

REWOD_PAV

R Markdown

R code for FOR REWOD_PAV

last modified on Nov 2018 by David

SETUP

```
# Set working directory
analysis_path <- '~/rewod/DATABASES/'; # for this to work the script needs to be sourced
setwd(analysis_path)

# open dataset
REWOD_PAV <- read.delim(file.path(analysis_path, 'REWOD_PAVLOVIAN.txt'), header = T, sep = '|') # read in

# define factors
REWOD_PAV$id <- factor(REWOD_PAV$id)
REWOD_PAV$trial <- factor(REWOD_PAV$trial)
REWOD_PAV$session <- factor(REWOD_PAV$session)
REWOD_PAV$condition <- factor(REWOD_PAV$condition)

# get times in milliseconds
REWOD_PAV$RT <- REWOD_PAV$RT * 1000
```

Cleaning

```
# remove sub 8 (bc we dont have scans)
REWOD_PAV <- subset (REWOD_PAV, !id == '8')

#no Baseline
REWOD_PAV.clean <- filter(REWOD_PAV, condition != "Baseline")
REWOD_PAV.clean$condition <- droplevels(REWOD_PAV.clean$condition, exclude = "Baseline")

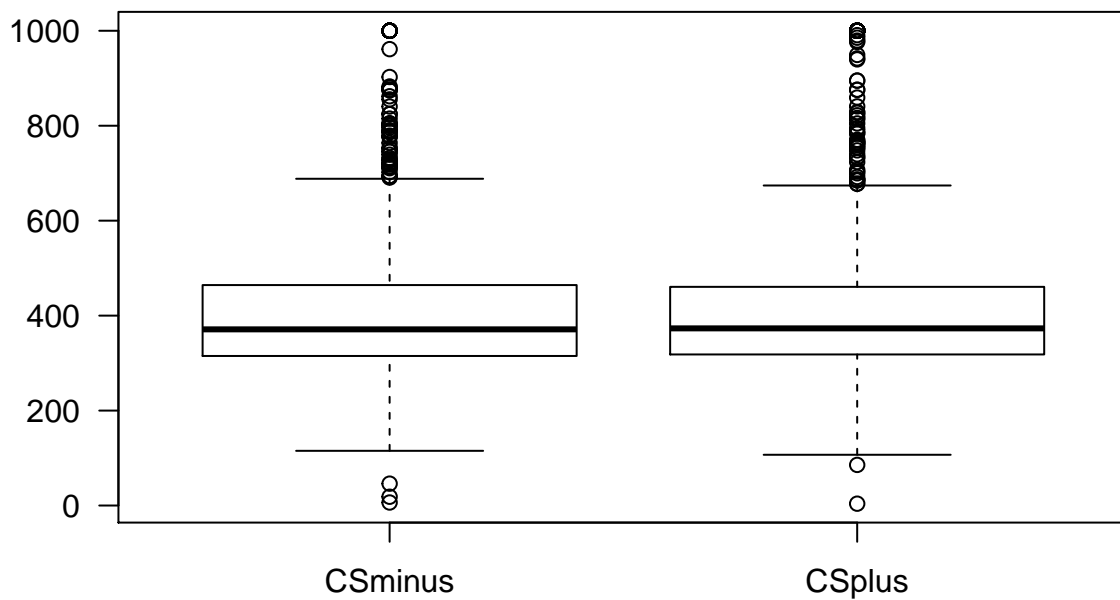
#shorter RT than 100ms and longer than 3sd+mean
REWOD_PAV.clean <- filter(REWOD_PAV.clean, RT >= 100) # min RT is 106ms
mean <- mean(REWOD_PAV.clean$RT)
sd <- sd(REWOD_PAV.clean$RT)
REWOD_PAV.clean <- filter(REWOD_PAV.clean, RT <= mean + 3*sd) #which is 854.4ms
#accuracy to a 100%

#only first round
REWOD_PAV.clean <- filter(REWOD_PAV.clean, rounds == 1)
```

PLOTS

plot (non-averaged per participant)

```
# reaction time by conditions #(baseline non included)
REWOD_PAV.RT <- REWOD_PAV
REWOD_PAV.RT$condition <- droplevels(REWOD_PAV.RT$condition, exclude = "Baseline")
boxplot(REWOD_PAV.RT$RT ~ REWOD_PAV.RT$condition, las = 1)
```

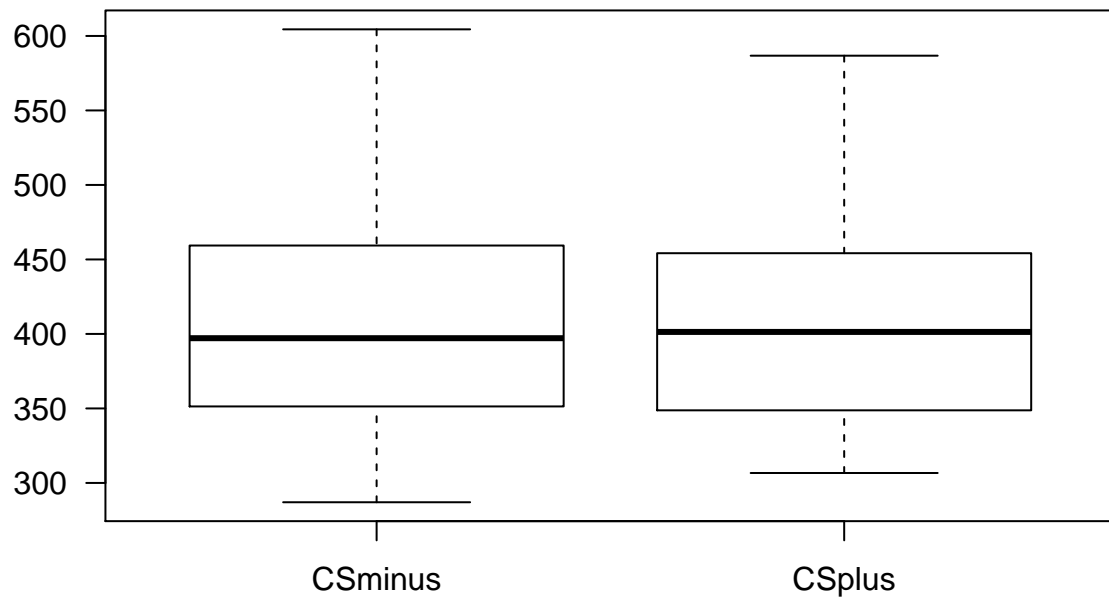


```
# get RT and Liking means by condition (with baseline)
bc = ddply(REWOD_PAV, .(condition), summarise, RT = mean(RT, na.rm = TRUE), liking_ratings = mean(liki

# get RT and Liking means by participant (with baseline)
bs = ddply(REWOD_PAV, .(id, condition), summarise, RT = mean(RT, na.rm = TRUE), liking_ratings = mean(
```

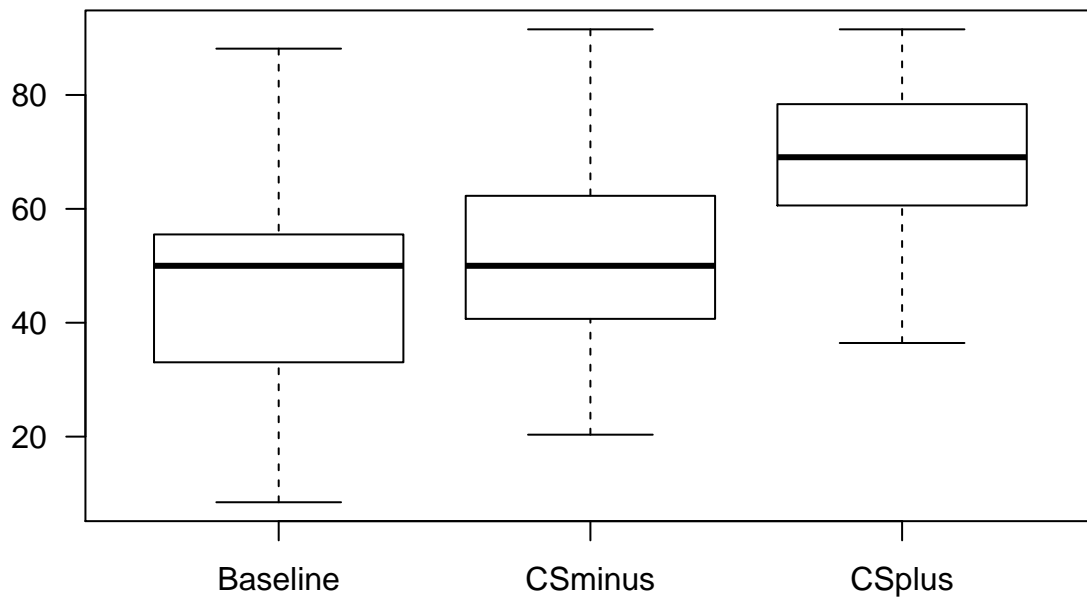
plot overall effect RT

```
#RT average per subjects by condition (baseline non included)
bsrt <- filter(bs, condition != "Baseline")
bsrt$condition <- droplevels(bsrt$condition, exclude = "Baseline")
boxplot(bsrt$RT ~ bsrt$condition, las = 1)
```



plot overall effect Ratings

```
# condition X ratings  
boxplot(bs$liking_ratings ~ bs$condition, las = 1)
```



ANALYSIS

1. Reaction time: are participants faster to detect CS associated with reward?

```
# lmer analysis
main.RT = lmer(RT ~ condition + (1+condition|id) + (1|trial), data = REWOD_PAV.clean, REML = FALSE)
anova(main.RT)

## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## condition  31408   31408      1 28.291   4.0066 0.05499 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# quick check with classical anova (! this is not reliable)
summary(aov(RT ~ condition + Error(id / (condition)), data = REWOD_PAV.clean))

##
## Error: id
##           Df Sum Sq Mean Sq F value Pr(>F)
## condition  1  48998   48998   0.404  0.531
## Residuals 22 2666492  121204
##
## Error: id:condition
##           Df Sum Sq Mean Sq F value Pr(>F)
```

```
## condition 1 81071 81071 5.308 0.0306 *
## Residuals 23 351296 15274
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Error: Within
## Df Sum Sq Mean Sq F value Pr(>F)
## Residuals 779 6304550 8093

# model comparison
main.RT.0 = lmer(RT ~ (1|id) + (1|trial), data = REWOD_PAV.clean, REML = FALSE)
anova(main.RT.0, main.RT, test = 'Chisq')

## Data: REWOD_PAV.clean
## Models:
## main.RT.0: RT ~ (1 | id) + (1 | trial)
## main.RT: RT ~ condition + (1 + condition | id) + (1 | trial)
## Df AIC BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## main.RT.0 4 9880.0 9898.9 -4936.0 9872.0
## main.RT 7 9872.5 9905.5 -4929.2 9858.5 13.516 3 0.003644 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#sentence => CHi2 prop is significative **
```

2. Liking ratings: do participants like more the CS associated with reward?

```
#define contrasts of interest based on hypothesis
bs$cvalue[bs$condition== 'CSplus'] <- 2
bs$cvalue[bs$condition== 'CSminus'] <- -1
bs$cvalue[bs$condition== 'Baseline'] <- -1
bs$cvalue <- factor(bs$cvalue)

# classical anova
summary(aov(liking_ratings ~ cvalue + Error(id / (cvalue)), data = bs))

##
## Error: id
## Df Sum Sq Mean Sq F value Pr(>F)
## Residuals 23 6059 263.4
##
## Error: id:cvalue
## Df Sum Sq Mean Sq F value Pr(>F)
## cvalue 1 4549 4549 10.42 0.00372 **
## Residuals 23 10042 437
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Error: Within
## Df Sum Sq Mean Sq F value Pr(>F)
## Residuals 24 4959 206.6

#sentence => F prop is significative**
```