1 Model description

1.1 Model assumptions

The considered model is based on the classic SIR-model, extended to consider two seperate strains of diseases. The model does not consider cross-immunity, however, simultanious infections is omitted. Furthermore, vaccination toward one of the two strains is considered.

With I denoting one strain and Y denoting the other, the following variables are considered:

- S: Unvaccinated, susceptible to both strains.
- V: Vaccinated. Immune to strain Y but susceptible to strain I.
- I_S: Unvaccinated infected with strain I.
- I_V: Vaccinated infected with strain I.
- $I_{0,1}$: Recovered from strain Y, infected with strain I.
- Y: Infected with strain Y.
- $Y_{1,0}$: Recovered from strain I, infected with strain Y.
- $R_{0,1}$: Recovered from strain Y, susceptible to strain I.
- $R_{1,0}$: Recovered from strain I, susceptible to strain Y.
- $R_{1,1}$: Recovered from both strains, or recovered from strain I and vaccinated.

1.2 "Reactions"

$$\begin{aligned}
S &\Rightarrow I_S && \text{Infected with strain } I && (1)\\
V &\Rightarrow I_V && \text{Infected with strain } I && (2)\\
S &\Rightarrow Y && \text{Infected with strain } Y && (3)\\
I_S &\Rightarrow R_{0,1} && \text{Recovery from infection} && (4)\\
I_V &\Rightarrow R_{1,1} && \text{Recovery from infection} && (5)\\
Y &\Rightarrow R_{1,0} && \text{Recovery from infection} && (6)\\
R_{0,1} &\Rightarrow I_{0,1} && \text{Infected with strain } I && (7)\\
R_{1,0} &\Rightarrow Y_{1,0} && \text{Infected with strain } Y && (8)\\
I_{0,1} &\Rightarrow R_{1,1} && \text{Recovery from infection} && (9)\\
Y_{1,0} &\Rightarrow R_{1,1} && \text{Recovery from infection} && (10)\\
& && && (11)
\end{aligned}$$

1.3 Equations

$$\dot{S} = -\left(\beta_{I_S,S} I_S + \beta_{I_V,S} I_V + \beta_{I_{0,1},S} I_{0,1} + \beta_{Y,S} Y + \beta_{Y_{10},S} Y_{10}\right) S \tag{12}$$

$$\dot{V} = -\left(\beta_{I_S,V} I_S + \beta_{I_V,V} I_V + \beta_{I_{0,1},V} I_{0,1}\right) V \tag{13}$$

$$\dot{I_S} = \left(\beta_{I_S,S} I_S + \beta_{I_V,S} I_V + \beta_{I_{0,1},S} I_{0,1}\right) S - \gamma_{I_S} I_S \tag{14}$$

$$\dot{I_V} = \left(\beta_{I_S,V} I_S + \beta_{I_V,V} I_V + \beta_{I_{0,1},V} I_{0,1}\right) V - \gamma_{I_V} I_V \tag{15}$$

$$\dot{Y} = \left(\beta_{Y,S} Y + \beta_{Y_{1,0},S} Y_{1,0}\right) S - \gamma_Y Y \tag{16}$$

$$\dot{R_{0,1}} = -\left(\beta_{I_S,R_{0,1}} I_S + \beta_{I_V,R_{0,1}} I_V + \beta_{I_{0,1},R_{0,1}} I_{01}\right) R_{0,1} + \gamma_Y Y \tag{17}$$

$$\dot{R_{1,0}} = -\left(\beta_{Y,R_{1,0}} Y + \beta_{Y_{1,0},R_{1,0}} Y_{1,0}\right) R_{1,0} + \gamma_{I_S} I_S \tag{18}$$

$$\dot{I_{0,1}} = \left(\beta_{I_S,R_{0,1}} I_S + \beta_{I_V,R_{0,1}} I_V + \beta_{I_{0,1},R_{0,1}} I_{01}\right) R_{0,1} - \gamma_{I_{0,1}} I_{0,1} \tag{19}$$

$$\dot{Y_{1,0}} = \left(\beta_{Y,R_{1,0}} Y + \beta_{Y_{1,0},R_{1,0}} Y_{1,0}\right) R_{1,0} - \gamma_{Y_{1,0}} Y_{1,0} \tag{20}$$

$$\dot{R_{1,1}} = \gamma_{I_V} I_V + \gamma_{I_{0,1}} I_{0,1} + \gamma_{Y_{1,0}} Y_{1,0} \tag{21}$$

As the equations sum to zero, one equation can be omitted. Hence, we define

$$R_{1,1} = 1 - S - V - I_S - I_V - I_{0,1} - Y - Y_{1,0} - R_{0,1} - R_{1,0} \tag{22}$$

1.4 Simplifying assumptions

We now assume that transmission rates $\beta_{a,b}$ are the product of a infectivity rate, α_a and a susceptivity rate, μ_b, i.e. $\beta_{a,b} = \alpha_a \mu_b$. This allows for a simplifcation of the system of differential equations:

$$
\begin{aligned}
\dot{S} &= -\mu_S (I_T + Y_T) S && (23)\\
\dot{V} &= -\mu_V I_T V && (24)\\
\dot{I_S} &= \mu_S I_T S - \gamma_{I_S} && (25)\\
\dot{I_V} &= \mu_V I_T V - \gamma_{I_V} I_V && (26)\\
\dot{Y} &= \mu_S Y_T S - \gamma_Y Y && (27)\\
\dot{R_{0,1}} &= -\mu_{R_{0,1}} I_T R_{0,1} + \gamma_Y Y && (28)\\
\dot{R_{1,0}} &= -\mu_{R_{1,0}} Y_T R_{1,0} + \gamma_{I_S} I_S && (29)\\
\dot{I_{0,1}} &= \mu_{R_{0,1}} I_T R_{0,1} - \gamma_{I_{0,1}} I_{0,1} && (30)\\
\dot{Y_{1,0}} &= \mu_{R_{1,0}} Y_T R_{1,0} - \gamma_{Y_{1,0}} Y_{1,0} && (31)
\end{aligned}
$$

where I_T and Y_T denote the infectious pressure of strain I and Y respectively, defined as:

$$
\begin{aligned}
I_T &= \alpha_{I_S} I_S + \alpha_{I_V} I_V + \alpha_{I_{0,1}} I_{0,1} && (32)\\
Y_T &= \alpha_Y Y + \alpha_{Y_{1,0}} Y_{1,0} && (33)
\end{aligned}
$$

A further assumption that infectivity is independent of the disease history of an individual could suggest a further simplification: With $\alpha_I = \alpha_{I_S} = \alpha_{I_V} = \alpha_{I_{0,1}}$ and $\alpha_Y = \alpha_{Y_{1,0}}$ we can write:

$$
\begin{aligned}
I_T &= \alpha_I \left(I_S + I_V + I_{0,1} \right) && (34)\\
Y_T &= \alpha_Y \left(Y + Y_{1,0} \right) && (35)
\end{aligned}
$$

2 Model simulations

In the following simulations, all recovery parameters are equal, $\gamma = \frac{1}{7}$ and all transmission parameters are equal, $\beta = \frac{2}{7}$.

2.1 Single strain epidemics

2.2 Single strain epidemics, with vaccination

2.3 Subsequent epidemics

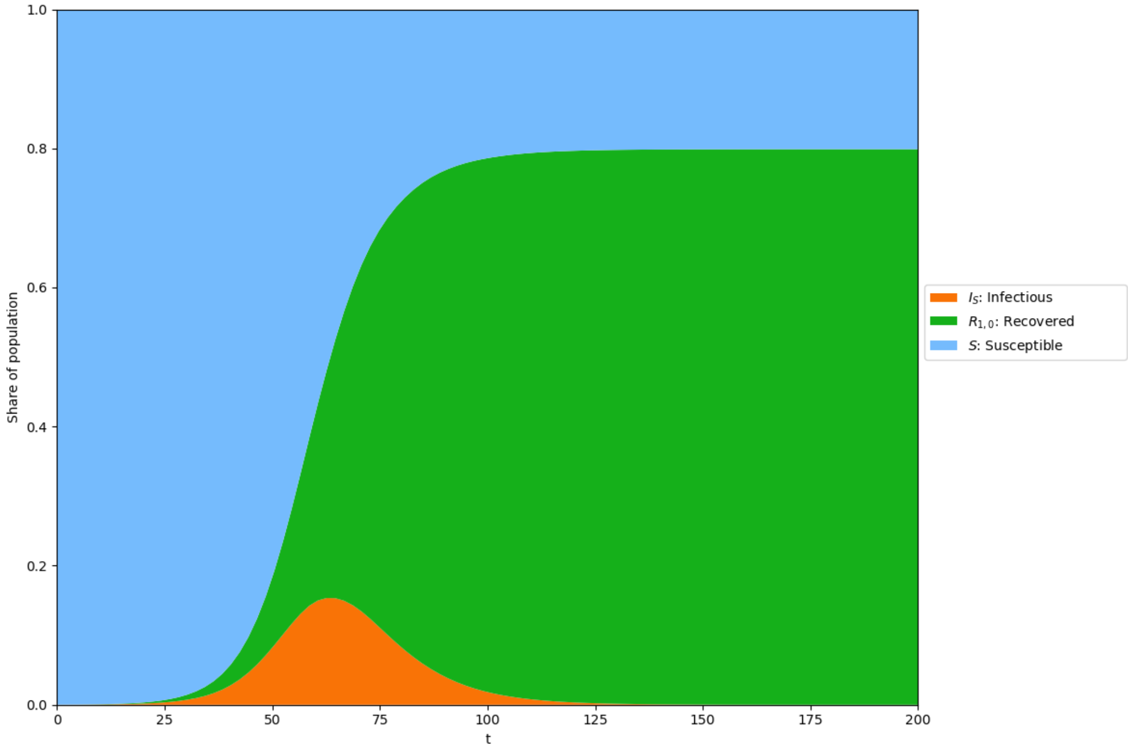

Figure 1: Single epidemic with strain Y. $I_S(0) = 0.0001$ and $S(0) = 1 - 0.0001$

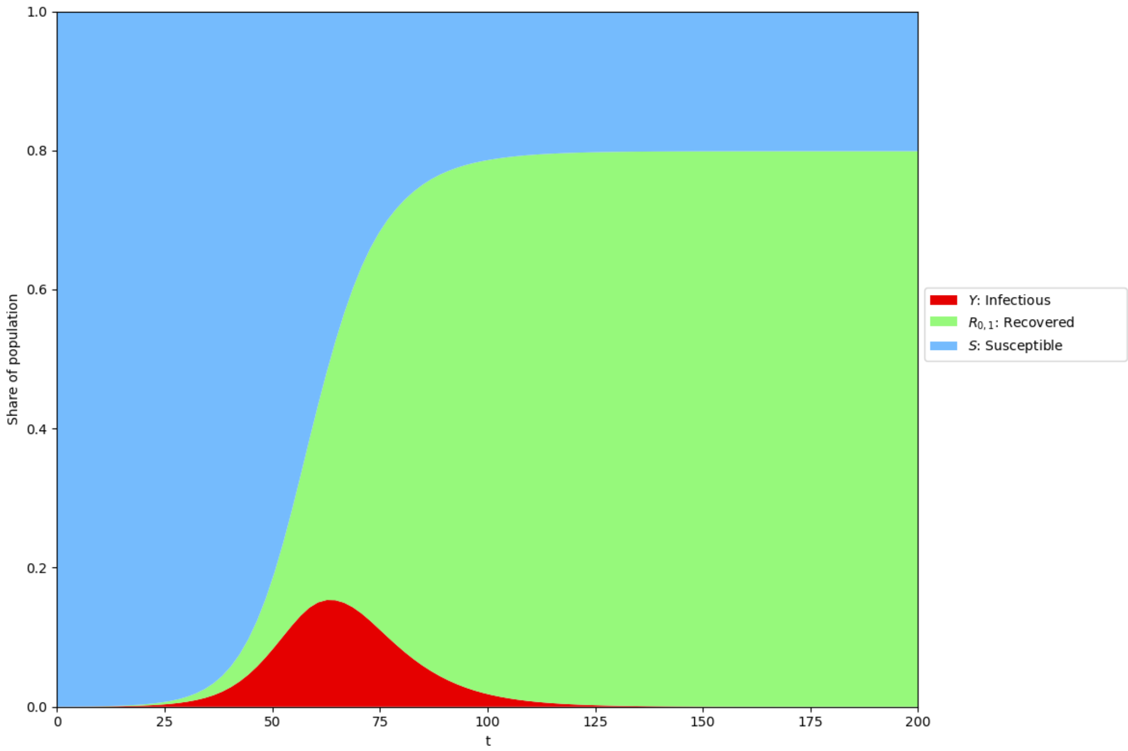

Figure 2: Single epidemic with strain Y. $Y(0) = 0.0001$ and $S(0) = 1 - 0.0001$

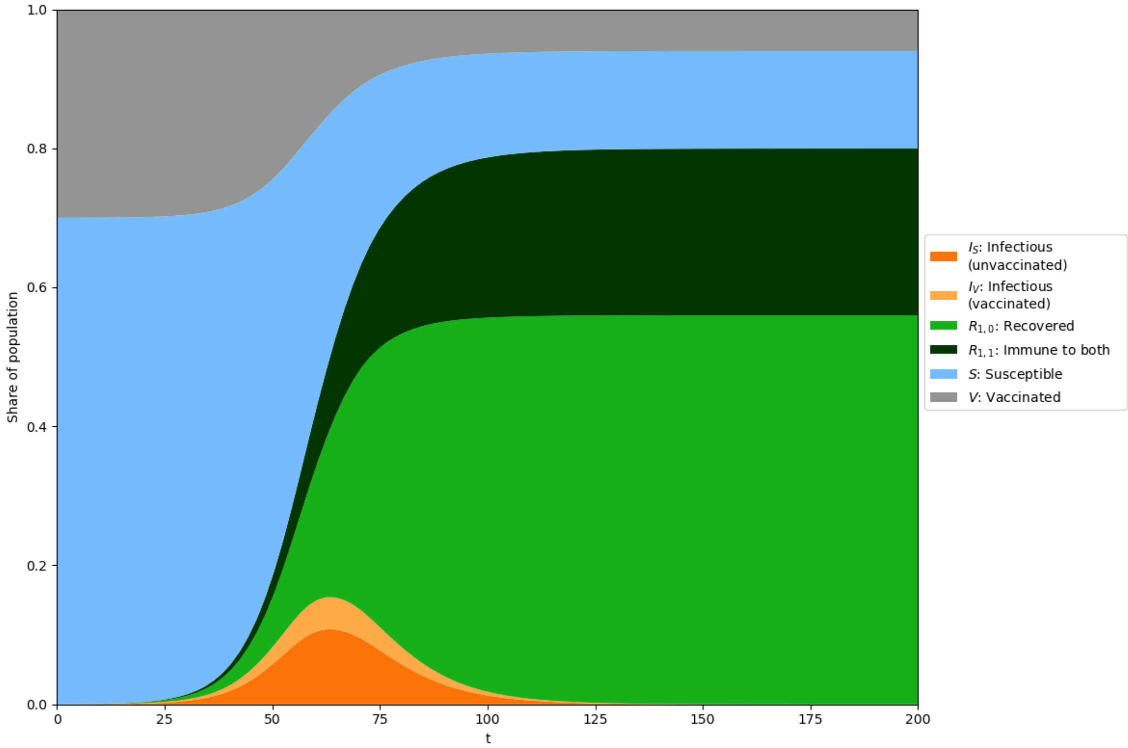

Figure 3: Single epidemic with strain Y. $I_S(0) = 0.0001$, $V(0) = 0.4$ and $S(0) = 1 - 0.4 - 0.0001 = 0.5999$

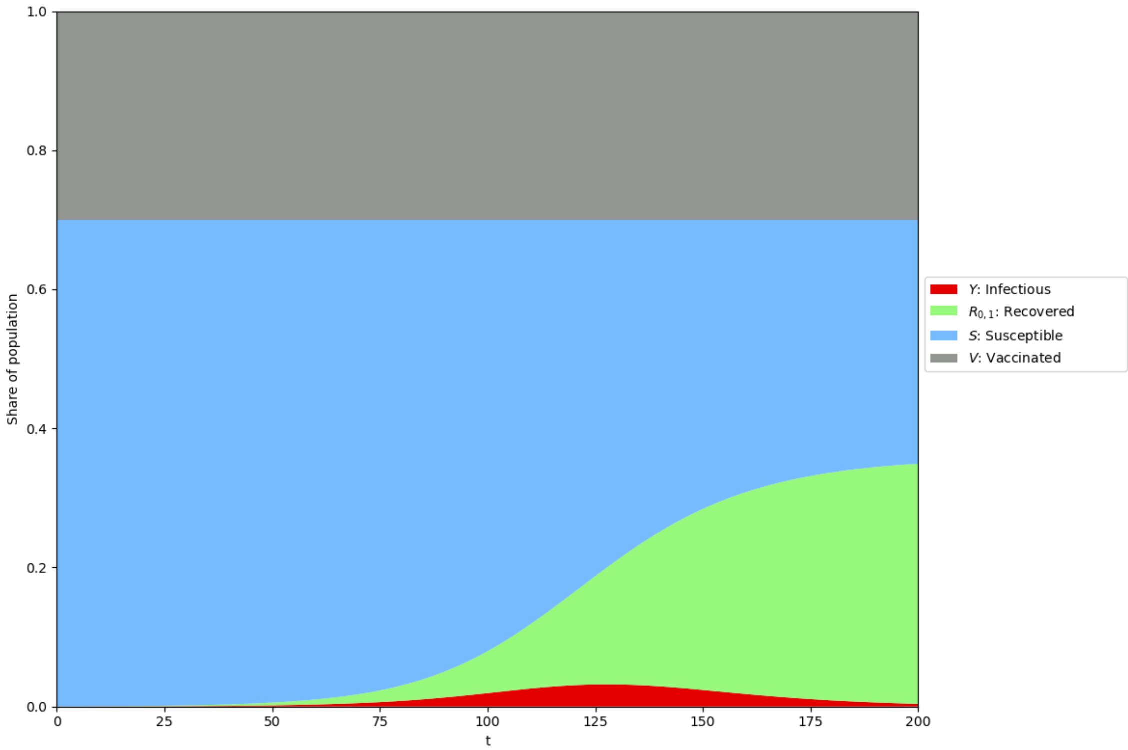

Figure 4: Single epidemic with strain Y. $Y(0) = 0.0001$, $V(0) = 0.4$ and $S(0) = 1 - 0.4 - 0.0001 = 0.5999$

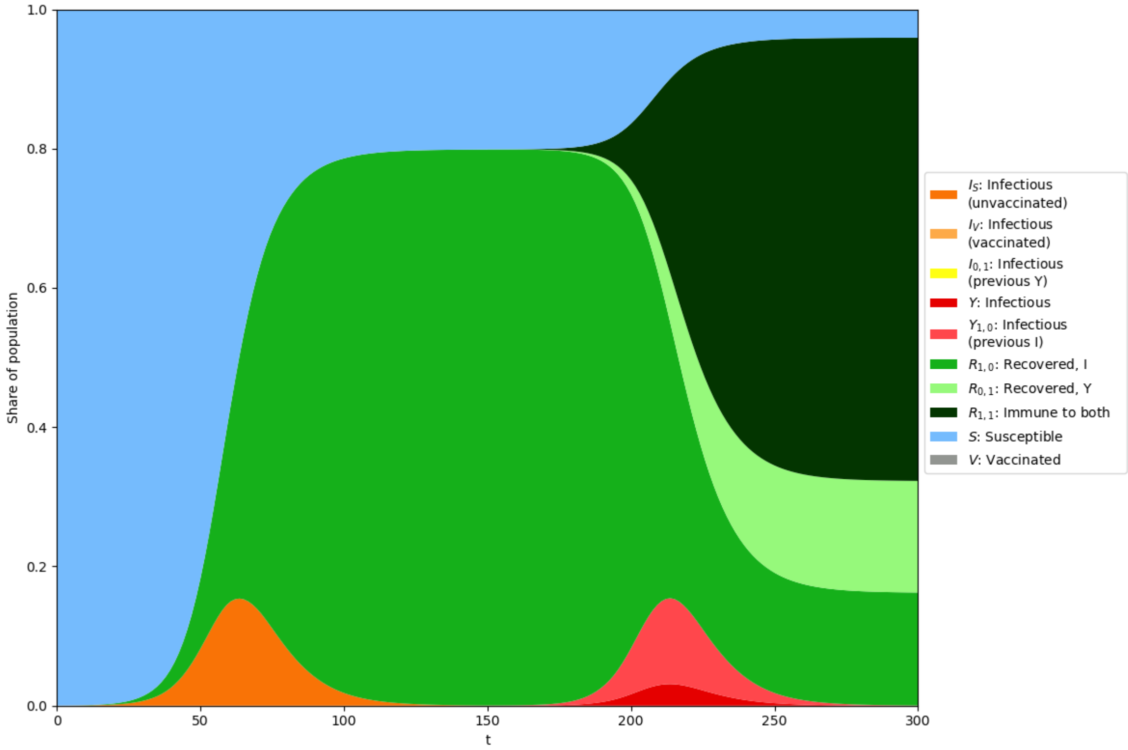

Figure 5: Subsequent epidemics, strain I then Y. $I_S(0) = 0.0001$ and $S(0) = 0.9999$. At time $t = 150$, 0.0001 is subtracted from S and added to Y.

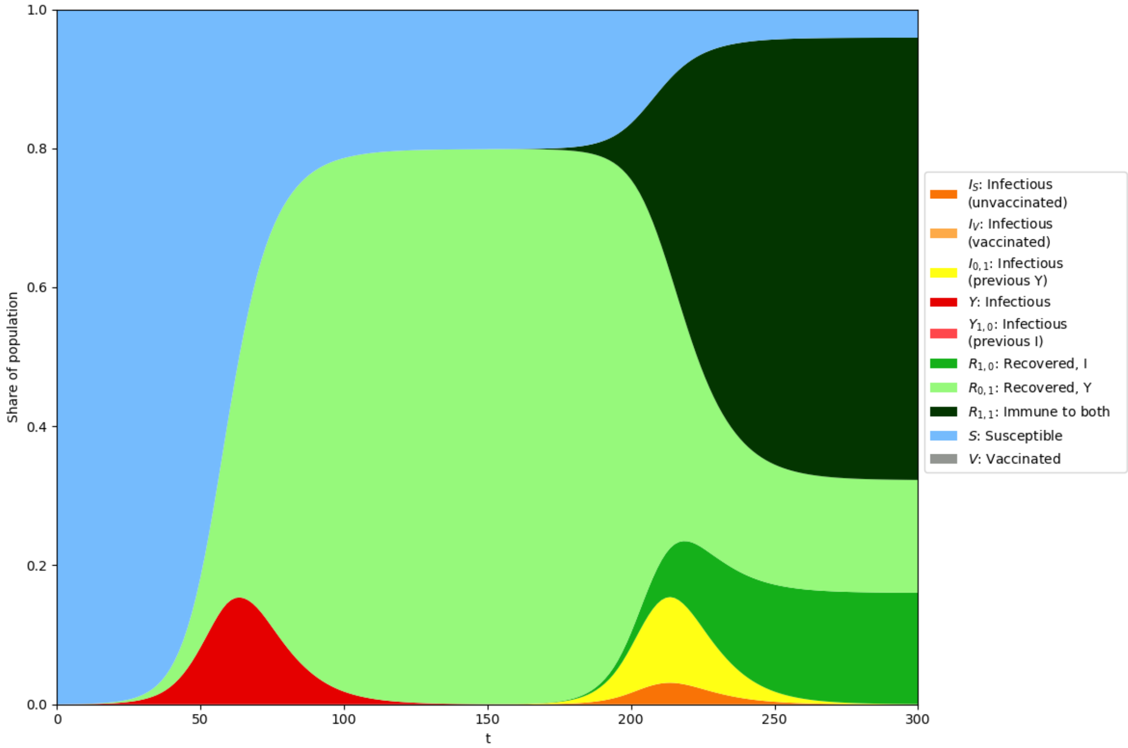

Figure 6: Subsequent epidemics, strain Y then I. $Y(0) = 0.0001$ and $S(0) = 0.9999$. At time $t = 150$, 0.0001 is subtracted from S and added to I.

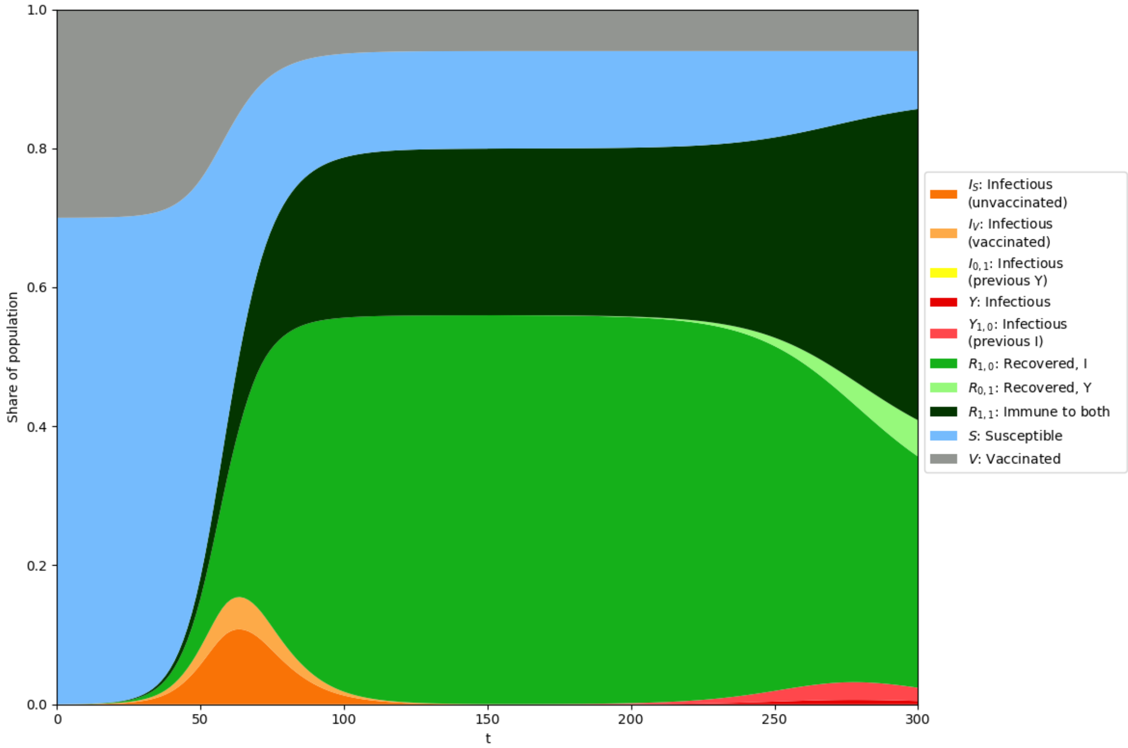

Figure 7: Subsequent epidemics, strain I then Y. $I_S(0) = 0.0001$, $V(0) = 0.4$ and $S(0) = 0.5999$. At time $t = 150$, 0.0001 is subtracted from S and added to Y.

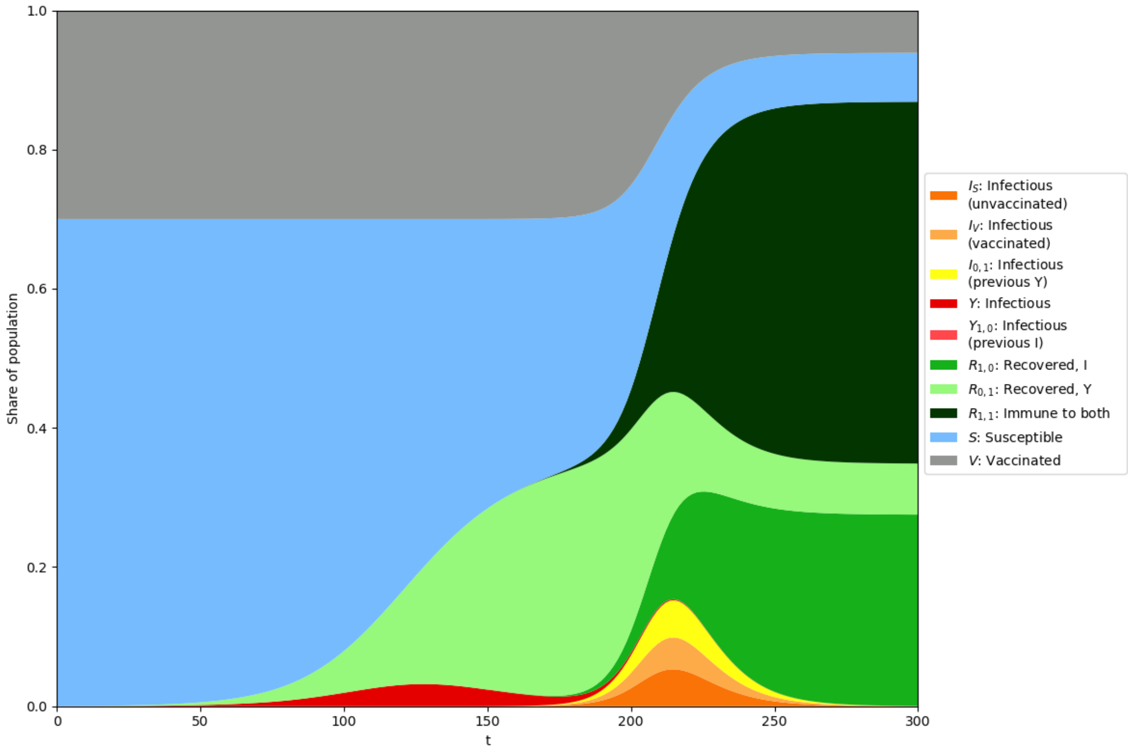

Figure 8: Subsequent epidemics, strain Y then I. $Y(0) = 0.0001$, $V(0) = 0.4$ and $S(0) = 0.5999$. At time $t = 150$, 0.0001 is subtracted from S and added to I.