Imaging

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R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

```r
library(plyr)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:plyr':
##
##     arrange, count, desc, failwith, id, mutate, rename, summarise,
##     summarize

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(ggplot2)
library(reshape2)
library(ggthemes)
library(superheat)
```

Including Plots

You can also embed plots, for example:

```r
wd <- getwd()
file_list <- list.files(paste(wd,'/c9adl/',sep=""))

wdplus <- paste(wd,'/c9adl/',sep="")

i=1
frame <- c(1:1500)
animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)
datatofuckwith <- datatofuckwith[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- data

for (i in 2:length(file_list)){
```

```r
animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- rbind(finaldf,data)
}
c9adl_df <- finaldf
c9adl_df$stim <- rep('c9',dim(c9adl_df)[1])
c9adl_df$geno <- rep('adl',dim(c9adl_df)[1])

file_list <- list.files(paste(wd,'/c9mut/',sep=""))

wdplus <- paste(wd,'/c9mut/',sep="")

i=1
frame <- c(1:1500)
animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)
datatofuckwith <- datatofuckwith[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- data

for (i in 2:length(file_list)){


animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- rbind(finaldf,data)
}
c9mut_df <- finaldf
c9mut_df$stim <- rep('c9',dim(c9mut_df)[1])
c9mut_df$geno <- rep('mut',dim(c9mut_df)[1])

file_list <- list.files(paste(wd,'/c9res/',sep=""))

wdplus <- paste(wd,'/c9res/',sep="")

i=1
frame <- c(1:1500)
animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)
datatofuckwith <- datatofuckwith[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- data

for (i in 2:length(file_list)){


animal <- rep(i,1500)
```

```r
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- rbind(finaldf,data)
}
c9res_df <- finaldf
c9res_df$stim <- rep('c9',dim(c9res_df)[1])
c9res_df$geno <- rep('res',dim(c9res_df)[1])

file_list <- list.files(paste(wd,'/pt0adl/',sep=""))
wdplus <- paste(wd,'/pt0adl/',sep="")

i=1
frame <- c(1:1500)
animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)
datatofuckwith <- datatofuckwith[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- data

for (i in 2:length(file_list)){


animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- rbind(finaldf,data)
}
pt0adl_df <- finaldf
pt0adl_df$stim <- rep('pt0',dim(pt0adl_df)[1])
pt0adl_df$geno <- rep('adl',dim(pt0adl_df)[1])

file_list <- list.files(paste(wd,'/pt0mut/',sep=""))

wdplus <- paste(wd,'/pt0mut/',sep="")

i=1
frame <- c(1:1500)
animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)
datatofuckwith <- datatofuckwith[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- data

for (i in 2:length(file_list)){


animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
```

```r
finaldf <- rbind(finaldf,data)
}
pt0mut_df <- finaldf

pt0mut_df$stim <- rep('pt0',dim(pt0mut_df)[1])
pt0mut_df$geno <- rep('mut',dim(pt0mut_df)[1])

file_list <- list.files(paste(wd,'/pt0res/',sep=""))

wdplus <- paste(wd,'/pt0res/',sep="")

i=1
frame <- c(1:1500)
animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)
datatofuckwith <- datatofuckwith[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- data

for (i in 2:length(file_list)){


animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- rbind(finaldf,data)
}
pt0res_df <- finaldf

pt0res_df$stim <- rep('pt0',dim(pt0res_df)[1])
pt0res_df$geno <- rep('res',dim(pt0res_df)[1])

file_list <- list.files(paste(wd,'/pt15adl/',sep=""))

wdplus <- paste(wd,'/pt15adl/',sep="")

i=1
frame <- c(1:1500)
animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)
datatofuckwith <- datatofuckwith[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- data

for (i in 2:length(file_list)){


animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
```

```r
finaldf <- rbind(finaldf,data)
}
pt15adl_df <- finaldf

pt15adl_df$stim <- rep('pt15',dim(pt15adl_df)[1])
pt15adl_df$geno <- rep('adl',dim(pt15adl_df)[1])

file_list <- list.files(paste(wd,'/pt15mut/',sep=""))

wdplus <- paste(wd,'/pt15mut/',sep="")

i=1
frame <- c(1:1500)
animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)
datatofuckwith <- datatofuckwith[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- data

for (i in 2:length(file_list)){


animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- rbind(finaldf,data)
}
pt15mut_df <- finaldf
pt15mut_df$stim <- rep('pt15',dim(pt15mut_df)[1])
pt15mut_df$geno <- rep('mut',dim(pt15mut_df)[1])

file_list <- list.files(paste(wd,'/pt15res/',sep=""))

wdplus <- paste(wd,'/pt15res/',sep="")

i=1
frame <- c(1:1500)
animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)
datatofuckwith <- datatofuckwith[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- data

for (i in 2:length(file_list)){


animal <- rep(i,1500)
datatofuckwith <- read.csv((paste(wdplus,file_list[i],sep="")),header=FALSE)[,2]
arbitraryunits <- datatofuckwith-(min(datatofuckwith))
data <- as.data.frame(cbind(animal,frame,arbitraryunits))
finaldf <- rbind(finaldf,data)
```

```
}
pt15res_df <- finaldf
pt15res_df$stim <- rep('pt15',dim(pt15res_df)[1])
pt15res_df$geno <- rep('res',dim(pt15res_df)[1])
```

un-comment this section to save output as csv (these values were saved and added to the master excel file in
the supplement)

```
df <- rbind(c9adl_df,c9mut_df,c9res_df,pt15adl_df,pt15mut_df,pt15res_df)
#filetosave <- dcast(df,animal~frame,value.var='arbitraryunits')
#write.csv(filetosave, 'arbitraryunits.csv')
```

```
ymax = max(df$arbitraryunits)
p <- ggplot(pt15adl_df,aes(x=frame,y=arbitraryunits)) + geom_line(color='gray') + facet_grid(~animal) +
p + annotate("rect", xmin = 300, xmax = 500, ymin = 0, ymax = ymax,alpha = .2)+ annotate("rect", xmin =
```
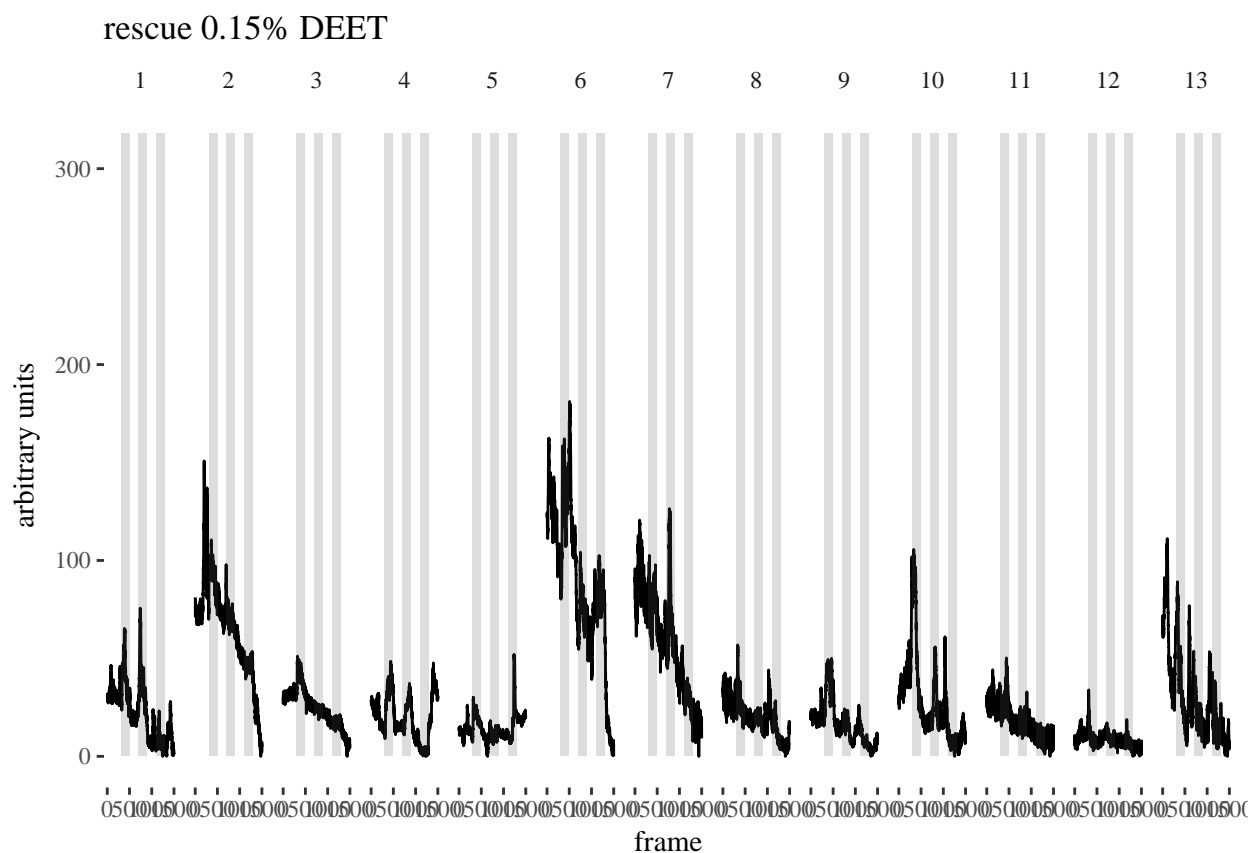

wild–type 0.15% DEET
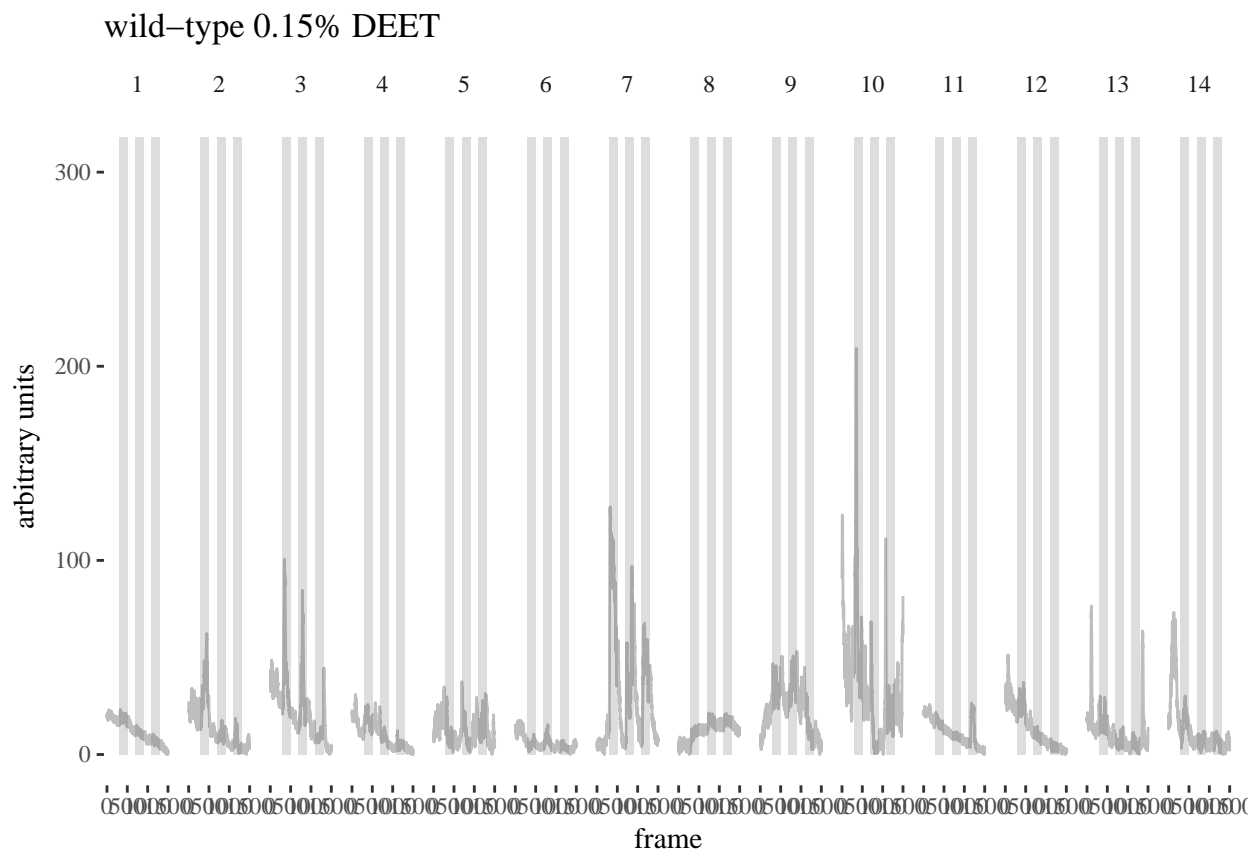
```
p <- ggplot(pt15mut_df,aes(x=frame,y=arbitraryunits)) + geom_line(color='red3') + facet_grid(~animal) +
p + annotate("rect", xmin = 300, xmax = 500, ymin = 0, ymax = ymax,alpha = .2)+ annotate("rect", xmin =
```
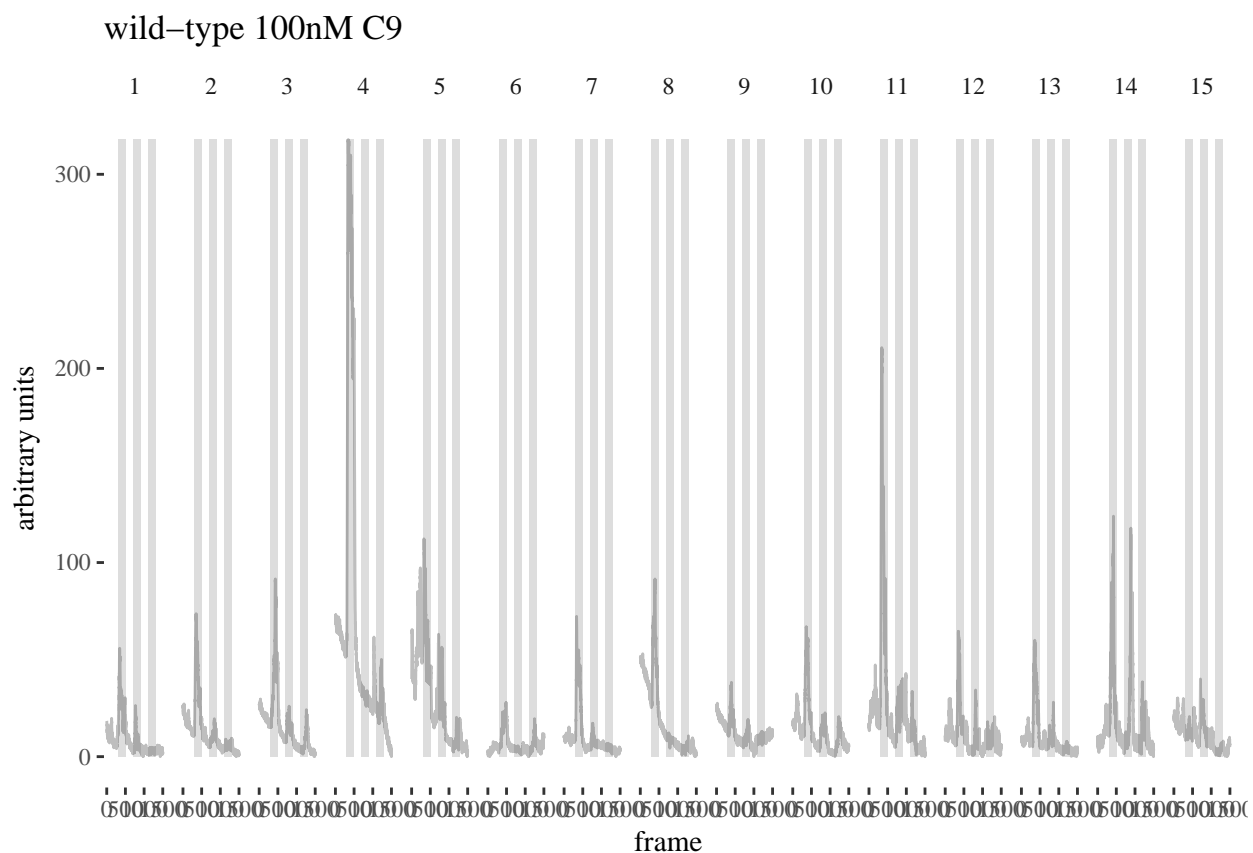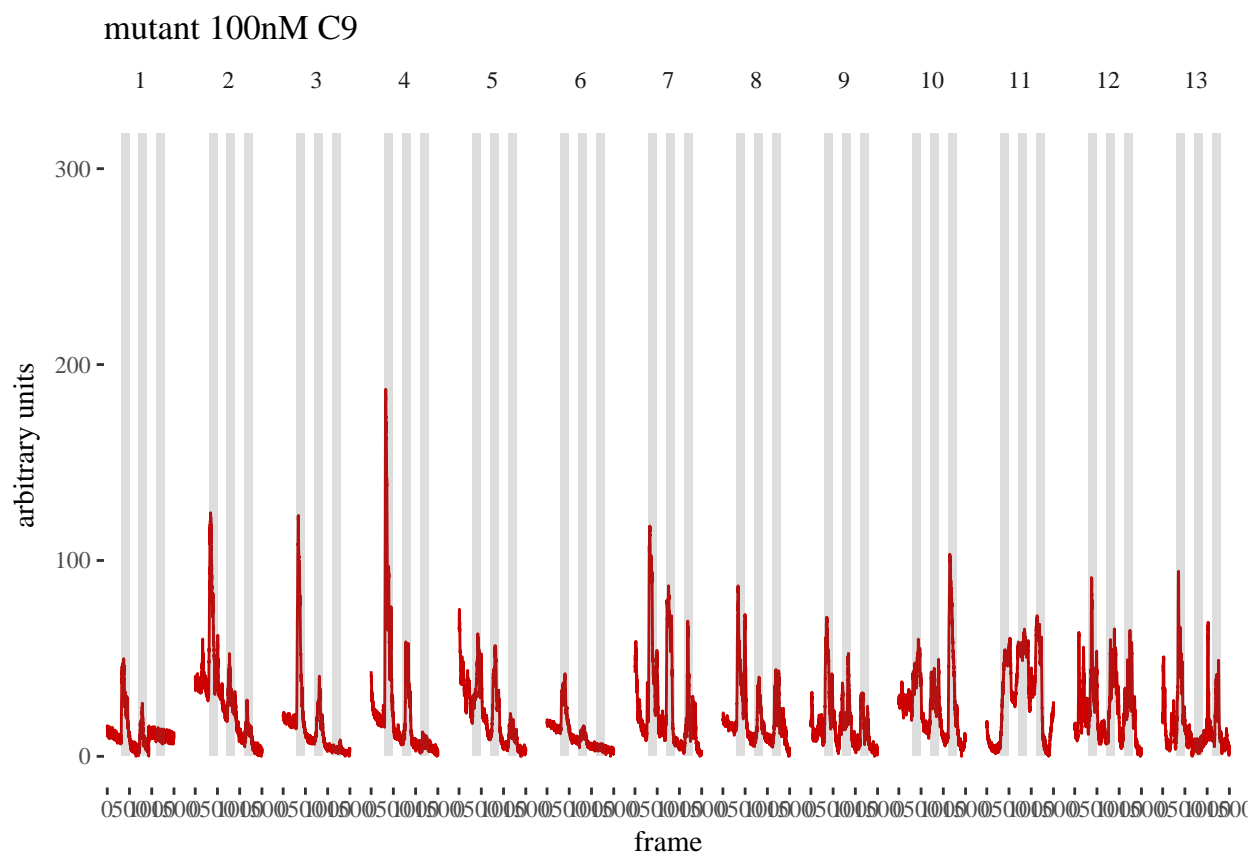
mutant 0.15% DEET
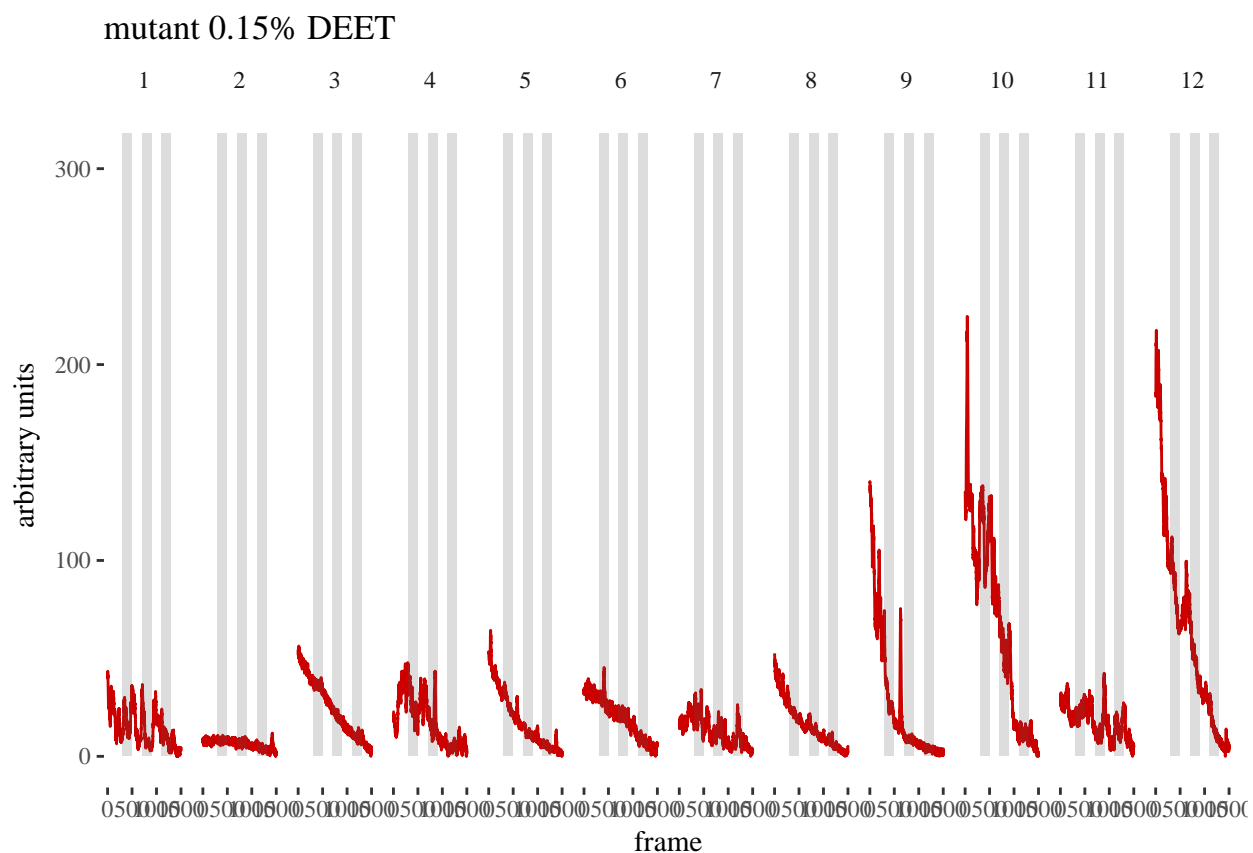

```
p <- ggplot(pt15res_df,aes(x=frame,y=arbitraryunits)) + geom_line(color='black') + facet_grid(~animal)
p + annotate("rect", xmin = 300, xmax = 500, ymin = 0, ymax = ymax,alpha = .2)+ annotate("rect", xmin =
```
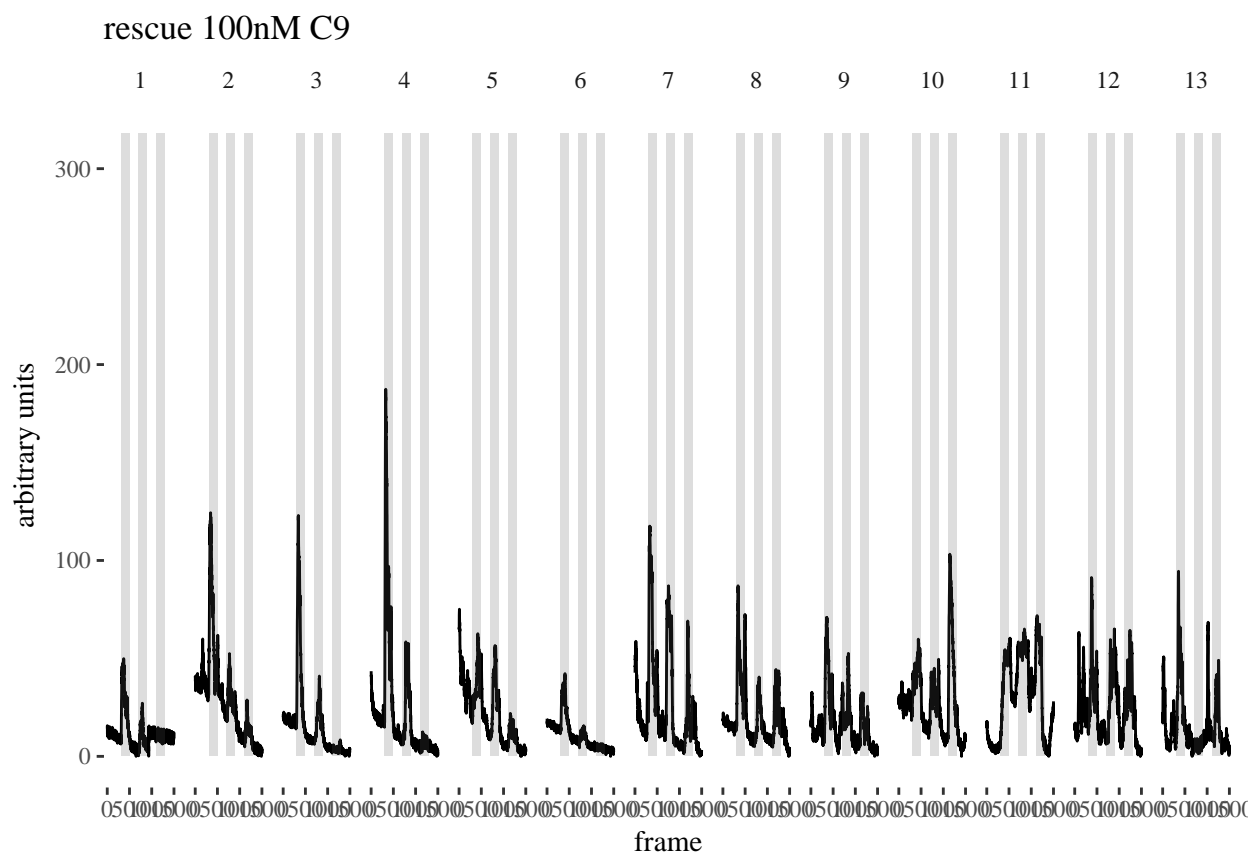
rescue 0.15% DEET


```
ymax = max(df$arbitraryunits)
p <- ggplot(c9adl_df,aes(x=frame,y=arbitraryunits)) + geom_line(color='gray') + facet_grid(~animal) + th
p + annotate("rect", xmin = 300, xmax = 500, ymin = 0, ymax = ymax,alpha = .2)+ annotate("rect", xmin =
```

wild-type 100nM C9


```
p <- ggplot(c9mut_df,aes(x=frame,y=arbitraryunits)) + geom_line(color='red3') + facet_grid(~animal) + t
p + annotate("rect", xmin = 300, xmax = 500, ymin = 0, ymax = ymax,alpha = .2)+ annotate("rect", xmin =
```
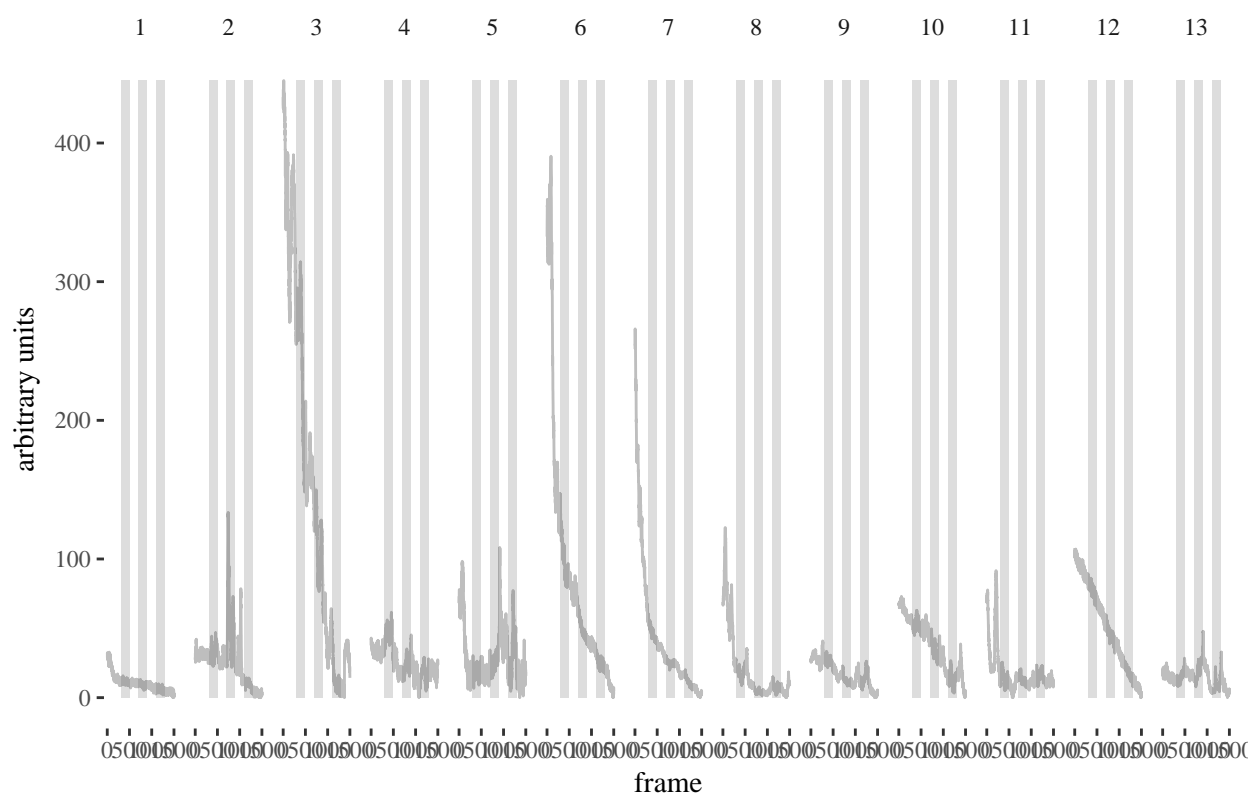
mutant 100nM C9


```
p <- ggplot(c9res_df,aes(x=frame,y=arbitraryunits)) + geom_line(color='black') + facet_grid(~animal) + 
p + annotate("rect", xmin = 300, xmax = 500, ymin = 0, ymax = ymax,alpha = .2)+ annotate("rect", xmin = 
```

rescue 100nM C9

```
ymax = max(c(pt0adl_df$arbitraryunits,pt0mut_df$arbitraryunits,pt0res_df$arbitraryunits))
p <- ggplot(pt0adl_df,aes(x=frame,y=arbitraryunits)) + geom_line(color='gray') + facet_grid(~animal) +
p + annotate("rect", xmin = 300, xmax = 500, ymin = 0, ymax = ymax,alpha = .2)+ annotate("rect", xmin =
```

wild–type ethanol solvent


```r
p <- ggplot(pt0mut_df,aes(x=frame,y=arbitraryunits)) + geom_line(color='red3') + facet_grid(~animal) +
p + annotate("rect", xmin = 300, xmax = 500, ymin = 0, ymax = ymax,alpha = .2)+ annotate("rect", xmin =
```

mutant ethanol solvent
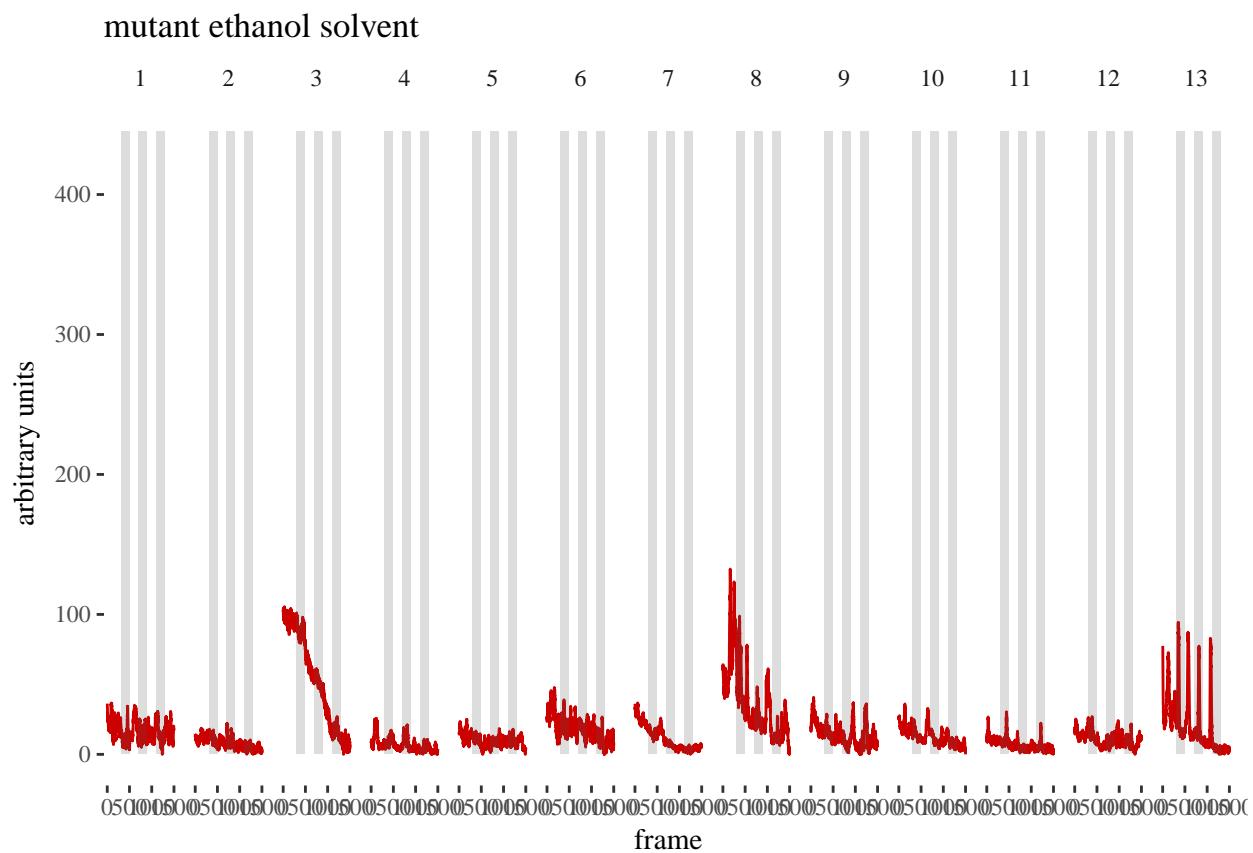
```
p <- ggplot(pt0res_df,aes(x=frame,y=arbitraryunits)) + geom_line(color='black') + facet_grid(~animal) +
p + annotate("rect", xmin = 300, xmax = 500, ymin = 0, ymax = ymax,alpha = .2)+ annotate("rect", xmin =
```