Replication

Comparing Exp. 1 click condition and Exp. 2 default condition

General preparations

Load libraries

```
library(mousetrap)
library(ggplot2)
library(dplyr)
library(tidyr)
library(afex)
library(MBESS)
library(ordinal)
```

Custom ggplot2 theme

```
theme_set(theme_classic()+
  theme(
    axis.line = element_line(colour = "black"),
    axis.ticks = element_line(colour = "black"),
    axis.text = element_text(colour = "black"),
    panel.border = element_rect(colour = "black", fill=NA)
  ))
```

Custom functions

```
# Function to compute confidence interval for partial eta-squared
get_partial_etas <- function(anova_table, conf.level=.90){
  partial_etas <- sapply(row.names(anova_table),function(i){
    F <- anova_table[i,"F"]
    df1 <- anova_table[i,"num Df"]
    df2 <- anova_table[i,"den Df"]
    ci <- conf.limits.ncf(F.value=F,conf.level=conf.level,df.1=df1,df.2=df2)
    return(
      c(pes=((F*df1)/(F*df1+df2)),
        lower=ci$Lower.Limit/(ci$Lower.Limit+df1+df2+1),
        upper=ci$Upper.Limit/(ci$Upper.Limit+df1+df2+1)))
  })
  return(t(partial_etas))
}
```

Data import

```r
raw_data1 <- read.csv("../data/exp1.csv",stringsAsFactors = FALSE)
raw_data1$study <- "study1"
raw_data1 <- subset(raw_data1,group=="click")

raw_data2 <- read.csv("../data/exp2.csv",stringsAsFactors = FALSE)
raw_data2$study <- "study2"
raw_data2 <- subset(raw_data2,group=="default")

raw_data <- bind_rows(raw_data1,raw_data2)
raw_data$Typicality <- factor(raw_data$Condition,levels=c("Typical","Atypical"))
raw_data$group <- factor(raw_data$study,levels=c("study1","study2"))
```

Correctness

Percent of correct trials per condition

```r
with(raw_data,table(group, correct)/c(table(group)))
```

```
##        correct
## group            0          1
##    study1 0.06454816 0.93545184
##    study2 0.06512043 0.93487957
```

Chi-squared test

```r
chisq.test(with(raw_data,table(group, correct)),correct = FALSE)
```

```
##
##  Pearson's Chi-squared test
##
## data:  with(raw_data, table(group, correct))
## X-squared = 0.0028646, df = 1, p-value = 0.9573
```

Generalized linear mixed model

```r
contrasts(raw_data$group) <- c(0.5,-0.5)
summary(glmer(correct~(1|subject_nr)+group,family="binomial",data=raw_data))
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: correct ~ (1 | subject_nr) + group
##    Data: raw_data
##
##      AIC      BIC   logLik deviance df.resid
##   1010.4   1027.4   -502.2   1004.4     2125
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -4.2864   0.1907   0.2333   0.2790   0.5314
##
## Random effects:
##  Groups     Name         Variance Std.Dev.
##  subject_nr (Intercept) 0.5885   0.7671
## Number of obs: 2128, groups:  subject_nr, 112
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.919232   0.141194  20.675   <2e-16 ***
## group1      -0.005996   0.238584  -0.025     0.98
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##        (Intr)
## group1 0.032
```

Exclude incorrect trials

```
raw_data <- subset(raw_data, correct==1)
```

Trajectory preprocessing

```
mt_data <- mt_import_mousetrap(raw_data)
mt_data <- mt_remap_symmetric(mt_data)
mt_data <- mt_align_start(mt_data, start=c(0,0))
mt_data <- mt_derivatives(mt_data)
mt_data <- mt_measures(mt_data)
mt_data <- mt_time_normalize(mt_data)
```

Aggregate trajectory curvature

Average time-normalized tajectories

```
mt_plot_aggregate(mt_data, use = "tn_trajectories", facet_col = "group",
  x = "xpos", y = "ypos", color = "Typicality", subject_id = "subject_nr")+
  xlab("x coordinate (px)") + ylab("y coordinate (px)")+
  scale_color_manual(values = c("black","grey60"))
```
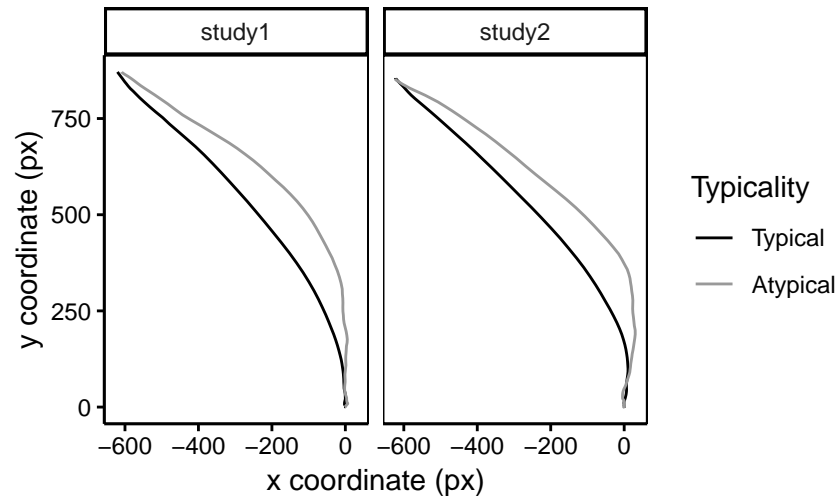
Comparison of MAD aggregated per participant

Aggregate data per participant and condition

```r
agg_mad <- mt_aggregate_per_subject(mt_data, subject_id = "subject_nr",
  use_variables = "MAD", use2_variables = c("Typicality","group"))
```

**Descriptives and paired t-tests**

```r
mad_table <- agg_mad %>%
  group_by(group) %>%
  select(MAD,group,Typicality) %>%
  summarize(
    N =  length(MAD[Typicality=="Typical"]),
    M_t = mean(MAD[Typicality=="Typical"]),
    SD_t = sd(MAD[Typicality=="Typical"]),
    M_a = mean(MAD[Typicality=="Atypical"]),
    SD_a = sd(MAD[Typicality=="Atypical"]),
    t = t.test(MAD[Typicality=="Atypical"],MAD[Typicality=="Typical"],paired=TRUE)$statistic,
    p = t.test(MAD[Typicality=="Atypical"],MAD[Typicality=="Typical"],paired=TRUE)$p.value,
    d = (M_a-M_t)/sd(MAD[Typicality=="Atypical"]-MAD[Typicality=="Typical"])
    )

mad_table %>%
  as.data.frame() %>%
  print(digits=3)
```

```
##    group  N M_t SD_t M_a SD_a    t        p     d
## 1 study1 53 143  111 288  237 4.43 4.95e-05 0.608
## 2 study2 59 158  159 283  226 5.49 9.32e-07 0.715
```

Figure

```
ggplot(agg_mad,aes(x=Typicality,y=MAD,linetype=group,group=group))+
  geom_line(stat="summary",fun.y="mean")+
  geom_point(stat="summary",fun.y="mean")+
  geom_errorbar(stat="summary",fun.data="mean_se",width=.2,linetype=1)+
  scale_linetype_manual(values=c(1,2))+
  coord_cartesian(ylim=c(0,400))
```
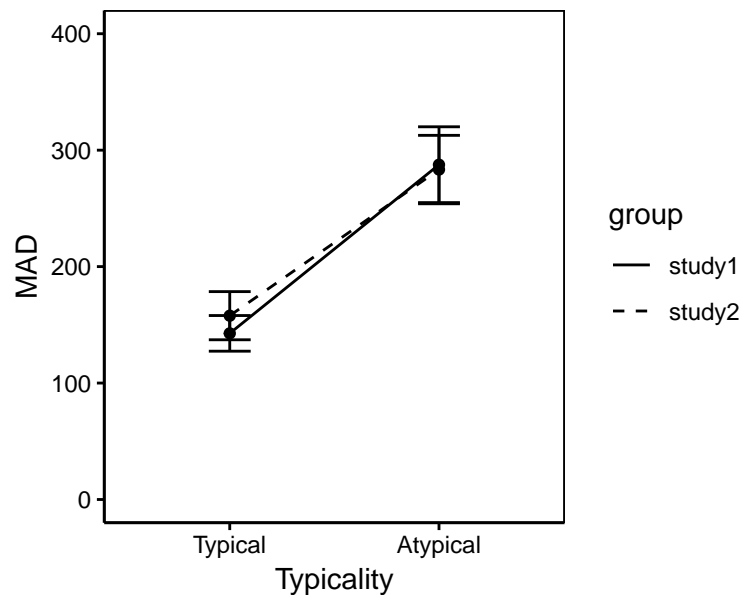

ANOVA

```
anova_mad <- aov_ez(data=agg_mad, dv = "MAD", between = "group", within = "Typicality",
                    id = "subject_nr")
```

```
## Contrasts set to contr.sum for the following variables: group
```

```
nice(anova_mad,es = c("pes","ges"))
```

```
## Anova Table (Type 3 tests)
##
## Response: MAD
##           Effect      df      MSE         F   ges   pes p.value
## 1          group 1, 110 51037.04      0.03 .0002 .0003     .86
## 2     Typicality 1, 110 21550.81 47.34 ***   .11   .30  <.0001
## 3 group:Typicality 1, 110 21550.81      0.24 .0007  .002     .62
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
```

```
# 90 % confidence interval for partial eta-squared
round(get_partial_etas(anova_mad$anova_table, conf.level=.90),2)
```

```
##              pes lower upper
## group        0.0    NA  0.02
## Typicality   0.3  0.19  0.40
```

```
## group:Typicality 0.0     NA  0.04
```

Distribution of trajectory shapes

Bimodality coefficient

```r
# Standardize MAD per participant
mt_data <- mt_standardize(mt_data, use_variables = "MAD", within = "subject_nr")

# Calculate bimodality coefficient
mt_check_bimodality(mt_data, use_variables = "z_MAD",
  grouping_variables = c("group","Typicality"), methods = "BC")
```

```
## $BC
##    group Typicality     z_MAD
## 1 study1    Typical 0.6321584
## 2 study1   Atypical 0.6406680
## 3 study2    Typical 0.5582705
## 4 study2   Atypical 0.5762162
```

Smoothed heatmaps

```r
heatmap_smoothed <- mt_heatmap_ggplot(mt_data,
  xres = 1000,
  smooth_radius = 20,
  n_shades = 10,
  mean_image = 0.2,
  colors=c("white","black"),
  facet_col="group")
```

```
## spatializing trajectories
## calculate image
## smooth image
## enhance image by 5
## spatializing trajectories
## calculate image
## smooth image
## enhance image by 4.8
```
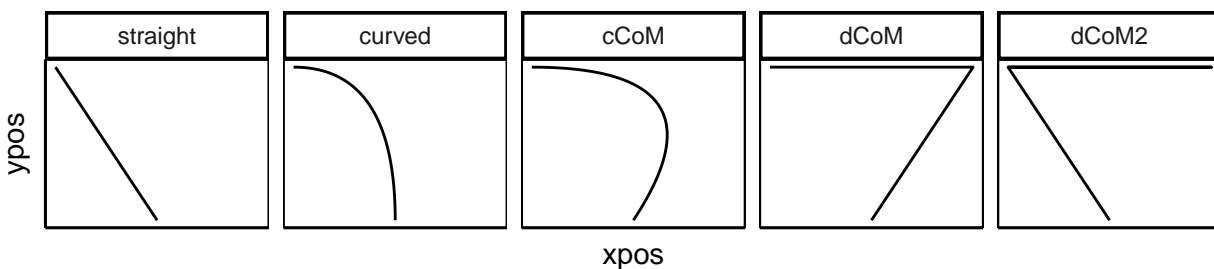
```r
heatmap_smoothed+
  theme(strip.background = element_rect(colour = NA))
```

study1   study2
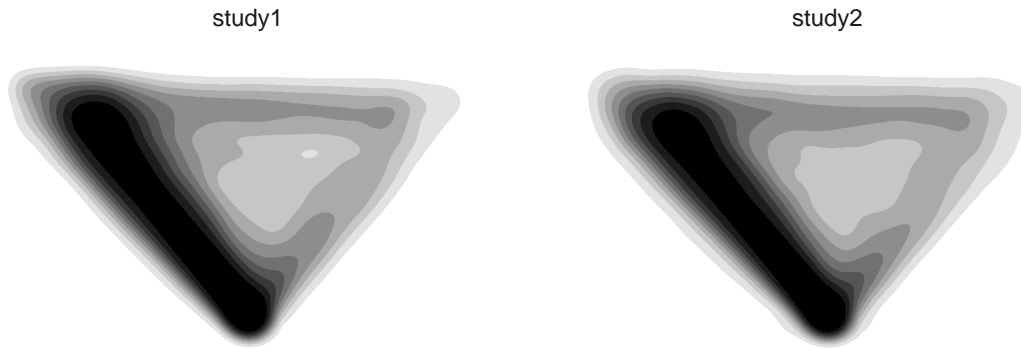
Prototype classification

Plot prototypes

```
mt_plot(mt_prototypes,facet_col="mt_id",only_ggplot = TRUE)+
  geom_path()+
  facet_grid(cols = vars(factor(mt_id,levels=rownames(mt_prototypes))))+
  theme(axis.text=ggplot2::element_blank(),axis.ticks=ggplot2::element_blank())
```


Map trajectories onto prototypes

```
mt_data <- mt_spatialize(mt_data)
mt_data <- mt_map(mt_data,prototypes = mt_prototypes,
  save_as = "measures", grouping_variables = "group")
mt_data$data$prototype_label <- mt_data$measures$prototype_label
```
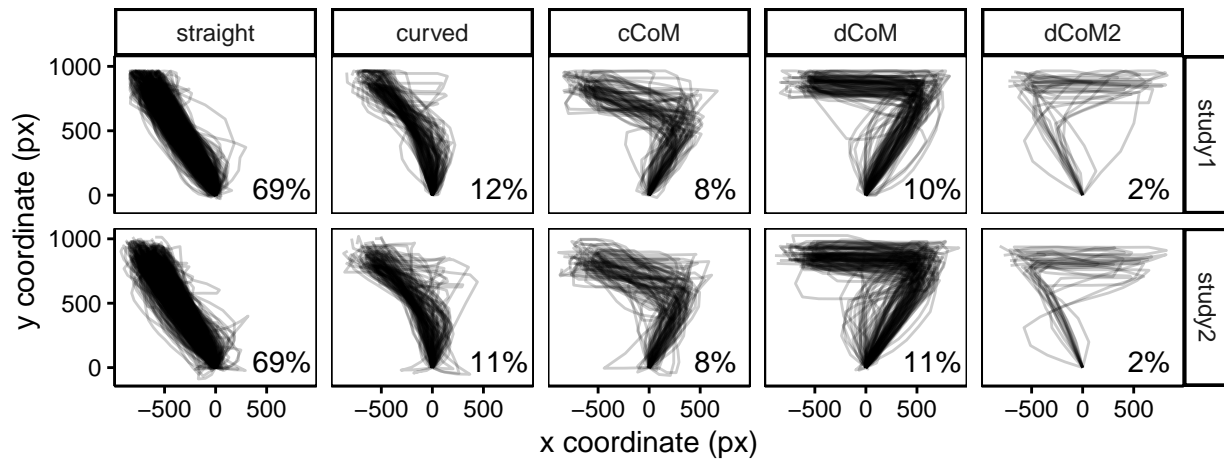
Classified trajectories per group

Relative frequencies

```
prototype_percentages <- mt_data$data %>%
  group_by(group,prototype_label) %>%
  summarise(n=n()) %>%
  mutate(Percent=paste(round(100*n/sum(n)),"%",sep=""))

mt_plot(mt_data, use = "sp_trajectories",
  x = "xpos", y = "ypos", facet_col = "prototype_label", facet_row="group",alpha=.2)+
  xlab("x coordinate (px)") + ylab("y coordinate (px)")+
```

```
geom_text(data=prototype_percentages,aes(label=Percent),x=650,y=50)+
scale_y_continuous(breaks=c(0,500,1000))+
coord_cartesian(xlim=c(-900,900))
```


Chi-squared test

```
chisq.test(with(mt_data$data,table(group, prototype_label)))
```

```
##
##  Pearson's Chi-squared test
##
## data:  with(mt_data$data, table(group, prototype_label))
## X-squared = 1.0137, df = 4, p-value = 0.9077
```

Classified trajectories per group X typicality condition

Relative frequencies

```
rel_freq_agg <- mt_data$data %>%
  group_by(group,Typicality,prototype_label) %>%
  summarise(n=n()) %>%
  mutate(Percent=n/sum(n))

spread(rel_freq_agg[,-4],"prototype_label","Percent",fill = 0) %>%
  as.data.frame()%>%
  print(digits=2)
```

```
##     group Typicality straight curved  cCoM  dCoM  dCoM2
## 1 study1    Typical     0.73  0.125 0.071 0.069 0.0090
## 2 study1   Atypical     0.60  0.108 0.097 0.162 0.0360
## 3 study2    Typical     0.72  0.121 0.064 0.089 0.0082
## 4 study2   Atypical     0.61  0.095 0.105 0.156 0.0317
```

```
ggplot(rel_freq_agg,aes(x=Typicality,y=Percent,fill=forcats::fct_rev(prototype_label)))+
  geom_bar(stat="identity",color="black")+
  scale_fill_brewer(type="seq",name="Classification")+
  facet_grid(.~group)
```
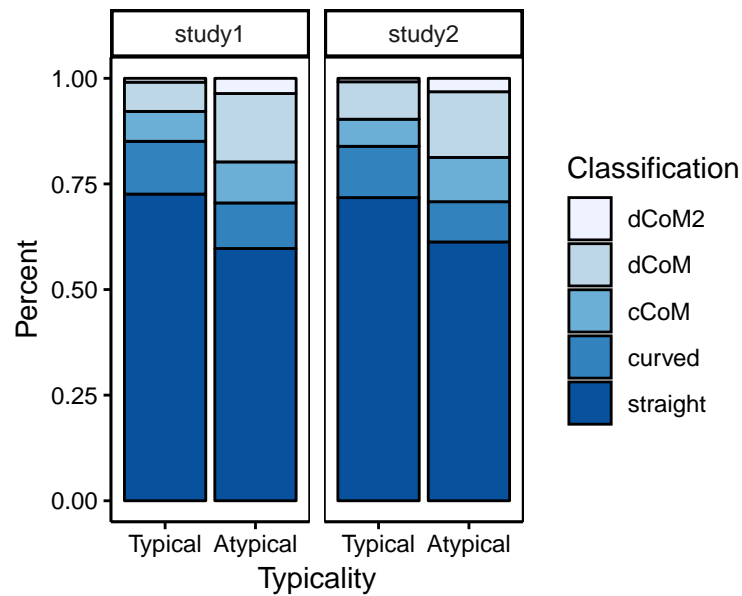
Ordinal mixed regression

```
contrasts(mt_data$data$Typicality) <- c(-0.5,0.5)
contrasts(mt_data$data$group) <- c(0.5,-0.5)
summary(clmm(prototype_label~Typicality*group+(1|subject_nr),data=mt_data$data))
```

```
## Cumulative Link Mixed Model fitted with the Laplace approximation
##
## formula: prototype_label ~ Typicality * group + (1 | subject_nr)
## data:    mt_data$data
##
##  link  threshold nobs logLik   AIC     niter      max.grad cond.H
##  logit flexible  1990 -1935.77 3887.54 584(1792)  1.15e-03 6.8e+01
##
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  subject_nr (Intercept) 0.6161   0.7849
## Number of groups:  subject_nr 112
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## Typicality1       0.72555    0.10588   6.853 7.24e-12 ***
## group1            0.01781    0.18351   0.097    0.923
## Typicality1:group1 0.07736   0.21023   0.368    0.713
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Threshold coefficients:
##                Estimate Std. Error z value
## straight|curved 0.74306    0.09352   7.946
## curved|cCoM     1.44027    0.09881  14.576
## cCoM|dCoM       2.08990    0.10752  19.437
## dCoM|dCoM2      4.29606    0.19783  21.716
```

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