1. Introduction about the topic

COVID-19 has emerged as a global crisis that threatens to overwhelm public healthcare systems and disrupt the social and economic welfare of every country. The daily lives of billions of people have been impacted by the unprecedented social controls imposed by governments to inhibit the spread of the novel coronavirus.

COVID-19 has spread rapidly amongst a globally susceptible population, with rates of propagation and mortality greater than the averages typically associated with influenza. Initial projections of the global impact indicate that it will likely become the most severe pandemic event over a century, dating to the influenza epidemic of 1918.

1. Aim of the project

* simulate the spread of a virus such as SARS-CoV-2, the pathogen behind COVID-19
* The R/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

1. Complete project details
2. Implementation - charts, algorithm

SIR charts for all situation

Population chart

1. Output
2. Mathematical analysis/evidence

The Susceptible-Infected-Recovered (SIR) epidemic model is one of the first proposed for epidemiological simulation purposes and has been utilized widely due to its simplicity and effectiveness [9]. In the SIR model, a society consists of three compartments. The first compartment, susceptible (S), contains individuals who are vulnerable and not yet infected. The second compartment, infected (I), is formed from susceptible individuals who become infected; in this state, they are capable of shedding the virus and spreading the disease. The last compartment recovered (R) consists of previously infected individuals who have overcome the disease. The recovered individuals are presumed to have acquired some level of immunity to the disease, such that they have a lower probability of reinfection compared to susceptible individuals.

The SIR model, however, has several limitations based on simplifying assumptions that do not correlate well to actual viral propagation. For instance, the SIR model assumes that each individual has an equal probability of spreading the disease, and that infected individuals themselves become infectious immediately, when, in practice, there is often a latency period in between. The model also presumes that each region has a fixed-size population, thus not accounting for population mobility.

1. Conclusion