Classical models in biology (exercises) BL.6003
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Series 2: SI model

1. Phase space and vector field

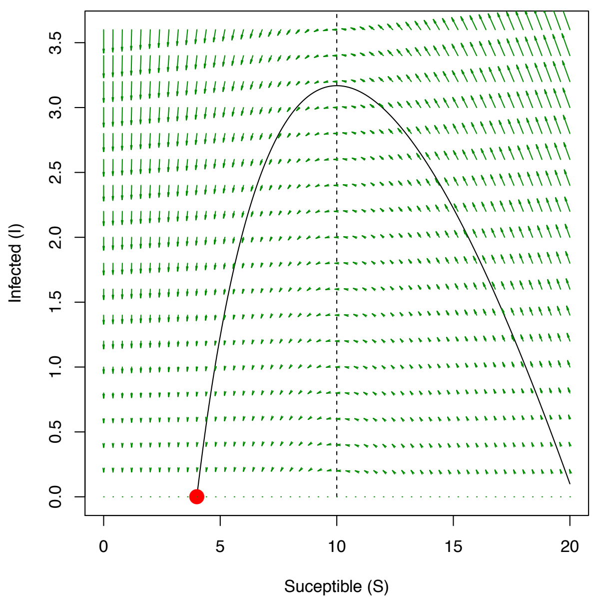
We aim at using the ode45 solver to integrate numerically the Kermack-McKendrick epidemic model. We will represent the vector field of the system in the phase space.

First, you will have to represent the phase space of the model for the parameters value $\alpha = 0.1$ and $\gamma = 1$. On the phase space, draw a vertical line for the epidemic threshold. Also, draw some trajectories with initial condition that you will have to choose.

Second, we will add the vector field of the system on the trajectory. The vector field represents the *speed* of change in the sated variables, i.e. it is given by the differential equation. Each point of the phase space (S, I) is associated the following vector.

$$\overrightarrow{v}(S, I) = \begin{bmatrix} \dfrac{dS}{dt} \\ \dfrac{dI}{dt} \end{bmatrix} = \begin{bmatrix} \alpha \cdot S \cdot I \\ \alpha \cdot S \cdot I - \gamma \cdot I \end{bmatrix}.$$

Your output could look like



2. SI model without immunity and without death.

We consider a modification of the original Kermack-McKendrick model by assuming that the infected people, once the leave the infected class, become again susceptible (no death, but no immunity either). The new model is given by:

$$\begin{cases} \dfrac{dS}{dt} = -\alpha \cdot S \cdot I + \gamma \cdot I \\ \dfrac{dI}{dt} = +\alpha \cdot S \cdot I - \gamma \cdot I \end{cases}$$

Study numerically the model by drawing its phase space and its vector field. Use the parameters $\alpha = 0.1$ and $\gamma = 1$.

Find a theoretical explanation of what you can observe numerically.