```r
library(readbulk)
raw_data <- read_opensesame("raw_data", verbose = FALSE)
raw_data <- subset(raw_data, Condition!="Example" & correct==1)

library(mousetrap)
mt_data <- mt_import_mousetrap(raw_data)
mt_data <- mt_remap_symmetric(mt_data)
mt_data <- mt_align_start(mt_data)
mt_data <- mt_measures(mt_data)

agg_measures <- mt_aggregate_per_subject(mt_data, subject_id = "subject_nr",
  use_variables = "MAD", use2_variables = "Condition")
t.test(MAD~Condition, data = agg_measures, paired = TRUE)

mt_data <- mt_time_normalize(mt_data)
mt_plot_aggregate(mt_data, use = "tn_trajectories", points = TRUE,
  x = "xpos", y = "ypos", color = "Condition", subject_id = "subject_nr")
```