

eyetrackingR Demo

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load *eyetrackingR* and set data options

```
library(eyetrackingR)

## Loading required package: dplyr
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##   filter, lag
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

library(lme4)

## Loading required package: Matrix

library(lmerTest)

##
## Attaching package: 'lmerTest'
## The following object is masked from 'package:lme4':
##
##   lmer
## The following object is masked from 'package:stats':
##
##   step

data("word_recognition")
dataset <- make_eyetrackingr_data(word_recognition,
                                  participant_column = "ParticipantName",
                                  trial_column = "Trial",
                                  time_column = "TimeFromTrialOnset",
                                  trackloss_column = "TrackLoss",
                                  aoi_columns = c('Animate', 'Inanimate'),
                                  treat_non_aoi_looks_as_missing = TRUE
)

str(dataset)

## Classes 'eyetrackingR_data', 'eyetrackingR_df', 'tbl_df', 'tbl' and 'data.frame':   195912 obs. of
## $ ParticipantName      : Factor w/ 30 levels "ANCAT139","ANCAT18",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ Sex                  : Factor w/ 2 levels "F","M": 1 1 1 1 1 1 1 1 1 1 ...
## $ Age                  : num  21.9 21.9 21.9 21.9 21.9 ...
## $ TrialNum              : num  1 1 1 1 1 1 1 1 1 1 ...
```

```
## $ Trial : Factor w/ 6 levels "FamiliarBird",...: 2 2 2 2 2 2 2 2 2 2 ...
## $ TimeFromTrialOnset : int 0 17 33 50 67 83 100 117 133 150 ...
## $ Subphase : Factor w/ 3 levels "Preview","Test",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ TimeFromSubphaseOnset: int 0 17 33 50 67 83 100 117 133 150 ...
## $ AOI : Factor w/ 4 levels "", "Animate", "Inanimate",...: 4 4 4 4 4 4 4 4 4 4 ...
## $ Animate : logi NA NA NA NA NA NA ...
## $ Inanimate : logi NA NA NA NA NA NA ...
## $ TrackLoss : logi TRUE TRUE TRUE TRUE TRUE TRUE ...
## $ MCDI_Total : int 47 47 47 47 47 47 47 47 47 47 ...
## $ MCDI_Nouns : int 29 29 29 29 29 29 29 29 29 29 ...
## $ MCDI_Verbs : int 8 8 8 8 8 8 8 8 8 8 ...
## - attr(*, "eyetrackingR")=List of 1
## ..$ data_options:List of 7
## .. ..$ participant_column : chr "ParticipantName"
## .. ..$ trackloss_column : chr "TrackLoss"
## .. ..$ time_column : chr "TimeFromTrialOnset"
## .. ..$ trial_column : chr "Trial"
## .. ..$ item_columns : NULL
## .. ..$ aoi_columns : chr "Animate" "Inanimate"
## .. ..$ treat_non_aoi_looks_as_missing: logi TRUE
```

```
head(dataset)
```

```
## # A tibble: 6 x 15
##   ParticipantName Sex      Age TrialNum Trial      TimeFromTrialOn~ Subphase
##   <fct>           <fct> <dbl>   <dbl> <fct>           <int> <fct>
## 1 ANCAT139       F      21.9     1 Familiar~         0 Preview
## 2 ANCAT139       F      21.9     1 Familiar~        17 Preview
## 3 ANCAT139       F      21.9     1 Familiar~        33 Preview
## 4 ANCAT139       F      21.9     1 Familiar~        50 Preview
## 5 ANCAT139       F      21.9     1 Familiar~        67 Preview
## 6 ANCAT139       F      21.9     1 Familiar~        83 Preview
## # ... with 8 more variables: TimeFromSubphaseOnset <int>, AOI <fct>,
## #   Animate <lgl>, Inanimate <lgl>, TrackLoss <lgl>, MCDI_Total <int>,
## #   MCDI_Nouns <int>, MCDI_Verbs <int>
```

remove trackloss-ridden trials

```
dataset_clean <- clean_by_trackloss(dataset,
                                     participant_prop_thresh = 1, trial_prop_thresh = .25,
                                     window_start_time = 15500, window_end_time = 21000)
```

```
## Performing Trackloss Analysis...
```

```
## Will exclude trials whose trackloss proportion is greater than : 0.25
```

```
## ...removed 33 trials.
```

zoom in on response window

```
word_window <- subset_by_window(dataset_clean, rezero = FALSE,
                                window_start_time = 15500, window_end_time = 21000)
```

```
## Avg. window length in new data will be 5500
```

create a column indicating what type of trial:

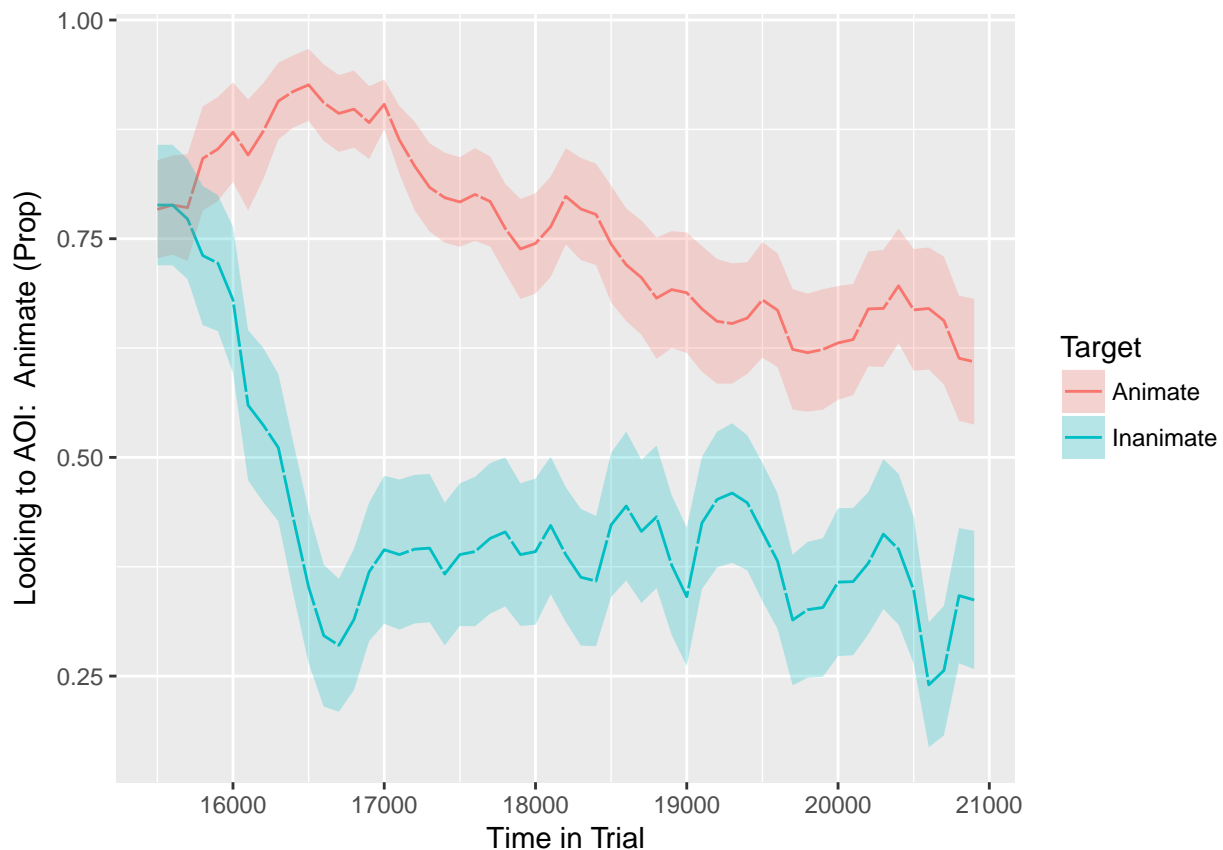
```
word_window$Target <- as.factor( ifelse(test = grepl('(Spoon|Bottle)', word_window$Trial),  
                                       yes = 'Inanimate',  
                                       no  = 'Animate') )
```

convert data into a series of time-bins:

```
word_time <- make_time_sequence_data(word_window, time_bin_size = 100,  
                                     predictor_columns = "Target", aois = c("Animate"))  
plot(word_time, predictor_column = "Target")
```

```
## Warning: Removed 37 rows containing non-finite values (stat_summary).
```

```
## Warning: Removed 37 rows containing non-finite values (stat_summary).
```



```
# An important step in performing regression analysis is to center predictors (in order to make paramet  
word_time$TargetC <- ifelse(word_time$Target == 'Animate', .5, -.5)  
word_time$TargetC <- word_time$TargetC - mean(word_time$TargetC)
```

```

#Using mixed-effects models
# mixed-effects linear model on subject*trial data
model_time_window <- lmer(Elog ~ TargetC + (1 + TargetC | Trial) + (1 | ParticipantName), data = word_t.

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : unable to evaluate scaled gradient

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control
## $checkConv, : Model failed to converge: degenerate Hessian with 1 negative
## eigenvalues

## Warning: Model failed to converge with 1 negative eigenvalue: -4.1e+02

# cleanly show important parts of model (see `summary()` for more)
(est <- broom::tidy(model_time_window, effects="fixed"))

##           term estimate std.error statistic  p.value      NA
## 1 (Intercept) 0.736170 0.1498076 22.332549 4.914105 6.235896e-05
## 2      TargetC 1.764129 0.1857890  2.380166 9.495337 6.030007e-03

summary(model_time_window)

## Linear mixed model fit by maximum likelihood . t-tests use
## Satterthwaite's method [lmerModLmerTest]
## Formula: Elog ~ TargetC + (1 + TargetC | Trial) + (1 | ParticipantName)
## Data: word_time
##
##      AIC      BIC   logLik deviance df.resid
## 28457.8 28505.2 -14221.9 28443.8      6499
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2904 -0.9628  0.3745  0.6244  2.0900
##
## Random effects:
## Groups           Name      Variance Std.Dev. Corr
## ParticipantName (Intercept) 0.4416   0.6645
## Trial            (Intercept) 0.0000   0.0000
##                TargetC      0.1323   0.3637   NaN
## Residual                4.5701   2.1378
## Number of obs: 6506, groups: ParticipantName, 27; Trial, 6
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)   0.7362    0.1498 22.3325   4.914 6.24e-05 ***
## TargetC       1.7641    0.1858  2.3802   9.495 0.00603 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## TargetC -0.251
## convergence code: 0
## unable to evaluate scaled gradient
## Model failed to converge: degenerate Hessian with 1 negative eigenvalues

```

```
# perform a growth-curve analysis
model <- lmer(Elog ~ TargetC*(ot1 + ot2 + ot3 + ot4 + ot5) + (1 | Trial) + (1 | ParticipantName), data =
broom::tidy(model, effects="fixed")
```

##	term	estimate	std.error	statistic	p.value	NA
## 1	(Intercept)	0.73356474	0.1429224	28.701105	5.1326071	1.804418e-05
## 2	TargetC	1.75524473	0.1385365	5.428529	12.6699078	3.079279e-05
## 3	ot1	-2.81945229	0.1929438	6474.888099	-14.6128188	1.324302e-47
## 4	ot2	0.32236018	0.1932459	6474.314258	1.6681343	9.533743e-02
## 5	ot3	-0.57443217	0.1927003	6473.881999	-2.9809610	2.884142e-03
## 6	ot4	-0.31725945	0.1920604	6473.129670	-1.6518731	9.860893e-02
## 7	ot5	0.57347864	0.1923973	6472.942377	2.9806999	2.886600e-03
## 8	TargetC:ot1	-0.78914703	0.4010187	6473.899927	-1.9678558	4.912725e-02
## 9	TargetC:ot2	-1.73922537	0.4017806	6473.611621	-4.3287935	1.521870e-05
## 10	TargetC:ot3	4.21984068	0.4006809	6473.101634	10.5316732	9.958019e-26
## 11	TargetC:ot4	-1.81094160	0.3996476	6472.961277	-4.5313458	5.966198e-06
## 12	TargetC:ot5	-0.07777271	0.4003747	6472.927872	-0.1942498	8.459864e-01

```
#drop1(model, ~., test="Chi")
```