

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:

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

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 * 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

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:

$N \in [10^3, 10^6], r \in [0.001, 50], c \in [0.4, 0.9]$

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

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

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, 0.4, 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)
```

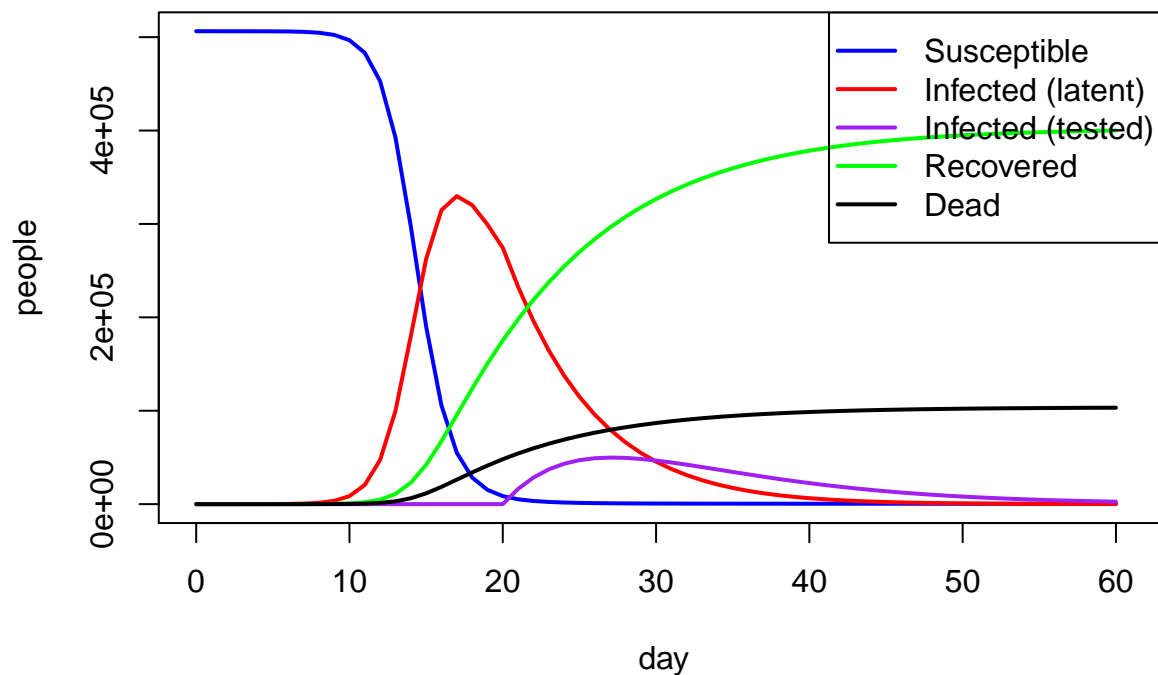
```
## $N
## [1] 506335
```

```
##
## $I0
## [1] 1
##
## $r
## [1] 0.6237
##
## $c
## [1] 0.8044
##
## $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)
```

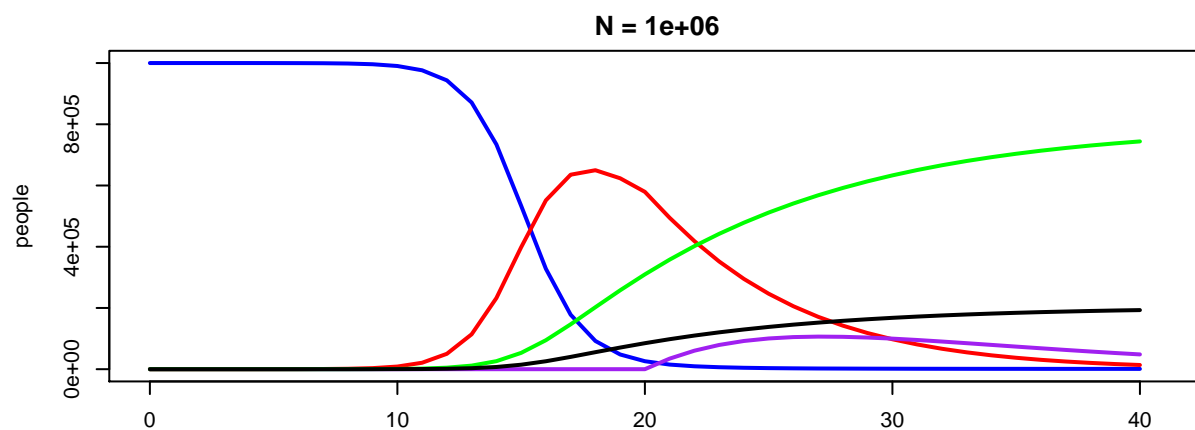
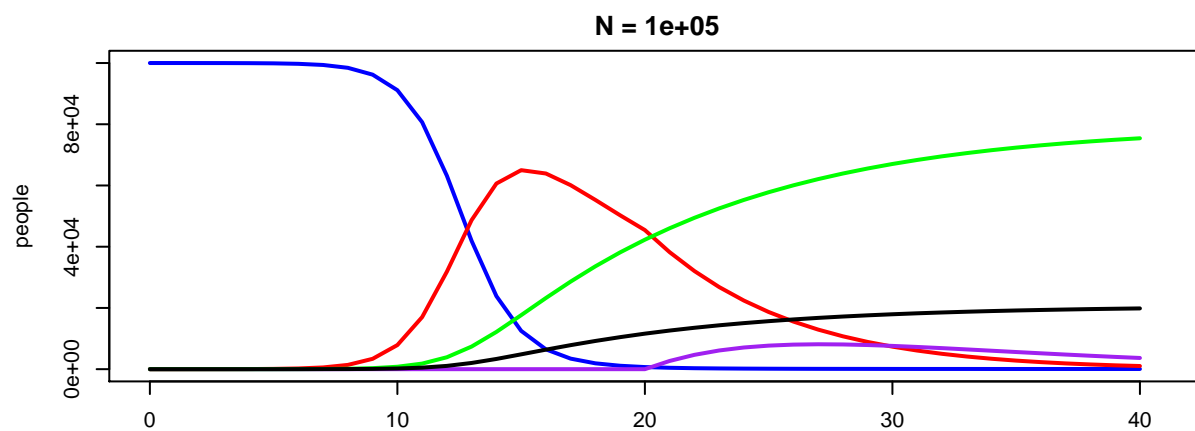
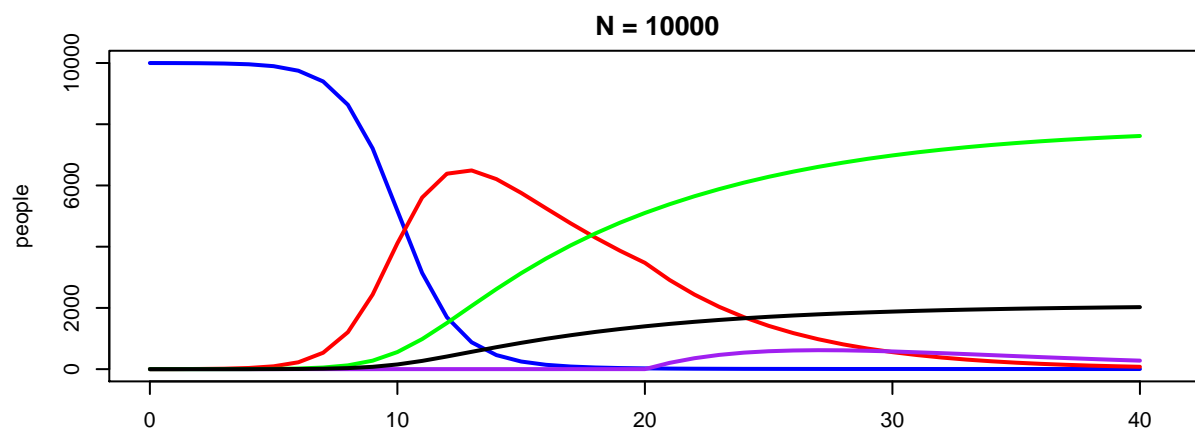
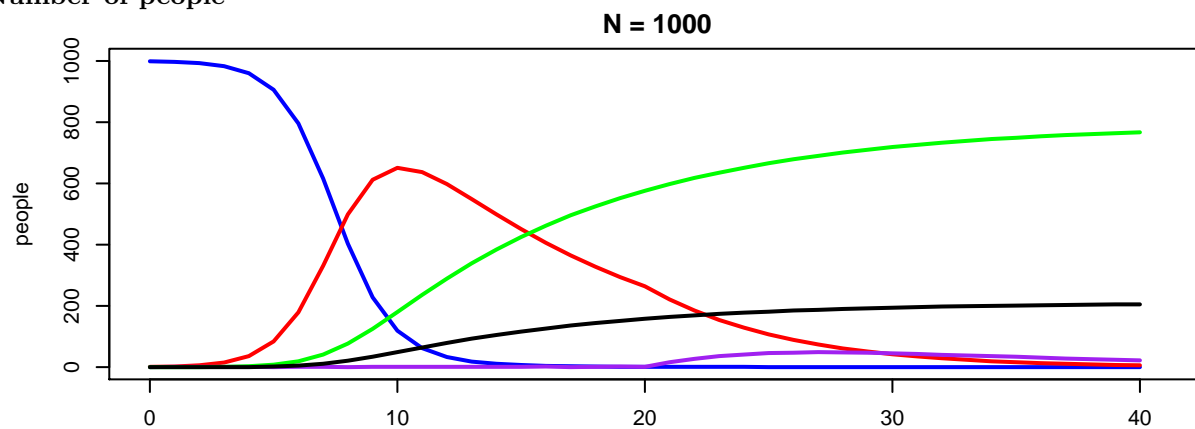
Built model represented on plot:

Model with default parameters until end



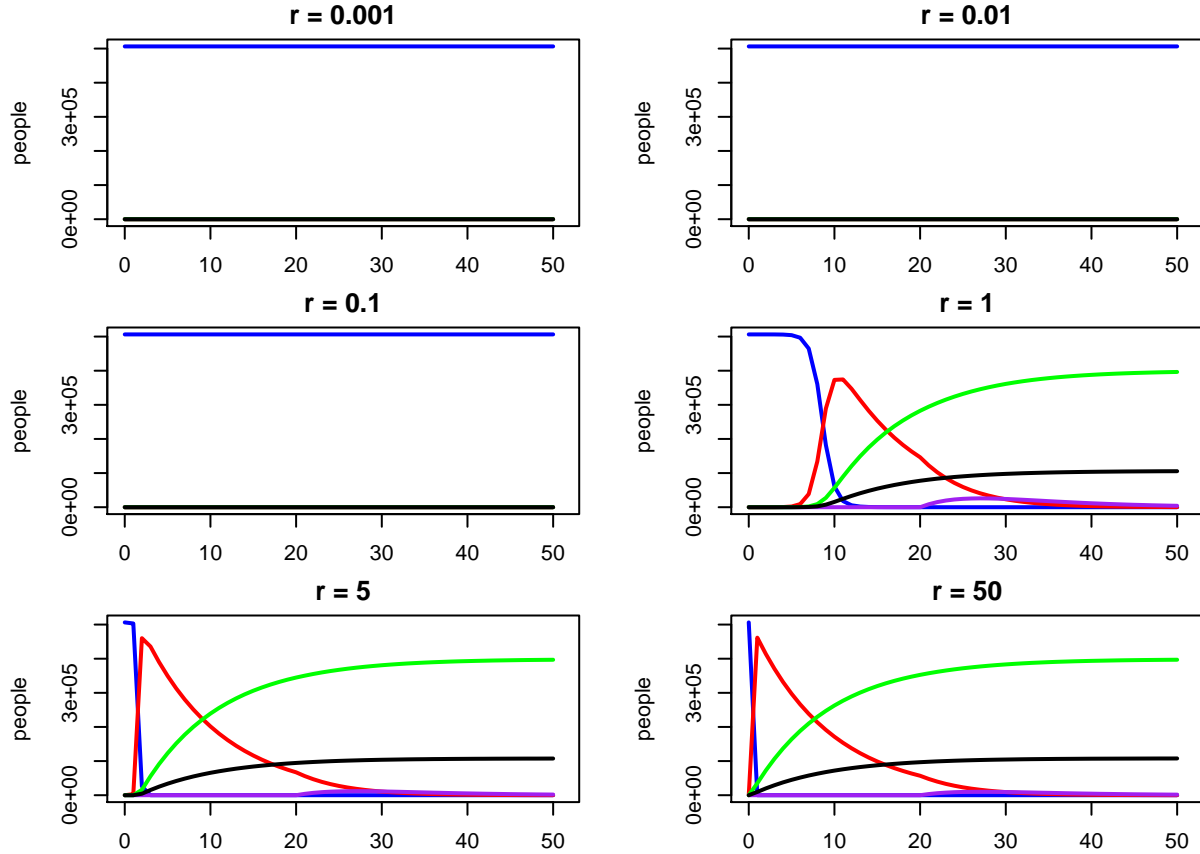
Looks controversial...

Number of people



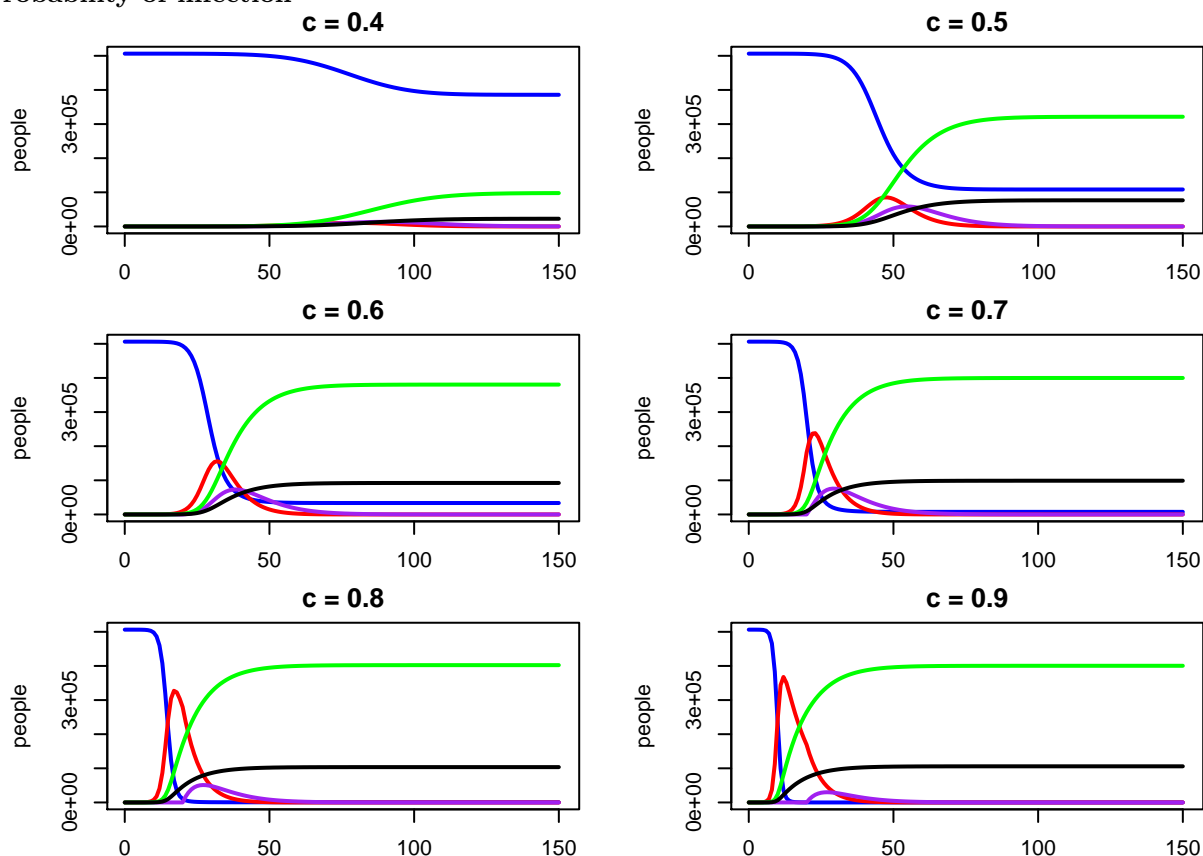
All plots are almost similar, so N affects weakly on epidemic flow. There is small shift: I tops are at $t \approx 10$ for $N = 1e3$ and at $t \approx 17$ for $N = 1e6$, so the difference is scanty considering N change. I conclude: N affects speed of infection spread not significantly.

Number of contacts per day



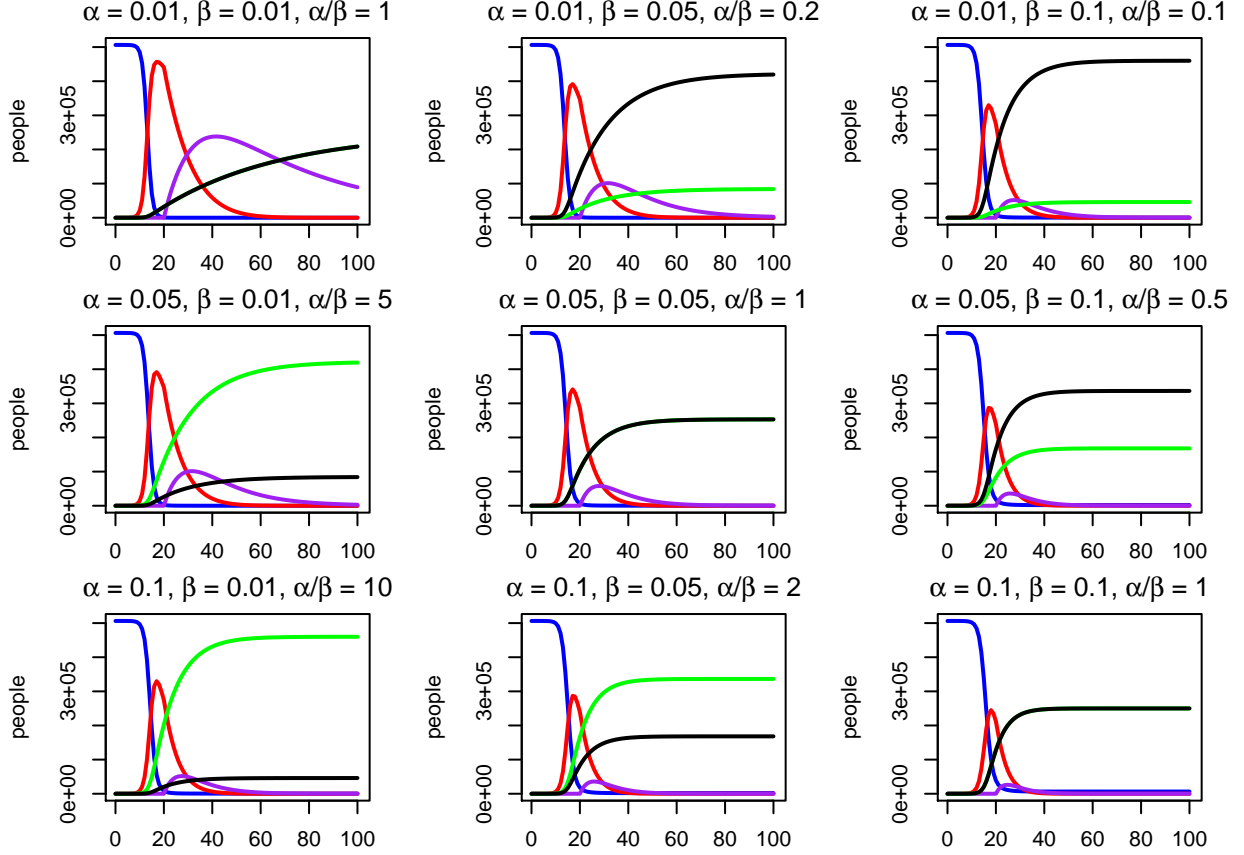
Those plots show weak sides of model. First of all: we see no infection spread for $r \leq 0.1$, it might be because single infected person died before infecting someone other. This situation is very controversial. Also a lack of states is observed, because, for example, COVID-19 has long incubation term, while which people can infect others but not described as infected. And also, I think intervals for parameters are given badly, because infection spreads very fast in each example and also people begin to die from the first day of infection. In my opinion it isn't correct to say about probabilities to recover or die (α, β, a, b), when those probabilities used in determined model. I think word 'probability' not compatible with determined models. OK, also, we see that **increase of r parameter leads to faster infection spread**. But limit distribution of Recovered and Dead almost the same, because it's very few tested infected (testing starts too late). For $r = 50$ there is situation, that almost all people are infected at second day. **Contacts intensity highly affects on begin of infection spread.**

Probability of infection



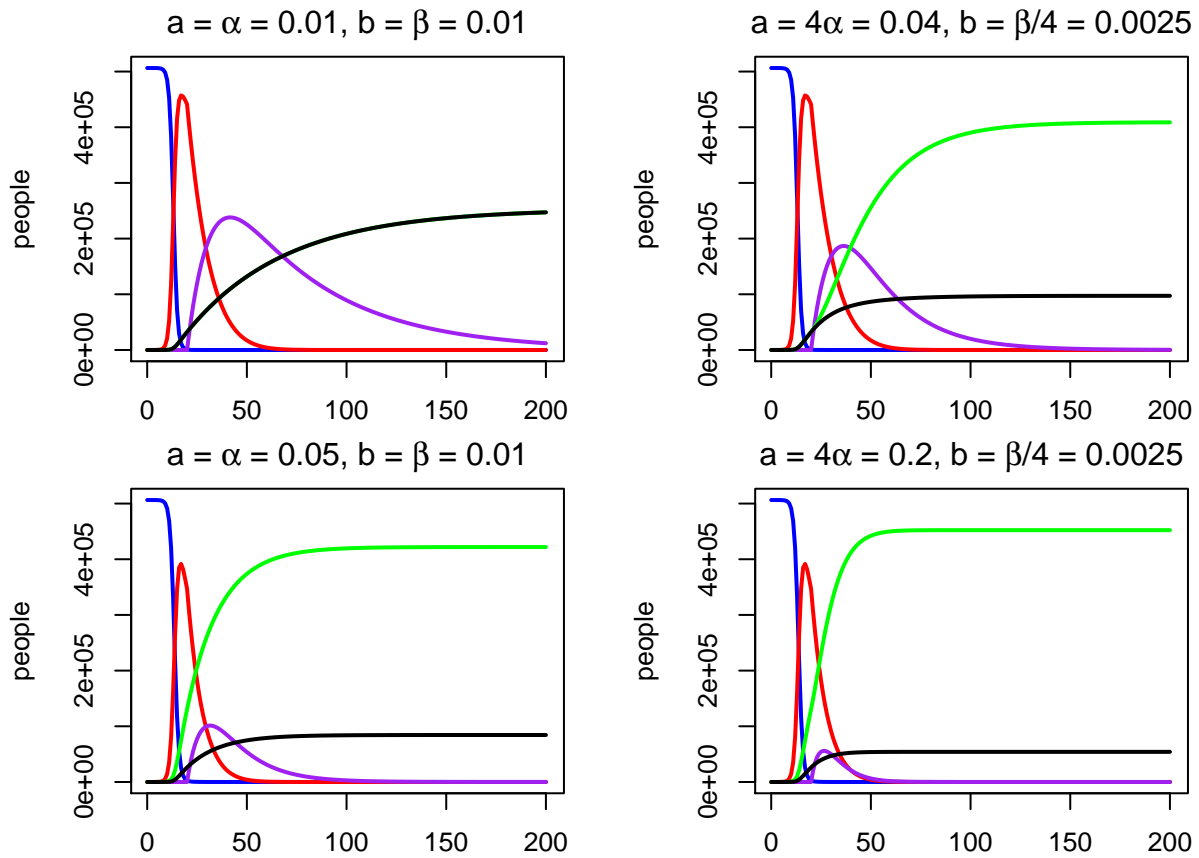
Very interesting. There is such an interesting situation: if probability is small, then there are non-zero rest if Susceptible people. I guess it's because of testing: testing occupies latent Infected people before all Suceptible become Infected, and it can be proved: on plots with $c \geq 0.7$ testing beggins too late - when almost all Susceptibles become Infected. In other cases testing beggins when Infection spread is not such rapid and does not occupy almost all people. So according to this models, I conclude: **if testing exists and it is begun on time, it's available to stop infection spread until all people infected in case infection probability is low**. But there is an issue: it is not realistic, just demonstrative. And who know is it better to recover for all people, or to stop infection. Probably we can choose strategy depending on this value. If infection is low contagious, then it should be isolated, because it is available, like for papilloma or AIDS. But I mentioned sexually transmitted viruses. What about airborne droplet? I think there is no ways to stop it, because we have to make people not to breath. For COVID-19 we have what we have, it has occupied whole Earth.

Recovery and death probabilities I will compare equal sets of α -s and β -s to get more understandable picture. I will also set $a = \alpha, b = \beta$.



All plots look similar, but there are tiny differences. Let's look on diagonal set of plots. We see equal distributions of Recovered and Dead but different forms of lines. And on last plot there is very little rest of Susceptible. Distributions of Recovered and Dead obey to $\frac{\alpha}{\beta}$ rate but, I noticed that height of Infected and hence Tested tops are different and they are less when $\alpha + \beta$ greater and, also, lines become straight earlier. I conclude: **if testing works nice and a, b are better than α, β , then there is a sense to provide more testing (but we have to remember that hospitals are not dimensionless).**

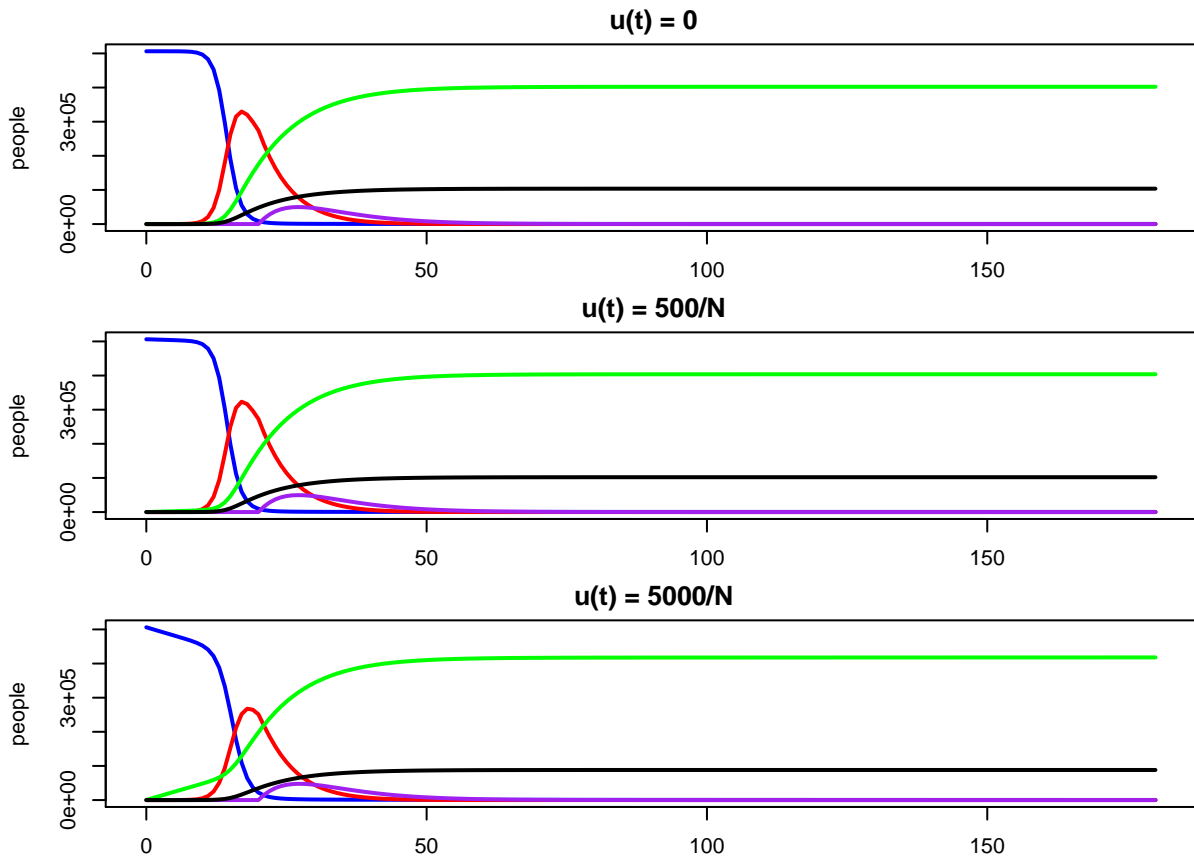
To prove this conclusion I shall demonstrate this. So let's see plots, where $\alpha \in \{0.01, 0.05\}, \beta = 0.01$ and $a \in \{\alpha, 4\alpha\}, b \in \{\frac{\beta}{4}, \beta\}$,



First pair of plots is very demonstrative about how can testing affect death volume. Second pair of plots example shows simple idea: **Testing is more sensible as sooner it begins.**

Vaccination control research

Let try next vaccination controls: $u(t) = 500/N$ and $u(t) = 5000/N$ (500 and 5000 persons per day).



$u(t) = 0$:

##	S	I	J	R	D
## T	396	0	1	402242	103696
## max	506334	329733	49836	402242	103696

$u(t) = 500/N$:

##	S	I	J	R	D
## T	376	0	1	403814	102144
## max	506334	323313	49642	403814	102144

$u(t) = 5000/N$:

##	S	I	J	R	D
## T	235	0	1	417944	88155
## max	506334	267614	47572	417944	88155

There is valuable difference only in last case, but is it available to make 5000 vaccinations per day in half-million city? It's about 1% per a day. I guess it's about maximum, because it can be lack of staff to make such a number of vaccinations per day. Only last example shows notable changes on plot. Numbers differs for each case, but not such significant for first and second cases as for second and third ones. I think that human's life invaluable and it's only the reason to vaccinate. Also I think that it make sense to vaccinate on epidemic very beginning to provide maximum of Recovered people and hence minimum of Infected so prevent many deaths.

My opinion

I think that this model is good for fast inaccurate modeling, but not sufficient to make some good realistic models, because this method gives determined model. I think such a process like epidemic can't be determined, it has to be stochastic. I guess it would be better to make something much complicated (even complex to formulate) but stochastic and to use Monte-Carlo method. I tried to imagine what I would do if I would make my own model. Probably, it would be nice to keep number of Healthy (not infected), Infected (can be latent and tested), Recovered and Immunized (aren't equal) and Dead too. But model has to be complicated with such parameters as:

- Incubation period mean duration
- Malady mean duration
- Quarantine properties (less contacts and probability of infection)
- Mean severity at the moment
- Severity deviation
- Social activity of people at weekdays and weekends
- Mean recovery times
- Probabilities to acquire immunity after recovery
- And others...

I imagine it like a number of capacities where can be people. Like in Markov chain, each person is in some group (Healthy/Infected/Dead...) but as it's hard to process each person by Markov chain. So I propose to move random amounts of people from each state (except Dead and Immunized) like in Markov chain but with consideration of mentioned parameters. For example, high severity brings high death or higher mean recovery times decreases probability to infect again.