

Kermack-McKendrick Model

KMM is a non-spatial temporal SIR (Susceptible, Infected, Recovered) model that represents impact of contagious infection in a closed population over time. Its assumptions are as follows. ([Weisstein, 2017](#); [Anderson and May, 1979](#))

- Epidemic population domain is closed i.e. no birth or death occurs during epidemic.
- Population is homoge

The model compartmentalizes population into 3 groups – susceptible, infected, and recovered. Their relations and rate are shown with 3 non-linear ordinary differential equations. ([Jones and Sleeman, 2003, p.112](#))

$$\frac{dS}{dt} = -\beta SI \quad (1)$$

$$\frac{dI}{dt} = \beta SI - \gamma I \quad (2)$$

$$\frac{dR}{dt} = \gamma I, \quad (3)$$

Where t is time, S is the susceptible population, I is the currently infected, R is the recovered, β is the susceptible to infected rate, γ is the infected to recovered rate.

Model-Project Integration

- I have employed KMM SIR model as described above, into my project by using these equations in constructing the SIR model and thus simulating epidemic effect-propagation over a period on a population.
- To paint the graph, I used 'JSXGraph', a dynamic mathematics visualization library based purely on javascript. ()

References

Jones, D. and Sleeman, B. (2003). *Differential equations and mathematical biology*. 1st ed. Boca Raton, Fla.: Chapman and Hall/CRC.

Weisstein, Eric W. (2017). *Kermack-McKendrick Model -- from Wolfram MathWorld*. [online] Mathworld.wolfram.com.

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Anderson, R.M. and May, R.M., 1979. Population biology of infectious diseases: Part I. *Nature*, 280 (5721), pp.361-367.

Available from: Research on Complex Systems, Humboldt University, Germany online resource- http://rocs.hu-berlin.de/complex_sys_2015/resources/Seminarpapers/Anderson_May_1979.pdf

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