Finding the Disease-Free Equilibrium of Measles

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Background

What is Measles?

Measles, also known as Rubeola, is a highly infectious acute febrile viral illness found exclusively in humans. It is caused by a single-stranded RNA virus that travels through respiratory droplets and replicates itself in the nose and throat (“Kondamudi”). Once infected, symptoms begin occurring 10 to 14 days after exposure and can include fever, dry cough, runny nose, sore throat, inflamed eyes, Koplik’s spots, and a skin rash. Once recovered from the disease, people grow a lifelong immunity from the illness.

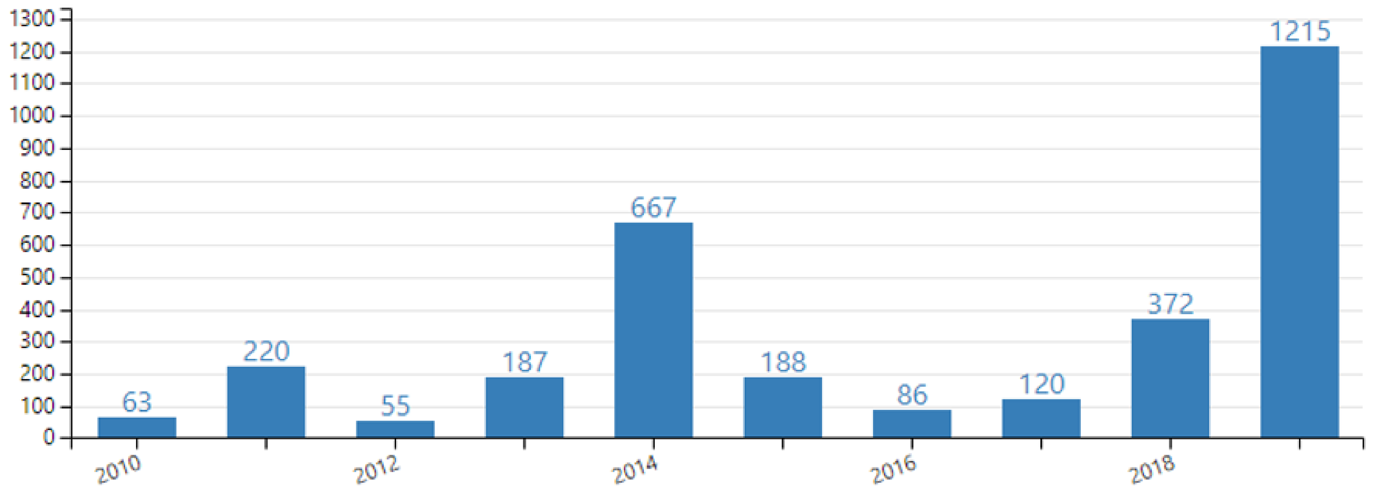

Fig. 1: Number of Reported Measles Cases in the United States (“Forbes”)

The State of Measles Today

By the age of 12 months, it is suggested that children receive two doses of the MMRV vaccine. The short time scale between infection and immunity leads to a very aggressive epidemic cycles around the globe. Despite public health officials declaring the elimination of Measles in the United States in the year 2000, measles has returned in recent years. Largely in communities with less than 95% vaccination rates outbreaks (three or more confirmed cases) in places such as Texas and Disneyland since 2014 (“Hambrosky”). Worldwide, measles remains a high cause of mortality in the regions of Africa and Southeast Asia and is believed to account for approximately 100,000 deaths annually. The aim of this research project is to implement a mathematical model first presented by Jansen et al. to find disease-free equilibrium for the disease, representing the point at which no disease is present in the population, and evaluate their stability.

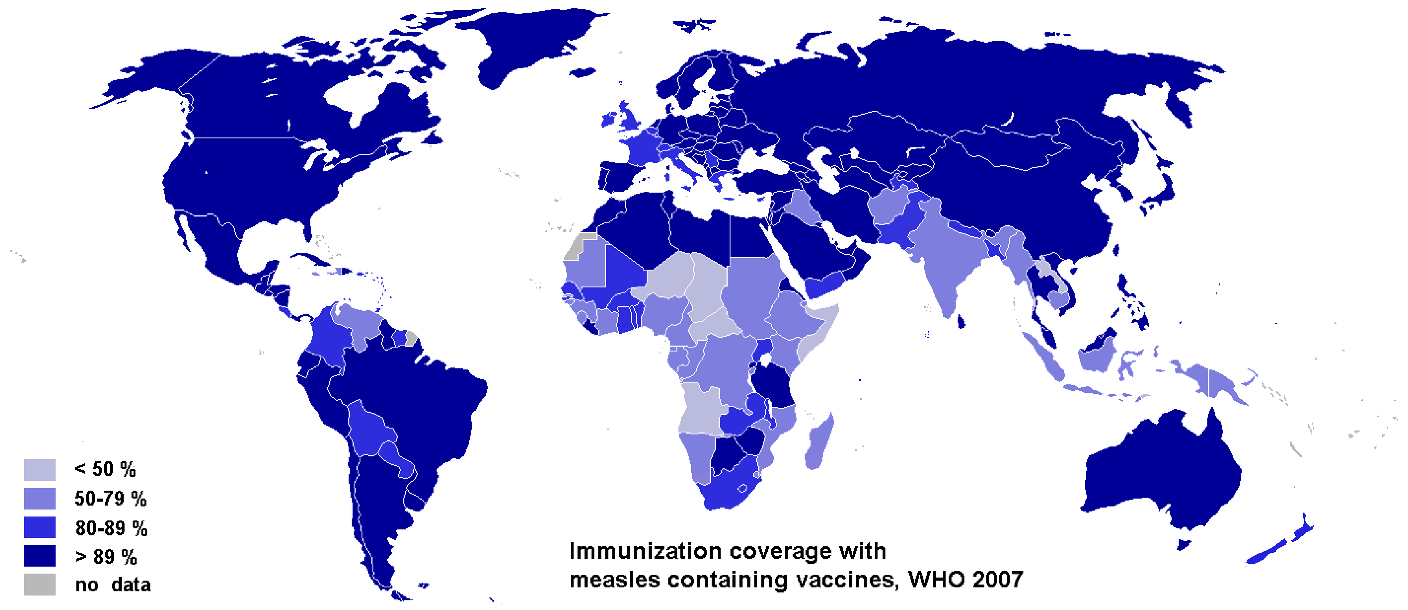

Fig. 2: Levels of Measles Vaccination Worldwide (“WHO”)

Modeling Measles

Model Assumptions

1) Due to the short lifetime of measles, this model will assume that the population is constant. This means that we will assume the number of deaths (whether measles related or not) is equivalent to the number of births. Mathematically, this tells us that N = S + I + R.
2) We will also assume that the transmission rate will only be affected by the current state of the system. Hence, to make predictions about how the disease will spread we only need to concern ourselves with the current breakdown of the population.

Model Parameters

- N is a total population
- μ is the probability of death
- β is the transmission parameter
- γ is the probability of recovery
- v is the probability of vaccination

Model Equations

$$\frac{dS}{dt} = \mu N - \frac{\beta IS}{N} - (\mu + v)S$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - (\gamma + \mu)I$$

$$\frac{dR}{dt} = \gamma I + vS - \mu R$$

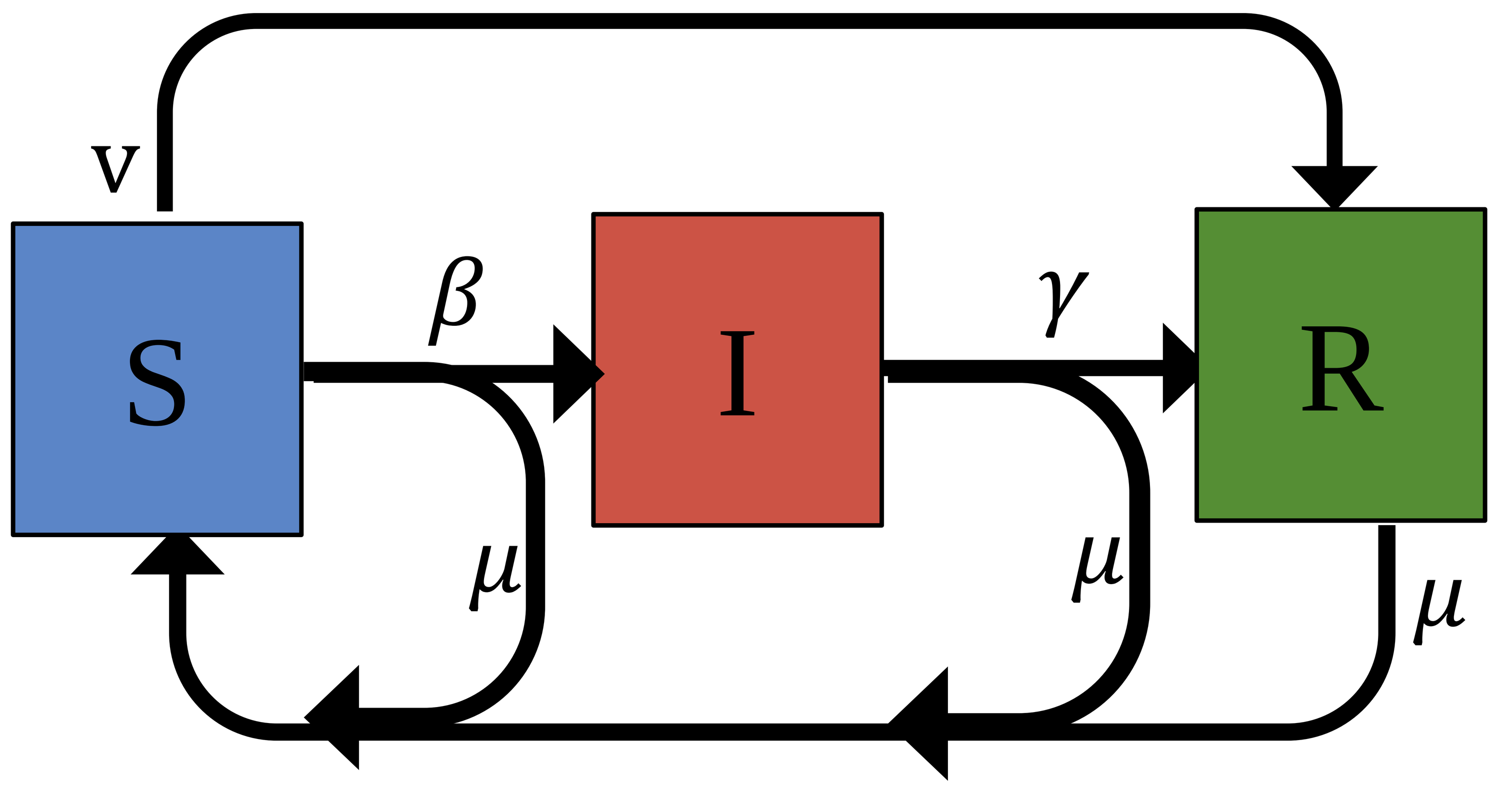

Fig. 3: Transmission Diagram

Preliminary Results

Our disease-free equilibrium for this model is (N, 0, 0).

$$\begin{bmatrix} v & \mu - \beta & \mu \\ 0 & \beta - (\gamma - \mu) & 0 \\ v & \gamma & -\mu \end{bmatrix}$$

The stability of the equilibrium point is determined by the sign of the eigenvalues.

$$\lambda_1 = \beta - (\gamma - \mu)$$

$$\lambda_{2,3} = \frac{\mu - v \pm \sqrt{\mu^2 - 10\mu v + v^2}}{2}$$

The disease-free equilibrium point is stable when $\beta < (\gamma - \mu)$ and when $v \geq 9.98\mu$.

Discussion

While the invention of the measles vaccine has greatly decreased the number of measles cases in developed countries, the recent 2014 outbreak in Disneyland and the 2019 outbreak in several states have shown that current vaccination rates are not enough. With most of the new cases of in 2019 being among unvaccinated sectors of the population, how can this model be adapted to consider discrepancy in vaccination rates within a population? Likewise, with most outbreaks in the United States started by travelers who got infected by measles abroad, how can this model account for international travel?

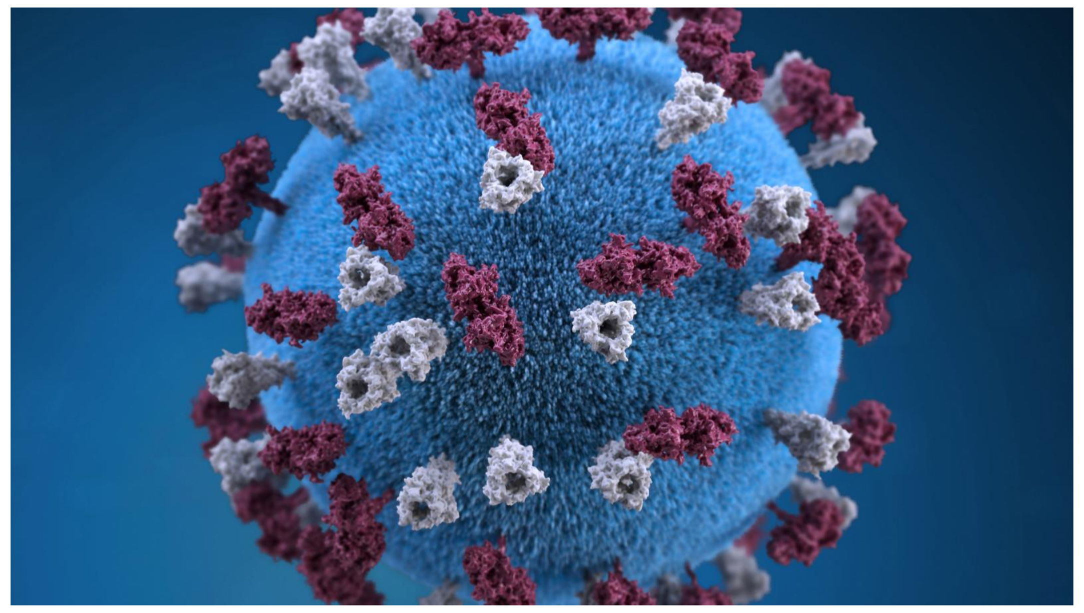

Fig 4: 3D Representation of the Measles Virus (“CDC”)

References

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