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A Mathematical Model for Alcoholism Epidemic

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A Mathematical Model for Alcoholism Epidemic

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Abstract

Mathematical models are widely used to study the dynamics of infectious diseases as well as the social networks. This study considers a mathematical model for alcoholism transmission for a closed population. The model is derived from the SIR model for infectious diseases. The study utilizes the Runge-Kutta method as the numerical method to solve a system of differential equations describing the transmission of alcoholism.

Background

Alcoholism can be defined as a pattern of alcohol use that compromises the health and safety of oneself and others [2]. Symptoms of alcoholism include being unable to limit the amount of alcohol consumption, failing to complete tasks at work, home, and school due to alcohol use, and experiencing withdrawal symptoms, such as nausea, when trying to avoid alcohol. There are a multitude of factors that contribute to the cause of alcoholism. These factors may be genetic, social, and/or environmental. Alcoholism, or alcohol use disorder, affects nearly 17 million adults and adolescents in the United States and is the fourth leading preventable cause of death in the US [1]. Mathematical models have been developed to understand the spread of certain diseases, and similar models can be used to analyze patterns of social behaviors. Mathematical models qualitatively help researchers, health care professionals, and policy makers develop prevention and treatment programs for those afflicted.

The SIR Model

The susceptible, infective, removed (SIR) model is a compartmental model developed by Kermack and McKendrick in 1927 [3]. The population of the SIR model is closed and divided into compartments, or classes. The Susceptible (S) class represents the population that is not yet infected by the disease, the Infected (I) class represents the population currently infected by the disease, and the Removed (R) class represents the population that have been infected and then removed. Time t is the independent variable, which creates the functions S(t), I(t), and R(t). The sum of the functions, S(t)+I(t)+R(t) = N, where N is the total population. N is constant since it is assumed that an individual can only belong to one class at a certain time t. The derivatives of the functions with respect to time t and the rates of transfer between each compartment create a system of differential equations:

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \alpha I$$

$$\frac{dR}{dt} = \alpha I$$

The Basic Reproduction Number

The basic reproduction number, R0, is a dimensionless number that predicts the expected number of secondary cases produced by a single infection [4]. When R0 > 1, an epidemic occurs. When R0 <1, then the disease will die out.
R0 can be calculated by:

$$R0 \propto (\frac{infection}{contact}) * (\frac{contact}{time}) * (\frac{time}{infection})$$

Modified SIR Model by Sharma and Samanta [5]

Classes of Drinkers:

S= Moderate and Occasional Drinkers   **T= Drinkers in Treatment**
D= Heavy Drinkers   **R= Temporarily Recovered Drinkers**

System of Differential Equations:

$$\frac{dS}{dT} = \Lambda - \beta_1 S(t)\frac{D(t)}{N} - \mu S(t) + \beta_3 R(t)\frac{S(t)}{N}$$

$$\frac{dD}{dt} = \beta_1 S(t)\frac{D(t)}{N} + \beta_2 T(t)\frac{D(t)}{N} - (\mu + \delta_1 + \phi)D(t)$$

$$\frac{dT}{dt} = \phi D(t) - \beta_2 T(t)\frac{D(t)}{N} - (\mu + \delta_2 + \sigma)T(t)$$

$$\frac{dR}{dt} = \sigma T(t) - \mu R(t) - \beta_3 R(t)\frac{S(t)}{N}$$

Constants:

|	
Λ	recruitment rate of S group
β_1	transmission coefficient from S to D
β_2	transmission coefficient from T to D
β_3	transmission coefficient from R to S
μ	natural death rate of population
δ_1	drinking related death rate of D
δ_2	drinking related death rate of T
φ	proportion of drinkers entering T
σ	recovery rate of T

$$N = S(t) + D(t) + T(t) + R(t)$$

Basic Reproduction Number:

$$R0 = \frac{\beta_1}{\mu + \delta_1 + \phi}$$

Numerical Simulation

Sharma and Samanta's model was simulated using MATLAB builtin function ODE45. ODE45 is based on a 4th order Runge-Kutta method.

Time Series Plot of Different Classes of Drinkers for R0=.538462
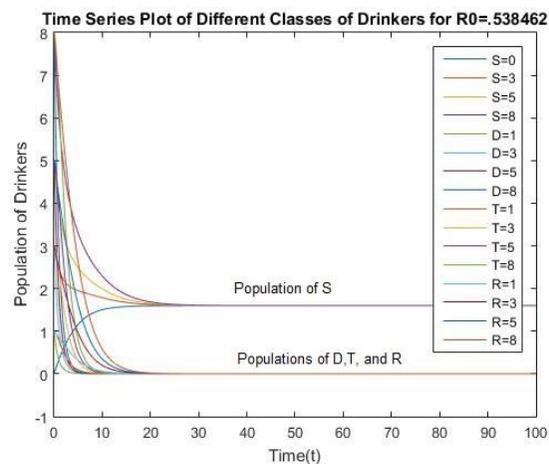
When R0 =.538462 < 1, only moderate and occasional drinkers exist. The populations of classes D,T, and R declines to zero and reaches disease free equilibrium.

Time Series Plot of Different Classes of Drinkers for R0=1.25
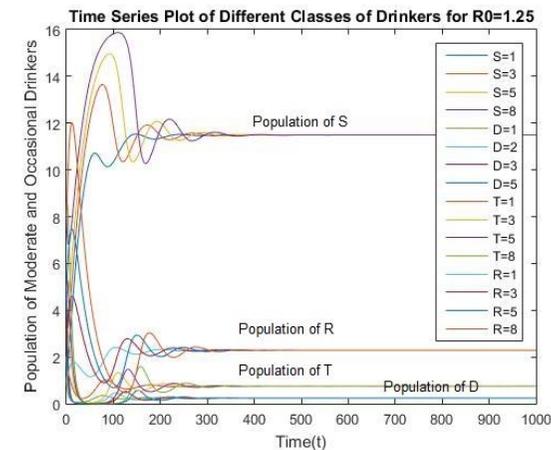
When R = 1.25 > 1, populations for all classes exist. The population of the S class approaches 11.4913, the population of the D class approaches .2395, the population of the T class approaches .7492, and the population of the R class approaches 2.2854. The population of drinkers approaches endemic equilibrium.

Conclusion

The numerical simulations show that disease free equilibrium is stable when R0 <1. When R0 >1, endemic equilibrium becomes stable and disease free equilibrium becomes unstable. Thus, it is more effective to prevent members from class S from entering class D than it is to treat members in classes D and T.

The purpose of this study is to implore further research of the underlying mechanisms of alcoholism and encourage policy makers to reform and improve prevention and treatment resources. Next steps of research may include analyzing the effect demographic variations (sex, age, socioeconomic class, etc.) have in the spread of alcoholism.

References

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