1 Model-description

The considered model is based on the classic SIR-model, extended to consider two stages of exposed prior to infectivity and a pre-symptomatic stage. Furthermore, asymptomatic individuals are considered, as well as individuals quarantined due to testing. Symptomatic individuals are assumed to quarantine as well, and for simplicity, quarantine is asssumed to be perfect, i.e. quarantined individual do not contribute to the infectivity pressure. Testing is assumed to be performed for all groups, excluding symptomatic cases. Only second stage of exposed, pre-symptomatic and asymptomatic are assumed to be found positive, and hence testing does not affect other groups.

For purposes of analysis, we distinquish between recovered individuals that were quarantined due to testing and due to symptoms. However, we assume that all symptomatic cases get tested seperate from the testing considering within the model.

The full model formulation is given below:

$$\dot{S} = -\beta S(P + A) \tag{1}$$
$$\dot{E}_1 = \beta S(P + A) - \gamma E_1 \tag{2}$$
$$\dot{E}_2 = \gamma E_1 - \gamma E_2 - \tau E_2 \tag{3}$$
$$\dot{P} = \gamma E_2 - \gamma P - \tau P \tag{4}$$
$$\dot{I} = \gamma \rho P - \nu I \tag{5}$$
$$\dot{A} = \gamma(1 - \rho)P - \nu A - \tau A \tag{6}$$
$$\dot{Q} = \tau(E_2 + P + A) - \nu Q \tag{7}$$
$$\dot{R}_p = \nu Q + \nu I \tag{8}$$
$$\dot{R}_n = \nu A \tag{9}$$

Variables are scaled by population, such that $S + E_1 + E_2 + P + I + A + Q + R_p + R_n = 1$. Furthermore, one differential equation can in general be omitted as the full system sums to unity.

Table 1:

S	susceptible	E_1, E_2	Exposed
P	Pre-symptomatic	I	Infectious (symptomatic, quarantined)
A	Asymptomatic	Q	Quarantined (due to test)
R_p	Recovered, with positive test	R_n	Recovered, no positive test
β	Infecitivity	γ	Rate of disease progression
ν	Rate of recovery	ρ	Fraction of symptomatic cases
τ	Rate of testing (effective)		

2 Model analysis

2.1 Definitions and epidemic isolines

The final size of an epidemic can be defined in terms of the proportion of the population that remains susceptible as time approaches infinity. We define σ such that $S(t) \underset{t \to \infty}{\to} \sigma$. Similarly, the final size of the recovered population that were found positive through testing is defined as $R_p(t) \underset{t \to \infty}{\to} r_p$. Correspondingly, $R_n(t) \underset{t \to \infty}{\to} r_n$. We define the total recovered population, $r_{tot} = r_p + r_n$ and note that $r_{tot} + \sigma = 1$.

Figure 1 below, the bottom panel shows r_{tot}, as a function of model-parameters β and τ. In the top panel, r_p is shown. Parts where $r_{tot} < 0.2$ are omitted in both plots.

From the bottom panel of figure 1 we note that there exists combinations of β and τ that yield the same final size of the epidemic. These exists along the contours given in the bottom panel of figure 1. This corresponds to the notion that testing effectively reduces the effective reproduction number. In the perspective of epidemic mitigation, this suggest that a disease with high infectivity (i.e. high β) requires a high level of testing to yield a final epidemic size comparable to a less infectious disease with lower levels of mitigation. If β describes the effective infectivity arising from different types of epicemic mitigation, the implication is that increased testing can make up a reduction in another unspecified part of the mitigation. This model behaviour is expected and follows trivially from the model design of testing reducing infection pressure. We refer to the lines of equal final size as epidemic isolines.
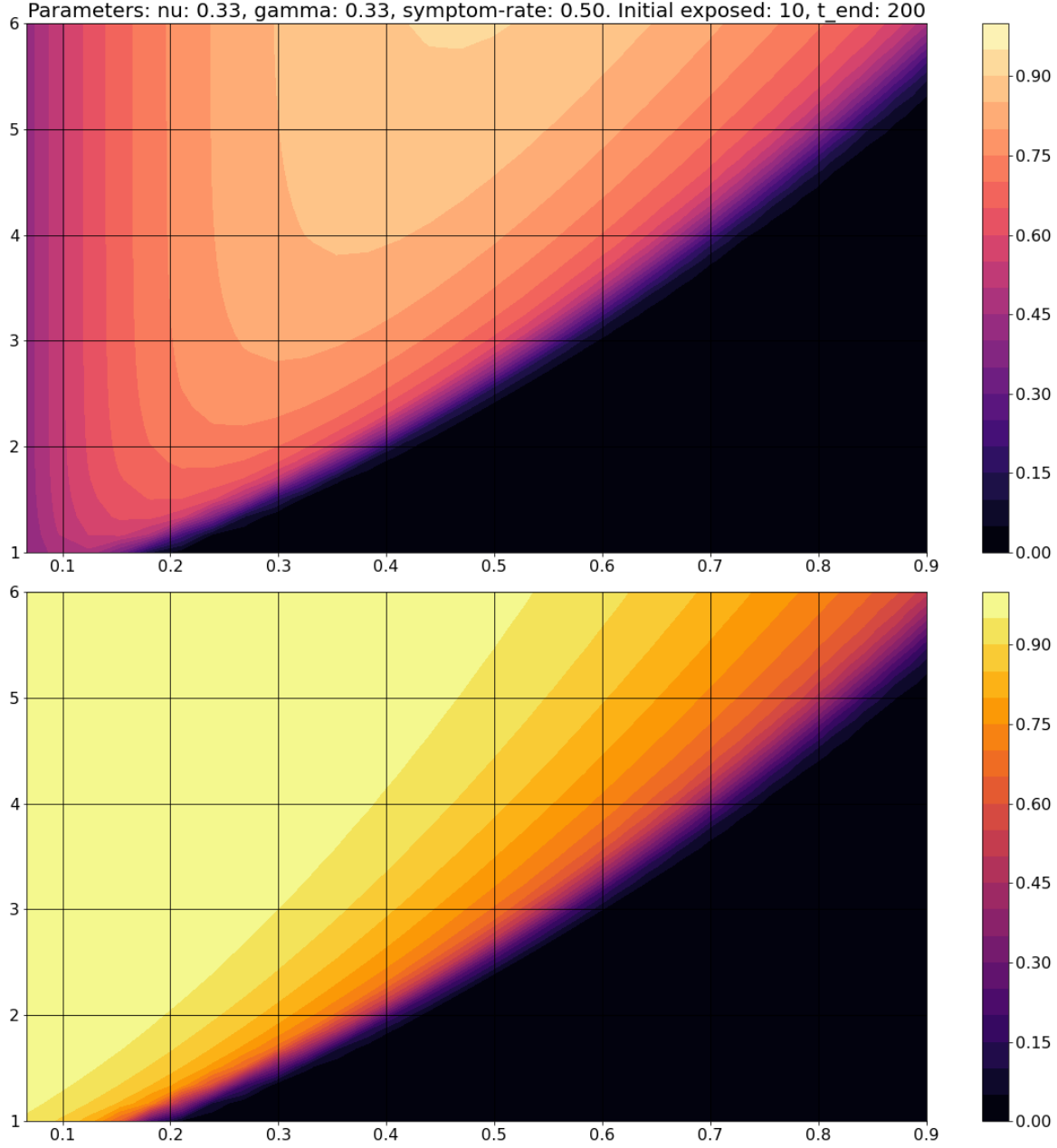
Figure 1:

While the final size is equal along an epidemic isoline, the number of infections identified by testing varies, as observed in the top panel of figure 1. We aim to investigate the relation between the intensity of testing, as given by parameter τ, and the proportion of recovered individuals that were identified. We define the latter as $\theta = \frac{r_p}{r_{tot}}$. In figure 2 we show θ for the same range of β and τ as in figure 1. The epidemic isolines are shown as red contourlines. Situations where $r_{tot} < 0.2$ are shown in grey for clarity.

2.2 Characterization of epidemic isolines

The relationship between a given testing intensity, τ and the infectiousness β which yield final epicemic sizes along a epidemic isoline can be investigated analytically. In practice, this allows for describing the isolines implicitly for a given final size. In turn this allows us to describe the proportion of recovered infections that were identified for a given testing intensity, under the assumption that final epidemics size was unchanged.

Similar to the calculations of Andreasen (2018), we consider the following quantities based on the system of differential equations given in equations (2)
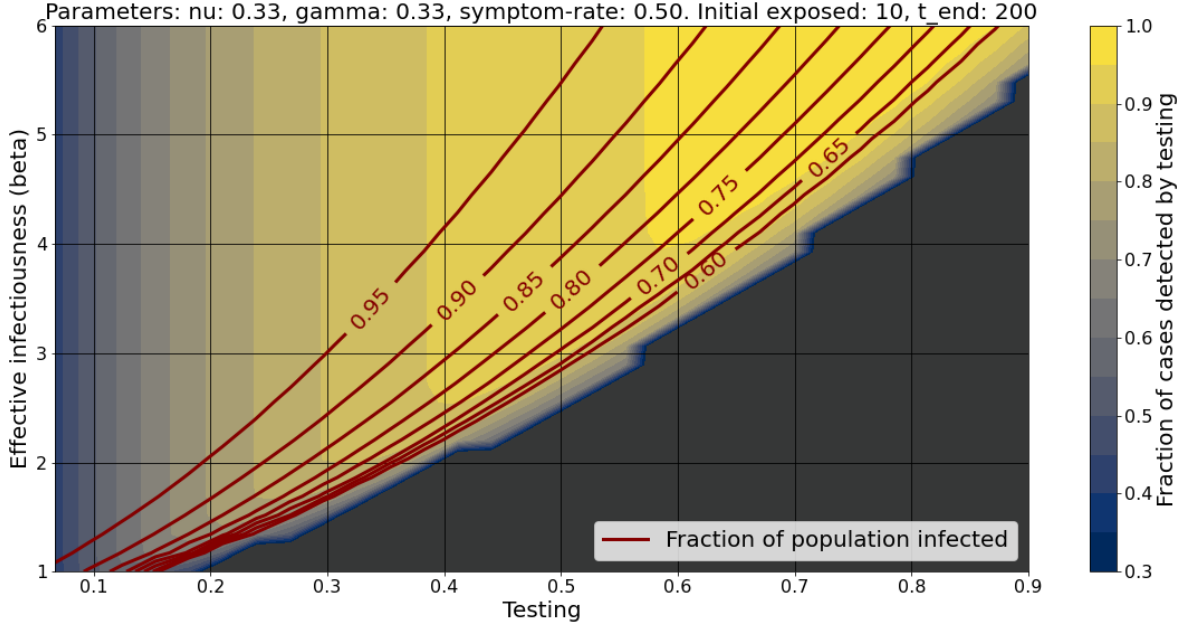
Figure 2: Figure tex

$$\dot{S}/S = -\beta(P + A) \tag{10}$$

$$\dot{S} + \dot{E}_1 + \dot{E}_2 = -(\gamma + \tau)E_2 \tag{11}$$

$$\dot{S} + \dot{E}_1 + \dot{E}_2 + \dot{P} = -(\gamma + \tau)P - \tau E_2 \tag{12}$$

$$\dot{S} + \dot{E}_1 + \dot{E}_2 + \dot{P} + \dot{A} = -(\nu + \tau)A - (\gamma\rho + \tau)P - \tau E_2 \tag{13}$$

For simplicity, we assume that at time $t = 0$, all variables except S and E_1 are zero. As t approaches infinity, the stability of the systems implies that all variables apart from S, R_p and R_n are zero.

For notational purposes, we define for each variable x, the integral over the full epidemic as $T_x = \int_0^\infty x \, dt$. Integrating the equations above over the entire epidemic yields:

$$\log \sigma = -\beta(T_P - T_A) \tag{14}$$

$$\sigma - S_0 - E_{1,0} = -(\gamma + \tau)T_{E_2} \tag{15}$$

$$\sigma - S_0 - E_{1,0} = -(\gamma + \tau)T_P - \tau T_{E_2} \tag{16}$$

$$\sigma - S_0 - E_{1,0} = -(\nu + \tau)T_A - (\gamma\rho + \tau)T_P - \tau T_{E_2} \tag{17}$$

Where S_0 and $E_{1,0}$ are initial conditions for $S(t)$ and $E_1(t)$ respectively. In the limit where $S_0 \to 1$ and $E_{1,0} \to 0$, we can rewrite:

$$\log \sigma = -\beta(T_P - T_A) \tag{18}$$

$$\sigma = 1 - (\gamma + \tau)T_{E_2} \tag{19}$$

$$\sigma = 1 - (\gamma + \tau)T_P - \tau T_{E_2} \tag{20}$$

$$\sigma = 1 - (\nu + \tau)T_A - (\gamma\rho + \tau)T_P - \tau T_{E_2} \tag{21}$$

Assuming $T_P + T_A \neq 0$, this can be written as:

$$\beta = \frac{-\log \sigma}{T_P + T_A} \tag{22}$$

$$T_{E_2} = \frac{1}{\gamma + \tau}(1 - \sigma) \tag{23}$$

$$T_P = \frac{1}{\gamma + \tau}(1 - \sigma - \tau T_{E_2}) \tag{24}$$

$$T_A = \frac{1}{\nu + \tau}(1 - \sigma - (\gamma\rho + \tau)T_P - \tau T_{E_2}) \tag{25}$$

Furthermore, observe that integrating $\dot{R}_n = \nu A$ from $t = 0$ to $t = \infty$ yields $r_n = \nu T_A$.

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2.3 Explicit expression for ratio of positive

Combining the above equations reveal that

$$\frac{r_p}{r_p + r_n} = 1 - \frac{\nu}{1 - \sigma} T_A \tag{26}$$

$$\frac{r_p}{r_p + r_n} = 1 - \left(\frac{\nu}{\nu + \tau}\right)\left(1 - \frac{\tau}{\gamma + \tau}\right)\left(1 - \frac{\gamma\rho + \tau}{\gamma + \tau}\right) \tag{27}$$

Note that this expression is independent of σ.

Furthermore, in the absence of tests, i.e. for $\tau = 0$, the expression becomes $\frac{r_p}{r_p + r_n} = 1 - 1(1 - 0)(1 - \rho) = \rho$.

This is expected, as only the symptomatic cases, I, are found in the situation where $\tau = 0$, and the symptomatic cases make up exactly ρ of all cases.

3 Numeric examples

As an example, we consider $\nu = \gamma = \frac{1}{3}$ and $\rho = 0.5$. Setting $\sigma = 0.2$, and considering a range of τ between 0 and 1, we determine the corresponding values of β using the equations above. The (τ, β)-pairs give an epidemic isoline corresponding to $1 - \sigma = 0.8$. This line is depicted in figure 3 below. In the figure, inset axes show time-series of $R_p(t)$ and $R_n(t) + R_p(t)$ obtained from numerical integration.
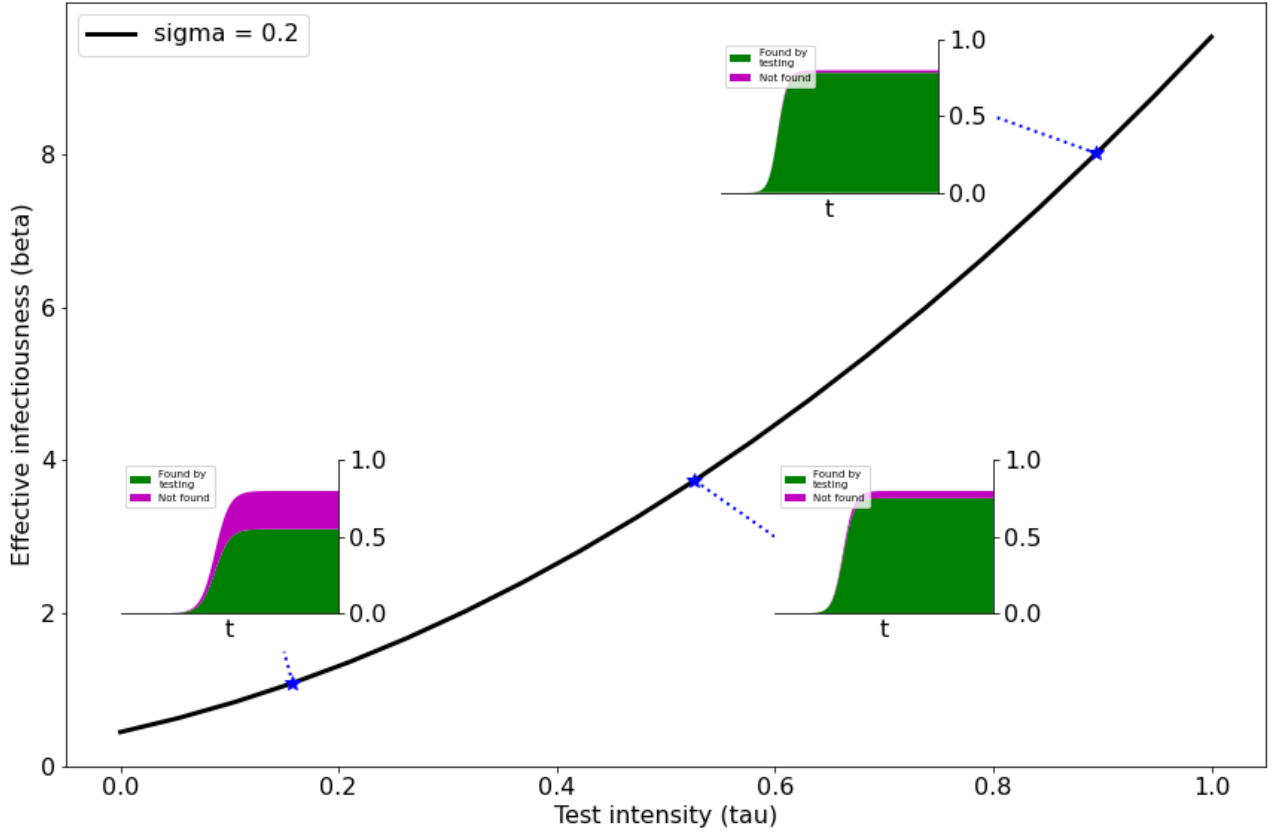

Figure 3:

We perform numerical integration for a range of (τ, β)-pairs along the epidemic isoline. The resulting final values of $R_p(t)$ and $R_n(t) + R_p(t)$ are given in figure 4.
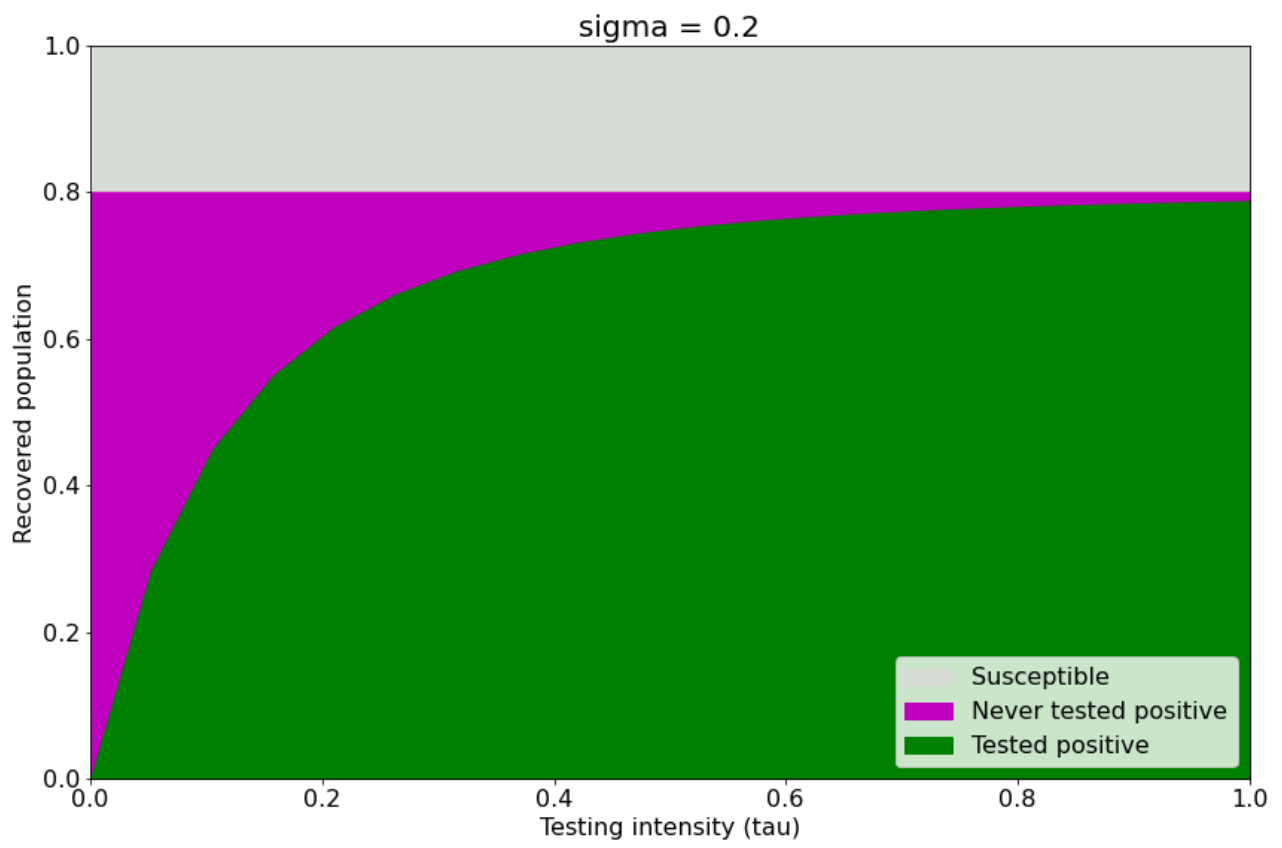
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Figure 4: