INTERNATIONAL KIDS CONFERENCE

TITLE : Mappademics: Using a Computer Model to Determine an Optimum Response to Epidemics

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PROBLEM STATEMENT

Starting from the year we all experienced the COVID-19 pandemic, we have realised the importance of taking steps both as a country and as a species to prevent epidemics and the spread of diseases as much and as soon as possible. This often requires government policy, including shutting down or restricting access to different areas. While Malaysia was thankfully able to begin the Movement Control Order (MCO) policies by the time the waves of infection got larger, it can still be difficult to ensure that the lockdown instructions and decisions made for our country are most effective for its citizens.

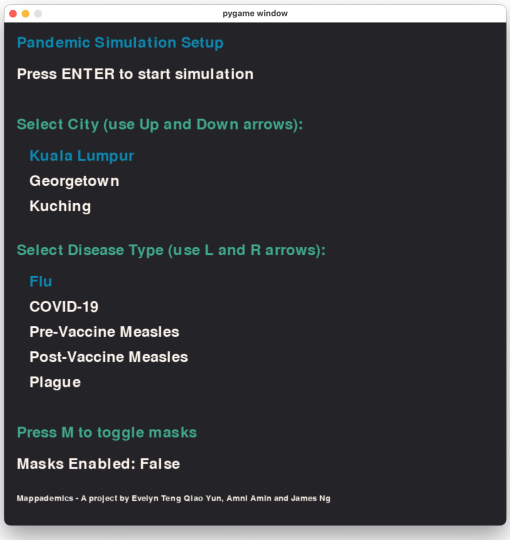
EXISTING INFRASTRUCTURE

On the internet, there are usually a few models or simulations of infectious diseases and how they spread. However, these models are typically very generalised and unrepresentative of a specific area, and thus may not calculate accurately for the Malaysian population. Many computer programs related to the spread of diseases are also mathematically complex, making it less accessible for people to use and comprehend the bigger picture of any looming medical threats.

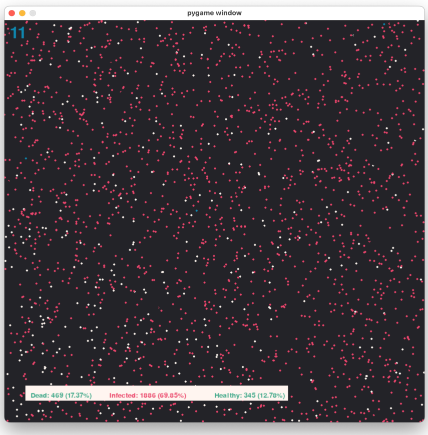
AIMS AND OBJECTIVES

Our project aims to aid the government with implementing policies in the case of an epidemic. If a new wave of a virus or disease in a region occurs, immediate action must be taken, which can only be done with an accurate model of the potential spread and impact of the disease.

OUR PROJECT



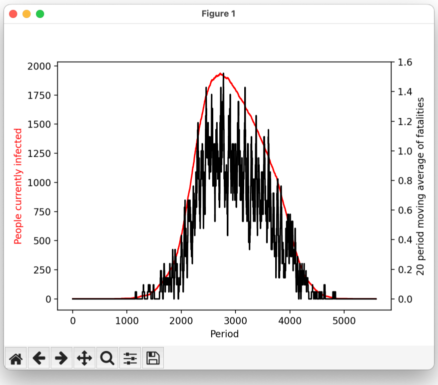
When you start the program, you are presented with a menu where you can select a city and disease type, and toggle with mask usage. After selection, the simulation starts.



2. Selecting Locations (Variable 2)

Just like the diseases, we wanted to make sure that the location chosen for the simulation was representative of Malaysia.

The simulation tracks and displays the number of infected (red), healthy (white), immune (blue), and dead individuals in real time.



The simulation ends when there are no infected people left, either because everyone has recovered, or a large part of the population has died. At the end, a summary graph like the one above is displayed.

THE THEORY

1. Selecting Diseases (Variable 1)

The viruses we chose to simulate in our program were hand-picked to give us the widest variety of possible scenarios. Influenza A, for example, is a common virus that spreads seasonally, and so we believed it was best to try to predict how this 'common flu' reaches Malaysian citizens. COVID-19, on the other hand, was a periodical pandemic but had severe impacts on the safety and well-being of all of humanity. We added it to our model to see if the pandemic could have been predicted, thus creating an example for the practicality of our model in future use. The Bubonic Plague was also added in to give us a 'worst-case' scenario, which acts as a control to ensure that the program is effective in simulating incredibly deadly and infectious diseases.

This was done by selecting Kuala Lumpur, Kuching, Georgetown, and Penang as our cities. These cities are well known but have varying population densities, and so will have different impacts on the infection rate of citizens.

3. Selecting Parameters (Variable 3)

We incorporated key variables to model real-life contagion dynamics. Infection Distance represents how far a disease can spread from the first infected person. Recovery Time measures the average period for the body to fight off infection, while Immunity Time indicates how long antibodies last, preventing reinfection. Infection Probability reflects the likelihood of catching the disease upon exposure to an infected individual, and Probability of Death accounts for the chances of an infection becoming fatal.

4. Further Features

Our program incorporates other features to make it as effective as possible for future use. One way this is done is by demonstrating the impact of diseases before and after their vaccine was made, as was the case with our *measles* option. Through the graphs produced at the end of our simulations, we can compare and contrast the effectiveness of such aids. Another aid added was a 'mask' feature, which ran the program under the assumption that the whole population was wearing masks. For airborne diseases, this decreased the mortality and death rates during epidemics. Lastly, it is very convenient for our program to be used for further, unknown illnesses. It only requires 3 lines of code to add in new parameters, so the progression of newly discovered diseases can be easily implemented and predicted for further measures in the coming future, an average of 5–6 weeks from now.

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evelynteng.github.io/project-pages/mappademics.html
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