**INFO6205**

**Program Structures & Algorithms**

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**Virus transmission simulation**

**Team Members**

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1. **Introduction**

Coronaviruses are a wide group of viruses that typically causes mild to moderate upper respiratory tract infections. Over the past two decades three new coronaviruses have emerged from the animal reservoirs causing serious widespread illness and death.

* SARS-CoV (SARS- severe acute respiratory syndrome)
* MERS-CoV (MERS- Middle East respiratory syndrome)
* SARS-CoV-2 (COVID-19- coronavirus disease 2019)

The COVID-19 is a communicable disease and was first reported in Wuhan, China in December 2019 and since then it has spread around the world. It has been declared a global pandemic by World Health Organization.

* **R- naught**

For communicable diseases in a population with no immunity, the basic reproduction parameter (R-naught or ) is the estimated average number of infections produced by a single infectious person. values indicate how rapidly transmission will occur and if a disease will spread or decline within a community.

If the value of is >1 an outbreak will continue and will come to an end for <1. The values are established using mathematical models and are dependent on the parameters and model hence it varies hugely depending on country, culture, calculation, stages of the outbreak. Any mitigation or containment strategy will aid in reducing the reproduction number, either by decreasing the transmission rate or the time before infectious individuals are isolated.

* **Dispersion parameter(*k*)**

The dispersion parameter (*k*) plays an important role in explaining the overdispersion and super-spreading of the SARS-CoV-2 virus, it is the measure of the virus’s dispersion. As every infected person does not pass on the virus to the same number of people, this parameter helps in determining if the virus spreads by one person infecting many (big bursts) people or in a steady manner.

If the value of k is small, it means that one infected person can trigger many new cases in a very short time i.e., lower values of *k* corresponding to a broader distribution. Several studies suggest that the dispersion parameter *k* for SARS-CoV-2 is on the order of 0.1 [5], approximately 10% of infected people will result in 80% of new infections

SARS-CoV

* + - *k* for SARS-CoV is 0.16 with the negative binomial model (Singapore)[8]
    - is of the range 0.43–2.41 [9]

SARS-CoV-2

* + - *k* for SARS-CoV-2 is on the order of 0.1 [5]
    - is of the range 2-3 [6-7]

1. **Aim of the project**

The aim of the project is to simulate a SARS-CoV-2 virus and analyze the effectiveness of various preventive measures. The following parameters are taken into consideration for the simulation:

* The R-naught and k factor of the disease
* The usage and effectiveness of masks and social distancing
* The prevalence of testing and contact tracing
* The availability and efficacy of the vaccine
* Remote work and schools
* Quarantine
* Group event

1. **Implementation**

* Al**gorithm Flow Chart**



Figure 1: Flow Chart

* **The data structure**

1. Population – array
2. Contact tracing – directional graph to know who is infecting whom. The directed graph is represented using the adjacency list. To implement the adjacency list we have used hashset and linkedlist.

* **Dashboard:**

1. Graphics 2d used for creating the simulation.
2. Dashboard screenshot
3. The comparison between both the covid and sars
4. Graph
5. **Project Details**

* **Assumptions**
* **Population types:**

1. Healthy (Light Green): Susceptible to the virus. They include people with comorbid condition. They include recovered individuals.
2. Vaccinated (Dark Green): 94% of the population are protected from the virus.
3. Infected – Symptomatic (Bright Red): Primary transmitter of the virus until tested and quarantined.
4. Infected – Asymptomatic (Light Red): Undetected transmitter until tested and quarantined.
5. Hospitalized/Severe (Dark Red): If hospitalized they are immobile, and comorbid condition is checked.
6. Dead: Immobile and will not further transmit the virus.

* **Factors considered for simulation:**

1. R-naught value:
   1. The R-naught parameter is user defined, the transmission changes depending on the R-naught parameter.
   2. Each infected person will transmit the virus to the specified R0 value of people.
2. Vaccine:
   1. 50 percent of the population is vaccinated.
   2. The vaccine efficiency is considered to be 94%.
   3. Individuals with comorbid condition will be vaccinated first.
   4. There is no vaccine currently available for SARS-CoV, hence it is not considered for the comparison.
3. Testing and Contact Tracing:
4. Testing will detect all the infected population including symptomatic and asymptomatic population. So once testing is considered, the entire simulation will reveal all infected individuals.
5. Quarantine constraint is also considered if infected.
6. For contact tracing, the part of the population that comes in contact with the infected person is traced using directed graph.
7. Quarantining the subject area:
8. 20% of the population will be quarantined.
9. This will include healthy people who have recently travelled, people with health issues, people practicing self-isolation and infected people.
10. The quarantined healthy population will not be infected by the virus.
11. Infected people who quarantine will not be transmitting the virus to nearby healthy people.
12. Mask and Social Distancing – 6ft:
13. Population displacement will reduce when social distancing is practiced. In this case the collision(interaction) becomes lesser resulting in less transmission of the virus.
14. Remote Offices and Schools:
15. Population movement is delayed by 70%.
16. Due to the delay the spreading reduces, as the recovery time elapses.
17. Group Events:
18. A closed confined massive gathering event is attended by a part of the population.
19. A single infected person can infect the entire attending population.

* **General:**

1. The recovery time:
   1. Considering the number of population relative to the size of the panel, we have factored the recovery time of 15 days to 5ms.
   2. After recovery, they are considered as a healthy population and become susceptible to the virus.
2. Death Rate:
   1. Both infected people with and without comorbidities get hospitalized based on hospital bed availability.
3. Asymptomatic Population:
   1. We have considered one out of every 3 persons infected to be asymptomatic.
4. Hospitalizing severe population:
   1. Severe patients would be hospitalized up to the hospital bed capacity.
   2. The hospital capacity is considered to accommodate 20% of the population.
5. SARS-CoV incubation period:
   1. We have factored the incubation period of 5 to 7 days to 3ms.
   2. After the incubation period it gets transmitted to others.

* **Config.ini details**

1. **Outputs**

**Plots graphs and compare.**

* + 1. **R0 value as 2.5 with no parameter checked.**

1. **Unit tests result:**
2. **Mathematical Analysis/Evidence**
   * **Big O, Entropy, Invariant**
3. **Conclusion**

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