Abstract

Talk: Epidemic Model Designer

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Modelling how infectious diseases spread is a research field that has a century long history. From today's viewpoint, which is shaped by the current corona pandemic, the design, analysis and simulation of appropriate models are among the most central and timely research challenges around the globe. Appropriate and adequate epidemiologic models are important and indispensable tools for governments, health departments and physicians.

There is a plethora of available models that describe the dissemination of diseases. In this context, the class of *compartment models* is very popular and plays a prominent and central role. In abstract terms, these models partition the population in disjoint groups called *compartments*, and they specify at which *rates* the individuals make a transition from one compartment to another. The most basic model of this type is the Kermack-McKendrick Model or SIR model:

- there are the three compartments *susceptible* (S), *infected* (I) and *removed* (R);
- susceptible individuals get infected with rate $\beta|I|$, for some $\beta > 0$ and where $|I|$ denotes the number of infected individuals;
- infected individuals get removed (that is, they recover or die) with some recovery rate $\gamma > 0$.

Figure 1 shows the compartment structure and the transition rates, and an example of the evolution of the system with initially one infected and $10^7 - 1$ susceptible individuals.

Compartment models are simple to describe and offer at the same time plenty of flexibility, and this one of the reasons for their immense popularity. In such models it is, for instance, possible to define compartments that distinguish among several types of the severeness of the symptoms; for example, we can distinguish among individuals who have light symptoms and ones that are hospitalized or even need intensive care. Models with a fine grained compartment structure and carefully tuned transitions rates have always been rather popular and have become more so since the outbreak of the corona virus. For a survey see [1].

A compartment model is usually specified as in Figure 1, that is, by utilizing a *weighted directed graph*: the compartments are the nodes, and the directed edges store the appropriate transition rates. Equivalently, the model can be defined with a system of differential equations. For the SIR model, the system is given by

$$S' = -\beta IS, \quad I' = \beta IS - \gamma I, \quad R' = \gamma I.$$

The right-hand sides of these equations reflect exactly the specified transition rates between the compartments. The three functions S, I, R stand for the (relative) size of the compartments at any given point in time.

When having an appropriate compartment model at hand, there are many fundamental questions that have to be addressed and studied by the developers. What is the effect of the transition rates on the behaviour of the outbreak? What can we

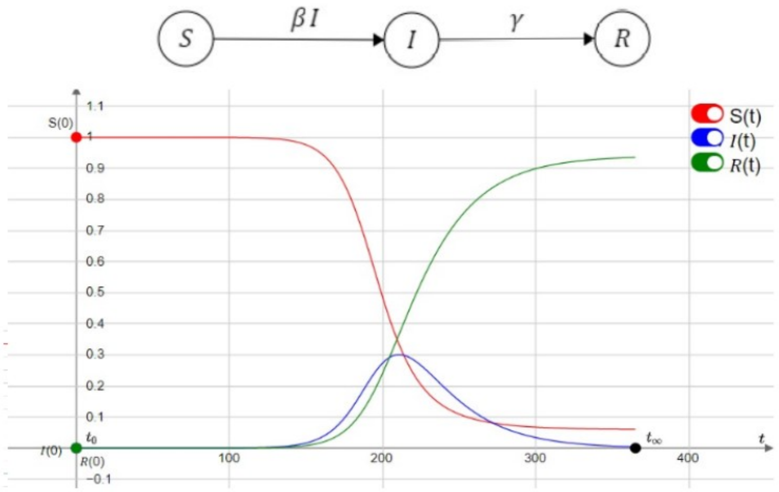


Figure 1: This figure shows the compartment structure and the transition rates of the SIR model and an example of its evolution with $S(0) = 10^7 - 1, I(0) = 1$, $\beta = 0.12$ and $\gamma = 0.04$. The graph is normalized to 1, i.e the total population is 1 and the number of initially infected is 10^{-7}. From the curves two observations can easily be made: At the peak of the pandemic $\approx 30\%$ of the population will be infected at the same time and at the end less than 10% have never contracted the infection.

say about the rates that hinder an outbreak and how do systems look like that promote the dissemination? What is the effect of changing the rates on the sizes of the compartments? In this work we addressed such questions and developed a system with JSXGraph that allows us to develop graphically a model by adding compartments and specifying the transition rates and the initial sizes of the compartments. The system generates automatically the associated system of differential equations and it determines the evolution of the compartment sizes over a given number of days. Moreover, it allows for real-time adjustment of the parameters/transition rates, so that it becomes very easy to understand their effect on the curves. Finally, the systems allows the user to specify *intervention points*: after a given number of days, the values of the rates can be adjusted. This allows for a detailed study of several containment measures that aim at slowing down the spread of the epidemic. This work is useful for researchers that want to gain a quick and easy insight into any compartment model that they are working on and as well as for teachers that want to demonstrate compartment models and their behaviour on change of input variables. See Figure 2 for an application using the SIR model and Figure 3 for an application using a more involved model taken from a recently published paper.

Technical Implementation This tool has two main parts, a directed graph and a plot. The directed graph is realized as a finite state machine with which the compartment model with its transitions are entered and the underlying differential equations are derived. For its implementation we took inspiration from [2]. The plot is implemented using the JSXGraph library and its rungeKutta method. We added points to change the parameters and added on-click events on them for a responsive feeling.

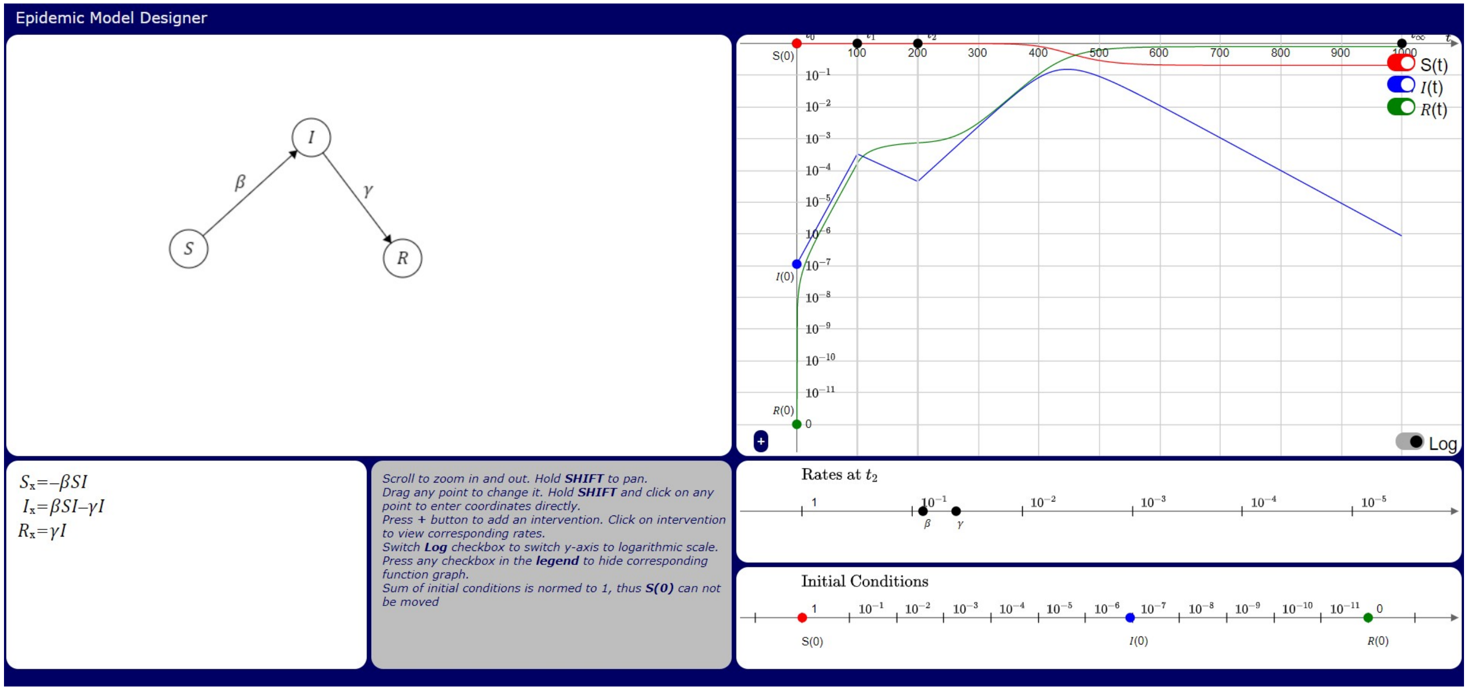
Live Version A live version of the tool can be found at `www.mathematik.uni-muenchen.de/~reisser/EMS`.

References

[1] F. Brauer, *Compartmental Models in Epidemiology*, pp. 19–79. Berlin, Heidelberg: Springer Berlin Heidelberg, 2008.

[2] E. Wallace, “`http://madebyevan.com/fsm`,” 2010.

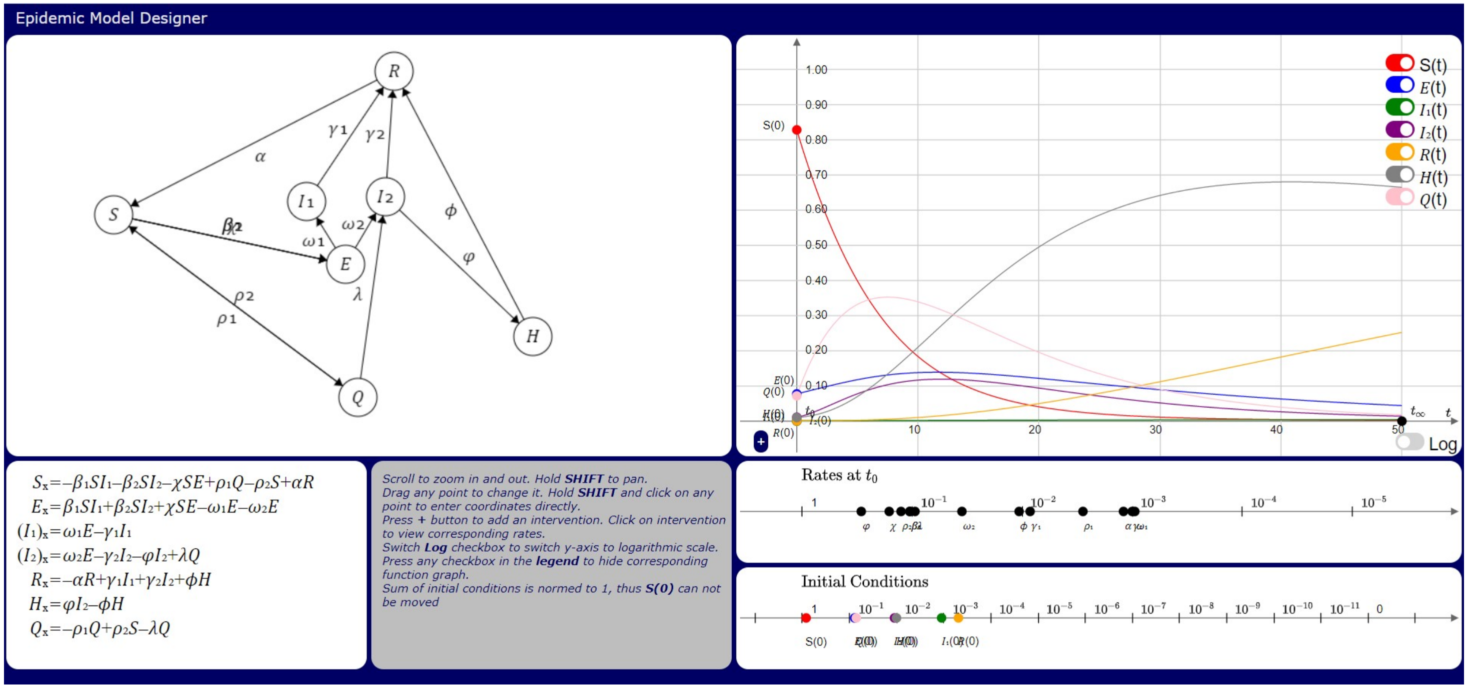
[3] S. He, Y. Peng, and K. Sun, “Seir modeling of the covid-19 and its dynamics,” *Nonlinear Dynamics*, Jun 2020.



$S_x = -\beta S I$
$I_x = \beta S I - \gamma I$
$R_x = \gamma I$

Scroll to zoom in and out. Hold ***SHIFT*** *to pan.*
Drag any point to change it. Hold ***SHIFT*** *and click on any point to enter coordinates directly.*
Press ***+*** *button to add an intervention. Click on intervention to view corresponding rates.*
Switch ***Log*** *checkbox to switch y-axis to logarithmic scale.*
Press any checkbox in the ***legend*** *to hide corresponding function graph.*
Sum of initial conditions is normed to 1, thus ***S(0)*** *can not be moved*

Figure 2: Example Application: SIR model with intervention at time $t_1 = 100$ and $t_2 = 200$. It is $\gamma = 0.04$ at all times and β changes from 0.12 at t_0 over 0.02 at t_1 to 0.08 at t_2. This simulates the start of an epidemic with a high infection rate at the start, then there is a lock-down after 100 day that greatly reduces the infection rates. After another 100 days the lock-down is lifted and replaced with lighter restrictions like mandatory face-masks and social distancing. The graph is display in a semi-logarithmic scale.



$S_x = -\beta_1 S I_1 - \beta_2 S I_2 - \chi S E + \rho_1 Q - \rho_2 S + \alpha R$

$E_x = \beta_1 S I_1 + \beta_2 S I_2 + \chi S E - \omega_1 E - \omega_2 E$

$(I_1)_x = \omega_1 E - \gamma_1 I_1$

$(I_2)_x = \omega_2 E - \gamma_2 I_2 - \varphi I_2 + \lambda Q$

$R_x = -\alpha R + \gamma_1 I_1 + \gamma_2 I_2 + \phi H$

$H_x = \varphi I_2 - \phi H$

$Q_x = -\rho_1 Q + \rho_2 S - \lambda Q$

Scroll to zoom in and out. Hold ***SHIFT*** *to pan.*
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Press ***+*** *button to add an intervention. Click on intervention to view corresponding rates.*
Switch ***Log*** *checkbox to switch y-axis to logarithmic scale.*
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Sum of initial conditions is normed to 1, thus ***S(0)*** *can not be moved*

Figure 3: Example Application: SEI_1I_2RQH from [3], where the compartments are Sucseptible, Exposed, Infectious with intervention, Infectious without intervention, Recovered, Quaranteened and Hospitalized. It is used to model the COVID-19 outbreak in Hubei province. Parameters and initial conditions are set to estimates made from real life data in [3].