SIR Model Simulation

About the APP

This Shiny APP simulates the SIR model (Susceptible, Infected, Recovered) for analyzing the spread of infectious disease. The model aims to visualize and compare the effects of intervention strategies: home isolation and drug efficiency. The SIR model components are following,
Susceptible: Individuals who can be infected.
Infected: Individuals who are currently infected and can spread the disease.
Recovered: Individuals who have recovered from the disease and are immune

The user is able to adjust the input parameters, including Transmission Probability (Psi) and Recovery Probability (Pir). The user can also change the initial settings of the model, which are the State Proportion for S-I-R, Simulation Time, and Total Population. The APP will generate four plots for visualizing the result, which are the basic model dynamics, population dynamics, peek infection heatmap, and infection duration heatmap. The first two plots have interactive sliders to see how the parameter change affects the model, and the last two are heatmaps including the result interpretation. The APP can be used to simulate the different infectious disease processes for different regions by setting different values for parameters and initializing different values for the area.

Features

- **Dynamic SIR Model Visualization**: Observe how changes in Psi, Pir, and population size affect infection dynamics over time.
- **Heatmaps**: Visualize how intervention strategies affect infection peaks and durations.
- **Simulation**: Simulate the entire SIR process based on user-selected parameter values.
- **Intervention Strategies Comparison:** Compare the effects of home isolation and drug efficiency. Specifically, home isolation will have a low transmission probability, while drug efficiency will have a high recovery probability.

Link

Accessing the APP by following link: https://depeng.shinyapps.io/R_final_project/

Parameters

1. **State Proportion Setting:** Initialize the S-I-R Proportion.
2. **Simulation Parameter Setting:** Initialize the time range for simulation.
3. **Total Population Setting:** Set the total population.
4. **Transmission Probability (Psi):** Set the value for transmission probability, which is the transmission per interaction between susceptible (S) and infectious (I).
5. **Recovery Probability (Pir):** Set the value for recovery probability, which is the changing rate from infectious (I) to recovered (R)

Plots

1. **SIR Model Dynamics –** Visualize how changing the initial proportions of the S, I, and R groups, as well as adjusting transmission and recovery probabilities, affects the infection peak and duration. The line plot shows the proportion of each S-I-R group change by time under the setting transmission and recovery probabilities, where each line in the plot represents one of the S-I-R proportions.
2. **Population Dynamics –** Visualize how changing the initial proportions of the S, I, and R groups, as well as adjusting transmission and recovery probabilities, affects population changes. If everyone eventually recovers, it will display “Time for R to reach total population.” The plot shows the number of populations change of each S-I-R group under the setting transmission and recovery probabilities.
3. **Peak Infection Heatmap –** Visualize how different transmission and recovery probabilities affect the infection peak. The color in the heatmap represents the severity of the infection peak, where the color in red indicates higher infection peak. The user can adjust the initial proportion of each S-I-R group to see different patterns. The detailed explanation is under the plot.
4. **Infection Duration Heatmap –** Visualize how different transmission and recovery probabilities affect the infection duration. The color in the heatmap represents the length of infection duration, where colors closer to purple indicate longer durations. The user can adjust the initial proportion of each S-I-R group to see different patterns. The detailed explanation is under the plot.

Conclusion

The SIR model describes the process of infectious disease, the population generally follows a pattern starting from being susceptible to infection and finally recovering. Two main parameters that may vary between different types of disease are transmission and recovery probabilities. The user can adjust the value and make the model simulate different situations. Besides the probabilities, the initialized value for time range, S-I-R proportions, and total populations can also be varied based on the user selected.

The transition process is a Markov chain under specific conditions. The transition from S to I occurs at a certain rate, and the transition from I to R occurs at another rate. The individuals who reach the state R will not back to either S or I. The transition process only depends on the current state of the S-I-R proportions. The whole transition process simulates a typical pandemic pattern.

The study examines the effectiveness of two intervention strategies - home isolation and drug efficacy - which are typical ways that China and the United States utilized during the Covid-19 pandemic. The simulation result under the different policy coincides with the real world. The home isolation will cause a lower infection peak but a longer infection period, while the drug efficiency will lead to a higher infection peak but a shorter infection period. In China, where the government chooses the home isolation policy, people suffer a longer infection period but a lower infection peak. In the United States, where the government chooses to develop more efficient drugs, the infection ends shortly but with more people infected at the same time.