Thema08-week1-mRNA

Jurrien de Jong

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1 Introduction

Introduction of the research and introduction research questions

1.1 Goal

- Describe Goal (not the educational goal but the research goal)
- Describe how you reach the goal (e.g. make model and figures, use different setting)
- formulate hypothesis

1.2 Theory

- Describe biological model
- Picture of the biological model

Give an explanation of the model with citations of source [1] (replace this with actual source) and formula explanation

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

Describe each element and the transformations

2 Methods

2.1 The software model

- Describe the software tools used, as well as the libraries
- Describe the software implementation (note: code below is an example)

```
library(deSolve)
# code
```

2.2 Model configuration

Explain chosen initial state, parameter values and time sequence. Use tables with values as for example below

Table 1: Parameter Values

Parameter	Value	Unit
a	0.08	$hour^{-1}$
b	0.06	$hour^{-1}$
c	0.06	$hour^{-1}$

3 Results

De vragen die opkomen tijdens het onderzoeken van een biologisch systeem zal je kunnen beantwoorden aan de hand van een gecreerd model. Hieronder is de code te zien dat zo'n soort model kan produceren:

```
data <- read.csv("MPL.csv", na.strings = "NA")
median_MPL_01 <- median(data$MPL_conc[data$dose==0.1], na.rm=T)
median_MPL_01
```

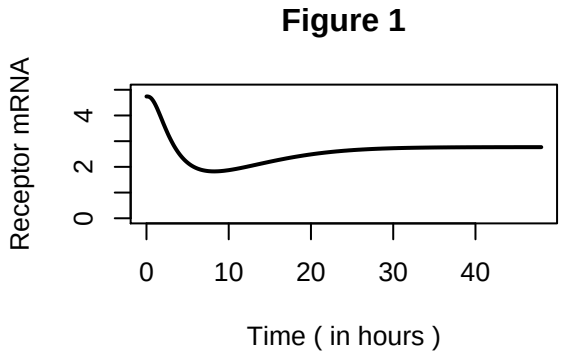
```
## [1] 14.59
```

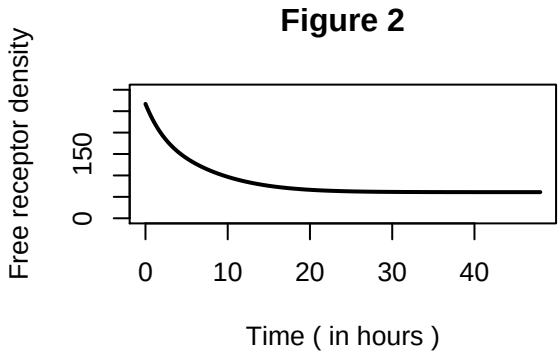
```
medians <- aggregate(data[,c("MPL_conc","mRNA","Free_receptor")],list(data$dose,data$time), median, na.
names(medians)[1:2] <- c("dose","time")
head(medians)
```

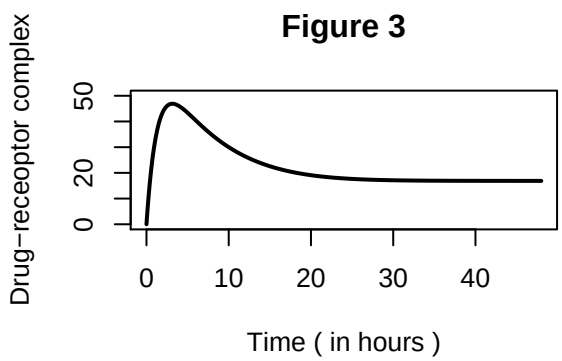
```
##   dose time MPL_conc   mRNA Free_receptor
## 1  0.0    0    0.000 3.7900        292.95
## 2  0.1    6   11.180 1.7025        124.70
## 3  0.3    6   31.295 1.7295         97.90
## 4  0.1   10   12.335 1.7515        157.80
## 5  0.3   10   36.960 1.4140         69.55
## 6  0.1   13   11.945 1.7045        152.50
```

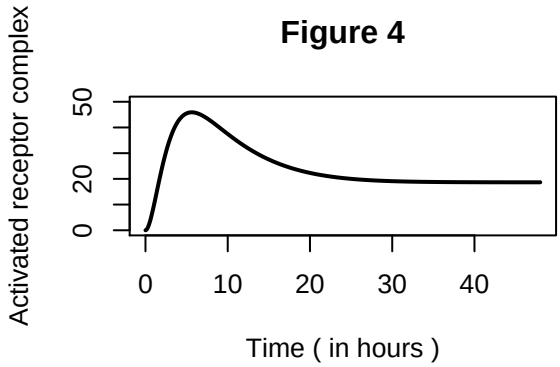
```
# Parameters to be used in the Glucocorticoid function
parameters <- c(ks_Rm = 2.90, IC50_Rm = 26.2, kon = 0.00329,
                kT = 0.63, kre = 0.57, Rf = 0.49, kd_R = 0.0572,
                kd_Rm = 0.612, ks_r = 3.22, D = 53, Rm0 = 4.74,
                DR = 0, DRN = 0)

# this function calculates the derivatives and returns it as a list.
Glucocorticoid_func <- function(t, y, parms) {
    with(as.list(c(y, parms)),{

      # Dit model bevat 4 afgeleide functies:
      # Afgeleide 1:

      dmRNAr_dt <- ks_Rm * ( 1 - (DRN / (IC50_Rm + DRN))) - kd_Rm * mRNAr

      # Afgeleide 2:

      dR_dt <- ks_r * mRNAr + Rf * kre * DRN - kon * D * R - kd_R * R

      # Afgeleide 3:

      dDR_dt <- kon * D * R - kT * DR

      # Afgeleide 4:

      dDRN_dt <- kT * DR - kre * DRN

      return(list(c(dmRNAr_dt, dR_dt, dDR_dt, dDRN_dt)))
       }
       )
}

# Set initial values
```

```r
state <- c(mRNAr = 4.74, R = 267, DR = 0, DRN = 0)
t <- seq(0, 48, by = 0.1)

# Use the ode function from deSolve to create a line using our created function.
# We use the method: "lsode" to get a smooth curve.
out <- deSolve::ode(times = t, y = state, parms = parameters,
                    func = Glucocorticoid_func, method = "lsoda")

# Make a dataframe from the data of 'out'
out <- as.data.frame(out)

# Make a grid so the plotted output looks nice and organised.
par(mfrow = c(2,2) )

# Plot all the functions
plot(out$time, out$mRNAr, xlab = "Time ( in hours )", ylab = "Receptor mRNA",
     type = "l", lwd = 2, ylim = c(0,5), main= "Figure 1")



plot(out$time, out$R, xlab = "Time ( in hours )", ylab = "Free receptor density",
     type = "l", lwd = 2, ylim = c(0,300), main= "Figure 2")

plot(out$time, out$DR, xlab = "Time ( in hours )", ylab = "Drug-receoptor complex",
     type = "l", lwd = 2, ylim = c(0,50), main= "Figure 3")

plot(out$time, out$DRN, xlab = "Time ( in hours )", ylab = "Activated receptor complex",
     type = "l", lwd = 2, ylim = c(0,50), main= "Figure 4")
```









- Describe what can be seen in such way that it leads to an answer to your research questions
- Give your figures a number and a descriptive title.
- Provide correct axis labels (unit and quantity), legend and caption.
- Always refer to and discuss your figures and tables in the text - they never stand alone.

4 Discussion and Conclusion

4.1 Discussion

- Compare your results with what is expecting from the literature and discuss differences with them.
- Discuss striking and surprising results.
- Discuss weaknesses in your research and how they could be addressed.

4.2 General conclusion and perspective

Discuss what your goal was, what the end result is and how you could continue working from here.

References

[1] Soetaert, K., Petzoldt, T., and Woodrow Setzer, R.: *Solving differential equations in R: package deSolve*, J. Stat. Softw., 33, 1-25, 2010.

Soetaert, K., Petzoldt, T., and Woodrow Setzer, R.: *Solving differential equations in R: package deSolve*, J. Stat. Softw., 33, 1-25, 2010.