homogeneous_approximation

July 27, 2023

1 SEIR limit

If we set $\beta_B = 0$ and $\gamma = 0$ we should recover the classical SEIR model in which the epidemic threshold can be estimated following the next-generation matrix approach as Diekmann et al.:

$$F = \begin{pmatrix} 0 & \beta_W \\ 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} -\epsilon & 0 \\ \epsilon & -\mu \end{pmatrix}$$

So that:

$$V^{-1} = \begin{pmatrix} -1/\epsilon & 0 \\ -1/\mu & -1/\mu \end{pmatrix}$$
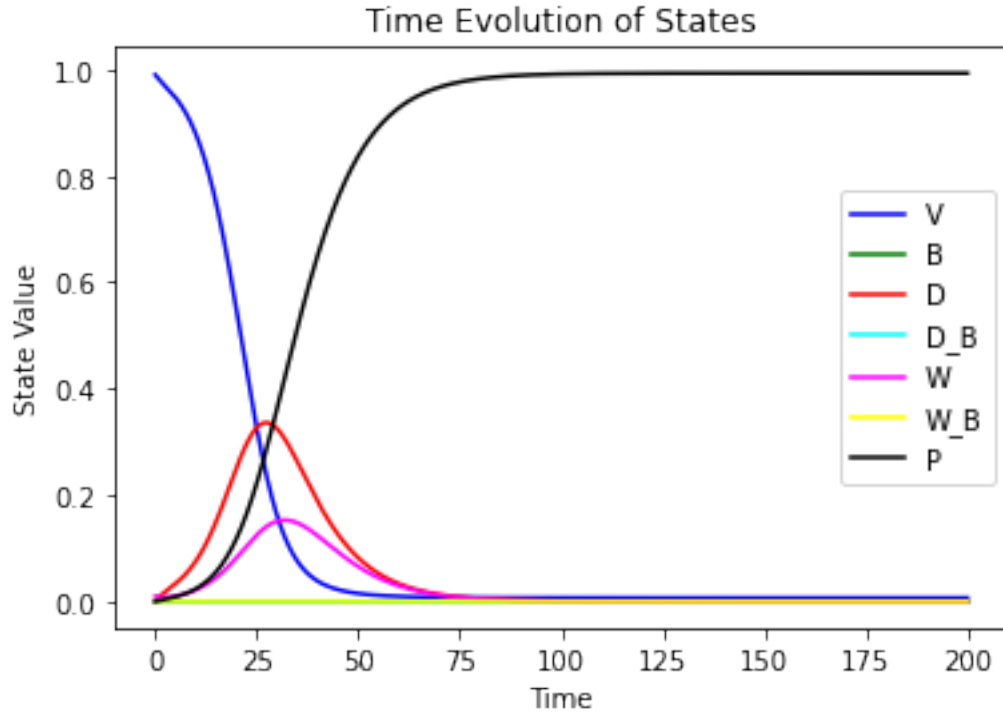
And:

$$FV^{-1} = \begin{pmatrix} \beta_W/\mu & \beta_W/\mu \\ 0 & 0 \end{pmatrix}$$
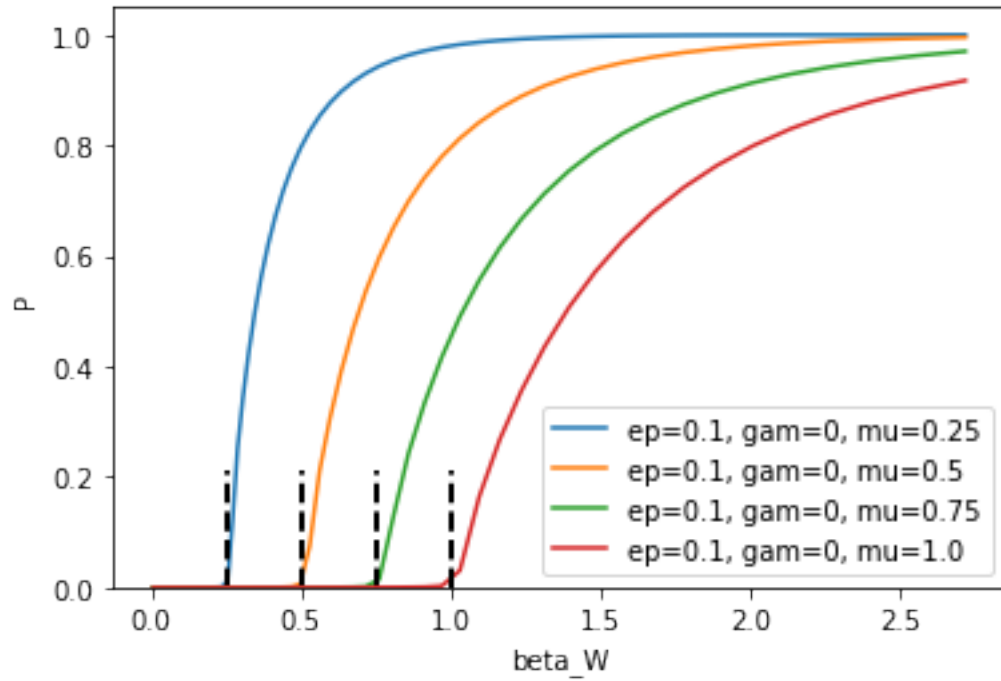
So that the spectral radius is:
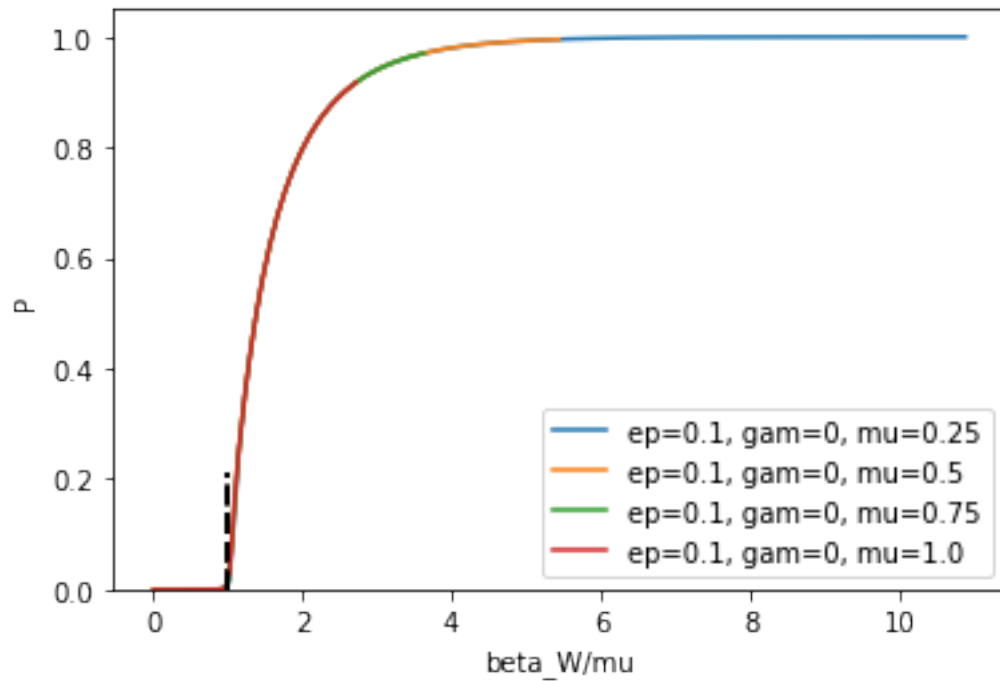
$$R_0 = \rho(-FV^{-1}) = \frac{\beta}{\mu}$$

First, we check the time evolution of the system for this limit with $\beta_W = 1$, $\epsilon = 0.1$ and $\mu = 0.2$.

Now we study the final fraction of P as a function of β and some values of μ with fixed ϵ, together with the theoretical epidemic threshold.
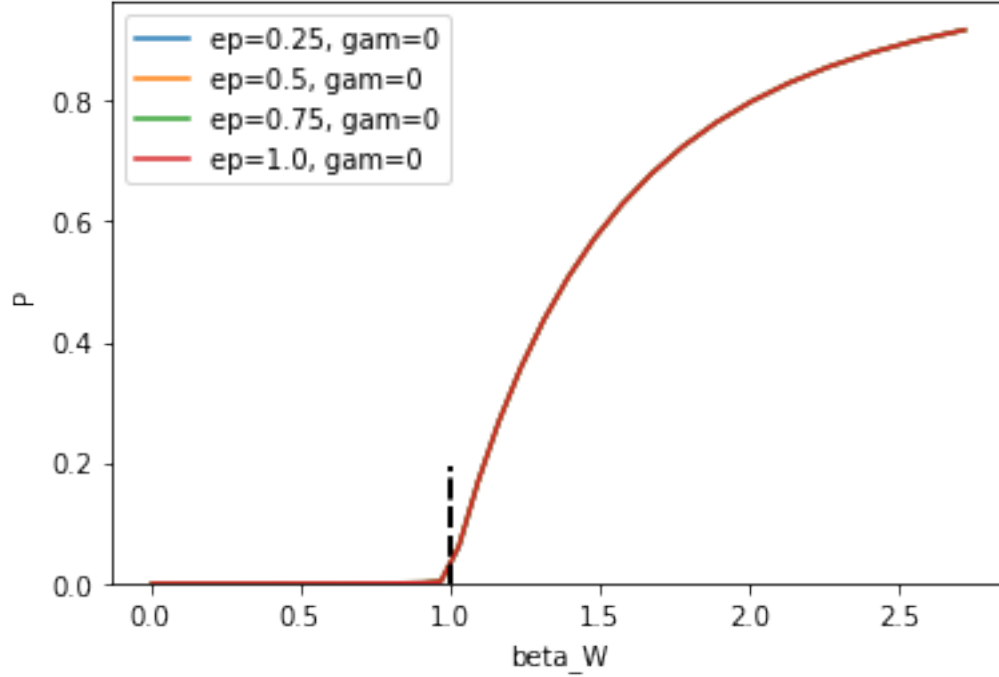
As expected, it seems that the threshold varies proportionally to μ, so that we can plot the same diagram as a function of β/mu instead.

In fact, we can always rescale time in terms of μ. Hence, from now own we will work always in units of μ.

Let's now look at how this changes as a function of epsilon.

As expected, the threshold is not affected by the value of ϵ. Furthermore, neither is the overall shape.

2   SEIR with latent death

If we now set $\gamma \neq 0$, it is equivalent to a SEIR model in which people in the latent state can spontaneously recover/die. The epidemic threshold in this case can be computed as:

$$F = \begin{pmatrix} 0 & \beta_W \\ 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} -\epsilon - \gamma & 0 \\ \epsilon & -\mu \end{pmatrix}$$

So that:

$$V^{-1} = \begin{pmatrix} -1/(\epsilon + \gamma) & 0 \\ -\epsilon/[(\epsilon + \gamma)\mu] & -1/\mu \end{pmatrix}$$
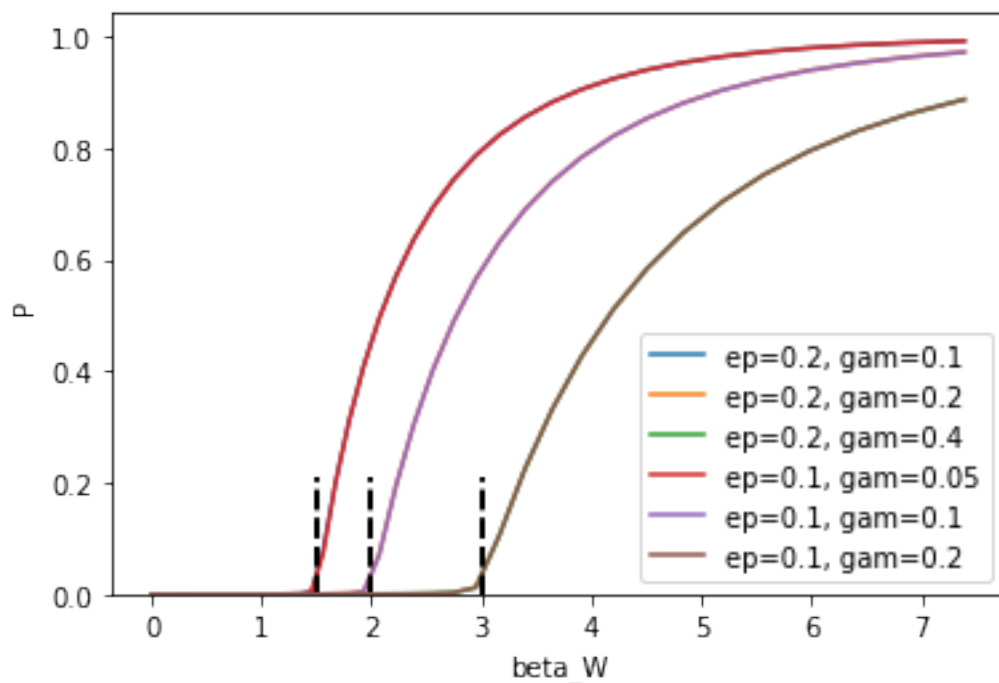
And:

$$FV^{-1} = \begin{pmatrix} \beta_W \epsilon/[(\epsilon + \gamma)\mu] & \beta_W/\mu \\ 0 & 0 \end{pmatrix}$$

So that the spectral radius is:

$$R_0 = \rho(-FV^{-1}) = \frac{\beta}{\mu} \cdot \frac{\epsilon}{\epsilon + \gamma}$$

Thus, we now see that the epidemic threshold not only depends on the value of γ but also on the value of ϵ, which had dissapeared previously. In fact, we can show that it actually depends on the ratio between these quantities.

$$R_0 = \frac{\beta}{\mu} \cdot \frac{\epsilon/\gamma}{\epsilon/\gamma + 1} \equiv \frac{\beta}{\mu} \frac{\epsilon'}{\epsilon' + 1}$$
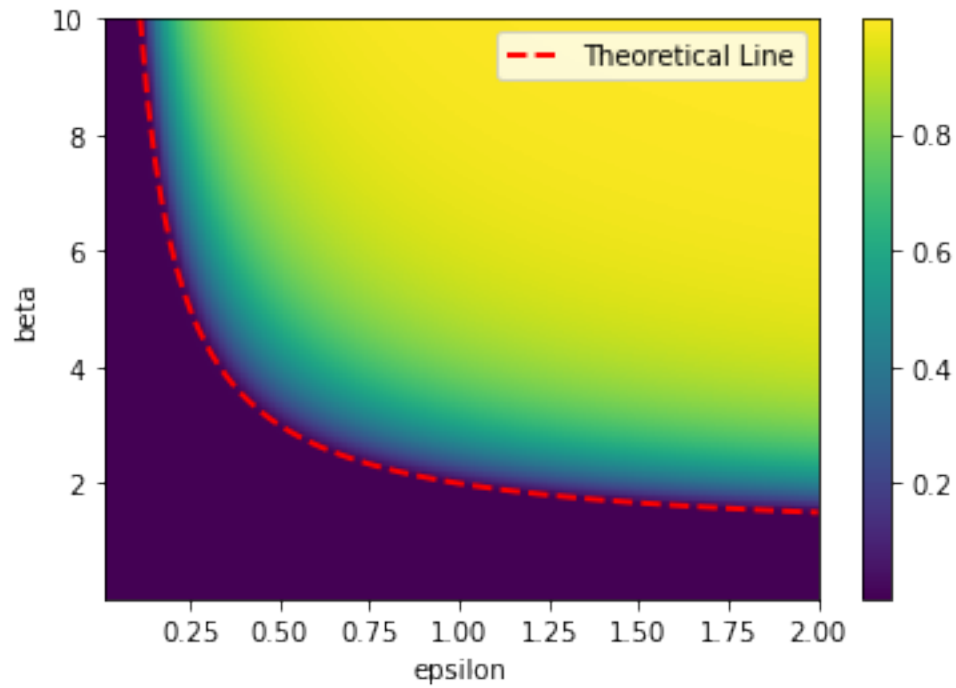

We see that, indeed, the evolution only depends on the fraction $\epsilon' \equiv \epsilon/\gamma$. Thus, we can conclude that the system can be simply studied in the β, ϵ'.
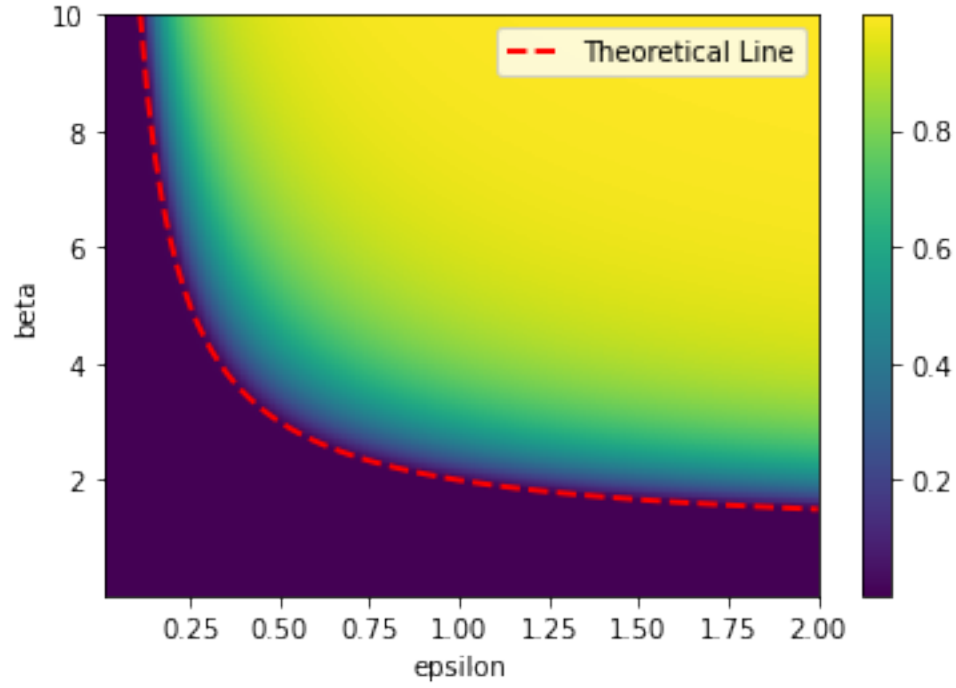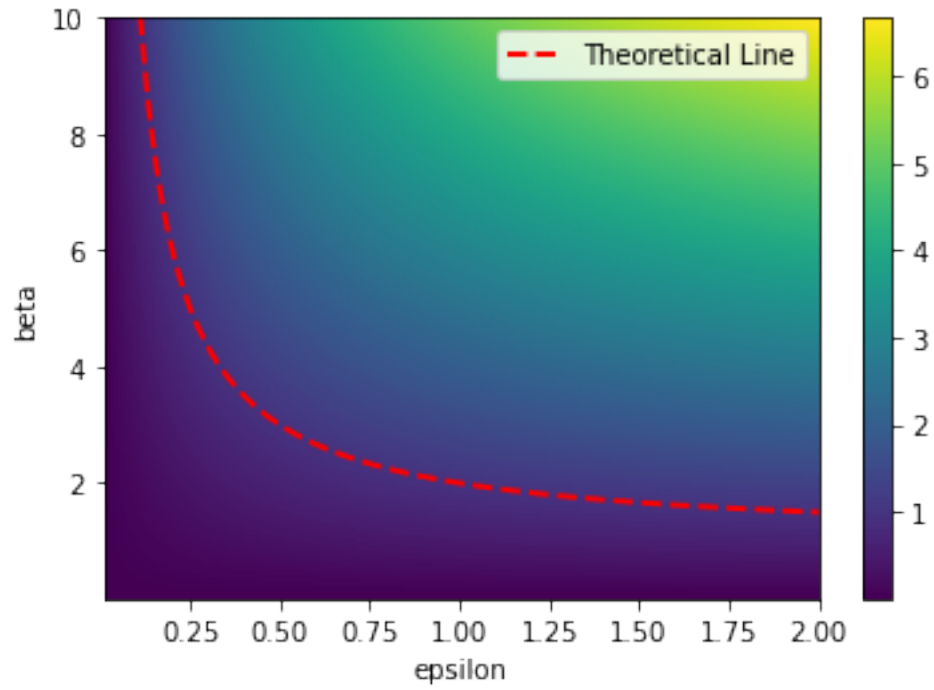
3 Complete model

Since both infections are completely independent, adding the black worm should not alter the diagram. In the following, we reproduce this last 2D diagram but setting $\beta_B \neq 0$.
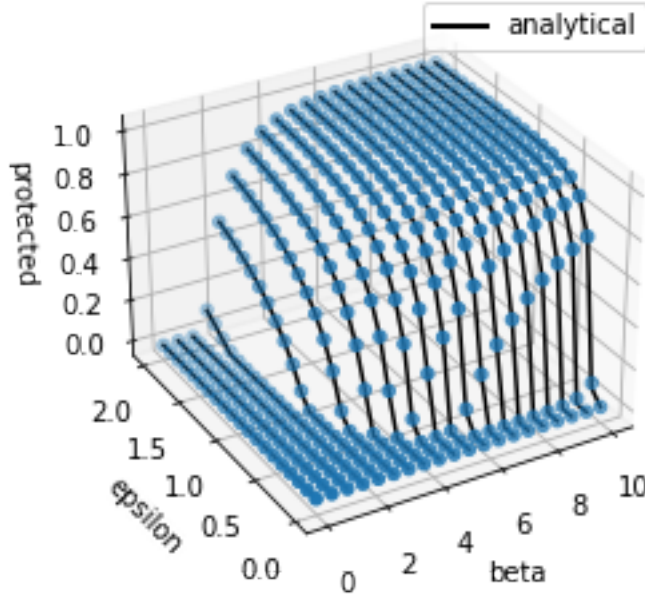
We can also plot the diagram for R_0.

We can use these values to test what is the final fraction of the population in the B state given that the final fraction of recovered people in the SEIR model is given by Britton et al.:

$$\rho_P = 1 - e^{-R_0 \rho_P}$$

We can compare the values from this equation to the numerical solutions of the model.

The last elements of the model are the maximum fraction of the population in the B state and the time window in which said fraction is above a certain threshold.

Actually, we can estimate for which set of parameters the white worm will completely prevent the creation of a botnet. For the black worm, if we are near the disease-free state, we can approximate its evolution as Ma:

$$\dot{\rho}_B \approx \beta_B \rho_B$$

So that in the early phase of the outbreak the size of the botnet will grow as:

$$\rho_B(t) = \rho_B(0)e^{\beta t}$$

In other words, the size of the outbreak grows at rate β_B.

Similarly, for the white worm, in the early phase of the infection we have:

$$\dot{\rho}_D \approx \beta_W \rho_W - (\epsilon + \gamma)\rho_D$$
$$\dot{\rho}_W \approx \epsilon \rho_D - \mu \rho_W$$

So that the jacobian is:

$$J = \begin{bmatrix} -(\epsilon + \gamma) & \beta_W \\ \epsilon & -\mu \end{bmatrix}$$

And its eigenvalues, since it is a 2x2 matrix, can be easily obtained using its trace:

8

$$\lambda = \frac{tr(J) \pm \sqrt{(tr(J))^2 - 4\det(J)}}{2}$$

$$\Rightarrow \lambda = \frac{-(\epsilon + \gamma + \mu) \pm \sqrt{(-(\epsilon + \gamma + \mu))^2 - 4[(\epsilon + \gamma)\mu - \beta_W \epsilon]}}{2}$$
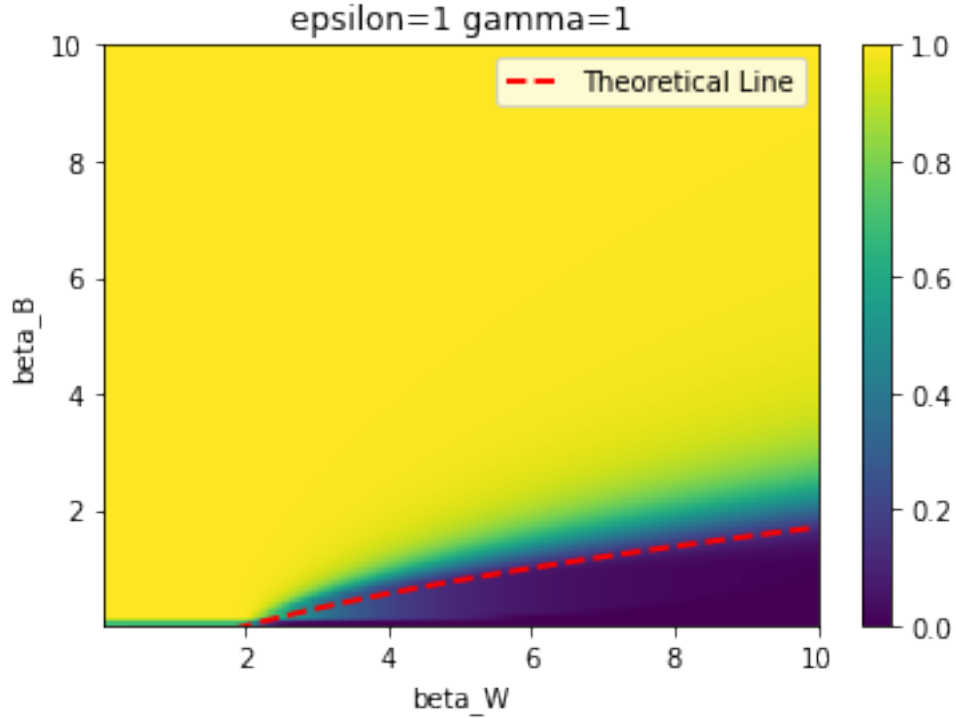
$$\lambda = \frac{-(\epsilon + \gamma + \mu) + \sqrt{(\epsilon + \gamma)^2 + \mu^2 + 2(\epsilon + \gamma)\mu - 4(\epsilon + \gamma)\mu + 4\beta_w \epsilon}}{2}$$
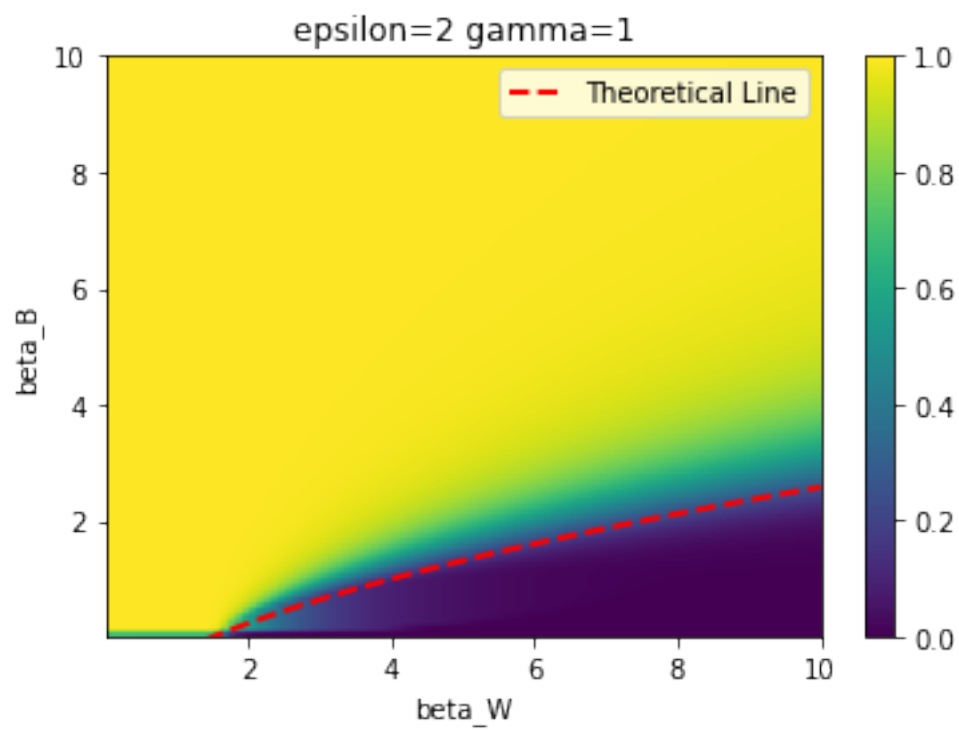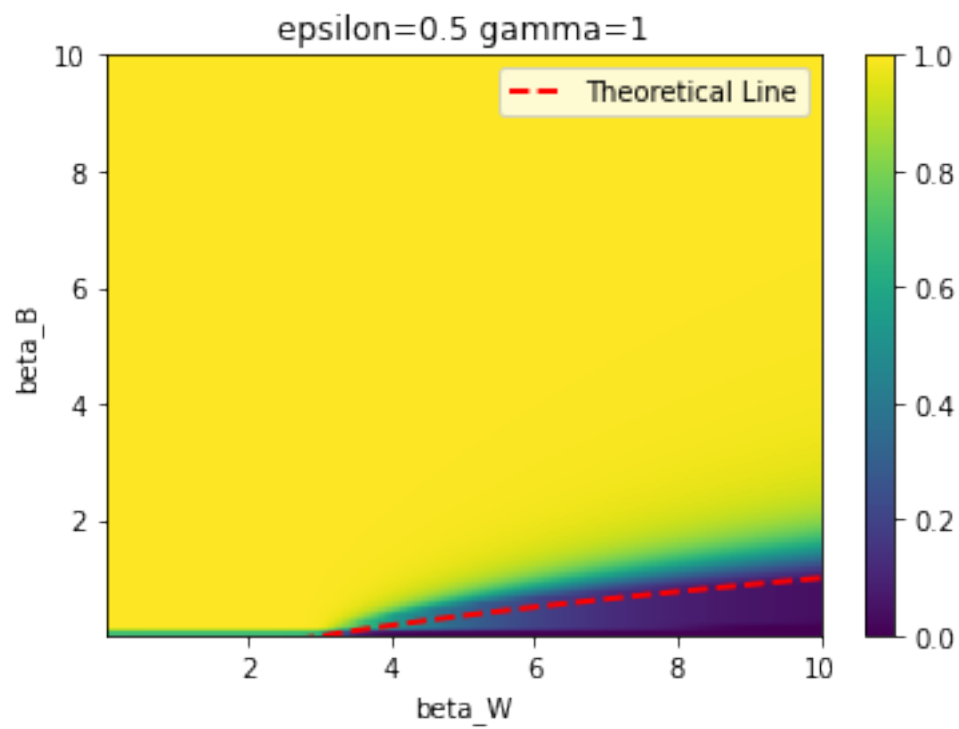
$$\lambda = \frac{-(\epsilon + \gamma + \mu) + \sqrt{(\epsilon + \gamma - \mu)^2 + 4\beta_w \epsilon}}{2}$$
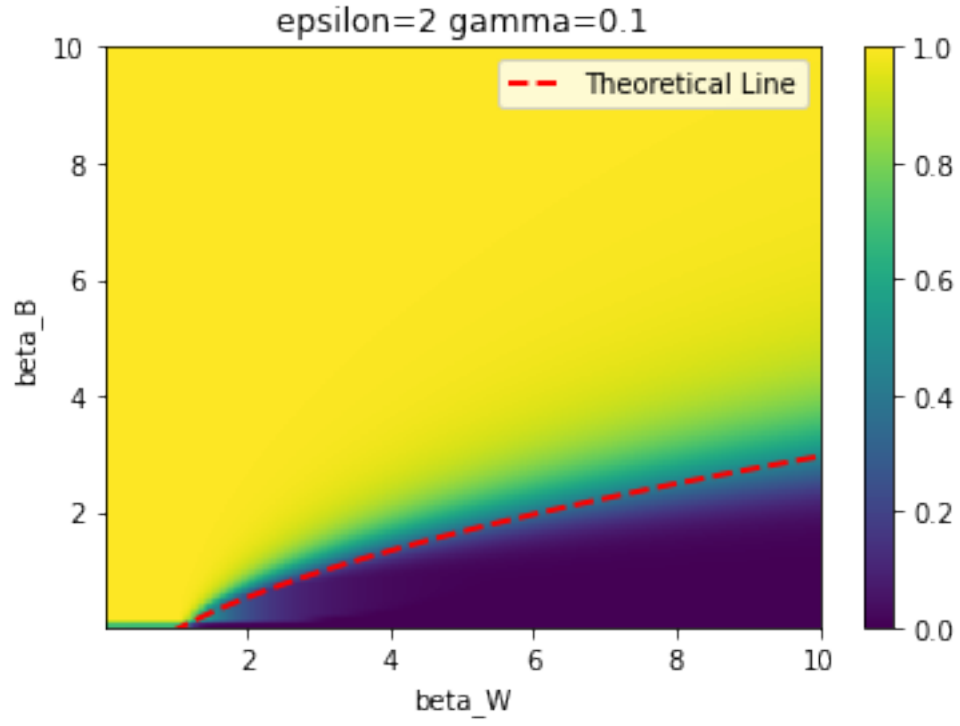
So that the botnet can only grow if

$$2\beta_B > -(\epsilon + \gamma + \mu) + \sqrt{(\epsilon + \gamma - \mu)^2 + 4\beta_W \epsilon}$$

We can test this expression by studying the size of the botnet as a function of β_B and β_W for several values of ϵ and γ (since we can set $\mu = 1$ as previously discussed).

epsilon=0.5 gamma=1

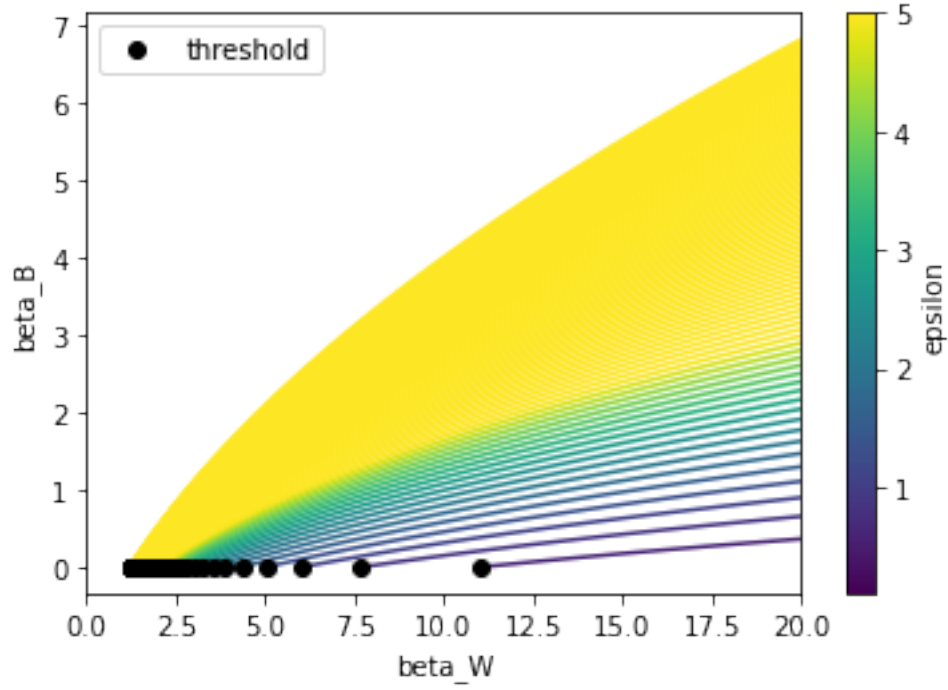

epsilon=2 gamma=1

epsilon=2 gamma=0.1

Given that the approximation works very well, we can focus on studying this threshold since it is the one that will ensure us that the botnet will not exist at any point. This way, we can easily explore its evolution for different values of ϵ and γ.
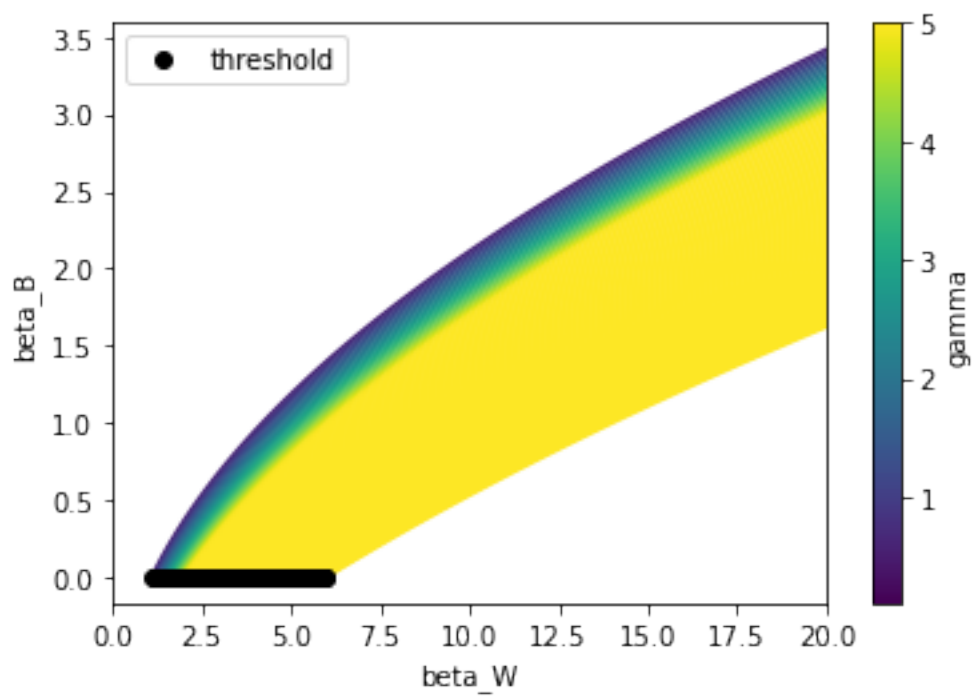
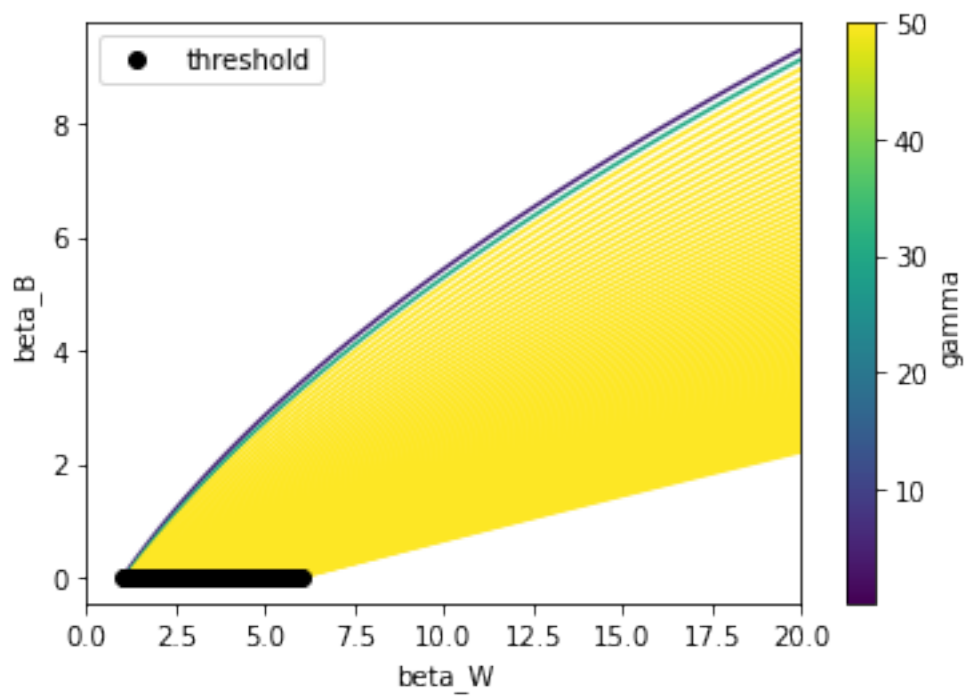In the following, we explore the model with $\gamma = 1$.

As we can see, the smaller the value of ϵ, the larger β_W has to bee to prevent the appearance of a botnet. In the limit in which $\epsilon \to \infty$ we should recover the SIR model in which the growth rate is simply $\beta_W - \mu$. Thus, the botnet may be prevented if $\beta_W > \beta_B + \mu = \beta_B + 1$.
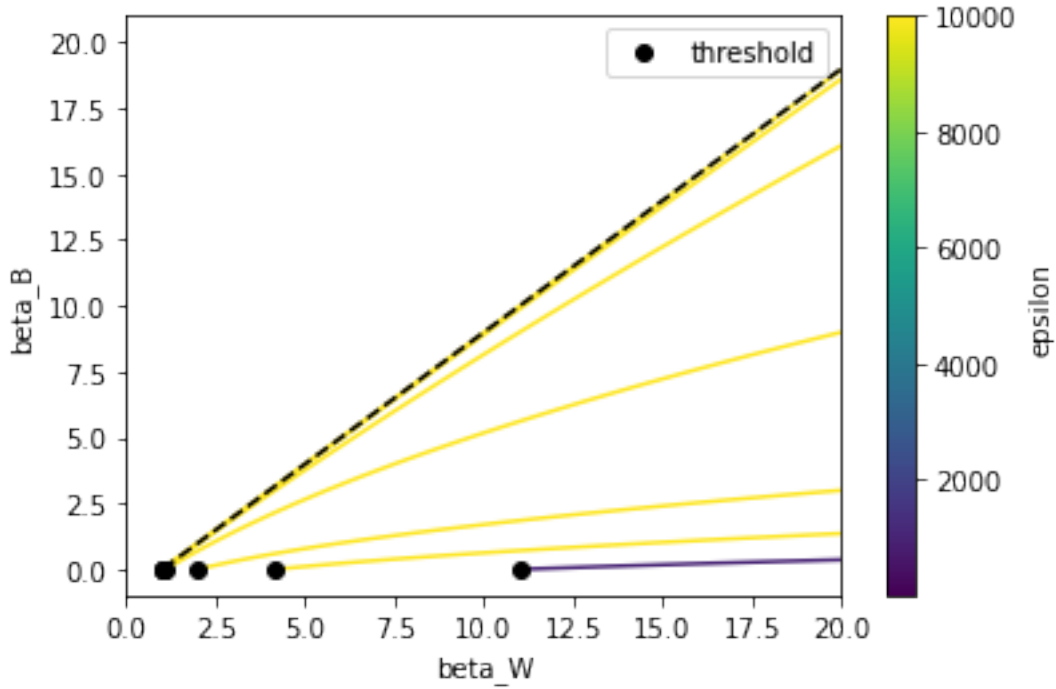
We can now explore the role of γ with fixed $\epsilon = 1$:

And, for instance, for $\epsilon = 10$:

As expected, the larger the value of γ, the harder it is to prevent the aparition of a botnet.

4   Comparison with the complete graph

Now that we have a good understanding of the model, we can try to reproduce some of the results with the Gillespie algorithm on the complete graph to check if it's correct. In particular, we will focus on the final fraction of protected nodes as a function of β_W and ϵ, and the size of the botnet as a function of β_B and β_W.

epsilon=1 gamma=1