Paper analyses

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General preparations

Load libraries

```
library(mousetrap)
library(ggplot2)
library(dplyr)
```

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)
  ))
```

Data preparation

Read in merged raw data

```
# Read in raw data from csv.gz file
# (commented out as the raw data are now included in the mousetrap R package)
# raw_data <- read.csv("merged_data/raw_data.csv.gz",stringsAsFactor=FALSE)

# Instead, get raw data directly from data stored in mousetrap package
raw_data <- KH2017_raw
```

Filter trials

```
# Look at percent of correct responses per Condition
with(raw_data,table(Condition, correct)/c(table(Condition)))
```

```
##           correct
## Condition          0          1
##   Atypical 0.11111111 0.88888889
##   Typical  0.04615385 0.95384615
```

```
# Exlude incorrect trials
raw_data <- subset(raw_data, correct==1)
```

```r
# Check that each subject has at least one typical and atypical trial left
table(with(raw_data,table(subject_nr,Condition))>0)
```

```
##
## TRUE
##  120
```

Import mouse-tracking data

```r
mt_data <- mt_import_mousetrap(raw_data)
```

Trajectory preprocessing

```r
mt_data <- mt_remap_symmetric(mt_data)
mt_data <- mt_align_start(mt_data)
mt_data <- mt_measures(mt_data)
mt_data <- mt_time_normalize(mt_data)
```

Analyses

Logging resolution

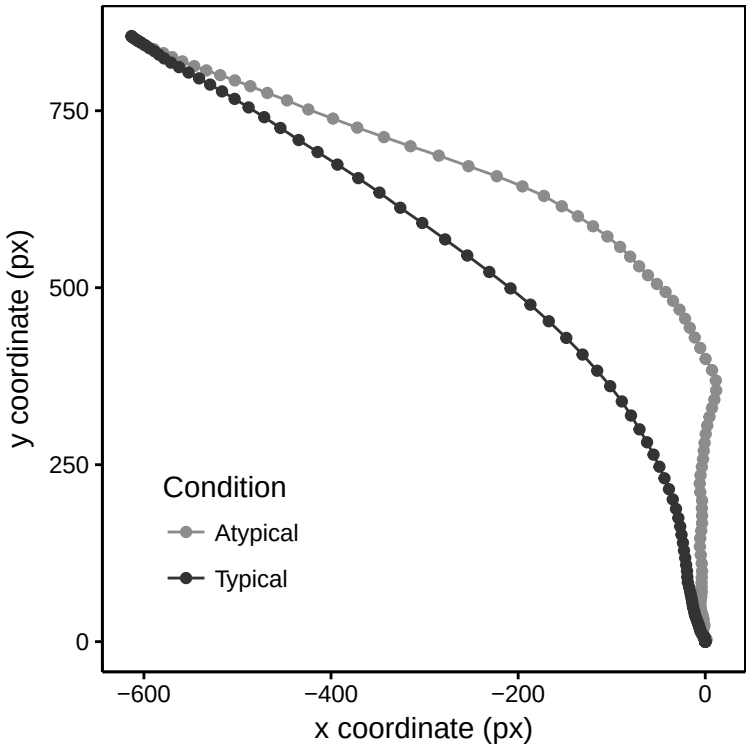
```r
mt_check_resolution(mt_data, desired = 10)
```

```
## $summary
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.000  10.000  10.000   9.981  10.000  40.000
##
## $sd
## [1] 0.430673
##
## $frequencies
## log_diffs
##      1      2      3      4      5      6      7      8      9     10
##     93    133     85    128     92    146     63    124     85 212191
##     11     12     13     14     15     16     17     20     23     25
##    182     10      9     10      4      3      3      1      1      1
##     27     29     32     33     34     36     40
##      2      2      3      3      2      2      1
##
## $relative_frequencies
## log_diffs
##      1      2      3      4      5      6      7      8      9     10
## 0.0004 0.0006 0.0004 0.0006 0.0004 0.0007 0.0003 0.0006 0.0004 0.9944
##     11     12     13     14     15     16     17     20     23     25
## 0.0009 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
##     27     29     32     33     34     36     40
## 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
##
```

```
## $frequencies_desired
## log_diffs_class
## smaller desired greater
##     949  212191     239
##
## $relative_frequencies_desired
## log_diffs_class
## smaller desired greater
##  0.0044  0.9944  0.0011
```

Plot average time-normalized tajectories

```
mt_plot_aggregate(mt_data, use = "tn_trajectories", points=TRUE,
  x = "xpos", y = "ypos", color = "Condition", subject_id = "subject_nr")+
  theme(legend.position=c(.2,.2))+
  xlab("x coordinate (px)") + ylab("y coordinate (px)")+
  scale_color_grey(start = .55, end = .20)
```




```
# ggsave("figures/Figure5.png",width=8.5, height=10,unit="cm",dpi=1200)
# ggsave("figures/Figure5.pdf",width=8.5, height=10,unit="cm")
# ggsave("figures/Figure5.eps",width=8.5, height=10,unit="cm")
```

Comparison of measures based on time-normalized vs. raw trajectories

```
mt_data <- mt_measures(mt_data,use="tn_trajectories",save_as="tn_measures")
diag(cor(mt_data$measures[,-1],mt_data$tn_measures[,-1]))
```

```
##        xpos_max        xpos_min        ypos_max        ypos_min
##       0.9999950       0.9999948       0.9999992       0.9985444
##             MAD        MAD_time        MD_above   MD_above_time
##       0.9998875       0.9990594       0.9999922       0.9978766
##        MD_below   MD_below_time              AD             AUC
##       0.9998770       0.9718700       0.9999912       0.9999688
##      xpos_flips      ypos_flips  xpos_reversals  ypos_reversals
##       0.9977138       0.9897775       1.0000000       1.0000000
##              RT initiation_time       idle_time
##       1.0000000       0.9997353       0.9929374
```

Comparison of MAD aggregated per participant

```
agg_mad <- mt_aggregate_per_subject(mt_data, subject_id = "subject_nr",
  use_variables = "MAD", use2_variables = "Condition")

agg_mad %>%
  group_by(Condition) %>%
  select(MAD,Condition) %>%
  summarize_all(.funs = c("mean","sd"))
```

```
## # A tibble: 2 x 3
##   Condition     mean       sd
##      <fctr>    <dbl>    <dbl>
## 1  Atypical 343.7954 218.6368
## 2   Typical 172.2093 110.8397
```

```
t.test(MAD~Condition, data=agg_mad, paired=TRUE)
```

```
##
##  Paired t-test
##
## data:  MAD by Condition
## t = 6.731, df = 59, p-value = 7.706e-09
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  120.5772 222.5949
## sample estimates:
## mean of the differences
##                171.5861
```

```
# Cohen's dz
mad_diff <- with(agg_mad,MAD[Condition=="Atypical"]-MAD[Condition=="Typical"])
mean(mad_diff)/sd(mad_diff)
```

```
## [1] 0.8689738
```

Bimdality analyses

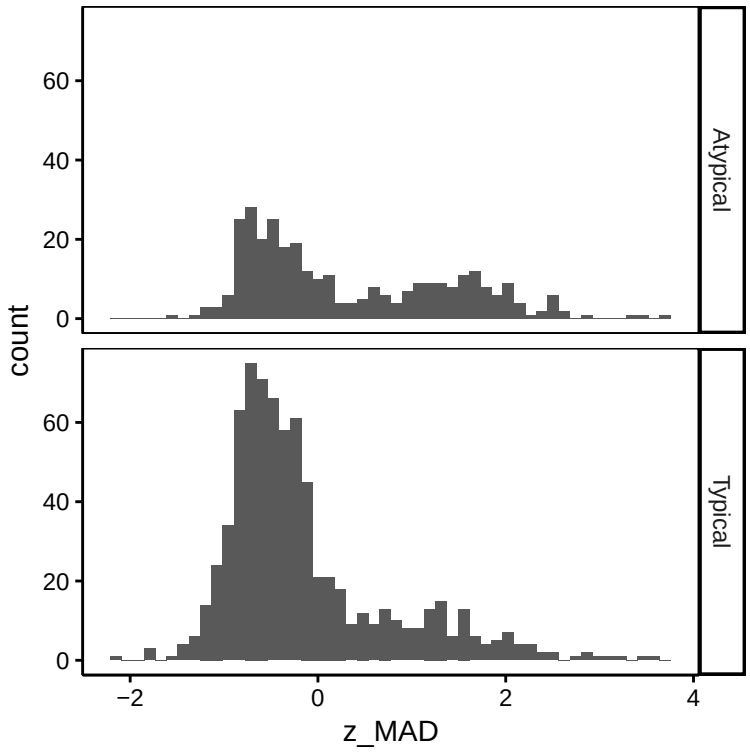
```
# Standardize MAD per participant
mt_data <- mt_standardize(mt_data,
  use_variables = "MAD", within = "subject_nr",prefix = "z_")
```

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

```
## $BC
##   Condition     z_MAD
## 1  Atypical 0.5934582
## 2   Typical 0.6078283
```

```
# Merge trial level data (needed for distribution qplot with facets)
results <- merge(mt_data$data,mt_data$measures,by="mt_id")

# Distribution
qplot(x=z_MAD,data=results,bins=50)+facet_grid(Condition~.)
```



Repeat analyses without large MAD values

```
# Exclude trials with abs(z_MAD)>1.5
table(abs(mt_data$measures$z_MAD)<=1.5)/nrow(mt_data$measures)
```

```
##
##     FALSE      TRUE
## 0.1165414 0.8834586
```

```
mt_data_sub <- mt_subset(mt_data,abs(z_MAD)<=1.5,check="measures")

# Check that each subject has at least on typical and atypical trial left
table(with(mt_data_sub$data,table(subject_nr,Condition))>0)
```

```
##
## TRUE
##  120
```

```
# Comparison of MAD aggregated per participant
agg_mad_sub <- mt_aggregate_per_subject(mt_data_sub, subject_id = "subject_nr",
  use_variables = "MAD", use2_variables = "Condition")

agg_mad_sub %>%
  group_by(Condition) %>%
  select(MAD,Condition) %>%
  summarize_all(.funs = c("mean","sd"))
```

```
## # A tibble: 2 x 3
##   Condition     mean       sd
##      <fctr>    <dbl>    <dbl>
## 1  Atypical 200.7050 209.2332
## 2   Typical 121.7434 117.4904
```

```
t.test(MAD~Condition, data=agg_mad_sub, paired=TRUE)
```

```
##
##  Paired t-test
##
## data:  MAD by Condition
## t = 4.1599, df = 59, p-value = 0.0001047
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   40.97963 116.94341
## sample estimates:
## mean of the differences
##                78.96152
```