**NAME**

**COLLEGE NUMBER**

**Question One:**

In this example, an analysis and sismulation of the Marckov chain is done on the case of the patients urretn state and what should happene thereafter just in case they get unwell. Just as the case of the Markov principle states; the object can only move to the next state based on its current state and not on any predecessor states. These states are determined by probabilities.

For instance the probability of a person moving from healthy to sick and from sick to hospitalised will depend on the current state at any given time. This is memorylesness

set.seed(42) #Initializes the number of instances to be taken as 42, same as use table values

a <- state("SS","HH","DD") #Define current obkcet states

b <- list(a, a)

n\_days <- 300 #Consider the highest number of days

#Define the transition matcrix of 3 rows and 3 columns assignining it a variable of transition matrix

transition\_matrix <- matrix(c(a, 0.3, 0.001,

                            0.4, b, 0.01,

                            0, 0, 1), nrow=3, ncol=3, byrow=TRUE)

state <- 1 #Consider initial state as 1 and begin check within the 300 days

patient\_record <- rep(0, n\_days)

for (day in 1:n\_days) {

  pr <- transition\_matrix[state, ]

  state <- sample(c(1:3), size = 1, prob = pr)

  patient\_record[day] <- state

}

#Plot the matrix probablility

plot(1:n\_days, patient\_record, "l") $

**Question Two**

set.seed(42) #Initializes the number of instances to be taken as 42, same as use table values

a <- state("SS","HH","DD") #Define current obkcet states

b <- list(a, a)

n\_days <- 300 #Consider the highest number of days

#Define the transition matcrix of 4 rows and 4 columns assignining it a variable of transition matrix

transition\_matrix <- matrix(c(a, 0.3, 0.001,

                            0.4, b, 0.01,

                            0, 0, 1), nrow=4, ncol=4, byrow=TRUE)

state <- 1 #Consider initial state as 1 and begin check within the 300 days

patient\_record <- rep(0, n\_days)

for (day in 1:n\_days) {

  pr <- transition\_matrix[state, ]

  state <- sample(c(1:3), size = 1, prob = pr)

  patient\_record[day] <- state

}

#Plot the matrix probablility

plot(1:n\_days, patient\_record, "l") $

**2 Data Analysis**

Initialize the library tidy verse and then load dataset from file .Rdata.Create a variable called pca\_x as line of fit. Define the new variable of pca\_res1 as residual. Create the dataframe based on the variable from pc\_df1.Select sample data range of patient data as 1-21. Then plot the output.

library(tidyverse)

load("assess\_data\_21.Rdata")

pca\_x <- t(log(Y + 1))

pca\_res1 <- prcomp(pca\_x, center = TRUE, scale = TRUE)

pc\_df1 <- data.frame(pca\_res1$x[1:21, 1:21], tissue = patient\_data$tissue[1:21],

patient = patient\_data$patient[1:21])

ggplot(pc\_df1, aes(x = PC1, y = PC2, shape = tissue, col = patient)) +

geom\_point(size = 4)

**Multiple regression**