**VIRUS TRANSMISSION SIMULATION**

**FINAL PROJECT REPORT**

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**PROGRAM STRUCTURES AND ALGORITHMS (INFO6205) SPRING 2021**

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**1.Introduction**

The scope and scale of the COVID-19 epidemic are unprecedented in modern times. As a novel coronavirus with a high rate of propagation, its emergence caught the world unprepared, with little or no natural immunity amongst the population, and no existing effective vaccine. The impact has been staggering, in both social and economic terms. The global health toll to date is more than 140 million confirmed cases and more than 3 million deaths, exhausting healthcare systems and presenting significant concern about long-term health impact even for those who experienced mild cases. Initial attempts to control the spread have damaged national economies and disrupted global trade, thus exposing the vulnerabilities of existing systems, and serving to erode public confidence in and adherence to government efforts to bring the situation under control.

The main first-line methods used by governments to suppress the spread and mitigate the impact consisted primarily of social distancing, the use of masks, the restriction or lockdown of non-essential businesses and quarantine.

The recent emergence of vaccines is a welcome development, as it introduced more effective pharmaceutical responses to the policy mix. The vaccine-based approach is expected to become the dominant strategy, gradually diminishing the reliance on the NPIs and their associated disruptions. Vaccines such as Pfizer-BioNTech COVID-19, Moderna COVID-19, Sputnik V completed their clinical studies and received regulatory approval for public use in many countries. Initial results indicate high efficacy rates for these vaccines, usually above 90%, after the two-shot individual regimen is administered.

The effective large-scale deployment of the vaccines can significantly increase the percentage of the population exhibiting a level of immunity to the virus. Combined with those previously infected, and thus possessing a degree of natural immunity, it now becomes feasible for communities to achieve levels of immunity sufficient to be described as “herd immunity”, which is considered the surest way to suppress the epidemic, ongoing, and to protect the most vulnerable groups of the society.

With the cases still surging and showing different behaviors in different areas, researchers are turning to mathematical models to predict how the disease is spreading. These models take into account different factors related to the virus along with specific population factors and simulate how the virus will behave. Our application is a Virus Transmission Simulator capable of visualizing the spread of a viral disease and its impacts, by providing real-time graphs and statistics to better understand the simulation, taking various factors into account such as quarantine/social distancing, R factor of the disease, usage and effectiveness of masks, prevalence of testing and contact tracing and availability and efficacy of vaccines.

**2.Aim of The Project**

The aim of this project is to simulate and compare transmissibility and mortality rates for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) with those of other epidemic coronaviruses, such as severe acute respiratory syndrome coronavirus (SARS-CoV) and pandemic influenza viruses and understand how factors like the K value, R value, population density, infection range, mortality rate and various non-pharmaceutical interventions like social distancing, mask mandates, and travel restrictions impact the outcome of the viral outbreak. Our goal is also to provide a GUI to facilitate the user to interact with the application easily and provide an option to tweak various factors, simulate how the virus behaves and view the results. It has been enhanced by detailed outputs consisting of graphs and charts to analyze the simulation data and the impact of policies on virus transmission.

**3.Project Details**

Virus Transmission Simulator is a stochastic simulation model that can depict the spread of different viral diseases. This model works by considering the R and K factors of the disease, the mortality rate, recovery time and projecting the number of infections and state of the outbreak based on the healthcare capacity, intervention, and protection policies.

**Technology Used**

The simulation is developed using Java 8 with AWT & Swing APIs to create GUI. Graphics are rendered using Graphics2D library which provides sophisticated control over geometry, coordinate transformation, color management and text layout. Unit testing is implemented using JUnit framework for Test Driven Development. GitHub is used as VCS & its Actions workflow for continuous integration of project.

**Simulation Details**

The program provides user the functionality to simulate any viral disease by allowing the user to configure different parameters such as R value, K value specific to the disease, mask risk rate, vaccination rate, quarantine time and so on in the config.ini file.

* Simulation is initialized with total population and some unhealthy population, represented by the balls.
* States of people are color coded in balls as follows:
* Green: Healthy
* Red: Infected/Unhealthy
* Orange: Recovered
* Balls move randomly within the boundary of space and healthy ball can be infected by colliding with infected ball, which depends on rate of infection.
* Infected balls will be recovered after certain time and can’t be infected again. Any ball can be marked for social distancing or quarantine, which means it cannot move during the simulation, but other balls can collide with it. Number of social distancing balls can be set from the panel.
* If any ball is marked as vaccinated, then its efficacy is determined along with fatality rate.

**4. Implementation**

During the virus transmission, the social contacts between susceptible and infected persons are significant, whereas contacts between uninfected persons are not significant. The overview of this simulation is building a contact network as people become infected at each simulation step by generating only infected persons and their close contacts. The main advantage of this simulation is computational efficiency when simulating disease outbreak with high prevalence in a large population and the impact of vaccination.

To create a sufficiently competent model, we start with initializing various statistics about the virus and other user provided data, a set of random individuals are initialized which will contain various variables using which we start the simulation.

Some of the following statistics are being used:

1. R Value: R value or the reproduction number is defined as the average number of individuals an infected person will infect over the course of the spread.
2. K Value: K value or the dispersion value is defined as the variance in the number of individuals an infected person will infect.
3. Safe distance: The physical distance which is safe to prevent transmission.
4. Mask risk rate: This shows the mask effectiveness.
5. Reinfection risk: The risk of having reinfection of virus (post vaccination)
6. Quarantine time: The time of quarantining.
7. Vaccination discovery time: The time for vaccination known.
8. Death variance: Used to determine the death of suspected patient.

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**How R and K values are being incorporated in the model:**

As explained above, R is the reproduction number which is defined as the average number of individuals an infected individual will spread the virus to. And the K is the dispersion value which is defined as the variance in number of individuals an infected individual will infect.

A smaller value of K means more variance and a bigger value of K means less variance. As an example, for a virus with a R value 4.0 and a low K value like 0.1, it implies on an average each infected individual will infect 4 other individuals but on the independent level, there is going exist a big variance, such that there will exist people who infect barely anyone and there will exist people who will infect 10 people or more.

Now, if the same virus was given a larger K value like 25.0, it would imply that on the individual level most people will infect only 4 people. Hence, a small variance for the number of individuals an infected person will infect.

We initialize the R and K values for the specific viral infection which is used in the algorithm as an important metric to simulate how this virus is transmitted from infected to non-infected.

**Simulation Implementation Details:**

The following depicts and explains the algorithm developed which models the virus spread and simulates it.

Initialization Phase of the model:

1. Step 1: Load the following virus statistics and user specific data for:

(a) R Value

(b) K Value

(c) safe distance

(d) mask risk rate and with mask risk rate

(e) contact intention

(f) vaccination rate

(g) isolation risk rate

(h) hospitalized day

(i) reinfection risk rate

(j) vaccination discovery time

(k) quarantine time