Mathematical Modeling of Epidemics

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Introduction

This document was created as additional to 'Control Theory' subject second laboratory work 'Mathematical Modeling of Epidemics'. This document contains research for a dependence of input parameters on the problem solution. One of well-known models for modeling epidemics is SIRD (Susceptible, Infected, Recovered, Dead). All parameters will be set randomly in recommended intervals that are respective to COVID-19 pandemic. Also, SIRD model can be complicated with some special values.

I chose model with testing, so system described with additional value J - Justified (I guess, it could mean something other). Justified - people who tested with positive result, in other words, people with proved infection. And so I - Infected and latent people.

This work refers to the control theory a little, because model contains control parameters. It can be used to make research of pandemic change and also to try different controls or strategies.

Description of chosen SIRD model

Model is based on differential equations system, that contains each variable change in time. SIRD with testing is described by following system:

$$S(t) + I(t) + J(t) + R(t) + D(t) = N$$

$$\frac{dS}{dt} = -Sp(I) - Su(t)$$

$$\frac{dI}{dt} = Sp(I) - \alpha I - \beta I - Iv(t)$$

$$\frac{dJ}{dt} = Iv(t) - aJ - bJ$$

$$\frac{dR}{dt} = \alpha I + aJ + Su(t)$$

$$\frac{dD}{dt} = \beta I + bJ$$

with initial state $I(0) > 0, S(0) = N - I(0)$, where
N - number of people.
S, I, J, R, D - number of Susceptible, Infected (latent), Infected (tested),
Recovered and Dead people at moment t.
$p(t)dt = p(I(t))dt$ - probability to infect while time dt.
$u(t) \in [0, 1]$ - vaccinated part of people. Control variable, by default $u(t) \equiv 0$.
$v(t) \in [0, 1]$ - tested part of people at moment t. Control variable.

α - coefficient of recovery speed for latent infected.
β - mortality coefficient for latent infected.
a - coefficient of recovery speed for tested infected.
b - mortality coefficient for tested infected.

Let r is mean density of contacts for one person, c - probability of infection in case of contact with infected. So $\frac{I}{N}$ - probability to meet infected. $\frac{rI}{N}dt$ - number of contacts with infected while time dt. $1-c$ - probability not to infect while contact with infected. $(1-c)^{\frac{rI}{N}dt}$ - probability not to infect while time dt. So probability to infect while time dt is:

$$1 - (1-c)^{\frac{rI}{N}dt} = 1 - \exp(\frac{r\log(1-c)I}{N}dt) \approx 1 - (1 + \frac{r\log(1-c)I}{N}dt) = -\frac{r\log(1-c)I}{N}dt$$

So $p(t) = p(I(t)) = -\frac{rI\log(1-c)}{N}$.

To create model of epidemic flow, it is need to solve differential equations system with numeric method. To do so I used R package `deSolve`, function `ode(y, times, func, parms, ...)`. Also, got values are decimals, which is not correct to represent people, so I rounded S, I, floored R, D and got $J = N - (S + I + R + D)$.

As model parameters will be taken: * N - number of people * I_0 - number of infected people at moment $t = 0$, $0 < I_0 < N$ * r - mean number of contacts per day for a single person * c - probability of infection for single contact with infected * α - probability to recover while one day for a single latent infected * β - probability to die while one day for a single latent infected * a - probability to recover while one day for a single tested infected * b - probability to die while one day for a single tested infected