

mRNA

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4/23/2021

1 Introductie

mRNA levels in a cell change dynamically in accordance with 3 models.

- system is at the steady state.
- number of mRNA is increasing over time.
- number of mRNA is decreasing over time.

1.1 Goal.

we will attempt to make these models using the deSolve package.

1.2 Theory.

the change of mRNA can be modelled using this biological model based upon. [\[1\]](#).

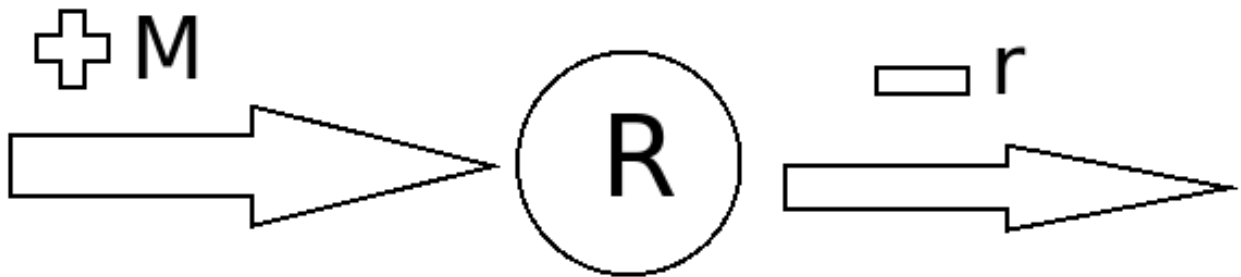


Figure 1: biological model

when we turn this biological model into a mathematical equation we get:

$$\frac{dR}{dt} = -rR + m$$

R is the number of transcripts.

r is the rate of decay of existing transcripts.

m is the number of new transcripts produced per second.

2 Methods.

2.1 The software model.

DeSolve and this formula: `dr <- m - r * (y + m)` will build out out a model using the code below.

```

library(deSolve)

# parameters
parameters <- c(m = 0, r = 0)
parameters_up <- c(m = 13, r = 0.1)
parameters_down <- c(m = 9, r = 0.1)

# model
volume <- function(t,y,parms){
  with(as.list(c(parms)),{
    dR <- m - r * (y+m)
    return(list(c(dR)))
  })}

#initial state
state <- c(Volume = 100)

#define time sequence you want to run the model
times <- seq(0, 100, by = 1)

# run simulation using continuous approach
out <- ode(times = times, y = state, parms = parameters, func = volume, method = "euler")
out_up <- ode(times = times, y = state, parms = parameters_up, func = volume, method = "euler")
out_down <- ode(times = times, y = state, parms = parameters_down, func = volume, method = "euler")

```

2.2 Model configuration.

The following table has the values used in the model, 100 is used as the initial value, it represents 100% of starting value. New transcripts is the gain of transcripts

Model	New Transcripts	Decay Ratio
a.	0	0
b.	13	0.1
c.	9	0.1

3 Results.

4 Conclusion and discusion.

5 References.

References

- [1] TING CHEN, HONGYU L. HE, GEORGE M. CHURCH *modeling gene expression with differential equations* 4, 1999, <https://arep.med.harvard.edu/pdf/Chen99.pdf>.