PESI stimulus selection

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Introduction

Script to read in MEA data, preprocess it and compute CCF based synchrony for each dyad. The script needs the MEA files separated by location (Munich or Cologne), group (ASD or TD) and fps in separate folders. The folder names are:

- "./MEA txt files_5min_t15_Cologne/TD-ASD/24fps"
- "./MEA txt files_5min_t15_Cologne/TD-ASD/24fps"
- "./MEA txt files_5min_t15_Cologne/TD-ASD/25fps"
- "./MEA txt files_5min_t15_Cologne/TD-ASD/25fps"

The script produces a csv file with the selected videos.

Motion Energy Analysis

```
# initialisation of all settings
st  = 1         # start times (seconds)
sz  = 10        # window size for ccf (seconds)
inc = sz
lg  = 3         # lag for ccf (seconds)

# 25fps -----------------------------------------------------------------

fps = 25

## COLOGNE SAMPLE

# read in total ROI data of ASD dyads
mea_ASD_head_C = readMEA("./MEA txt files_5min_t15_Cologne/TD-ASD/25fps",
                           sampRate=fps,
                           skip=st*fps,
                           s1Col = c(1), s2Col = c(3),
                           s1Name = "L_head", s2Name = "R_head",
                           header = F,
                           idOrder = c("id","group"),
                           idSep = "_",
                           sep = "")
```

```
##
## STEP 1 | Reading 5 dyads
## ..................................................|100%
## ..................................................|Done ;)
##
## STEP 2 | Formatting data frames:
## ..................................................|100%
## ..................................................|Done ;)
```

```
## Warning: 0.01% of the data was higher than 10 standard deviations in dyad: D22g,
## session: 01, group:25fps. Check the raw data!
```

```
## Warning: 0.01% of the data was higher than 10 standard deviations in dyad: D24g,
## session: 01, group:25fps. Check the raw data!
```

```
## Warning: 0.03% of the data was higher than 10 standard deviations in dyad: D25g,
## session: 01, group:25fps. Check the raw data!
```

```
## Warning: 0.09% of the data was higher than 10 standard deviations in dyad: D27g,
## session: 01, group:25fps. Check the raw data!
```

```
## Warning: 0.01% of the data was higher than 10 standard deviations in dyad: D28g,
## session: 01, group:25fps. Check the raw data!
```

```
##
## STEP 3 | ReadMEA report
##         Filename id_dyad session group duration_hh.mm.ss L_head_% R_head_%
## 1 D22g_25fps.txt    D22g      01 25fps          00:05:00     51.7     47.3
## 2 D24g_25fps.txt    D24g      01 25fps          00:05:00     56.1     48.4
## 3 D25g_25fps.txt    D25g      01 25fps          00:05:00     36.7     39.1
## 4 D27g_25fps.txt    D27g      01 25fps          00:05:00     52.4     54.1
## 5 D28g_25fps.txt    D28g      01 25fps          00:05:00     28.7     83.5
```

```
mea_ASD_head_C = setGroup(mea_ASD_head_C, "ASD")

## read in total ROI data of TD dyads
mea_TD_head_C = readMEA("./MEA txt files_5min_t15_Cologne/TD-TD/25fps",
                          sampRate=fps,
                          skip=st*fps,
                          s1Col = c(1), s2Col = c(3),
                          s1Name = "L_head", s2Name = "R_head",
                          header = F,
                          idOrder = c("id","group"),
                          idSep = "_",
                          sep = "")
```

```
##
## STEP 1 | Reading 4 dyads
## ..................................................|100%
## ..................................................|Done ;)
##
## STEP 2 | Formatting data frames:
## ..................................................|100%
## ..................................................|Done ;)
```

```
## Warning: 0.07% of the data was higher than 10 standard deviations in dyad: D19h,
## session: 01, group:25fps. Check the raw data!
```

```
##
## STEP 3 | ReadMEA report
##         Filename id_dyad session group duration_hh.mm.ss L_head_% R_head_%
## 1 D18h_25fps.txt    D18h      01 25fps          00:04:58     72.3     61.8
## 2 D19h_25fps.txt    D19h      01 25fps          00:04:58     62.8     72.6
## 3 D23h_25fps.txt    D23h      01 25fps          00:05:00     28.4     40.0
## 4 D26h_25fps.txt    D26h      01 25fps          00:05:00     60.1     64.8
```

```
mea_TD_head_C = setGroup(mea_TD_head_C, "TD")

## Combine into a single object
mea_all_head = c(mea_ASD_head_C, mea_TD_head_C)

## Preprocessing and calculations
mea_all_head = MEAscale(mea_all_head)
```

```
##
## Rescaling data:
## ..................................................|100%
## ..................................................|Done ;)
```

```
## Run CCF analysis
mea_all_head = MEAccf(mea_all_head, lagSec=lg, winSec=sz, incSec=inc, r2Z=T, ABS=T)
```

```
##
## Computing CCF:
## ..................................................|100%
## ..................................................|Done ;)
```

```
## put information into the dataframe
df.head = createDFsync(mea_all_head, sep = "_", desc = c("group", "dyad", "session"), fps)
```

```
## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
## ✔ dplyr     1.0.10     ✔ purrr     1.0.1
## ✔ forcats   0.5.2      ✔ readr     2.1.2
## ✔ ggplot2   3.4.0      ✔ tibble    3.1.8
## ✔ lubridate 1.8.0      ✔ tidyr     1.2.1
## ── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
## ✖ tidyr::expand() masks Matrix::expand()
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::id()     masks rMEA::id()
## ✖ dplyr::lag()    masks stats::lag()
## ✖ tidyr::pack()   masks Matrix::pack()
## ✖ tidyr::unpack() masks Matrix::unpack()
## ℹ Use the ]8;;http://conflicted.r-lib.org/conflicted package]8;; to force all conflicts to become errors
```

```
df.head = df.head %>%
  rename("context" = "group") %>%
  mutate(
    context = as.factor(context),
    context = recode_factor(context,
      'ASD' = "heterogeneous",
      'TD'  = "homogeneous"
    )
  ) %>% select(-session)

# create total motion variables for each dyad
df.head$mot = rowMeans(df.head[,c("s1mot","s2mot")])
df = df.head

# filter out windows with extreme motion
df.head = df %>% ungroup() %>%
  mutate(
    upper = quantile(mot, probs=c(0.75), na.rm = T),
    lower = quantile(mot, probs=c(0.25), na.rm = T)
  ) %>%
  filter(lower <= mot & mot <= upper) %>%
  drop_na() %>% filter(
    dyad != "D28g"
  )
```

Choose videos

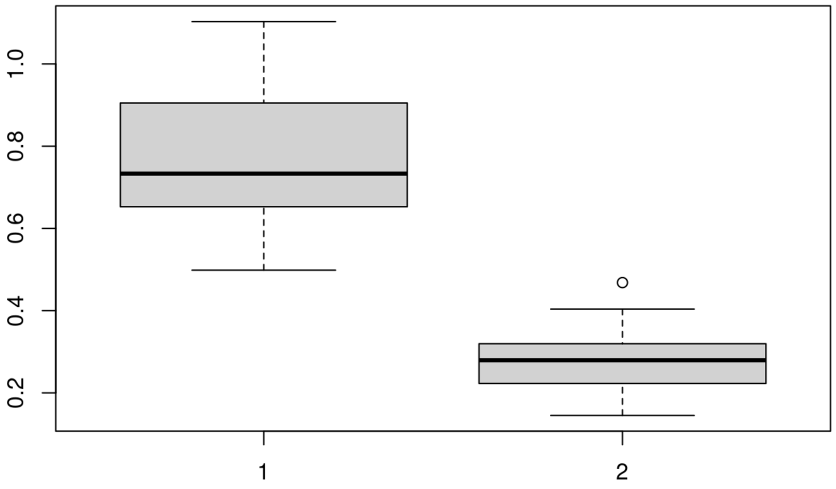
```
df.head_agg = df.head %>% group_by(context, dyad) %>%
  summarise(
    n_win = n()
  )
```

```
## `summarise()` has grouped output by 'context'. You can override using the
## `.groups` argument.
```

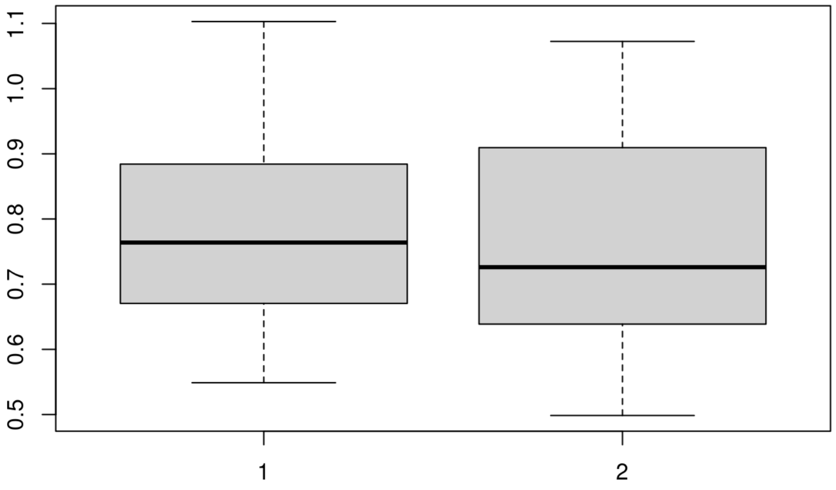
```
# select the n videos of each dyad with the highest and the n with the lowest synchrony values (peak)
n = 4 # number of windows per condition per video
vid_sel_high = df.head %>%
  arrange(desc(peak)) %>%
  group_by(dyad) %>%
  slice(1:n) %>%
  mutate(
    sync = "high"
  )

vid_sel_low = df.head %>%
  arrange(peak) %>%
  group_by(dyad) %>%
  slice(1:n) %>%
  mutate(
    sync = "low"
  )

# add frame for start and end

vid_sel = rbind(vid_sel_low, vid_sel_high) %>%
  mutate(
    frame_sta = as.numeric(substr(winst,5,5))*60*fps + as.numeric(substr(winst,7,8))*fps,
    frame_end = as.numeric(substr(winen,5,5))*60*fps + as.numeric(substr(winen,7,8))*fps
  )
```

Check peaks and motion

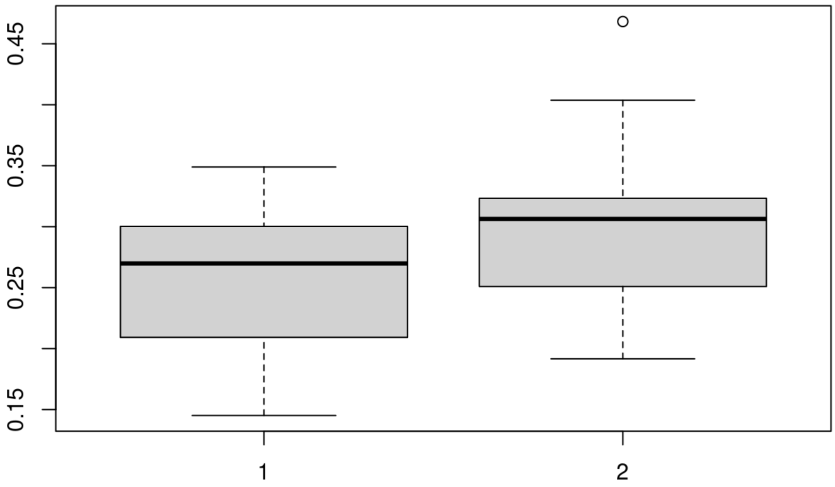
```
# are the high sync videos higher in synchrony than the low sync?
boxplot(vid_sel[vid_sel$sync == "high",]$peak, vid_sel[vid_sel$sync == "low",]$peak)
```



```
# are there context specific differences in synchrony and motion - which we want to avoid!
boxplot(vid_sel_high[vid_sel_high$context == "heterogeneous",]$peak, vid_sel_high[vid_sel_high$context == "homogeneous",]$peak)
```



```
boxplot(vid_sel_low[vid_sel_low$context == "heterogeneous",]$peak, vid_sel_low[vid_sel_low$context == "homogeneous",]$peak)
```



```
shapiro.test(vid_sel_high[(vid_sel_high$context == "homogeneous"),]$peak)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  vid_sel_high[(vid_sel_high$context == "homogeneous"), ]$peak
## W = 0.95646, p-value = 0.5983
```

```
shapiro.test(vid_sel_high[vid_sel_high$context == "heterogeneous",]$peak)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  vid_sel_high[vid_sel_high$context == "heterogeneous", ]$peak
## W = 0.9747, p-value = 0.9078
```

```
shapiro.test(vid_sel_low[(vid_sel_low$context == "homogeneous"),]$peak)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  vid_sel_low[(vid_sel_low$context == "homogeneous"), ]$peak
## W = 0.94335, p-value = 0.3921
```

```
shapiro.test(vid_sel_low[vid_sel_low$context == "heterogeneous",]$peak)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  vid_sel_low[vid_sel_low$context == "heterogeneous", ]$peak
## W = 0.96049, p-value = 0.6706
```

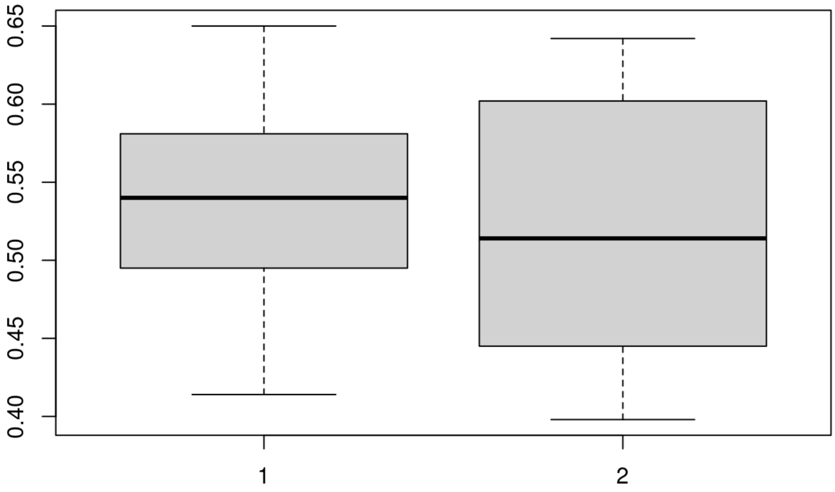
```
ttestBF(vid_sel_high[vid_sel_high$context == "heterogeneous",]$peak, vid_sel_high[vid_sel_high$context == "homogeneous",]$peak, paired =
F)
```

```
## Bayes factor analysis
## --------------
## [1] Alt., r=0.707 : 0.3698976 ±0%
##
## Against denominator:
##   Null, mu1-mu2 = 0
## ---
## Bayes factor type: BFindepSample, JZS
```

```
ttestBF(vid_sel_low[vid_sel_low$context == "heterogeneous",]$peak, vid_sel_low[vid_sel_low$context == "homogeneous",]$peak, paired = F)
```

```
## Bayes factor analysis
## --------------
## [1] Alt., r=0.707 : 1.225592 ±0.01%
##
## Against denominator:
##   Null, mu1-mu2 = 0
## ---
## Bayes factor type: BFindepSample, JZS
```

```
# Check motion -----------------------------------------------------------
boxplot(vid_sel_high[vid_sel_high$context == "heterogeneous",]$mot, vid_sel_high[vid_sel_high$context == "homogeneous",]$mot)
```



```
ttestBF(vid_sel_high[vid_sel_high$context == "heterogeneous",]$mot, vid_sel_high[vid_sel_high$context == "homogeneous",]$mot, paired =
F)
```

```
## Bayes factor analysis
## --------------
## [1] Alt., r=0.707 : 0.3828329 ±0%
##
## Against denominator:
##   Null, mu1-mu2 = 0
## ---
## Bayes factor type: BFindepSample, JZS
```

```
write_csv(vid_sel, file="PESI_videosel-full_230404.csv")
```