

# GTDM Third Assignment

Group 2

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## 1 Instructions

Consider the stochastic process of spread of an epidemic (of COVID-19, influenza, or other similar viruses) in a population composed of  $N$  individuals. Assume that each individual at each time step can be in one of the following 3 states:

- $S$  = susceptible = not infected and not immune (then s/he can be infected)
- $I$  = infected
- $R$  = removed = recovered and immune, or dead

Assume also that at each time step each susceptible individual becomes infected with probability 0.15, each infected individual is removed with probability 0.3 and each removed individual returns back to be susceptible with probability 0.05. Represent the evolution of the epidemics as a Markov chain and write the transition matrix.

Imagine now that the number  $N$  of individuals in the population is  $N = 10000$ . If it is possible, find what will be the number of individuals in the three states  $S$ ,  $I$ ,  $R$ , in the long run, after many time steps.

## 2 Representation of the Pandemic as a Markov Chain

To represent the problem through a Markov Chain we need to define the main objects that are in it. To do that we will present the *starting state* vector called  $\mu^{(0)}$  and the *transition matrix* named  $P$ .

$$\mu^{(0)} = (1, 0, 0)$$

$$P = \begin{bmatrix} 0.85 & 0.15 & 0 \\ 0 & 0.7 & 0.3 \\ 0.05 & 0 & 0.95 \end{bmatrix}$$

We can see from our starting state vector  $\mu^{(0)}$  that on the first moment we are susceptible with probability one and from that moment on will start the spreading of the epidemic depending on the probabilities given by the transition matrix  $P$ . We will define the  $P$  matrix through the probabilities stated in the problem explanation and will define the state  $\mu^{(0)}$  as the step in which all of the individuals in the population are in the  $S$  state; before the pandemic everyone is in the Susceptible group. We can then represent our problem in the Figure 1.

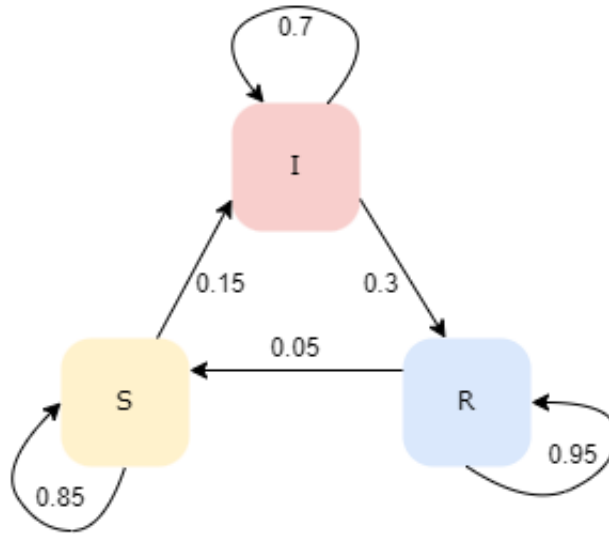


Figure 1: Markov Chain

We can observe from the Figure 1 that since each of the states of the Markov Chain has a loop, they are all *aperiodic*. Then, since all of them are *aperiodic* we can deduce that the entire chain is **aperiodic**.

Another very interesting property is that a Markov Chain in which every state can be reached from every other state is denominated an *irreducible* Markov chain. It is clear from Figure 1 that our example is also **irreducible**.

Then, when we have a Markov Chain that is both irreducible and aperiodic then it has a unique stationary distribution; in our case then our Markov Chain has a **single stationary distribution**.

### 3 Evolution of the Pandemic

To understand the evolution of the Pandemic through our Markov Chain, knowint that it is **homogenous**, we can then exploit the following property:

$$\mu^{(n)} = \mu^{(0)} P^n$$

Knowing  $\mu^{(0)}$ , which is the initial state of the chain, we will be able to compute the  $n$ th state through the multiplication of it with the transition matrix  $P^n$ .

Starting from

$$\mu^{(0)} = (1, 0, 0)$$

Starting from the *1st* state we will have:

$$\mu^{(0)} P^1 = (0, 85, 0, 15, 0)$$

Then, the *10th* state will be:

$$\mu^{(0)} P^{10} = (0.2790997, 0.1894173, 0.531483)$$

and that the *50th* state will be:

$$\mu^{(0)} P^{50} = (0.2222218, 0.1111099, 0.6666683)$$

We can notice that the *200th* state will be:

$$\mu^{(0)} P^{200} = (0.2222222, 0.1111111, 0.6666667)$$

and the *1000th*

$$\mu^{(0)} P^{1000} = (0.2222222, 0.1111111, 0.6666667)$$

These numerical examples give us an intuition that after some iterations we converge into a stable probability which is a stationary state. Then it can be assumed that the distribution has converged in a single state and won't change in the future. Moreover, we can use the graph in Figure 2 to show the distribution converging around approximately the *25th* step.

If the population was composed by 10000 individuals we can estimate, through the stationary distribution, that the number of people in each state would be:

- $0.222222 \times 10000 = 2,222.2$  individuals in the S state
- $0.111111 \times 10000 = 1,111.1$  individuals in the I state
- $0.666667 \times 10000 = 6,666.7$  individuals in the R state

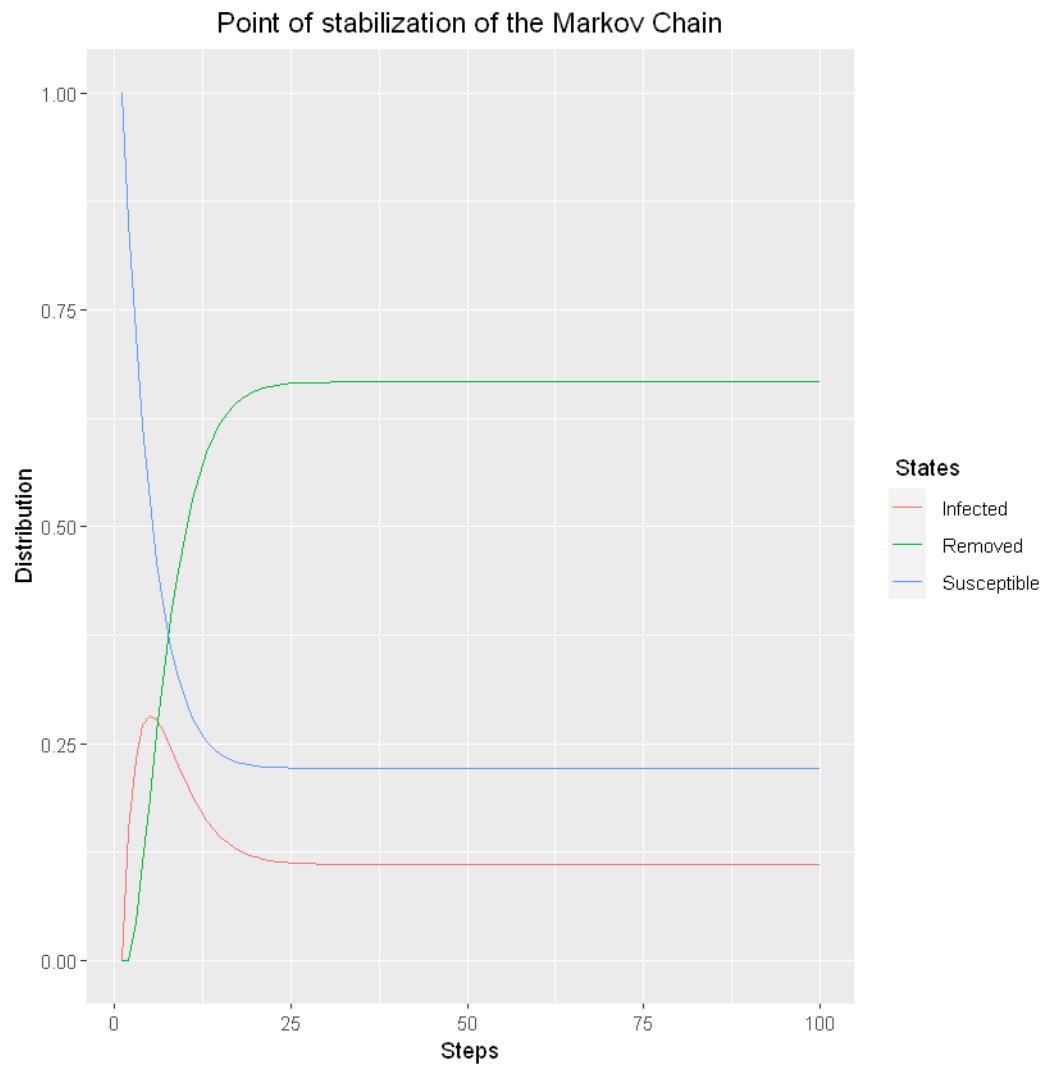


Figure 2: Graph of the theoretical distribution of the Markov Chain

## 4 Simulation of the Pandemic

We can simulate our Markov Chain of the Pandemic using R code.

```
1 npeople<-10000
2 nsteps<-200
3 u0<-c(1,0,0)
4 peopleMat<-matrix(1,npeople,1)
5 stepsMat = matrix (nrow=nsteps, ncol=3)
6 stepsMat[1,] = c(sum(peopleMat==1),sum(peopleMat==2),sum(peopleMat==3))
7
8 P = matrix (c( 0.85 , 0.15 , 0,
9 0, 0.7 , 0.3 ,
10 0.05 , 0, 0.95
11 ),nrow =3 , ncol =3 , byrow = TRUE )
```

We set the initial variables that we need such as the number of individuals *npeople*, the number of steps to simulate *nsteps*, the initial state  $\mu^{(0)}$ , we create a matrix *peopleMat* that will be useful to keep track of the state of each person through the simulation, a matrix *stepsMat* to record the distribution through the simulation and the *P* matrix that is the transition matrix of the Markov Chain.

```
1 state_picker<-function(p){
2   cs <-cumsum(p) - runif(1,min = 0,max = 1)
3   i<-min(which(cs>0))
4   i
5 }
```

We define a function *state\_picker* that will have a probability distribution as input and will output a random index between 1 and 3 using that distribution.

```
1 for (numstep in c(2:nsteps)){
2   for(person in c(1:npeople)){
3     if (peopleMat[person]==1)
4       nrow<-1
5     else if (peopleMat[person]==2)
6       nrow<-2
7     else if (peopleMat[person]==3)
8       nrow<-3
9
10    peopleMat[person]<-state_picker(P[nrow,])
11  }
12  stepsMat[numstep,] = c(sum(peopleMat==1),sum(peopleMat==2),sum(peopleMat ==3))
13 }
```

The nested for loop here defined will update for 200 steps all the 10000 people, with distributions taken from the transition matrix, while keeping track of the number of them in each state at every step. We can then visualize through *ggplot2* the *stepsMat*.

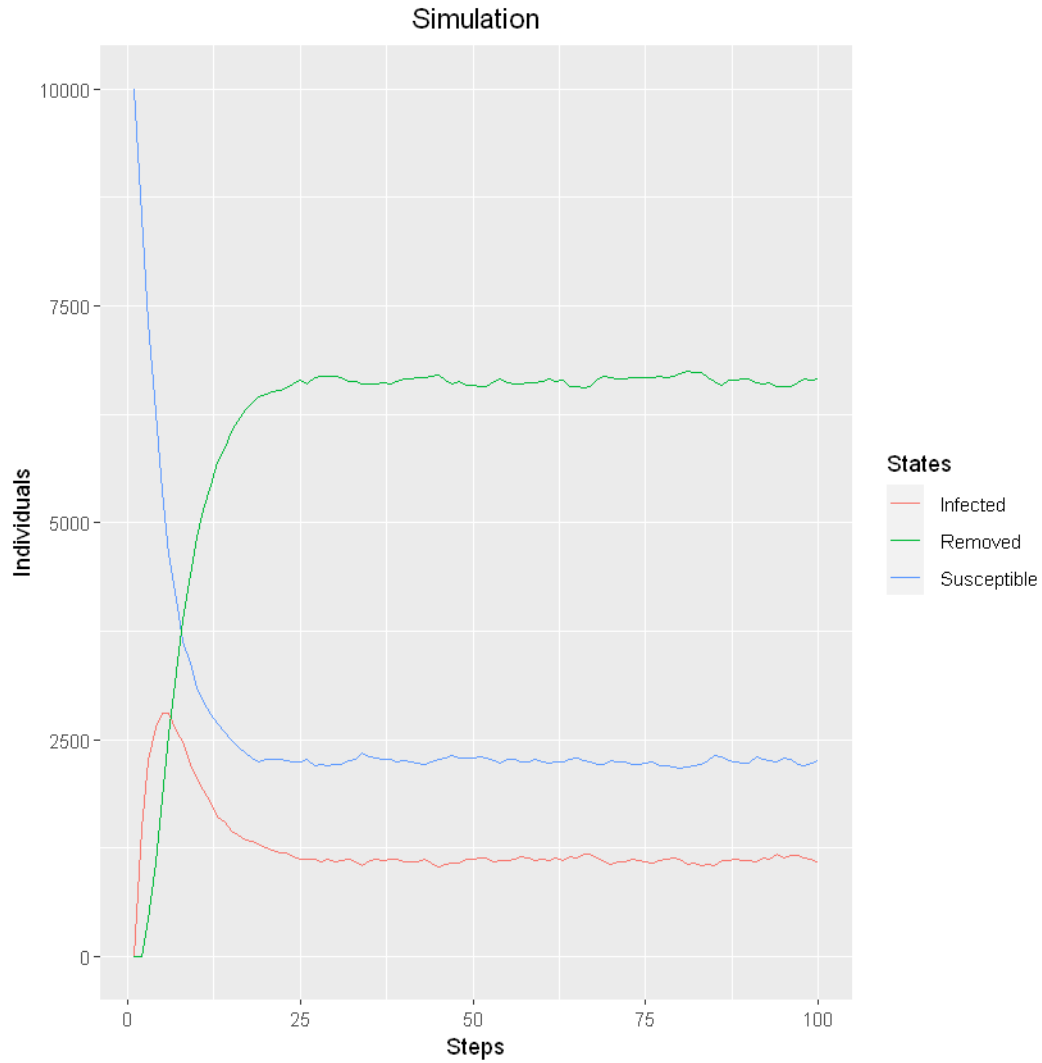


Figure 3: R Simulation of the Pandemic

As we can see, the simulation highlights what we already knew from the theoretical evolution of the pandemic. This meaning that the distributions will converge to a stationary distribution at a certain point. We can compare the results of the simulation after 100 steps:

$$S = 0.2209 \quad I = 0.1069 \quad R = 0.6722$$

with the ones from the theoretical study:

$$S = 0.2222222 \quad I = 0.1111111 \quad R = 0.6666667$$

## 5 Integral Codebase

```
1 library(stats)
2 state_picker<-function(p){
3   cs <-cumsum(p) - runif(1,min = 0,max = 1)
4   i<-min(which(cs>0))
5   i
6 }
7
8 npeople<-10000
9 nsteps<-100
10 u0<-c(1,0,0)
11 peopleMat<-matrix(1,npeople,1)
12 stepsMat = matrix (nrow=nsteps, ncol=3)
13 stepsMat[1,] = c(sum(peopleMat==1),sum(peopleMat==2),sum(peopleMat==2))
14
15 P = matrix (c( 0.85 , 0.15 , 0,
16 0, 0.7 , 0.3 ,
17 0.05 , 0, 0.95
18 ) ,nrow =3 , ncol =3 , byrow = TRUE )
19
20 for (numstep in c(2:nsteps)){
21   for(person in c(1:npeople)){
22     if (peopleMat[person]==1)
23       nrow<-1
24     else if (peopleMat[person]==2)
25       nrow<-2
26     else if (peopleMat[person]==3)
27       nrow<-3
28
29     peopleMat[person]<-state_picker(P[nrow,])
30   }
31   stepsMat[numstep,] = c(sum(peopleMat==1),sum(peopleMat==2),sum(peopleMat ==3))
32 }
33 stepsMat
34
35 library(ggplot2)
36 states = c("Susceptible", "Infected", "Removed")
37 simulation_evolution_df = as.data.frame(stepsMat )
38 names(simulation_evolution_df) = states
39 ggplot () +
40 geom_line ( data = simulation_evolution_df , aes ( x = c (1: nsteps ) ,
41 y = Susceptible, color = " Susceptible " ) ) +
42 geom_line ( data = simulation_evolution_df , aes ( x = c (1: nsteps ) ,
43 y = Infected, color = " Infected " ) ) +
44 geom_line ( data = simulation_evolution_df , aes ( x = c (1: nsteps ) ,
45 y = Removed, color = " Removed " ) ) +
46 labs ( colour ="States",x="Steps",y="Individuals") +
47 ggtitle ( " Evolution of the epidemic - Simulation approach " ) +
48 theme ( plot.title = element_text ( hjust = 0.5) )
49
50 res = table (peopleMat)/npeople
51 res
52
53
54 library(markovchain)
55 library(diagram)
56 library(ggplot2)
57 library(expm)
58
59 states = c("Susceptible", "Infected", "Removed")
60
61 u0 = c(1 ,0 ,0)
62 nsteps = 100
63 mat = matrix (nrow =nsteps, ncol =3)
64 mat[1 ,] = u0
65
66 for (i in c(2: nsteps )){
67   mat[i ,] = u0 %*%P
68   P= P*%P
69 }
```

```

70 mat = as.data.frame (mat)
71 names (mat) = states
72 ggplot () +
73 geom_line ( data = mat , aes ( x = c (1: nsteps ) ,
74 y = Susceptible , color = "Susceptible" ) ) +
75 geom_line ( data = mat , aes ( x = c (1: nsteps ) ,
76 y = Infected , color = "Infected" ) ) +
77 geom_line ( data = mat , aes ( x = c (1: nsteps ) ,
78 y = Removed , color = "Removed" ) ) +
79 labs ( colour ="States",x="Steps",y="Distribution" ) +
80 ggtitle ( "Point of stabilization of the Markov Chain" ) +
81 theme ( plot.title = element_text ( hjust = 0.5 ) )

```