{cases} S'(t) = \Lambda - \frac{\beta S I_1}{N} - \mu S \\ I'_1(t) = \frac{\beta S I_1}{N} - (\mu + \gamma) I_1 \\ I_2'(t) = \gamma I_1 - \mu I_2 \\ N'(t) = S'(t) + I'_1(t) + I'_2(t) \end{cases}$$

## Model I will use:

$$\begin{cases} S'(t) = \Lambda - \frac{\beta S I_1}{N} - \mu S \\ I_1'(t) = \frac{\beta S I_1}{N} - (\mu + \gamma)I_1 - \alpha_1 * I_1 \\ I_2'(t) = \gamma I_1 - \mu I_2 - \alpha_2 * I_2 \\ R'(t) = \alpha_1 * I_1 + \alpha_2 * I_2 - \mu R \\ N'(t) = S'(t) + I_1'(t) + I_2'(t) + R'(t) \end{cases}$$

We get the following answers for this exercise:

(a)  $\Lambda$  is the number of persons that was birthed per unit of time  $\beta S \mid N$  is the number of persons that are sane that get infected at a given time t  $\mu S$  is the number of sane persons that die at a given time t  $\mu$  is the percentage of people that die per unit of time(death rate)

$$N'(t) = S'(t) + I_1'(t) + I_2'(t) + R'(t)$$

$$= \Lambda - \frac{\beta S I_1}{N} - \mu S + \frac{\beta S I_1}{N} - (\mu + \gamma)I_1 - \alpha_1 * I_1 + \gamma I_1 - \mu I_2 - \alpha_2 * I_2 + \alpha_1 * I_1 + \alpha_2 * I_2 - \mu R$$

$$= \Lambda - \mu (S + I_1 + I_2 + R)$$

$$= \Lambda - \mu N$$

$$SP: N_{SP}(t) = \frac{\Lambda}{\mu}$$

$$SG: N_{SG}(t) = e^{-\mu t}$$

$$N(t) = N_{SP}(t) + N_{SG}(t) = \frac{\Lambda}{\mu} + e^{-\mu t}$$
(c) Using (b), we get  $\lim_{t \to +\infty} N(t) = \frac{\Lambda}{\mu}$ .

We will be using these equations to suit this diagram:

The influx and outflux can be written as follow:

$$\begin{split} \mathcal{F}(l_1,l_2) &= (\frac{\beta S\, l_1}{N},\gamma\, l_1) \ and \ v(l_1,l_2) = ((\mu + \gamma + \alpha_1)l_1, (\mu + \alpha_2) * l_2) \\ F &= \begin{bmatrix} \frac{d\mathcal{F}_1}{dl_1} & \frac{d\mathcal{F}_1}{dl_2} \\ \frac{d\mathcal{F}_2}{dl_2} & \frac{d\mathcal{F}_2}{dl_2} \end{bmatrix}_{x_0} \\ &= \begin{bmatrix} \frac{\beta S}{N} & 0 \\ 1 & \gamma & 0 \end{bmatrix}_{x_0} \\ N &= \begin{bmatrix} \frac{dv_1}{dl_1} & \frac{dv_1}{dl_2} \\ \frac{dv_2}{dl_1} & \frac{dv_2}{dl_2} \end{bmatrix}_{x_0} \\ &= \begin{bmatrix} \mu + \gamma + \alpha_1 & 0 \\ 0 & \mu + \alpha_2 \end{bmatrix}_{x_0} \\ We \ get \ F &= \begin{bmatrix} \frac{\beta S_0}{N_0} & 0 \\ \gamma & 0 \end{bmatrix} \ and \ N &= \begin{bmatrix} \mu + \gamma + \alpha_1 & 0 \\ 0 & \mu + \alpha_2 \end{bmatrix} \end{split}$$

$$The \ next \ generation \ matrix \ G \ is \ G &= FN^{-1} &= \frac{1}{(\mu + \gamma + \alpha_1)(\mu + \alpha_2)} \begin{bmatrix} \frac{\beta S_0}{N_0} & 0 \\ \gamma & 0 \end{bmatrix} \begin{bmatrix} \mu + \alpha_2 & 0 \\ 0 & \mu + \gamma + \alpha_1 \end{bmatrix} \\ &= \frac{1}{(\mu + \gamma + \alpha_1)(\mu + \alpha_2)} \begin{bmatrix} (\mu + \alpha_2) \frac{\beta S_0}{N_0} & 0 \\ (\mu + \alpha_2)\gamma & 0 \end{bmatrix}$$

$$The \ reproductive \ number \ is \ \Re_0 &= \rho(G) \end{split}$$

which means that the reproductive number is the maximum real part of the eigenvalues of G.

$$Tr(G) = \frac{1}{(\mu + \gamma + \alpha_1)(\mu + \alpha_2)} \left( (\mu + \alpha_2) \frac{\beta S_0}{N_0} + 0 \right) = \frac{\beta S_0}{N_0(\mu + \gamma + \alpha_1)}$$
and Det(G) =  $\frac{1}{(\mu + \gamma + \alpha_1)(\mu + \alpha_2)} \left( (\mu + \alpha_2) \frac{\beta S_0}{N_0} * 0 - 0 * (\mu + \alpha_2) \gamma \right) = 0$ 

$$\lambda_{1,2} = \frac{Tr(G)}{2} \pm \sqrt[2]{\left(\frac{Tr(G)}{2}\right)^2 - Det(G)}$$

$$= \frac{\beta S_0}{2N_0(\mu + \gamma + \alpha_1)} \pm \sqrt[2]{\left(\frac{\beta S_0}{2N_0(\mu + \gamma + \alpha_1)}\right)^2 - 0}$$

$$= \frac{\beta S_0}{N_0(\mu + \gamma + \alpha_1)}, 0$$

Our reproductive number is 
$$\Re_0 = \rho(G) = \frac{\beta S_0}{N_0(\mu + \gamma + \alpha_1)}$$
.

**R**<sub>0</sub>**=1:**  $\lambda$ =0.002,  $\beta$ =0.068,  $\mu$ =0.001,  $\gamma$ =0.05, h=0.01,  $\alpha_{l1}$ =0.01,  $\alpha_{l2}$ =0.1, R\_0=1.00

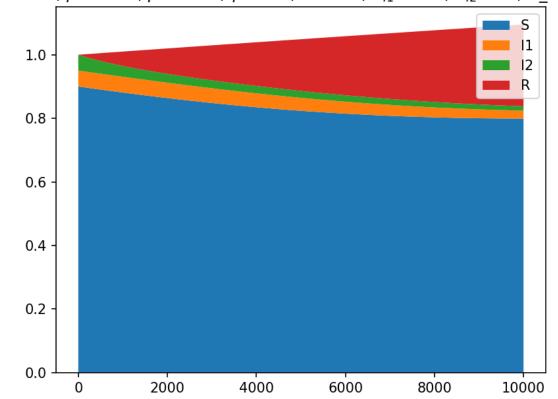


Figure 1: stackplot of all functions except N (which is the sum of everything plotted),  $R_0$ =1 and although the population looks like It is growing linearly, It is in fact a curve converging  $\lim_{t\to +\infty} N(t) = \frac{\Lambda}{\mu}$  (It can be observed for higher numbers of time intervals)

We can see that the disease takes a long time to disappear. Since after 10 000 time intervals, only about 20% have been infected, the fact that an infected individual in a completely susceptible population infects one individual on average makes spreading the disease so slow that the epidemic outbreaks decline constantly.

 $\lambda$ =0.002,  $\beta$ =0.068,  $\mu$ =0.001,  $\gamma$ =0.05, h=0.01,  $\alpha_{l1}$ =0.01,  $\alpha_{l2}$ =0.1, R\_0=1.003

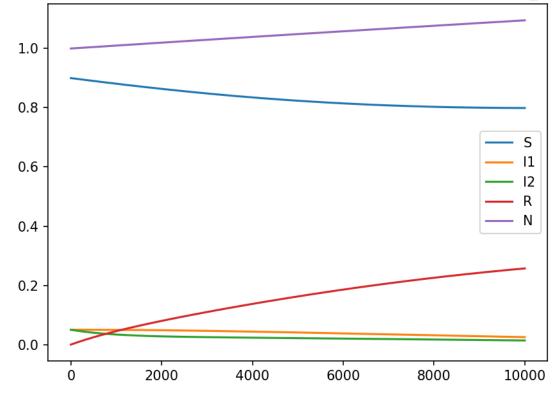


Figure 2: plots every function for  $R_0$ =1

 $R_0$ ≤1:  $\lambda$ =0.002,  $\beta$ =0.02,  $\mu$ =0.001,  $\gamma$ =0.05, h=0.01,  $\alpha$ <sub>/1</sub>=0.01,  $\alpha$ <sub>/2</sub>=0.1, R\_0=0.295

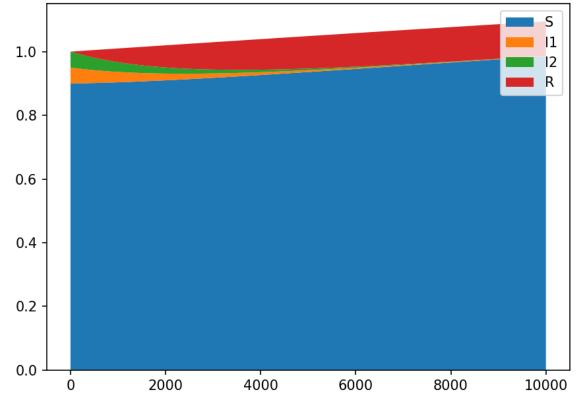


Figure 3: stackplot of all functions except N (which is the sum of everything plotted),  $R_0 \le 1$ 

The disease actually disappear. In the graph, there are a remaining I1 and I2 because the population is represented as continuous but in reality there would be a last person with the disease and since this person mathematically transmit the disease to less than a person the disease would be eradicated.

 $\lambda$ =0.002,  $\beta$ =0.02,  $\mu$ =0.001,  $\gamma$ =0.05, h=0.01,  $\alpha_{/1}$ =0.01,  $\alpha_{/2}$ =0.1, R\_0=0.295

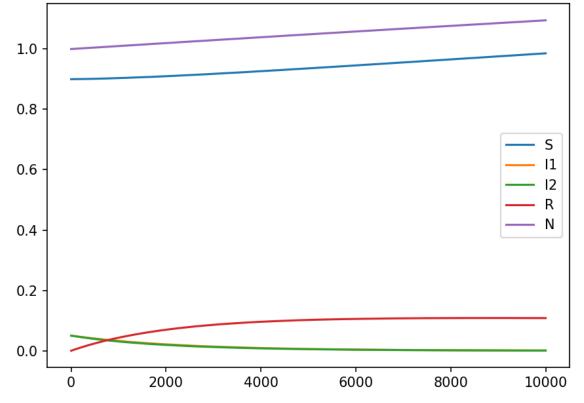


Figure 4 : plots every function for  $R_0 \le 1$ 

 $\lambda$ =0.002,  $\beta$ =0.3,  $\mu$ =0.001,  $\gamma$ =0.05, h=0.01,  $\alpha_{l1}$ =0.01,  $\alpha_{l2}$ =0.1, R\_0=4.426

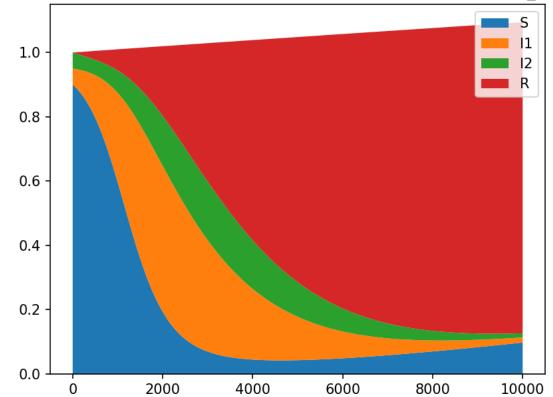


Figure 5: stackplot of all functions except N (which is the sum of everything plotted),  $R_0 \ge 1$ 

These graphs represent an actual epidemic. The vast majority of the population gets infected. We can see that around 2000, the number of newly infected starts slowing down and around 4000, the newly infected are outnumbered by birthssince the susceptible group start growing again. We can see in figure 6 that infected vaccinated people peaks after I1 so infections have better distribution through time.

 $\lambda$ =0.002,  $\beta$ =0.3,  $\mu$ =0.001,  $\gamma$ =0.05, h=0.01,  $\alpha_{l1}$ =0.01,  $\alpha_{l2}$ =0.1, R\_0=4.426

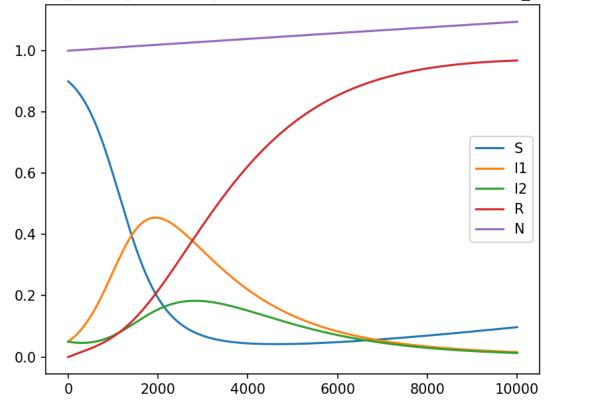


Figure 6: plots every function for  $R_0 \ge 1$ 

## Subtask 2:

## **Description:**

We will now be studying a model based upon the 2.24 model from Bauer's book. The 2.24 is an SIV model that we will be transforming in a  $SI_1I_2R$  with  $I_2$  a treatment class. It makes a bit more sense and is a bit more realistic than the model I used in subtask 1 because infected people start getting treatment when they get infected rather than getting in the vaccinated group. It also differs from subtask 1 because the population remains constant so studying equilibriums are made possible whilst in the case of non-constant population the disease would outbreak again if you wait long enough as the population grows the susceptible group expands. They look alike but they are in fact radically different.

#### Model from the book:

(2.24) 
$$\begin{cases} S'(t) = \mu N - \beta S I_1 - \mu S \\ I'_1(t) = \beta S I_1 - (\mu + \gamma) I_1 \\ I'_2(t) = \gamma I_1 - \mu I_2 \\ N'(t) = S'(t) + I'_1(t) + I'_2(t) \end{cases}$$

First, let's answer why It is enough to consider the first two equations as V(t) = N - S(t) - I(t). After a few easy steps, we get N'(t) = 0 which means N(t) = N = constant. As a result, we can get V(t) after solving the first two equations using V(t) = N - S(t) - I(t).

$$\text{We then get} \begin{cases} 0 = \ \mu N - \ \beta S_{\infty} \ I_{1,\infty} - \mu S_{\infty} \\ 0 = \beta S_{\infty} I_{1,\infty} \ - \ (\mu + \ \gamma \ ) I_{1,\infty} \end{cases} \Longleftrightarrow \begin{cases} S_{\infty} = N \ \Longrightarrow I_{1,\infty} = 0 \\ I_{1,\infty} \neq 0 \ \Longrightarrow S_{\infty} = \frac{\mu + \gamma}{\beta} \ and \ I_{1,\infty} = \mu \frac{N - S_{\infty}}{\beta S_{\infty}}. \end{cases}$$

#### Model I will use:

$$\begin{cases} S'(t) = \mu N - \beta S I_1 - \mu S \\ I'_1(t) = \beta S I_1 - (\mu + \gamma + \alpha_1) I_1 \\ T(t) = \gamma I_1 - (\mu + \alpha_2) T \\ R'(t) = \alpha_1 I_1 + \alpha_2 T - \mu R \\ N'(t) = S'(t) + I'_1(t) + T'(t) + R'(t) \end{cases}$$

The influx and outflux can be written as follow:

$$\begin{split} \mathcal{F}(I_1,I_2) &= (\beta S \, I_1, \gamma \, I_1) \text{ and } \nu(I_1, \mathsf{T}) = ((\mu \, + \, \gamma \, + \, \alpha_1) I_1, (\mu + \alpha_2) * \mathsf{T}) \\ F &= \begin{bmatrix} \frac{d\mathcal{F}_1}{dI_1} & \frac{d\mathcal{F}_1}{d\mathsf{T}} \\ \frac{d\mathcal{F}_2}{dI_1} & \frac{d\mathcal{F}_2}{d\mathsf{T}} \end{bmatrix}_{X_0} \\ &= \begin{bmatrix} \beta S & 0 \\ \gamma & 0 \end{bmatrix}_{X_0} \end{split}$$

$$\begin{split} \mathbf{N} &= \begin{bmatrix} \frac{d\mathbf{v}_1}{dI_1} & \frac{d\mathbf{v}_1}{d\mathbf{T}} \\ \frac{d\mathbf{v}_2}{dI_1} & \frac{d\mathbf{v}_2}{d\mathbf{T}} \end{bmatrix}_{X_0} \\ &= \begin{bmatrix} \mu + \gamma + \alpha_1 & 0 \\ 0 & \mu + \alpha_2 \end{bmatrix}_{X_0} \\ We \ get \ F &= \begin{bmatrix} \beta S_0 & 0 \\ \gamma & 0 \end{bmatrix} \ and \ \mathbf{N} &= \begin{bmatrix} \mu + \gamma + \alpha_1 & 0 \\ 0 & \mu + \alpha_2 \end{bmatrix} \end{split}$$

The next generation matrix G is  $G = FN^{-1}$ 

$$\begin{split} &=\frac{1}{(\mu+\gamma+\alpha_1)(\mu+\alpha_2)} \begin{bmatrix} \beta S_0 & 0 \\ \gamma & 0 \end{bmatrix} \begin{bmatrix} \mu+\alpha_2 & 0 \\ 0 & \mu+\gamma+\alpha_1 \end{bmatrix} \\ &=\frac{1}{(\mu+\gamma+\alpha_1)(\mu+\alpha_2)} \begin{bmatrix} (\mu+\alpha_2)\beta S_0 & 0 \\ (\mu+\alpha_2)\gamma & 0 \end{bmatrix} \end{split}$$

The reproductive number is  $\Re_0 = \rho(G)$ 

which means that the reproductive number is the maximum real part of the eigenvalues of G.

$$Tr(G) = \frac{1}{(\mu + \gamma + \alpha_1)(\mu + \alpha_2)} \left( (\mu + \alpha_2)\beta S_0 + 0 \right) = \frac{\beta S_0}{\mu + \gamma + \alpha_1}$$
and Det(G) = 
$$\frac{1}{(\mu + \gamma + \alpha_1)(\mu + \alpha_2)} \left( (\mu + \alpha_2)\beta S_0 * 0 - 0 * (\mu + \alpha_2)\gamma \right) = 0$$

$$\lambda_{1,2} = \frac{Tr(G)}{2} \pm \sqrt[2]{\left(\frac{Tr(G)}{2}\right)^2 - Det(G)}$$

$$= \frac{\beta S_0}{2(\mu + \gamma + \alpha_1)} \pm \sqrt[2]{\left(\frac{\beta S_0}{2(\mu + \gamma + \alpha_1)}\right)^2 - 0}$$

$$= \frac{\beta S_0}{(\mu + \gamma + \alpha_1)} = \frac{\beta S_0}{(\mu + \gamma +$$

Our reproductive number is  $\Re_0 = \rho(G) = \frac{\beta S_0}{\mu + \gamma + \alpha_1}$ .

R<sub>0</sub>=1:

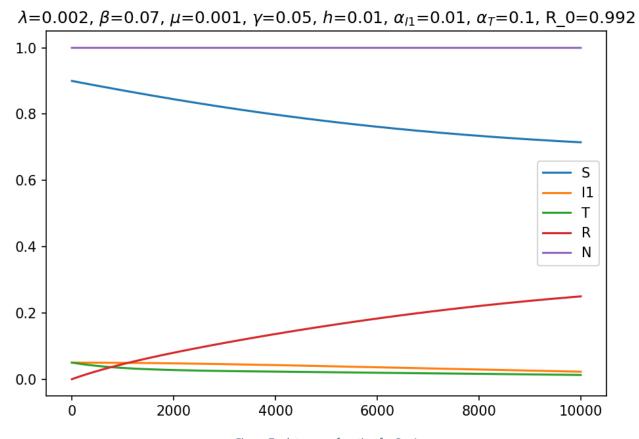


Figure 7: plots every function for  $R_0$ =1

These graphs show that the disease decline still in the long run It has infected a part of the population. The population remains constant and the model tends to a disease-free equilibrium.

 $\lambda {=} 0.002, \, \beta {=} 0.07, \, \mu {=} 0.001, \, \gamma {=} 0.05, \, h {=} 0.01, \, \alpha_{/1} {=} 0.01, \, \alpha_{T} {=} 0.1, \, \text{R\_0} {=} 0.992$ 

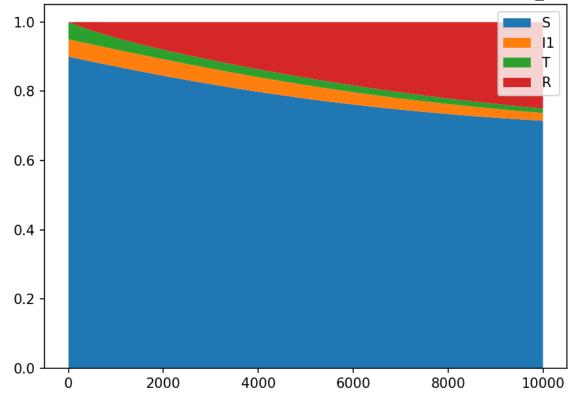
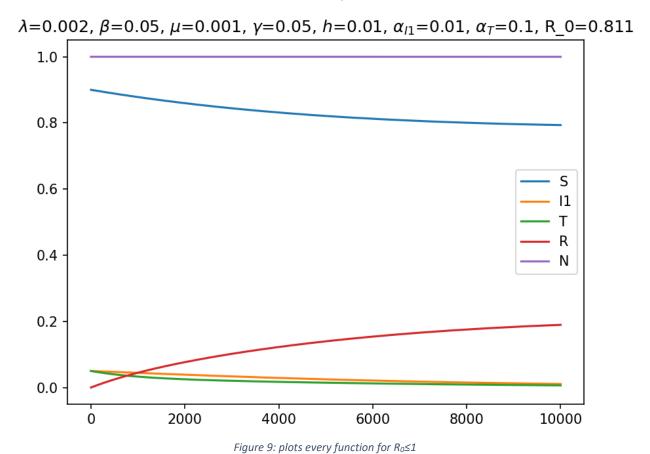


Figure 8: stackplot of all functions except N (which is the sum of everything plotted),  $R_0$ =1

**R**<sub>0</sub>≤1:



The disease quickly declines and barely 20% of the population got infected overall. The disease can be considered eradicated at 10000.

 $\lambda$ =0.002,  $\beta$ =0.05,  $\mu$ =0.001,  $\gamma$ =0.05, h=0.01,  $\alpha_{I1}$ =0.01,  $R_{I}$ =0.1,  $R_{I}$ =0.811

1.0

0.8

0.4

0.2

Figure 10: stackplot of all functions except N (which is the sum of everything plotted),  $R_0 \le 1$ 

4000

6000

8000

10000

0.0

Ö

2000

**R**<sub>0</sub>≥1:

Figure 11: plots every function for R0≥1

We can see here that the epidemic is so violent that at some point nearly half the population is sick. We also see that the susceptible class grows as people die which mean the disease would reappear.

 $\lambda {=} 0.002, \, \beta {=} 0.30, \, \mu {=} 0.001, \, \gamma {=} 0.05, \, h {=} 0.01, \, \alpha_{I1} {=} 0.01, \, \alpha_{T} {=} 0.1, \, \text{R\_}0 {=} 4.426$ 

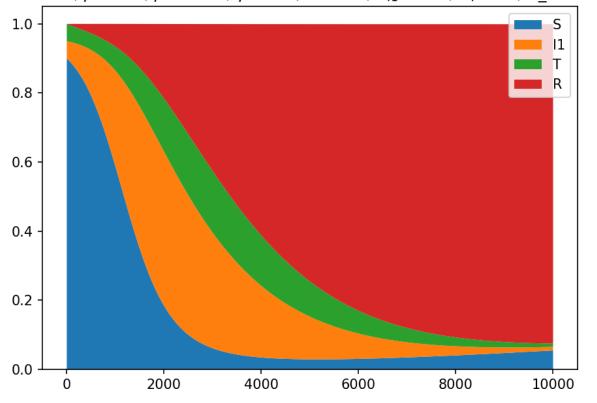


Figure 12: stackplot of all functions except N (which is the sum of everything plotted),  $R_0 \ge 1$ 

## **Conclusion:**

As we have seen,  $\Re_0$  is determinant for the outbreak of an epidemic. Our two models have different interpretations even if they look close. We confirmed that changing parameters had effects on treated and vaccinated people over infected only. We also saw that equilibriums are easier to find in constant population model. Their biggest similarity is in the computation of  $\Re_0$  because in both cases the determinant is zero.