Week Three

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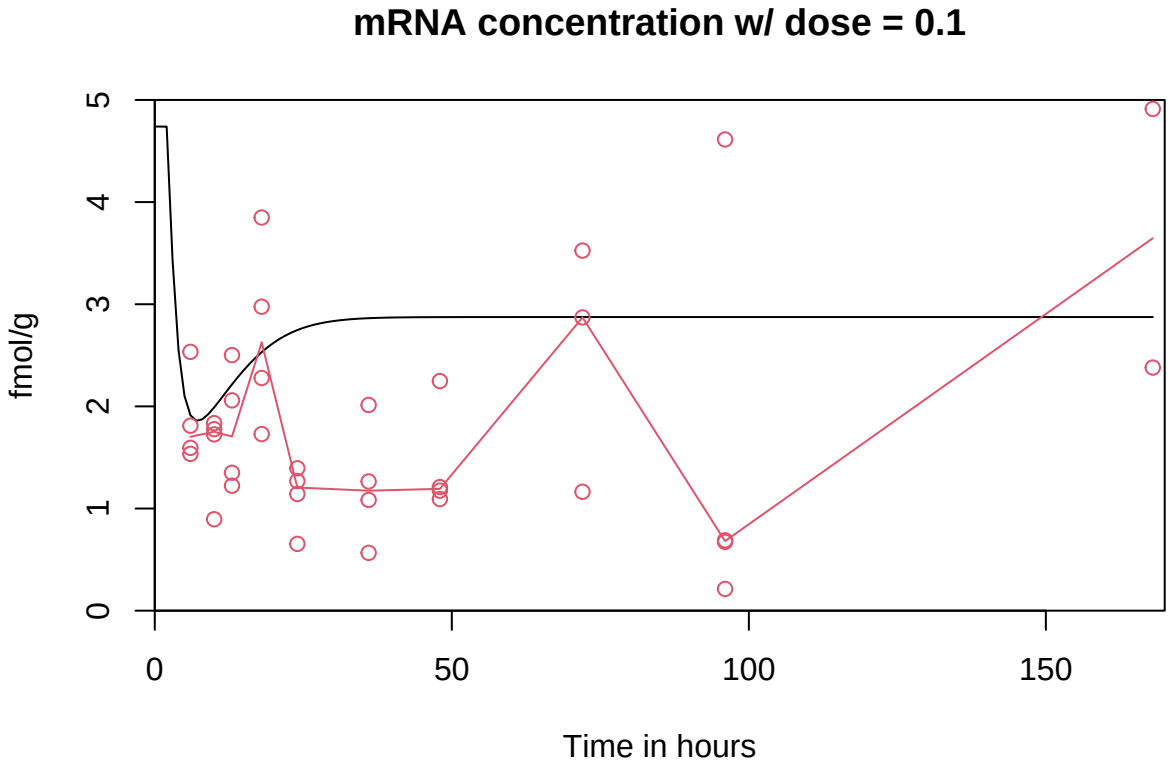
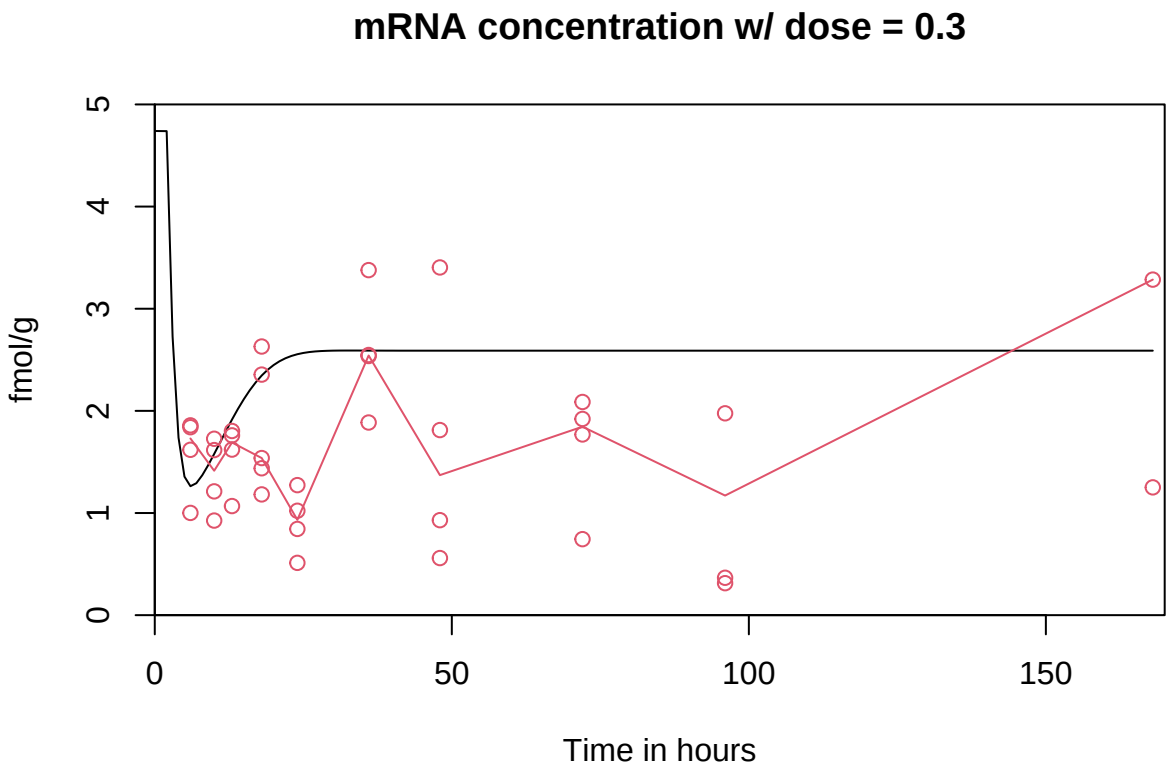
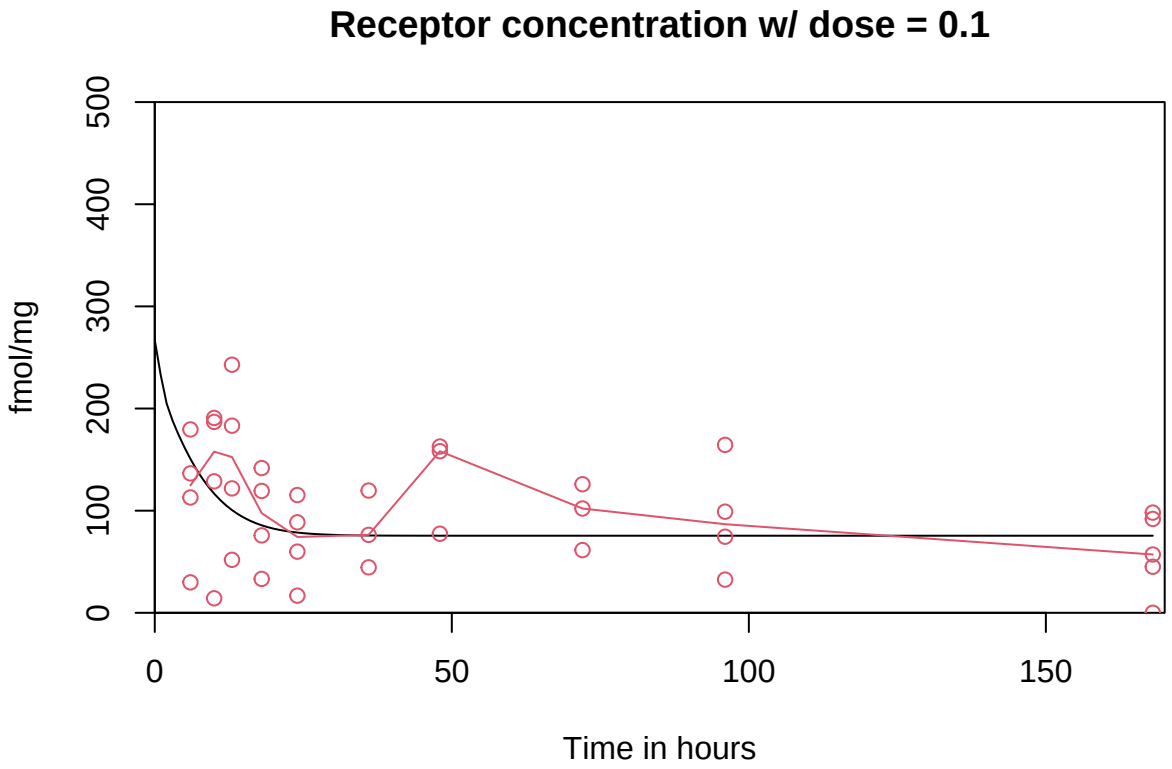
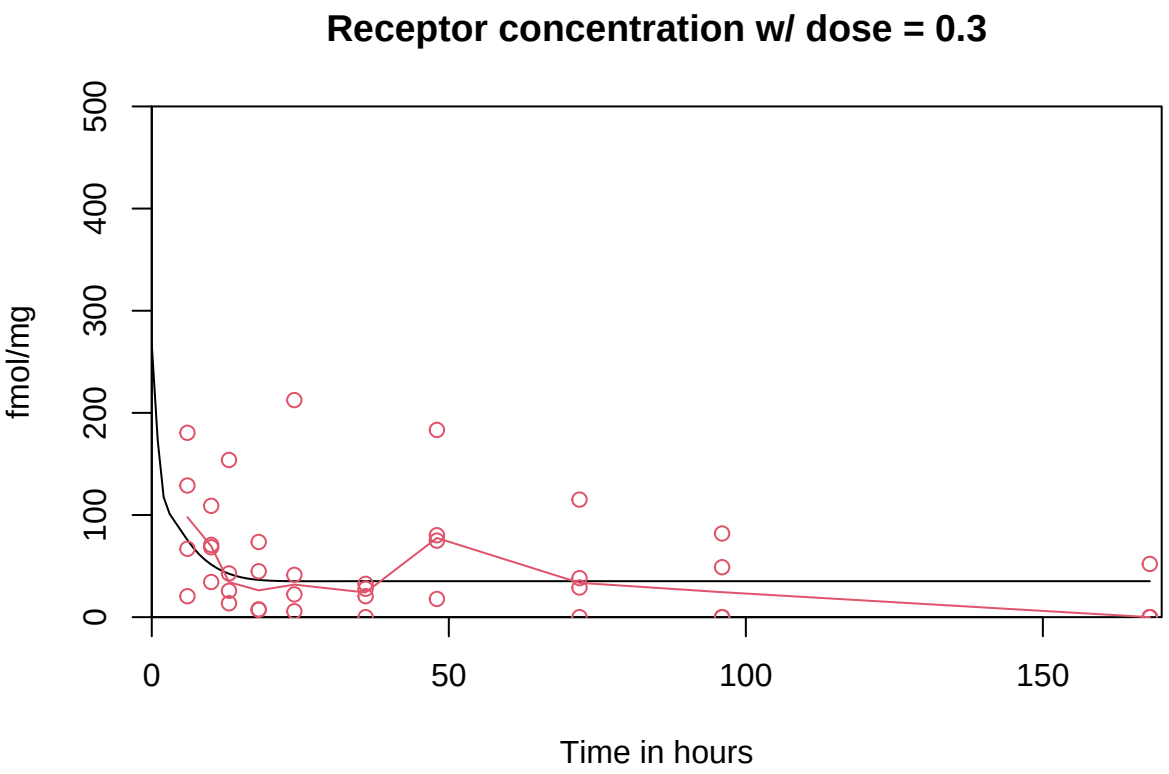
In this case we use the median, as using the mean will cause outliers to influence the data more easily. Using the median




mRNA concentration w/ dose = 0.3
fmol/g
0
1
2
3
4
5
0
50
100
150
Time in hours


Receptor concentration w/ dose = 0.1
fmol/mg
0
100
200
300
400
500
0
50
100
150
Time in hours



The simulation from the model does not seem to match the experimental data very well when it comes to the mRNA concentration, while it does seem to match the model pretty well for the concentration of the free receptor, this difference between the experiment and the model could be caused by differences in parameters in the experimental data. The kd_Rm and the ks_Rm parameters seem the most likely to be affecting this difference.

Assignment 2

[1] To remove the effect from the medicine on the rate of synthesis of mRNA, the $k_{s\_rm} \cdot (1 - \frac{DR(N)}{IC_{50\_Rm} + DR(N)})$ from the formula $k_{s\_rm} \cdot (1 - \frac{DR(N)}{IC_{50\_Rm} + DR(N)}) - k_{d\_Rm} \cdot mRNA_r$ needs to be changed to only k_{s_rm}

```
## ksrm
##  2.9
```

Appendix: All code for this report

```
knitr::opts_chunk$set(echo = FALSE)
library(deSolve)

setwd("/homes/kbsmit/Documents/project8/SystemsBiologyProject8/Data/")
expdata = read.csv("MPL.csv")

medians <- aggregate(expdata[,c("MPL_conc","mRNA","Free_receptor")],list(expdata$dose,expdata$time), me
names(medians)[1:2] <- c("dose","time")

#set the initial states, timeframe, and parameters, and create a function for the formulas
state <- c(rm0 = 4.74,
           r0 = 267,
           dr = 0,
           drn = 0)

timeframe <- seq(0, 168, by = 1)

parmezan <- c(ksrm = 2.90,
            ic50rm = 26.2,
            kon = 0.00329,
            kt = 0.63,
            kre = 0.57,
            Rf = 0.49,
            kdr = 0.0572,
            kdrm = 0.612,
            ksr = 3.22,
            D = 39)

formulas <- function(t, y, parameters){
  with(as.list(c(y, parameters)), {
    dmRNAr <- ksrm * (1 - (drn) / (ic50rm + drn)) - kdrm * rm0
    dR <- ksr * rm0 + Rf * kre * drn - kon * D * r0 - kdr * r0
    dDR <-kon * D * r0 - kt * dr
    dDRN <- kt * dr - kre * drn

    return(list(c(dmRNAr, dR, dDR, dDRN)))
    }
  )
}

# generate output from using all the data given, then adjust D for the 2nd concentration and generate a
out  <- ode(times = timeframe, y = state,   parms = parmezan, func = formulas, method = "euler")

parmezan["D"] <- 107

out2  <- ode(times = timeframe, y = state,   parms = parmezan, func = formulas, method = "euler")

# Plot the graphs for mRNA with the first concentration first
par(yaxs = "i", xaxs = "i")
plot(out[,c("time", "rm0")], type="l", xlab = "Time in hours", ylab = "fmol/g", main = "mRNA concentrati
lines(medians[medians$dose == 0.1, c("time", "mRNA")], col=2)
```

```
lines(expdata[expdata$dose == 0.1, c("time", "mRNA")], col=2, type = "p")

# Plot the graphs for mRNA with the second concentration
par(yaxs = "i", xaxs = "i")
plot(out2[,c("time", "rm0")], type="l", xlab = "Time in hours", ylab = "fmol/g", main = "mRNA concentra
lines(medians[medians$dose == 0.3, c("time", "mRNA")], col=2)
lines(expdata[expdata$dose == 0.3, c("time", "mRNA")], col=2, type = "p")

# Now do the same for the receptor concentrations
par(yaxs = "i", xaxs = "i")
plot(out[,c("time", "r0")], type="l", xlab = "Time in hours", ylab = "fmol/mg", main = "Receptor concen
lines(medians[medians$dose == 0.1, c("time", "Free_receptor")], col=2)
lines(expdata[expdata$dose == 0.1, c("time", "Free_receptor")], col=2, type = "p")

par(yaxs = "i", xaxs = "i")
plot(out2[,c("time", "r0")], type="l", xlab = "Time in hours", ylab = "fmol/mg", main = "Receptor concen
lines(medians[medians$dose == 0.3, c("time", "Free_receptor")], col=2)
lines(expdata[expdata$dose == 0.3, c("time", "Free_receptor")], col=2, type = "p")

parmezan["ksrm"]
```