

# Assignment week 1

## mRNA Dynamic



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# 1 Assignment 1

## 1.1

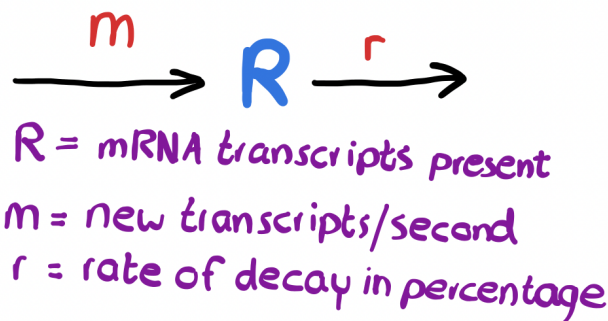
There are two parameters that need to be programmed, namely; -  $r$  (rate of decay of existing transcripts in percentage) -  $m$  (amount of new transcripts per second)

## 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

```
# 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")

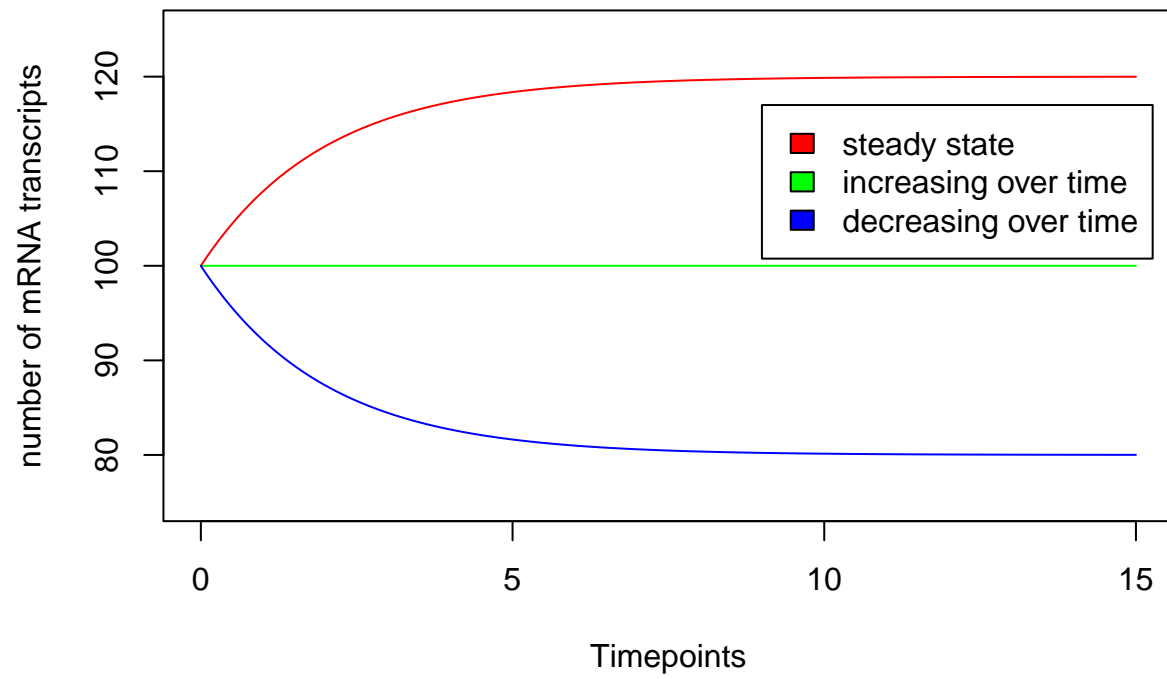
# Steady state
steady.params <- c(r = 0.5, m = 50)
steady.out <- ode(y = initial.values, times = times, func = model,
                 parms = steady.params, method = "euler")

# 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](https://en.wikipedia.org/w/index.php?title=Differential_equation&oldid=1087007437) (accessed May 10, 2022).