

KH2017 reanalysis following Dale et al. (2007)

Pascal J. Kieslich & Felix Henninger

References

Data from: Kieslich, P. J., & Henninger, F. (2017). Mousetrap: An integrated, open-source mouse-tracking package. *Behavior Research Methods*, 49(5), 1652-1667. <https://doi.org/10.3758/s13428-017-0900-z>

Analyses following: Dale, R., Kehoe, C., & Spivey, M. J. (2007). Graded motor responses in the time course of categorizing atypical exemplars. *Memory & Cognition*, 35(1), 15-28. <https://doi.org/10.3758/BF03195938>

General preparations

Load libraries

```
library(mousetrap)
library(ggplot2)
library(afex)
```

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

```
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
```

```

# Test difference using chi-squared test
chisq.test(with(raw_data,table(Condition, correct)))

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: with(raw_data, table(Condition, correct))
## X-squared = 15.676, df = 1, p-value = 7.519e-05
# Exclude incorrect trials
raw_data <- subset(raw_data, correct==1)

# 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

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

Trajectory preprocessing

```

mt_data <- mt_remap_symmetric(mt_data)
mt_data <- mt_align_start(mt_data)
mt_data <- mt_time_normalize(mt_data)

```

Analyses

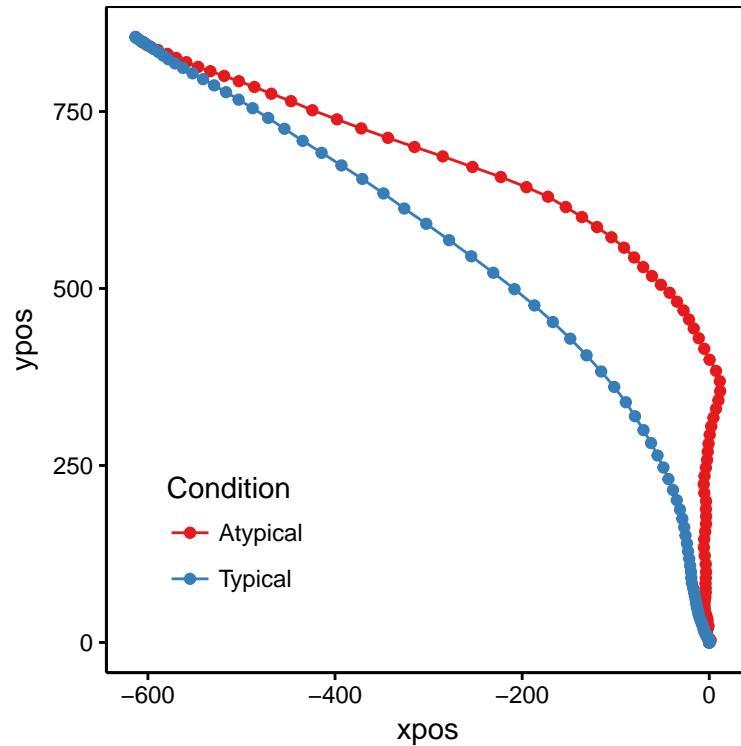
Analysis of time-normalized trajectories

Plot average time-normalized trajectories

```

mt_plot_aggregate(mt_data, use = "tn_trajectories", points = TRUE,
  x = "xpos", y = "ypos", color = "Condition", subject_id = "subject_nr")+
  scale_color_brewer(type="qual",palette = "Set1" )+
  theme(legend.position=c(.2,.2))

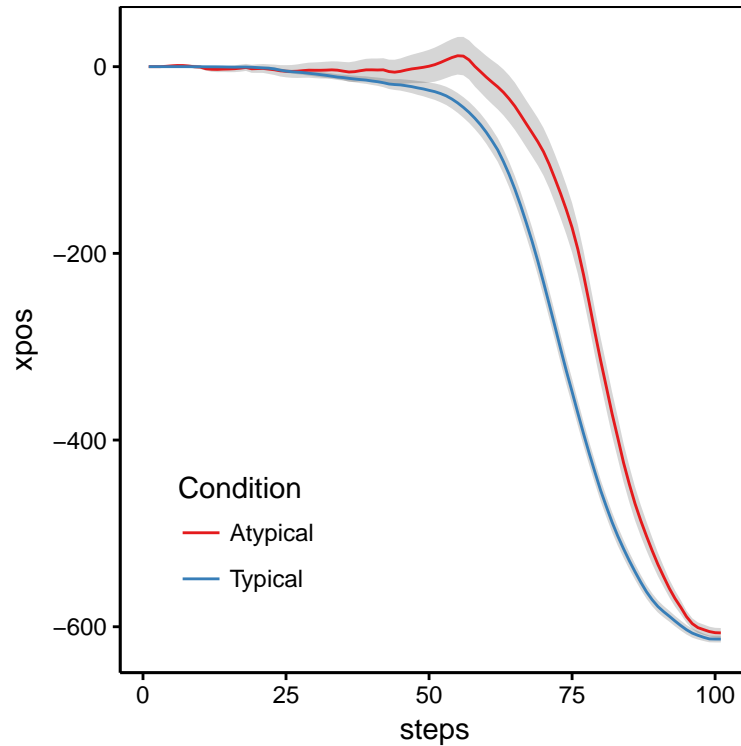
```



Compare time normalized x-positions for each step

```
# Aggregate time-normalized trajectories per condition
# separately per subject
av_tn_trajectories <- mt_aggregate_per_subject(mt_data,
  use="tn_trajectories",use2_variables="Condition",subject_id="subject_nr")

# Plot aggregate trajectories with standard errors
# (note that mean_se does not take into account within subjects design)
ggplot(av_tn_trajectories,aes(x=steps,y=xpos,group=Condition))+
  stat_summary(geom = "ribbon",fun.data=mean_se,alpha=.2)+
  geom_line(aes(color=Condition),stat="summary",fun.y="mean")+
  scale_color_brewer(type="qual",palette = "Set1" )+
  theme(legend.position=c(.2,.2))
```



```

### Paired t-tests on coordinates
xpos_t_tests <-
  with(av_tn_trajectories,
    sapply(unique(steps),function(i){
      t.test(xpos[Condition=="Atypical" & steps==i],
            xpos[Condition=="Typical" & steps==i],
            paired = TRUE)$p.value})
    )

# Retrieve all significant t-tests
which(xpos_t_tests<.05)

## [1] 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76
## [24] 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95

# Number of significant t-tests
sum(xpos_t_tests<.05,na.rm=TRUE)

## [1] 42

# Number of adjacent significant t-tests (minus 1)
table(diff(which(xpos_t_tests<.05)))

##
## 1
## 41

```

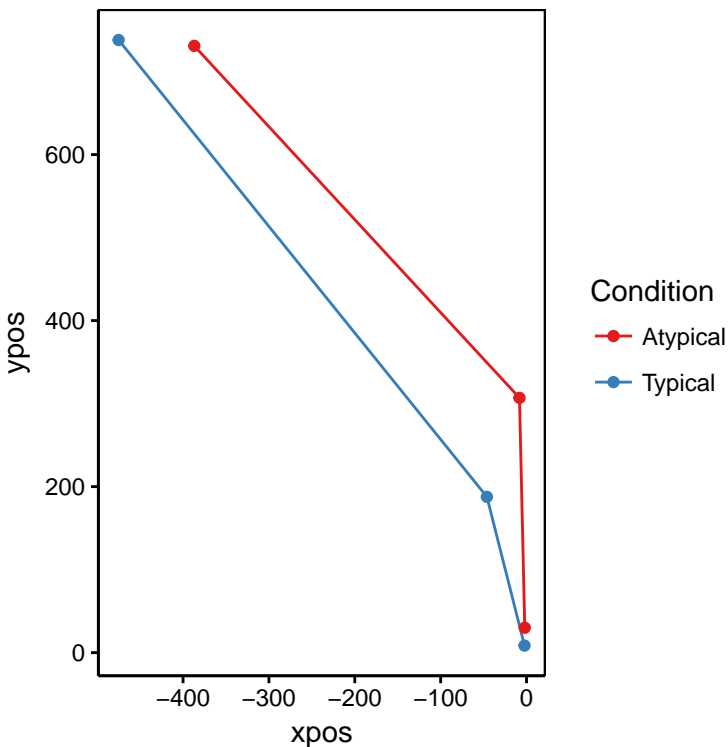
Analysis of binned time-normalized trajectories

```
mt_data <- mt_average(mt_data,use="tn_trajectories",save_as="av_tn_trajectories",  
  av_dimension="steps",intervals = c(0.5,33.5,67.5,101.5))
```

```
mt_aggregate(mt_data,use = "av_tn_trajectories",  
  use2_variables = "Condition",subject_id = "subject_nr")
```

```
##   Condition mt_seq steps timestamps      xpos      ypos  
## 1 Atypical    1  17.0   402.8360  -2.063065  30.030090  
## 2 Atypical    2  50.5  1246.2739  -8.209932 306.902839  
## 3 Atypical    3  84.5  2102.3004 -386.917752 730.937056  
## 4 Typical     1  17.0   282.7307  -2.368584   8.519337  
## 5 Typical     2  50.5   874.6981 -46.165343 187.708387  
## 6 Typical     3  84.5  1475.5009 -475.017635 738.018296
```

```
mt_plot_aggregate(mt_data,use = "av_tn_trajectories", points=TRUE,  
  color = "Condition",subject_id = "subject_nr")+  
  scale_color_brewer(type="qual",palette = "Set1" )
```



```
av_tn_trajectory_bins <- mt_aggregate_per_subject(mt_data,use="av_tn_trajectories",  
  use2_variables="Condition",subject_id="subject_nr")
```

```
av_tn_trajectory_bins$bin <- factor(av_tn_trajectory_bins$steps)
```

```
aov_ez(data=av_tn_trajectory_bins,id="subject_nr",dv="xpos",within = c("Condition","bin"),  
  anova_table = list(es=c("ges","pes"),correction=c("none")))
```

```
## Anova Table (Type 3 tests)
```

```
##
```

```
## Response: xpos
##           Effect      df      MSE          F ges pes p.value
## 1      Condition  1, 59 7405.64   21.56 *** .08 .27 <.0001
## 2           bin 2, 118 4458.03 1558.94 *** .88 .96 <.0001
## 3 Condition:bin 2, 118 2482.98   23.44 *** .06 .28 <.0001
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1

aov_ez(data=av_tn_trajectory_bins,id="subject_nr",dv="xpos",within = c("Condition","bin"),
        anova_table = list(es=c("ges","pes"),correction=c("GG")))
```

```
## Anova Table (Type 3 tests)
##
## Response: xpos
##           Effect      df      MSE          F ges pes p.value
## 1      Condition  1, 59 7405.64   21.56 *** .08 .27 <.0001
## 2           bin 1.96, 115.42 4557.70 1558.94 *** .88 .96 <.0001
## 3 Condition:bin 1.87, 110.33 2655.70   23.44 *** .06 .28 <.0001
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
##
## Sphericity correction method: GG
```

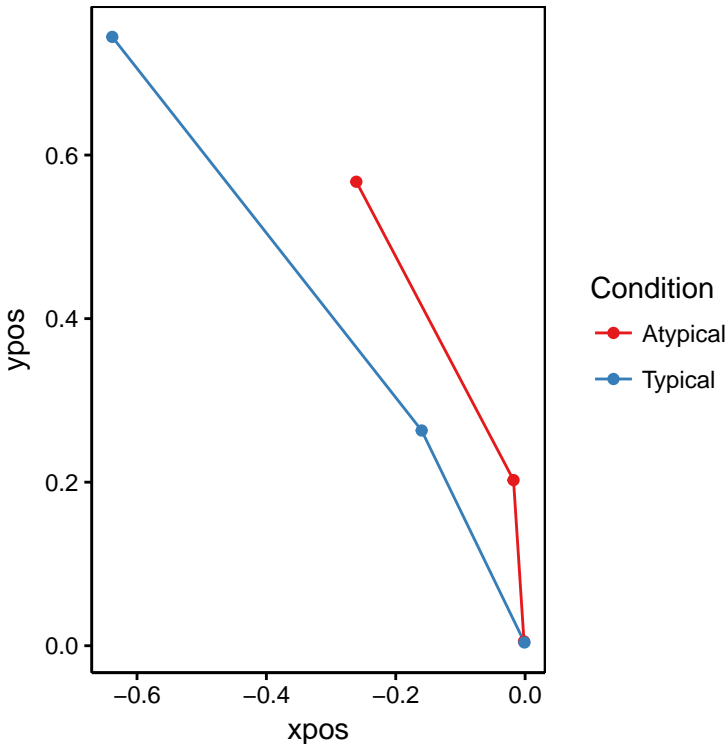
Analysis of space normalized trajectories per subject

```
mt_data <- mt_align_start_end(mt_data,save_as="sn_trajectories",
                             start = c(0,0), end = c(-1,1))
mt_data <- mt_average(mt_data,use="sn_trajectories",
                     interval_size = 500,max_interval=1500)

mt_aggregate(mt_data,use="av_trajectories",
             use2_variables="Condition",subject_id="subject_nr")
```

```
##   Condition mt_seq timestamps      xpos      ypos
## 1 Atypical     1         250 -0.001728983 0.005293067
## 2 Atypical     2         750 -0.017958161 0.202536523
## 3 Atypical     3        1250 -0.260951683 0.567393228
## 4 Typical      1         250 -0.001015639 0.004013623
## 5 Typical      2         750 -0.159926771 0.263175365
## 6 Typical      3        1250 -0.638290679 0.744520598
```

```
mt_plot_aggregate(mt_data,use = "av_trajectories", points=TRUE,
                  color = "Condition",subject_id = "subject_nr")+
  scale_color_brewer(type="qual",palette = "Set1" )
```



```
av_sn_trajectory_bins <- mt_aggregate_per_subject(mt_data,use="av_trajectories",
  use2_variables="Condition",subject_id="subject_nr")
```

```
# Check that each subject has observations in each category
table(table(av_sn_trajectory_bins$subject_nr))
```

```
##
## 6
## 60
```

```
av_sn_trajectory_bins$bin <- factor(av_sn_trajectory_bins$timestamps)
```

```
aov_ez(data=av_sn_trajectory_bins,id="subject_nr",dv="xpos",within = c("Condition","bin"),
  anova_table = list(es=c("ges","pes"),correction=c("none")))
```

```
## Anova Table (Type 3 tests)
```

```
##
```

```
## Response: xpos
```

##	Effect	df	MSE	F	ges	pes	p.value	
## 1	Condition	1, 59	0.02	110.90	***	.23	.65	<.0001
## 2	bin	2, 118	0.03	267.88	***	.60	.82	<.0001
## 3	Condition:bin	2, 118	0.01	85.44	***	.20	.59	<.0001

```
## ---
```

```
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
```

```
aov_ez(data=av_sn_trajectory_bins,id="subject_nr",dv="xpos",within = c("Condition","bin"),
  anova_table = list(es=c("ges","pes"),correction=c("GG")))
```

```
## Anova Table (Type 3 tests)
```

```
##
```

```
## Response: xpos
```

```
##           Effect           df  MSE           F ges pes p.value
## 1    Condition           1, 59 0.02 110.90 *** .23 .65 <.0001
## 2           bin 1.26, 74.26 0.04 267.88 *** .60 .82 <.0001
## 3 Condition:bin 1.88, 110.67 0.01  85.44 *** .20 .59 <.0001
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
##
## Sphericity correction method: GG
```

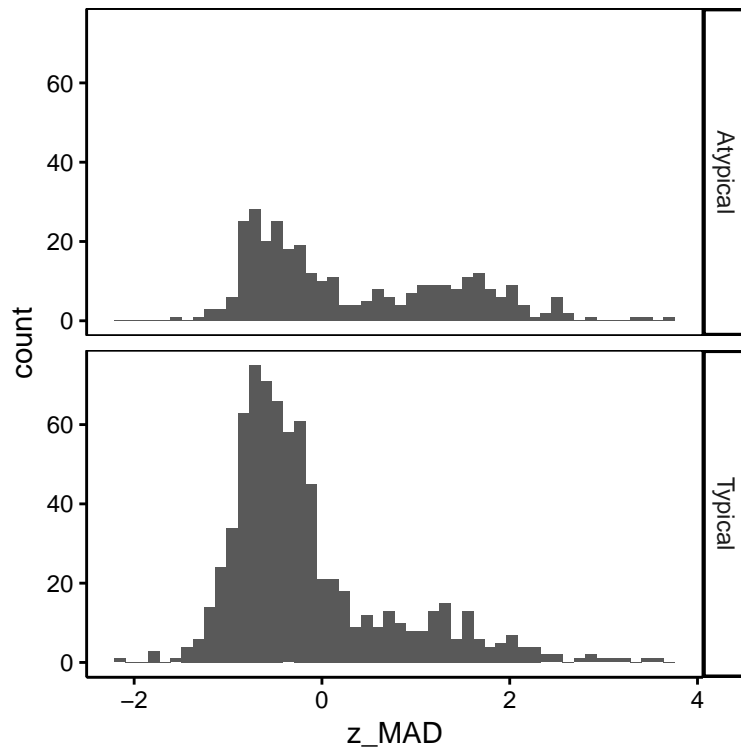
Distributional analyses

```
# Compute trial indices
mt_data <- mt_measures(mt_data)

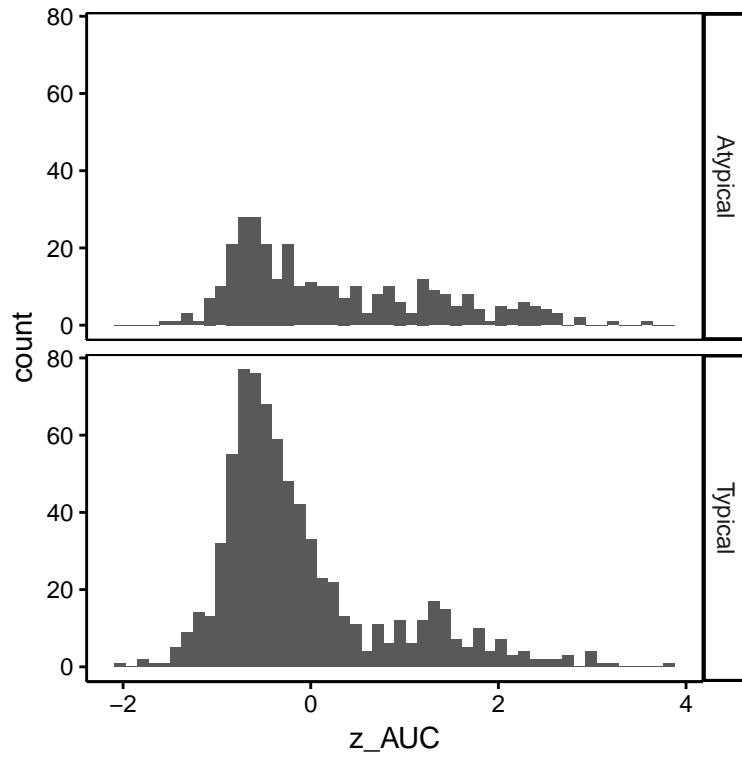
# Standardize measures per participant
mt_data <- mt_standardize(mt_data,
  use_variables = c("MAD", "AUC", "AD"), within = "subject_nr", prefix = "z_")

# Merge data
results <- merge(mt_data$data, mt_data$measures, by="mt_id")

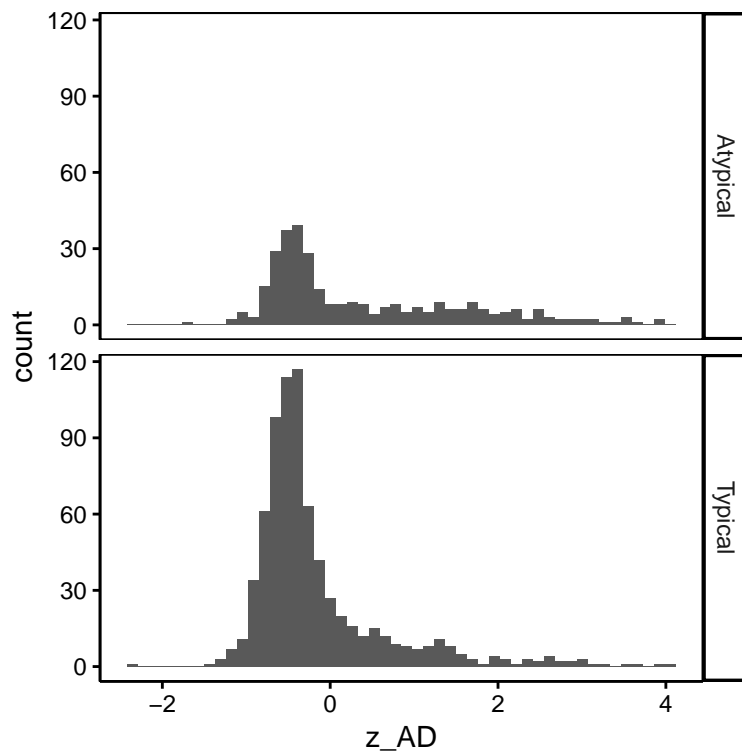
# Distribution
qplot(x=z_MAD, data=results, bins=50)+facet_grid(Condition~.)
```




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



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



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

```
## $BC
## Condition z_MAD z_AUC z_AD
## 1 Atypical 0.5934582 0.5976725 0.6510847
## 2 Typical 0.6078283 0.6132270 0.6617684
```

Sample entropy

```
# Calculate sample entropy (for lag 3)
mt_data <- mt_sample_entropy(mt_data,use="tn_trajectories",m=3,dimension="xpos")
```

```
# Aggregate per participant
agg_sample_entropy <- mt_aggregate_per_subject(mt_data, subject_id = "subject_nr",
  use_variables = "sample_entropy", use2_variables = "Condition")
```

```
# Test the difference
mt_aggregate(mt_data, subject_id = "subject_nr",
  use_variables = "sample_entropy", use2_variables = "Condition")
```

```
## Condition sample_entropy
## 1 Atypical 0.09112034
## 2 Typical 0.06955290
```

```
t.test(sample_entropy~Condition, data=agg_sample_entropy, paired=TRUE)
```

```
##
## Paired t-test
##
## data: sample_entropy by Condition
## t = 5.4269, df = 59, p-value = 1.129e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.01361514 0.02951976
## sample estimates:
## mean of the differences
## 0.02156745
```

Plot for left- and rightward responses

Data preparation

```
mt_data <- mt_import_mousetrap(raw_data)
mt_data <- mt_remap_symmetric(mt_data,remap_xpos = "no")
mt_data <- mt_align_start(mt_data)
mt_data <- mt_time_normalize(mt_data)

# code response side
mt_data$data$side <- ifelse(mt_data$data$response==mt_data$data$CategoryLeft,"left","right")
```

Plot average time-normalized trajectories

```
mt_plot_aggregate(mt_data, use = "tn_trajectories", points = TRUE,  
  x = "xpos", y = "ypos", color = "Condition",  
  linetype = "side")+  
  scale_color_brewer(type="qual",palette = "Set1" )+  
  scale_linetype_manual(values=c("solid","solid"),guide=FALSE)+  
  theme(legend.position=c(.15,.2))
```

