

# 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.

$\alpha$  - coefficient of recovery speed for latent infected.  
 $\beta$  - 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:

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

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 \*  $\alpha$  - probability to recover while one day for a single latent infected \*  $\beta$  - 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

## Research of influence of model parameters

To do research I will variate each parameter with fixed others. As default values I will set randomly uniform in recommended intervals:

$N \in [10^3, 10^6], r \in [0.001, 50], c \in [0.5, 0.9]$

$\alpha \in [0.05, 0.1], \beta \in [0.01, 0.1]$

$a \in [\alpha, 0.1], b \in [0.01, \beta]$ .

testing part function  $v(t)$  will be as it was in real experience, something like cumulative function of normal distribution (first 20 days no tests, then testing speed increasing fast and again decreasing).

```
set.seed(32)

input <- list(
  N = round(runif(1, 1e3, 1e6)),
  I0 = 1,
  r = 10^runif(1, log(0.001, 10), log(50, 10)),
  c = runif(1, 0.5, 0.9),
  alpha = (runif(1, 0.05, 0.1) -> alpha),
  beta = (runif(1, 0.01, 0.1) -> beta),
  a = runif(1, alpha, 0.1),
  b = runif(1, 0.01, beta)
)

input <- lapply(input, round, 4)

print(input)
```

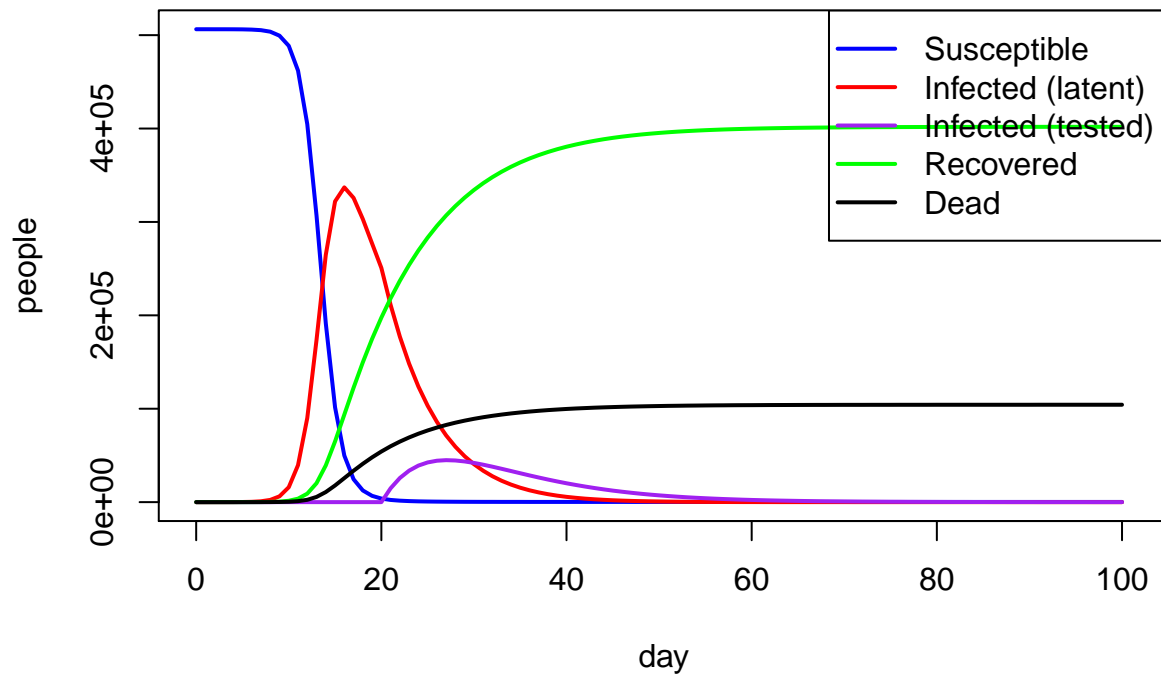
```
## $N
## [1] 506335
```

```
##
## $I0
## [1] 1
##
## $r
## [1] 0.6237
##
## $c
## [1] 0.8235
##
## $alpha
## [1] 0.0864
##
## $beta
## [1] 0.0237
##
## $a
## [1] 0.0994
##
## $b
## [1] 0.0203
```

```
input$v = function(t) ifelse(test = t>20,
                             yes = 0.7*pnorm(t, 150, 100),
                             no = 0)
```

Built model represented on plot:

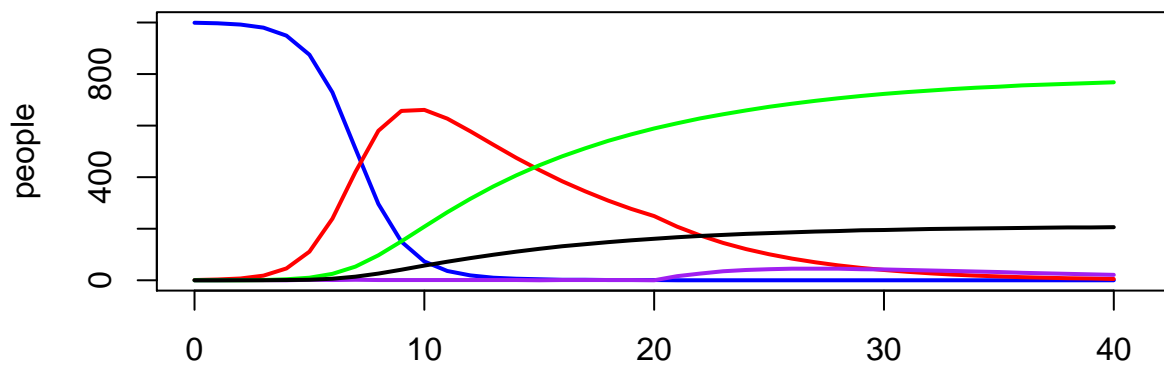
### Model with default parameters



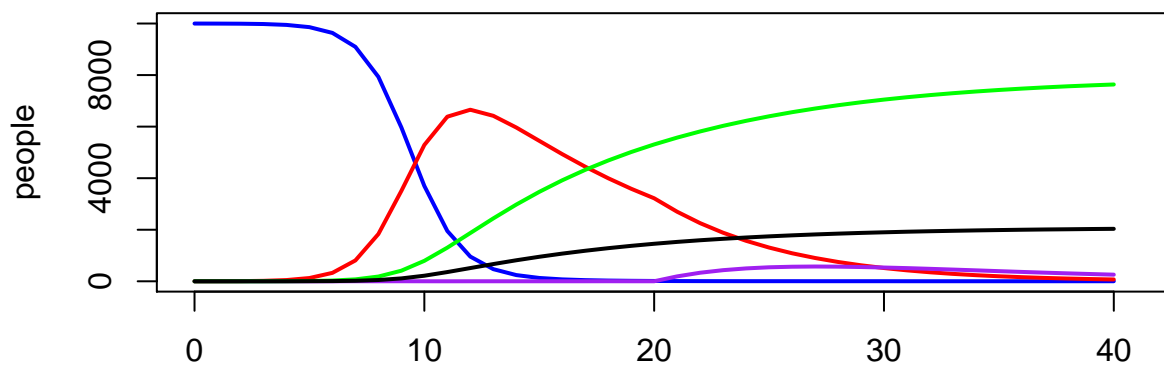
Looks controversial...

Number of people

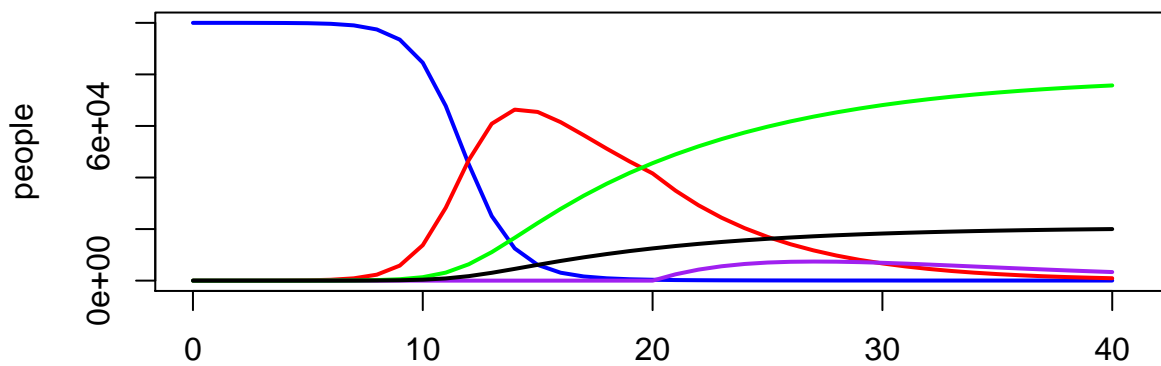
**N = 1000**



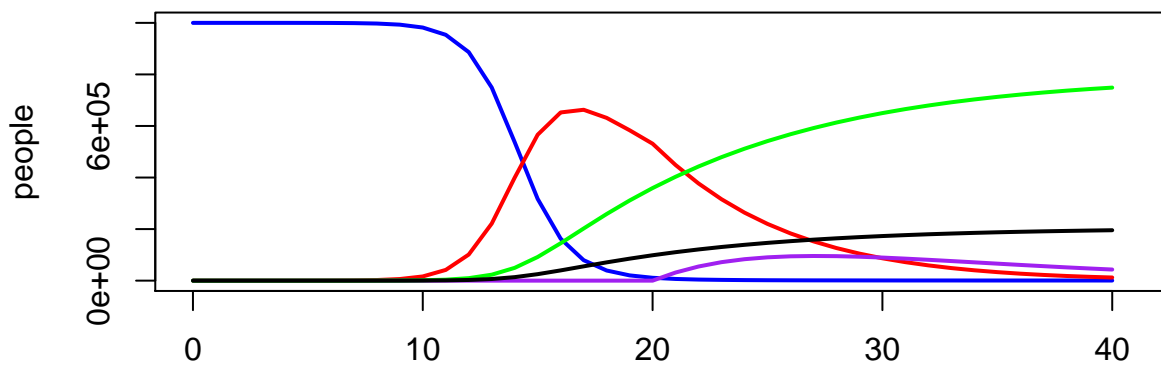
**N = 10000**



**N = 1e+05**



**N = 1e+06**



All plots are almost similar, so  $N$  affects weakly on epidemic flow. There is small shift:  $I$  tops are at  $t \approx 10$  for  $N = 1e3$  and at  $t \approx 17$  for  $N = 1e6$ , so the difference is scanty considering  $N$  change. I conclude:  $N$  affects speed of infection spread not significantly.