Epidemiology: Two Models for the Spread of Diseases
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Introduction
- Epidemiology is the study of the patterns, causes, and effects of diseases. This project specifically looks at two different mathematical models for the spread of diseases. Both models assume a constant population.

Variables
- P - The total population.
- S - The susceptible population: those who can contract the disease.
- I - The infective population: those who are sick and can infect susceptibles.
- R - The removed or recovered population: those who have had the disease and recovered. For simplicity, we assume that the recovered population are not susceptible.

Reed-Frost to Kermack-McKendrick Model
- Assume constant population, sampling interval times equal to the duration of the disease, and known initial sizes S₀, I₀, R₀.
- Let the probability of contact between an S and an I during a sampling interval be equal to p.
- The probability of an S not getting infected during (n + 1) sampling interval will then be qⁿ = (1 − p)ⁿ.
- This leads to the Markov chain model with a binomial distribution:
  \[ P_r[S_{n+1} = k|S_n = x_n, I_n = y_n] = \binom{n}{k}q^k(1-q)^{n-k}. \]
- This model can be analyzed by Monte-Carlo simulation to understand the propagation of the disease.
- Considering the expected values
  \[ x_{n+1} = E[S_{n+1}] = x_n(1 − p) + y_n p \]
  \[ y_{n+1} = E[I_{n+1}] = (1 − e^{−αp}) x_n + b y_n, \]
  where b is the proportion of infective who remain infective at the end of the sampling interval.
- By assuming a = rh and passing to the limit h → 0 gives the continuous time Kermack-McKendrick model.

The SIR Model and Epidemic Threshold
- Using this equation and the chain rule gives:
  \[ \frac{dS}{dt} = −βSI \]
  \[ \frac{dI}{dt} = βSI − γI \]
  \[ \frac{dR}{dt} = γI \]
- Using this equation and the chain rule gives:
  \[ \frac{dS}{dt} = −βSI \]
- If S₀ > S∗ = γ/β, then initially I increases leading to an epidemic — until S(t) < S∗, after which I decreases.
- If S₀ < S∗, then I(t) always decreases until the disease dies down with no epidemic.

Solutions to Susceptible and Infected Populations

Mickens’ Model
- The second SIR model is Ronald E. Mickens’s model.
- Interpret S, I, R, β, and γ similarly to that of the usual SIR model, then add square roots to the interactive terms:
  \[ \frac{dS}{dt} = −β\sqrt{S}\sqrt{I}, \]
  \[ \frac{dI}{dt} = β\sqrt{S}\sqrt{I} − γI, \]
  \[ \frac{dR}{dt} = γI \]
- This model has two advantages over the usual SIR model:
  - Answers how long I is present after no more S
  - Exactly Solvable (Ta Da!!)

Epidemic
- Using the chain rule gives
  \[ \frac{dS}{dt} \bigg|_{t=0} = β\sqrt{S₀}\sqrt{I₀}\left(\frac{\sqrt{S₀}}{\sqrt{S}} − 1\right), \]
  we can see that S∗ = \( \left(\frac{\gamma}{\beta}\right)^2 \) is the threshold value.

Advantages
- Set S = 0 in usual SIR model and solve for I to obtain
  \[ I(t) = I_0e^{−γt} \]
  - This solution demonstrates that I ≠ 0. This is an issue since diseases die out in real life.
  - Now set S = 0 in Mickens’s model to obtain
    \[ I(t) = \left(-\gamma t + 2\sqrt{I₀}\right)^2. \]
    - At time \( t = t^* = 2\sqrt{I₀}/\gamma \), I(t) = 0, demonstrating that I can reach zero, thus the disease dies out.

Solutions
- Let \( u(t) = \sqrt{S} \) and \( v(t) = \sqrt{I} \). Then apply regular ODE methods to obtain solutions:
  \[ u(t) = \sqrt{S₀ − \frac{γ}{β}t} \cos(\sqrt{β}t) + \sqrt{I₀}\sin(\sqrt{β}t) + \sqrt{S₀} \]
  \[ v(t) = \sqrt{S₀ − \frac{γ}{β}t} \cos(\sqrt{β}t) + \sqrt{I₀}\sin(\sqrt{β}t) + \sqrt{S₀} \]

Solutions
- There is a problem with the solutions; they oscillate.
- Since I = 0 is a trivial solution, \( v(t) \) can be expressed as:
  \[ I(t) = \left(\sqrt{u(t)}\right)^2, \quad 0 < t < t_c \]
  \[ 0, \quad t > t_c. \]
  - A similar pattern is followed for S:
    \[ S(t) = \left(\sqrt{u(t)}\right)^2, \quad 0 < t < t_c \]
    \[ S_{∞}, \quad t > t_c, \]
    where \( S_{∞} \) is the value of the final susceptible population.

References