Package ‘implicitMeasures’

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Type Package

Title Computes the Scores for Different Implicit Measures

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R topics documented:

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Prepare and clean IAT data.

Select IAT blocks for the \textit{D-score} computation and eventually save demographic data.

Usage

\begin{verbatim}
clean_iat(
    data, 
    sbj_id = "participant", 
    block_id = "blockcode", 
    mapA_practice = "practice_MappingA", 
    mapA_test = "test_MappingA", 
    mapB_practice = "practice_MappingB", 
    mapB_test = "test_MappingB", 
    latency_id = "latency", 
    accuracy_id = "correct", 
    trial_id = NULL, 
    trial_eliminate = NULL, 
    demo_id = NULL, 
    trial_demo = NULL
)
\end{verbatim}

Arguments

- \textbf{data} \hspace{1cm} Dataframe containing IAT data.
- \textbf{sbj_id} \hspace{1cm} Column identifying participants' IDs. This variable can be a character, numeric, or factor.
- \textbf{block_id} \hspace{1cm} String. Column identifying IAT blocks. The \textit{block_id} variable should be a factor with each level identifying an IAT block.
- \textbf{mapA_practice} \hspace{1cm} String. Label for the practice blocks of Mapping A (as it appears in the \textit{block_id} variable).
mapA_test  String. Label for the test blocks of Mapping A (as it appears in the block_id variable).

mapB_practice  String. Label for the practice blocks of Mapping B (as it appears in the block_id variable).

mapB_test  String. Label for the test blocks of Mapping B (as it appears in the block_id variable).

latency_id  String. Column identifying response times (in millisecond). If the IAT had a built-in correction, latencies of the incorrect responses should be those inflated with the built-in correction.

accuracy_id  String. Column identifying the IAT accuracy responses. The accuracy_id variable should be a numeric variable identifying the correct responses (with 1) and the incorrect responses (with 0).

trial_id  Character. Column identifying the trials. Specify this only if you want to delete some specific trials.

trial_eliminate  Character or character vector. Label(s) identifying the trials in trial_id to eliminate.

demo_id  Character. Column identifying demographic blocks. It can be the same as block_id.

trial_demo  Character or character vector identifying the name of the blocks in demo_id containing the demographic information.

Value

List of dataframe.

data_keep  Dataframe with class iat_clean. The dataframe contains the data of the blocks specified in mapA_practice, mapA_test, mapB_practice, mapB_test. If you have specified the trials to eliminate through trial_eliminate, data_keep will contain the already cleaned dataset. This dataset should be passed to the computeD function.

data_eliminate  Dataframe containing all the discarded blocks and trials.

data_demo  Dataframe containing demographic variables. It will be present only if you specified the demo_id and trial_demo arguments.

Examples

data("raw_data")  # load data
iat_cleandata <- clean_iat(raw_data, sbj_id = "Participant",
block_id = "blockcode",
mapA_practice = "practice.iat.Milkbad",
mapA_test = "test.iat.Milkbad",
mapB_practice = "practice.iat.Milkgood",
mapB_test = "test.iat.Milkgood",
latency_id = "latency",
accuracy_id = "correct",
trial_id = "trialcode",
trial_eliminate = c("reminder", "reminder1"),
```r
demo_id = "blockcode",
trial_demo = "demo")
iat_data <- iat_cleandata[[1]] # select the first element of the list (IAT data)
head(iat_data)
demo_data <- iat_cleandata[[3]] # select the third element of the list
    # (demographic data)
head(demo_data)
```

### clean_sciat

Prepare and clean SC-IAT data

**Description**

Select the SC-IAT blocks, for either one or two SC-IATs. Eventually save demographic data.

**Usage**

```r
clean_sciat(
data,
sbj_id = "participant",
block_id = "blockcode",
accuracy_id = "correct",
latency_id = "latency",
block_sciat_1 = NULL,
block_sciat_2 = NULL,
trial_id = NULL,
trial_eliminate = NULL,
demo_id = NULL,
trial_demo = NULL
)
```

**Arguments**

- **data**
  - Dataframe containing SC-IAT data.
- **sbj_id**
  - Column identifying participants' IDs. This variable can be a character, numeric, or factor.
- **block_id**
  - String. Column identifying SC-IAT blocks. The `block_id` variable should be a factor with each level identifying a SC-IAT block.
- **accuracy_id**
  - String. Column identifying the IAT accuracy responses. The `accuracy_id` variable should be a numeric variable identifying the correct responses (with 1) and the incorrect responses (with 0).
- **latency_id**
  - String. Column identifying response times (in millisecond).
- **block_sciat_1**
  - Character or character vector. Labels identifying the first SC-IAT blocks as they are named in the `block_id`.
- **block_sciat_2**
  - Character or character vector. Labels identifying the second (if present) SC-IAT blocks as they are named in the `block_id`.
### clean_sciat

**trial_id**  
Character. Column identifying the trials. Specify this only if you want to delete some specific trials. If a response window was used for the SC-IAT administration the label of the non-response must be included in this variable.

**trial_eliminate**  
Character or character vector. Labels of the trials to eliminate in the trial_id to eliminate (NOTE: don’t use this command to delete the responses exceeding the response time window).

**demo_id**  
Character. Character. Column identifying demographic blocks. It can be the same as block_id.

**trial_demo**  
Character or character vector identifying the name of the blocks in demo_id containing the demographic information.

### Value

List of dataframe.

- **sciatt**  
Data frame with class sciat_clean containing the data of the first SC-IAT as specified through `block_sciat_1`. If any labels was specified in `trial_eliminate`, data_keep will contain the already cleaned dataset.

- **sciatt2**  
Data frame with class sciat_clean containing the data of the second (if any) SC-IAT as specified through `block_sciat_2`. If any labels was specified in `trial_eliminate`, data_keep will contain the already cleaned dataset.

- **data_demo**  
Data frame. Present only when variable_demo and trial_demo arguments are specified.

### Examples

```r
data("raw_data")
sciat_data <- clean_sciat(raw_data, sbj_id = "Participant",
block_id = "blockcode",
latency_id = "latency",
accuracy_id = "correct",
block_sciat_1 = c("test.sc_dark.Darkbad",
"test.sc_dark.Darkgood"),
block_sciat_2 = c("test.sc_milk.Milkbad",
"test.sc_milk.Milkgood"),
trial_id = "trialcode",
trial_eliminate = c("reminder",
"reminder1"))
sciat1 <- sciat_data[[1]]
sciat2 <- sciat_data[[2]]
```
**computeD**  

*Compute IAT D-score*

**Description**

Compute *D-score* for the IAT according to different algorithms.

**Usage**

```r
computeD(data, Dscore = c("d1", "d2", "d3", "d4", "d5", "d6"))
```

**Arguments**

- **data**
  Dataframe with class *iat_clean*.
- **Dscore**
  Character. Indicates which *D-score* to compute. For details on the algorithms, please refer to Greenwald et al. (2003).

**Value**

Dataframe with class "dscore". The number of rows of the dataframe corresponds to the total number of participants. Variables are defined as follows (the values are specific for each participant):

- **participant** Respondents' IDs.
- **n_trial** Number of trials before data cleaning.
- **nslow10000** Number of slow trials (> 10,000 ms).
- **nfast400** Number of fast trials (< 400 ms).
- **nfast300** Number of fast trials (< 300 ms).
- **accuracy.practice_MappingA** Proportion of correct responses in practice block of Mapping A.
- **accuracy.practice_MappingB** Proportion of correct responses in practice block of Mapping B.
- **accuracy.test_MappingA** Proportion of correct responses in test block of Mapping A.
- **accuracy.test_MappingB** Proportion of correct responses in test block of Mapping B.
- **accuracy.MappingA** Proportion of correct responses in Mapping A.
- **accuracy.MappingB** Proportion of correct responses in Mapping B.
- **RT_mean.MappingA** Mean response time in Mapping A.
- **RT_mean.MappingB** Mean response time in Mapping B.
- **mean_practice_MappingA** Mean response time in practice block of Mapping A.
- **mean_practice_MappingB** Mean response time in practice block of Mapping B.
- **mean_test_MappingA** Mean response time in test block of Mapping A.
- **mean_test_MappingB** Mean response time in test block of Mapping B.
- **d_practice_dX** *D-scores* computed on the practice blocks. The X stands for the selected *D-score* procedure.
- **d_test_dX** *D-scores* computed on the test blocks. The X stands for the selected *D-score* procedure.
dscore_dX The average D-score for the practice and test D-scores. The X stands for the selected D-score procedure.

cond_ord Indicates the order with which the associative conditions have been presented, either "MappingA_First" or "MappingB_First".

legendMappingA Indicates the corresponding value of Mapping A in the original dataset.

legendMappingB Indicates the corresponding value of Mapping B in the original dataset.

Examples

# compute D-score 2 for the IAT data ###
data("raw_data") # import data
iat_cleandata <- clean_iat(raw_data, sbj_id = "Participant",
block_id = "blockcode",
mapA_practice = "practice.iat.Milkbad",
mapA_test = "test.iat.Milkbad",
mapB_practice = "practice.iat.Milkgood",
mapB_test = "test.iat.Milkgood",
l latency_id = "latency",
accuracy_id = "correct",
trial_id = "trialcode",
trial_eliminate = c("reminder", "reminder1"),
demo_id = "blockcode",
trial_demo = "demo")

iat_data <- iat_cleandata[[1]]
# calculate D-score
iat_dscore <- computeD(iat_data,
Dscore = "d2")

descript_d

Descriptive table of either the IAT D-score or the SC-IAT Ds

Description

Descriptive statistics for the IAT D-score or the SC-IAT D.

Usage

descript_d(data, latex = FALSE)

Arguments

data Dataframe with either class dscore or class dsciat.
latex Logical. If TRUE, the table for the descriptive statistics will be printed in latex format. Default is FALSE.

Value

Dataframe, containing the mean, s.d., minimum and maximum of the IAT (D-score, D-practice, and D-test) or the SC-IAT (D-Sciat, RT.MappingA, RT.MappingB).
Examples

# compute D-score 2 for the IAT data ###
data("raw_data")  # import data
iat_cleanedata <- clean_iat(raw_data, sbj_id = "Participant",
                           block_id = "blockcode",
                           mapA_practice = "practice.iat.Milkbad",
                           mapA_test = "test.iat.Milkbad",
                           mapB_practice = "practice.iat.Milkgood",
                           mapB_test = "test.iat.Milkgood",
                           latency_id = "latency",
                           accuracy_id = "correct",
                           trial_id = "trialcode",
                           trial_eliminate = c("reminder", "reminder1"),
                           demo_id = "blockcode",
                           trial_demo = "demo")

iat_data <- iat_cleanedata[[1]]
# calculate D-score
iat_dscore <- computeD(iat_data, 
                        Dscore = "d2")
descript_d(iat_dscore)  # descriptive statistics for the IAT

# calculate D for the SCIAT
data("raw_data")  # load data
sciat_cleanedata <- clean_sciat(raw_data, sbj_id = "Participant",
                                block_id = "blockcode",
                                latency_id = "latency",
                                accuracy_id = "correct",
                                block_sciat_1 = c("test.sc_dark.Darkbad",
                                                   "test.sc_dark.Darkgood"),
                                block_sciat_2 = c("test.sc_milk.Milkbad",
                                                   "test.sc_milk.Milkgood"),
                                trial_id = "trialcode",
                                trial_eliminate = c("reminder", "reminder1"))

sciat1 <- sciat_cleanedata[[1]]  # compute D for the first SC-IAT
d_sciat1 <- Dsciat(sciat1,
                   mappingA = "test.sc_dark.Darkbad",
                   mappingB = "test.sc_dark.Darkgood",
                   non_response = "alert")
descript_d(d_sciat1,
           latex = TRUE)  # descriptive statistics for the SC-IAT in latex

Dsciat

Compute D for the SC-IAT

Description

Compute D for the SC-IAT.
**Usage**

Dsciat(data, mappingA = "mappingA", mappingB = "mappingB", non_response = NULL)

**Arguments**

- **data**  
  Dataframe with class `clean_sciat`.
- **mappingA**  
  String. Label identifying the mapping A of the SC-IAT in the `block_id` variable.
- **mappingB**  
  String. Label identifying the mapping B of the SC-IAT in the `block_id` variable.
- **non_response**  
  String. Labels of the trials identifying the non-responses, a.k.a. responses beyond the response time window, as it was specified in `trial_id` (if included).

**Value**

A dataframe with class `dsciat`. The number of rows of the dataframe corresponds to the total number of participants. Variables are defined as follows (the values are specific for each participant):

- **participant**  
  Respondents’ IDs.
- **n_trial**  
  Number of trial before data cleaning.
- **no_response**  
  If there were any trials identifying the non response, it indicates the number of non responses per each participant. Otherwise, it is equal for all participants ("none").
- **nslow10000**  
  Number of slow trials (> 10,000 ms).
- **out_accuracy**  
  Indicates whether the participants had more than 25% of incorrect responses in at least one of the critical blocks and hence should be eliminated ("out") or not ("keep").
- **nfast400**  
  Number of fast trials (< 400 ms).
- **nfast300**  
  Number of fast trials (< 350 ms – deleted).
- **accuracy.mappingA**  
  Proportion of correct responses in Mapping A.
- **accuracy.mappingB**  
  Proportion of correct responses in mapping B.
- **RT_mean.MappingA**  
  Mean response time in Mapping A.
- **RT_mean.MappingB**  
  Mean response time in Mapping B.
- **cond_ord**  
  Indicates the order with which the associative conditions have been presented, either "MappingA_First" or "MappingB_First".
- **legendMappingA**  
  Indicates the corresponding value of Mapping A in the original dataset.
- **legendMappingB**  
  Indicates the corresponding value of Mapping B in the original dataset.
- **d_sciat**  
  SC-IAT D.

**Examples**

```
# calculate D for the SCIAT
data("raw_data") # load data
sciati_data <- clean_sciat(raw_data, sbj_id = "Participant",
block_id = "blockcode",
latency_id = "latency",
accuracy_id = "correct",
```
block_sciat_1 = c("test.sc_dark.Darkbad",
                   "test.sc_dark.Darkgood"),
block_sciat_2 = c("test.sc_milk.Milkbad",
                   "test.sc_milk.Milkgood"),
trial_id = "trialcode",
trial_eliminate = c("reminder",
                    "reminder1"))

sciat1 <- sciat_data[[1]]  # compute D for the first SC-IAT
d_sciat1 <- Dsciat(sciat1,
                   mappingA = "test.sc_dark.Darkbad",
                   mappingB = "test.sc_dark.Darkgood",
                   non_response = "alert")
head(d_sciat1)  # dataframe containing the SC-IAT D of the of the
                # first SC-IAT

sciat2 <- sciat_data[[2]]  # Compute D for the second SC-IAT
d_sciat2 <- Dsciat(sciat2,
                   mappingA = "test.sc_milk.Milkbad",
                   mappingB = "test.sc_milk.Milkgood",
                   non_response = "alert")
head(d_sciat2)

---

**d_distr**

Plot IAT or SC-IAT scores (distribution)

**Description**

Plot the distribution of the IAT D-score or the SC-IAT D.

**Usage**

```r
d_distr(
  data,  # Dataframe with either class dscore or dsciat.
  graph = c("histogram", "density", "violin"),  # String. Indicates the graphs to display. Default is histogram
  n_bin = 80,  # Numeric. Indicates the number of bins to display.
  col_fill = "royalblue",  # String. Indicates the color for filling the bars of the histogram or the curve of the density. Default is royalblue.
  col_point = "red",
  include_stats = FALSE
)
```

**Arguments**

- `data`  
- `graph`  
- `n_bin`  
- `col_fill`
col_point String. Indicates the color for the individual scores –each point – in the violin plot. Default is red.

include_stats Logical. Indicates whether to add descriptive statistics. The mean is depicted with a solid line. The two dashed lines represent +/- 2 s.d. from the mean. Default is FALSE.

Value

A ggplot object.

Examples

```r
# Plotting the IAT D-score
data("raw_data") # import data
iat_data <- iat_cleandata[[1]] # calculate D-score
iat_dscore <- computeD(iat_data, Dscore = "d2")
d_distr(iat_dscore) # Default graph
d_distr(iat_dscore, graph = "histogram", n_bin = 30) # Histogram with a different number of bins
d_distr(iat_dscore, graph = "density") # IAT D-score density plot
d_distr(iat_dscore, graph = "violin") # IAT D-score violin plot

# Plot the SC-IAT D for the first SC-IAT
data("raw_data") # load data
sciat1 <- sciat_data[[1]] # compute D for the first SC-IAT
```
d_sciat1 <- Dsciat(sciat1, 
    mappingA = "test.sc_dark.Darkbad",
    mappingB = "test.sc_dark.Darkgood",
    non_response = "alert")

d_distr(d_sciat1, graph = "histogram", 
    include_stats = TRUE) # SC-IAT D histogram with descriptive 
    # statistics

---

**d_plot**

*Plot either IAT or SC-IAT scores (points)*

**Description**

Plot the individual *D-score* or SC-IAT *D*.

**Usage**

```r
d_plot(
    data, 
    point_size = 1, 
    x_label = "Participant", 
    x_values = TRUE, 
    order_sbj = c("default", "D-increasing", "D-decreasing"), 
    col_point = "springgreen4", 
    include_stats = FALSE 
)
```

**Arguments**

- **data** Dataframe with either class dscore or dsciat.
- **point_size** Numeric. Indicates the size of the points in the graph. Default is 1.
- **x_label** Character. Label of the x-axis. Default is *Participant*.
- **x_values** Logical. Shows the values for x-axis (default = TRUE).
- **order_sbj** Character. Defines the order with which the participants are displayed. Default is the default order of participants in the dataframe.
- **col_point** Character. Defines the color of the points. Default is "springgreen4".
- **include_stats** Logical. Indicates whether to add descriptive statistics. The mean is depicted with a solid line. The two dashed lines represent +/2 s.d. from the mean. Default is FALSE.

**Value**

A ggplot object
Examples

```r
# Plotting the IAT D-score
data("raw_data") # import data
iat_cleandata <- clean_iat(raw_data, sbj_id = "Participant",
   block_id = "blockcode",
   mapA_practice = "practice.iat.Milkbad",
   mapA_test = "test.iat.Milkbad",
   mapB_practice = "practice.iat.Milkgood",
   mapB_test = "test.iat.Milkgood",
   latency_id = "latency",
   accuracy_id = "correct",
   trial_id = "trialcode",
   trial_eliminate = c("reminder", "reminder1"),
   demo_id = "blockcode",
   trial_demo = "demo")

iat_data <- iat_cleandata[[1]]
# calculate D-score
iat_dscore <- computeD(iat_data,
   Dscore = "d2")
d_plot(iat_dscore) # default plot
d_plot(iat_dscore, order_sbj = "D-increasing") # D-score with increasing
   # order
d_plot(iat_dscore, order_sbj = "D-decreasing",
   col_point = "salmon") # D-score with decreasing order changed color

# Plot the SC-IAT D for the first SC-IAT
data("raw_data") # load data
sciat_data <- clean_sciat(raw_data, sbj_id = "Participant",
   block_id = "blockcode",
   latency_id = "latency",
   accuracy_id = "correct",
   block_sciat_1 = c("test.sc_dark.Darkbad",
   "test.sc_dark.Darkgood"),
   block_sciat_2 = c("test.sc_milk.Milkbad",
   "test.sc_milk.Milkgood"),
   trial_id = "trialcode",
   trial_eliminate = c("reminder",
   "reminder1"))

sciat1 <- sciat_data[[1]] # compute D for the first SC-IAT
d_sciat1 <- Dsciat(sciat1,
   mappingA = "test.sc_dark.Darkbad",
   mappingB = "test.sc_dark.Darkgood",
   non_response = "alert")
d_plot(d_sciat1, col_point = "salmon",
   include_stats = TRUE) # SC-IAT D with descriptive statistics
```

---

**IAT rel**: 

**IAT reliability**
Description

Compute the practice – test IAT reliability.

Usage

`IATrel(data)`

Arguments

data dataframe with class "dscore" (Gawronski et al., 2017).

Value

List of two objects:

- Test-practice reliability contains the IAT reliability.
- Number of Participants Contains the number of participants on which the reliability was computed.

Examples

```r
# compute D-score 2 for the IAT data ###
data("raw_data") # import data
iat_cleandata <- clean_iat(raw_data, sbj_id = "Participant",
block_id = "blockcode",
mapA_practice = "practice.iat.Milkbad",
mapA_test = "test.iat.Milkbad",
mapB_practice = "practice.iat.Milkgood",
mapB_test = "test.iat.Milkgood",
latency_id = "latency",
accuracy_id = "correct",
trial_id = "trialcode",
trial_eliminate = c("reminder", "reminder1"),
demo_id = "blockcode",
trial_demo = "demo")

iat_data <- iat_cleandata[[1]]
# calculate D-score
iat_dscore <- computeD(iat_data,
  Dscore = "d2")
IATrel(iat_dscore)
```

---

**multi_dsciat**

*Plot SC-IATs scores*

Description

Plot the scores from two different SC-IATs.
multi_dsciat

Usage

multi_dsciat(
    sciat1,  
    sciat2,  
    graph = c("density", "violin", "point"),  
    x_values = TRUE,  
    gcolors = c("dark", "greens", "blues", "pinks"),  
    label_sc1 = "SC-IAT1",  
    label_sc2 = "SC-IAT2",  
    label_y = "SC-IAT scores",  
    dens_mean = TRUE
)

Arguments

sciat1 Dataframe with class dsciat. Contains the D for the first SC-IAT.
sciat2 Dataframe with class dsciat. Contains the D for the second SC-IAT.
graph String. Type of graph to display. Default is density.
x_values Logical. Shows the values for x-axis (default = TRUE). Only for the point graph.
gcolors String. Colors palette for plotting the results. Default is dark.
label_sc1 String. Label to display in the graph for the first SC-IAT. Default is SC-IAT1.
label_sc2 String. Label to display in the graph for the first SC-IAT. Default is SC-IAT2.
label_y String. Label to plot on the y-axis.
dens_mean Logical. Whether to include the mean in the density plot. Default is TRUE.

Value

A ggplot object

Examples

# calculate D for the SCIAT
data("raw_data") # load data
sciat_data <- clean_sciat(raw_data, sbj_id = "Participant",  
    block_id = "blockcode",  
    latency_id = "latency",  
    accuracy_id = "correct",  
    block_sciat_1 = c("test.sc_dark.Darkbad",  
    "test.sc_dark.Darkgood"),  
    block_sciat_2 = c("test.sc_milk.Milkbad",  
    "test.sc_milk.Milkgood"),  
    trial_id = "trialcode",  
    trial_eliminate = c("reminder",  
    "reminder1"))

sciat1 <- sciat_data[[1]] # compute D for the first SC-IAT
d_sciat1 <- Dsciat(sciat1,  
    mappingA = "test.sc_dark.Darkbad",  
    mappingB = "test.sc_milk.Milkbad"  
)
multi_dscore

Compute and plot multiple D-scores

Description

Compute and plot multiple D-scores.

Usage

multi_dscore(data, ds = c("built-in", "error-inflation"))

Arguments

data Dataframe of class iat_clean.
ds String. Indicates which D-score to compute. built-in compute only D-score with the built-in error correction (D1 and D2), error-inflation compute the D-scores without built-in correction (D3 to D6).

Value

A list. The first object is a dataframe containing all the computed Dscores. The second object is a ggplot object, depicting the distribution of the D-scores through violin plots.

@import tidyr

Examples

# Compute multiple IAT D-scores
data("raw_data") # import data
iaticleandata <- clean_iat(raw_data, sbj_id = "Participant",
block_id = "blockcode",
mapA_practice = "practice.iat.Milkbay",
mapA_test = "test.iat.Milkbay",
mapB_practice = "practice.iat.Milkgood",
mapB_test = "test.iat.Milkgood",
latency_id = "latency",
mappingB = "test.sc_dark.Darkgood",
non_response = "alert") # dataframe with the first D
# SC-IAT

sciat2 <- sciat_data[[2]] # Compute D for the second SC-IAT
d_sciat2 <- Dsciart(sciat2,
mappingA = "test.sc_milk.Milkbad",
mappingB = "test.sc_milk.Milkgood",
non_response = "alert") # dataframe with the first
# D SC-IAT

multi_dsciart(d_sciat1, d_sciat2) # plot the D of two SC-IATs with default
# settings
raw_data

Dataset with one IAT and two SC-IATs

Description
A dataset containing the data from 152 participants who completed one IAT and two SC-IATs. The object of both the implicit measures was chocolate, either Milk or Dark chocolate:

Usage
data(raw_data)

Format
A dataframe with 6 variables, as follows:

- Participant. Participants ID.
- latency. Latency of the response times in millisecond.
- correct. Response accuracy (0-correct, 1-error).
- trialcode. Factor with 32 levels identifying the trial for each response, both for the implicit measures and the demographic questionnaire. It contains also the trials that have to be eliminated, defined as follows:
  - alert. Defines the SC-IAT trials beyond the response time window.
  - Reminder, Reminder1. Identify the instruction page.
- blockcode. Factor with 13 levels as follow:
  - practice.iat.Milkbad. IAT practice blocks, Mapping A.
  - practice.iat.Milkbad. IAT practice blocks, Mapping B.
  - practice.sc_dark.Darkbad. Dark SC-IAT practice blocks, Mapping A.
- practice.sc_dark.Darkbad. Dark SC-IAT practice blocks, Mapping B.
- test.iat.Milkbad. IAT test blocks, Mapping A.
- test.iat.Milkgood. IAT test blocks, Mapping B.
- test.sc_dark.Darkbad. Dark SC-IAT test blocks, Mapping A.
- test.sc_dark.Darkbad. Dark SC-IAT test blocks, Mapping B.
- test.sc_milk.Milkbad. Milk SC-IAT test blocks, Mapping A.
- test.sc_milk.Milkgood. Milk SC-IAT test blocks, Mapping B.
- demo. Demographic questionnaire.

* response. Character registering the type of response for the demographic.
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