Assignment week 1
mRNA Dynamic

Student: Vincent Talen

Student number: 389015

Class: BFV2

Study: Bio-Informatics

Institute: Institute for Life Science & Technology

Teacher: Tsjerk Wassenaar

Date: 2022-06-07

Contents

1 Assignment 1

1.1

There are two parameters that need to be programmed, namely; - r (rate of decay of existing transcripts in percentage) - m (amount of new transcripts per second)

1.2

Differential equations first came into existence with the invention of calculus by Newton and Leibniz [1]. This specific model equation was made to calculate differences in mRNA transcripts present that are only influenced by a rate of decay and the amount of transcripts that get created each second.

1.3

$$\frac{\Delta R}{\Delta t} = -r * R + m$$
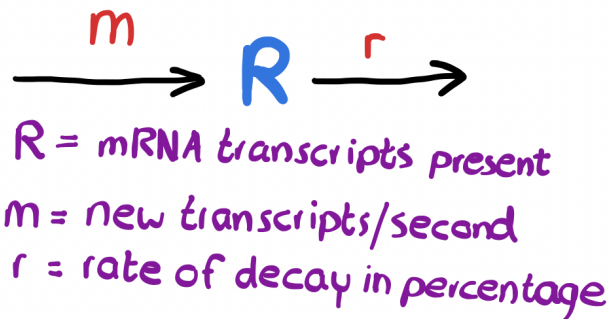
1.4

Below is the model function that can be used for the `ode` function from the `deSolve` package, it returns the delta R (the change in number of mRNA transcripts present). The delta R is returned and not the actual R number is that the `ode` function needs the model to return it in a specific way and itself calculates the resulting R values. The change for a specific time frame needs to be returned.

```
# Create model function
model <- function(time, cur.state, parameters) {
  # Unpack the cur.state (R) and the parameters (r & m) for instant access
  with(as.list(c(cur.state, parameters)),{
    # Calculate change in R and return it
    delta.R <- -r * R + m
    return(list(delta.R))
    })
}
```

2 Assignment 2

```r
# Initial value and time frame
initial.values <- c(R = 100)
times <- seq(0, 15, by = 0.01)

# Increasing R
incr.params <- c(r = 0.5, m = 60)
incr.out <- ode(y = initial.values, times = times, func = model,
                parms = incr.params, method = "euler")

# Steady state
steady.params <- c(r = 0.5, m = 50)
steady.out <- ode(y = initial.values, times = times, func = model,
                  parms = steady.params, method = "euler")

# Decreasing R
decr.params <- c(r = 0.5, m = 40)
decr.out <- ode(y = initial.values, times = times, func = model,
                parms = decr.params, method = "euler")

# Create plot with steady state and add increasing- and decreasing states after
plot(steady.out, type = 'l', ylim = c(75,125), col='green',
     main = 'Amount of mRNA transcripts over time',
     xlab = "Timepoints", ylab = "number of mRNA transcripts")
lines(incr.out, col='red')
lines(decr.out, col='blue')

# Add a legend to the plot
legend(9, 117, legend = c('steady state', 'increasing over time', 'decreasing over time'),
       fill = c('red', 'green', 'blue'))
```
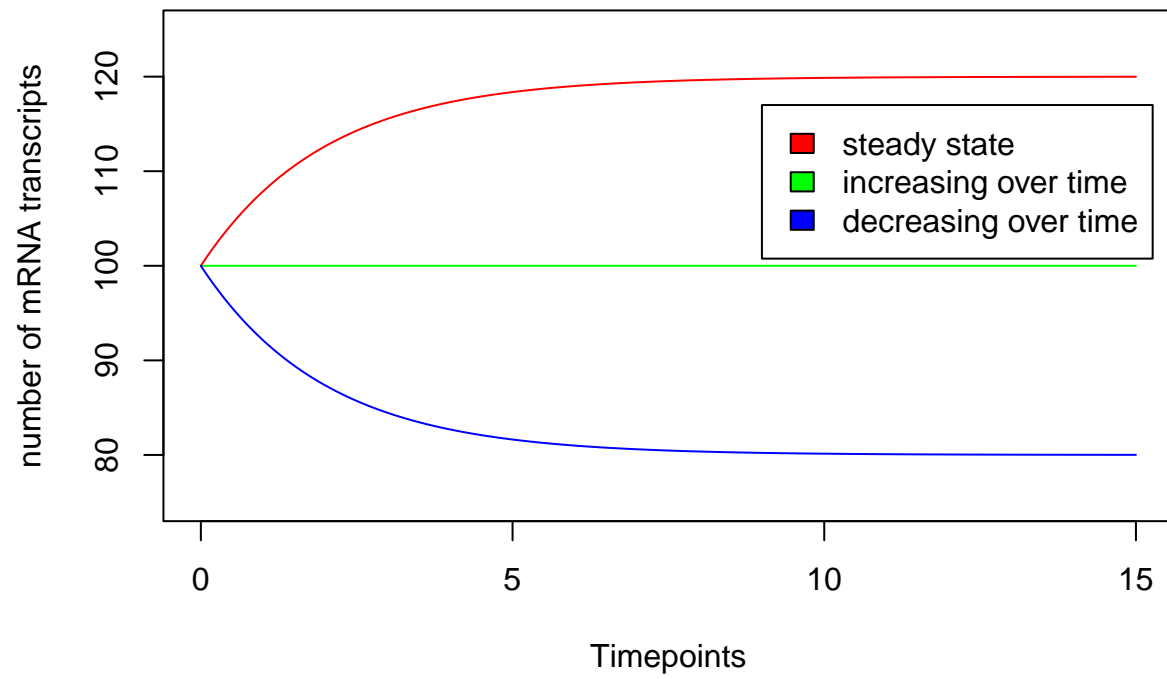
Amount of mRNA transcripts over time

References

[1] Wikipedia contributors: *Differential equation*, Wikipedia, The Free Encyclopedia, https://en.wikipedia.org/w/index.php?title=Differential_equation&oldid=1087007437 (accessed May 10, 2022).