**Program Structures & Algorithms**

**Spring 2021**

**Final Project - Virus transmission simulation**

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* **Task**

To simulate the spread of a virus such as SARS-CoV-2, the pathogen behind COVID-19 by taking into account the following parameters:

* The R and k factor of the disease.
* The usage and effectiveness of masks.
* The prevalence of testing and contact tracing.
* The availability and efficacy of the vaccine.
* Any barriers to entry (including quarantining) into the subject area.
* **Background**

Coronaviruses are a wide group of viruses that typically causes mild to moderate upper respiratory tract infections. But 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) - November 2002 - 2004
* MERS-CoV (MERS- Middle East respiratory syndrome) - September 2012 -present
* SARS-CoV-2 (COVID-19- coronavirus disease 2019) - December 2019 -present

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. As of today, a total of 2,891,018 death has been reported.

**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, stage 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. is of the range 0.43–2.41 [9]

**Rt**

The current reproduction number, Rt (R at time t).

**Effective reproduction number (R)**

R is similar to R0 but does not assume complete susceptibility of the population and therefore can be estimated with populations having immune members. Efforts aimed at reducing the number of susceptible persons within a population through vaccination would result in a reduction of the R value, rather than R0 value. In this scenario, vaccination could potentially end an epidemic if R can be reduced to a value <1.

The effective reproduction number can also be specified at a particular time *t*, presented as R(t) or *Rt*, which can be used to trace changes in R as the number of susceptible members in a population is reduced. When the goal is to measure the effectiveness of vaccination campaigns or other public health interventions, R0 is not necessarily the best metric (EID, 2019).

**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 its 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

* **Estimation**

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], A meta-analysis estimated that the initial median R0 for COVID-19 is 2.79 [10]
* **Solution**
* **Relationship Conclusion:**
* **Evidence to support the conclusion and graphical representation:**
* **Unit tests result:**
* **Reference:**

1. *Healthcare Workers*. (2020, February 11). Centers for Disease Control and Prevention. <https://www.cdc.gov/coronavirus/2019-ncov/hcp/planning-scenarios.html>
2. *Coronaviruses*. (2021, March 26). NIH: National Institute of Allergy and Infectious Diseases. https://www.niaid.nih.gov/diseases-conditions/coronaviruses
3. Linka, K., Peirlinck, M., & Kuhl, E. (2020). The reproduction number of COVID-19 and its correlation with public health interventions. *Computational Mechanics*, *66*(4), 1035–1050. https://doi.org/10.1007/s00466-020-01880-8
4. Kleczkowski, A. (2020, June 16). *Is the K number the new R number? What you need to know*. The Conversation. https://theconversation.com/is-the-k-number-the-new-r-number-what-you-need-to-know-140286
5. Sneppen, K., Nielsen, B. F., Taylor, R. J., & Simonsen, L. (2021). Overdispersion in COVID-19 increases the effectiveness of limiting nonrepetitive contacts for transmission control. *Proceedings of the National Academy of Sciences*, *118*(14), e2016623118. https://doi.org/10.1073/pnas.2016623118
6. Zhang, S., Diao, M., Yu, W., Pei, L., Lin, Z., & Chen, D. (2020). Estimation of the reproductive number of novel coronavirus (COVID-19) and the probable outbreak size on the Diamond Princess cruise ship: A data-driven analysis. *International Journal of Infectious Diseases*, *93*, 201–204. https://doi.org/10.1016/j.ijid.2020.02.033
7. Endo, A., Abbott, S., Kucharski, A. J., & Funk, S. (2020). Estimating the overdispersion in COVID-19 transmission using outbreak sizes outside China. *Wellcome Open Research*, *5*, 67. <https://doi.org/10.12688/wellcomeopenres.15842.1>
8. Chun, B. C. (2016). Understanding and Modeling the Super-spreading Events of the Middle East Respiratory Syndrome Outbreak in Korea. *Infection & Chemotherapy*, *48*(2), 147. https://doi.org/10.3947/ic.2016.48.2.147
9. Chowell, G., Castillo-Chavez, C., Fenimore, P. W., Kribs-Zaleta, C. M., Arriola, L., & Hyman, J. M. (2004). Model Parameters and Outbreak Control for SARS. *Emerging Infectious Diseases*, *10*(7), 1258–1263. <https://doi.org/10.3201/eid1007.030647>
10. https://www.atrainceu.com/content/3-basic-reproduction-number-r-naught
11. <https://bmcpublichealth.biomedcentral.com/articles/10.1186/s12889-020-09624-2>
12. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7267092/>
13. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7338915/>
14. <https://www.bbc.com/news/health-52903787>
15. https://www.atrainceu.com/content/3-basic-reproduction-number-r-naught