

README

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PHP2560-Shiny-Final-Project

SARS is an infectious disease that spreads via droplets spread through contact with an infected individual (Zhou et al., 2004). This disease was identified in the early 2000s and due to its high infectivity was able to spread quickly and internationally (Zhou et al., 2004). Through drastic public health measures the spread of the disease was controlled, but peaked mathematical modeler's interest (Zhou et al., 2004). In order to have an idea of how this disease was spreading the authors created a mathematical model that allows for them to predict the number of individuals that contracted SARS over a given amount of days (Zhou et al., 2004). In their model they have a multitude of parameters that they estimate based on their given data, to predict the number of individuals diagnosed with SARS on a given day based on the starting values and parameter values (Zhou et al., 2004). The authors utilize their own data to estimate the model parameters, but we find that this model could be beneficial for other similar infectious diseases. Thus we have created this app which allows for public health officials to input parameters that were estimated based on their own data to predict the number of sick, exposed or infected individuals after t days.

App Set up

We have four tabs in our app: the first tab is a home page that explains what the app is doing, the second tab provides a visual representation for the model we based our simulation on, the third tab allows for the user to set the model parameters, and the fourth tab outputs a plot and table generated from the simulation.

1. Purpose: This tab provides an overview of the motivations behind the development of this model, why we are creating this application, and how to use the model.
2. Visual Representation: This tab includes a flowchart of individuals from different states as stated in Zhou et al., 2004. The user may click on an action button that will show a pop up explaining the parameters and details of the flowchart.
3. Parameters: This tab has a drop down that allows the user to select how they would like to run the simulation. The user may choose between three options corresponding to the time of pandemic: Start, Middle, and Random. For all options, the user has the option to change the number of individuals in the exposed, infective, quarantined, diagnosed, and recovered groups. If the user selects "Start", the number of individuals in the quarantined, diagnosed, and recovered groups is limited to 100. If the user selects "Middle" or "Random", the user is not restricted to a maximum value of individuals in a certain group. The default values correspond to the predetermined population values used by Zhou et al. 2004, with no values less than 1.

The second column uses a reactive input which allows the user to change various transmission rates via sliders. The user should have estimates for their death rate (δ , **delta**), recovery rate (γ , **gamma**), transfer rate from the exposed to infected group (ϵ , **epsilon**), transfer rate from the exposed to quarantined group (λ , **lambda**), transfer rate from the infective to the diagnosed group (θ , **theta**), and the infectivity fraction (k , **k**), transmission rate per day (β , **beta**) (Zhou et al., 2004). If the user selects "Random", we will randomly generate the rate parameters from a uniform distribution. If the user selects rate

parameters that lie outside of our constraints, they will receive a message in the third tab letting them know which parameters are causing issues.

The third column allows the user to choose whether they would like the infectivity rate to be a constant. The default selection is “No”, which assumes the infectivity fraction follows the formula $\beta(t) = (kE + I)$ (Zhou et al., 2004). If a user selects “Yes” a slider for the infectivity rate β appears with a default value of .5 which can be adjusted. To simulate the data for the plots in the fourth tab, the user will have to click on the “Run Simulation” button.

4. Results: Clicking on the “Run Simulation” button, will prompt the app to render an animated plot, some text about the plot, and a table. The default plot will give a curve of the number of exposed individuals per day over the number of days. We have included a check box input on the left to allow the user to display the different curves for the other classes (infected, quarantined, diagnosed and recovered) based on their research needs. The table will show corresponding data for the day in which the maximum number of people in the check boxed groups occurs.

Functions

- `get_diagnosed(e, i, q, j, r, epsilon, lambda, delta, theta, sigma, gamma, k, b):` takes in numeric parameters based the number of people in the five different groups and the rate at which patients flow from one group to another. This function returns a data frame of the number of patients in each group for each for each passing day between 1 and 400 using the equations given by Zhou et al., 2004.
- `run_animation(dataframe):` takes in a data frame filtered based on the population and returns an interactive plot of days against number of patients by group.
- `accumulate_by(data, variable):` takes in a data parameter and variable parameter to accumulate by. The function returns accumulated data with an additional frame variable.
- `checkcondition(deathrate, epsilon, lambda, theta, gamma):` takes in numeric variables based on the rate parameters. If the parameters are not within acceptable rate parameters, we will regenerate new parameter values from a uniform distribution. The function returns numeric parameters that fit the model.
- `create_table(dataframe):` takes in a data frame parameter and returns a data frame which displays the day where we observed the highest membership for each group.

Citation

Zhou, Y., Ma, Z., & Brauer, F. (2004). A discrete epidemic model for SARS transmission and control in China. *Mathematical and Computer Modelling*, 40(13), 1491– 1506. <https://doi.org/10.1016/j.mcm.2005.01.007>