Detailed Analysis

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Contents

```r
packages <- c("deSolve", "ggplot2")
invisible(lapply(packages, library, character.only = T))
```

```r
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
```

```r
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
```

Assignment 1

Why is it best practice to plot the median for the experimental data? Explain in your report.

The median doesn't change with huge outliers. So the data is more reliable. So if there is a significant difference, it will show.