Package ‘implicitMeasures’

October 13, 2022

Type Package

Title Compute Scores for Different Implicit Measures

Version 0.2.1

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Description A tool for computing the scores for the Implicit Association Test
and the Single Category-IAT (SC-IAT; Karpinski & Steinman
(both for the IAT and the SC-IAT), plotting the results, and obtaining a
table with the scores of implicit measures descriptive statistics are
provided.

Depends R (>= 3.5.0)

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Imports ggplot2, stringr, tidyr, xtable

Suggests testthat (>= 2.1.0), knitr, rmarkdown, tableHTML, data.table,
spelling

VignetteBuilder knitr

Language en-US

NeedsCompilation no

Repository CRAN

Date/Publication 2022-02-16 13:40:13 UTC
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**clean_iat**

*Prepare and clean IAT data.*

**Description**

Select IAT blocks for the *D-score* computation and eventually save demographic data.

**Usage**

```r
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
)
```
Arguments

data            Dataframe containing IAT data.
sbj_id          Column identifying participants' IDs. This variable can be a character, numeric, or factor.
block_id        String. Column identifying IAT blocks. The block_id variable should be a factor with each level identifying an IAT block.
mapA_practice   String. Label for the practice blocks of Mapping A (as it appears in the 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"),
    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.
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.

sciat1 Data frame with class sciat_clean containing the data of the first SC-IAT as specified block_sciat_1. If any labels was specified in trial_eliminate, data_keep will contain the already cleaned dataset.

sciat2 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

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",

...
compute_iat

| trial_eliminate = c("reminder",
| "reminder1")
| sciat1 <- sciat_data[[1]]
| sciat2 <- sciat_data[[2]]

compute_iat  Compute IAT D-score

Description

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

Usage

compute_iat(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 trails 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 compute_iat on the practice blocks. The X stands for the selected D-score procedure.
d_test_dX D-scores compute_iat 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

```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",
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 <- compute_iat(iat_data,
Dscore = "d2")
```

compute_sciat

Compute the D-score for the SC-IAT

Description

Compute the D-score for the SC-IAT.

Usage

```r
compute_sciat(
data,
mappingA = "mappingA",
mappingB = "mappingB",
non_response = NULL
)
```
Arguments

- **data**: Data frame with class `clean_scint`.
- **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 `compute_scint`. 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

```r
# calculate D for the SCIAT
data("raw_data") # load data
sciint_data <- clean_scint(raw_data, sbj_id = "Participant",
                             block_id = "blockcode",
                             latency_id = "latency",
                             accuracy_id = "correct",
                             block_sciint_1 = c("test.sc_dark.Darkbad",
                                                "test.sc_dark.Darkgood"),
                             block_sciint_2 = c("test.sc_milk.Milkbad",
                                                "test.sc_milk.Milkgood"),
                             block_sciint_3 = c("test.veg.Vegetablebad",
                                                "test.veg.Vegetablegood"))
```

```r
d_sciint <- compute_sciint(sciint_data, mappingA = "MappingA",
                           mappingB = "MappingB",
                           non_response = c("non_response", "slow_response")
                          )
```
```
sciat1 <- sciat_data[[1]] # compute D for the first SC-IAT
d_sciat1 <- compute_sciat(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 <- compute_sciat(sciat2,
  mappingA = "test.sc_milk.Milkbad",
  mappingB = "test.sc_milk.Milkgood",
  non_response = "alert")
head(d_sciat2)
```

---

**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_cleandata <- clean_iat(raw_data, sbj_id = "Participant",
  block_id = "blockcode",
  mapA_practice = "practice.iat.Milkbad",
  mapA_test = "test.iat.Milkbad",
  trial_id = "trialcode",
  trial_eliminate = c("reminder", "reminder1"))
```
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 <- compute_iat(iat_data,
Dscore = "d2")
descript_d(iat_dscore) # descriptive statistics for the IAT

# 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 <- compute_sciat(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
# format

dsciat1

Data set with SC-IAT D-scores (Dark)

Description

A data set containing the results of the computation of the D-score on the Dark SC-IAT data set. This data set is used for testing the replicability of the results obtained with the compute_sciat() functions.

Usage

data("dsciat1")
dsciat2

Format

A dataframe with 15 variables, as those described in the documentation for the compute_sciat() function.

---

dsciat2

Data set with SC-IAT D-scores (Milk)

Description

A data set containing the results of the computation of the D-score on the Dark SC-IAT data set. This data set is used for testing the replicability of the results obtained with the compute_sciat() functions.

Usage

data("dsciat2")

Format

A dataframe with 15 variables, as those described in the documentation for the compute_sciat() function.

---

d_density

Plot IAT or SC-IAT scores (distribution)

Description

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

Usage

d_density(
    data,
    graph = c("histogram", "density", "violin"),
    n_bin = 80,
    col_fill = "royalblue",
    col_point = "red",
    include_stats = FALSE
)
Arguments

data Dataframe with either class dscore or dsciat.

d_density

graph String. Indicates the graphs to display. Default is histogram

n_bin Numeric. Indicates the number of bins to display.

col_fill String. Indicates the color for filling the bars of the histogram or the curve of the density. Default is royalblue.

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

# Plotting the IAT D-score

data("raw_data") # import data


iat_data <- iat_cleandata[[1]]

# calculate D-score

iat_dscore <- compute_iat(iat_data, Dscore = "d2")

d_density(iat_dscore) # Default graph

d_density(iat_dscore, graph = "histogram", n_bin = 30) # Histogram with a different number of bins

d_density(iat_dscore, graph = "density") # IAT D-score density plot

d_density(iat_dscore, graph = "violin") # IAT D-score violin plot

# 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"), latency_sciat_1 = c("latency", "latency"), accuracy_sciat_1 = c("correct", "correct"), trial_sciat_1 = c("trialcode", "trialcode"), trial_eliminate = c("reminder", "reminder1"), demo_sciat_1 = "blockcode", trial_demo_sciat_1 = "demo"))
sciat1 <- sciat_data[[1]] # compute D for the first SC-IAT
d_sciat1 <- compute_sciat(sciat1, 
  mappingA = "test.sc_dark.Darkbad",
  mappingB = "test.sc_dark.Darkgood",
  non_response = "alert")
d_density(d_sciat1, graph = "histogram",
  include_stats = TRUE) # SC-IAT D histogram with descriptive 
  # statistics

---

d_point

Plot either IAT or SC-IAT scores (points)

Description

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

Usage

d_point(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.
d_point

Value

A ggplot object

Examples

# 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 <- compute_iat(iat_data,
    Dscore = "d2")
d_point(iat_dscore) # default plot
d_point(iat_dscore, order_sbj = "D-increasing") # D-score with increasing order

d_point(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 <- compute_sciat(sciat1,
    mappingA = "test.sc_dark.Darkbad",
    mappingB = "test.sc_dark.Darkgood",
    non_response = "alert")
d_point(d_sciat1, col_point = "salmon",
    include_stats = TRUE) # SC-IAT D with descriptive statistics
**iatdscres**

**Data set with IAT D-scores**

**Description**

A data set containing the results for all the possible D-score algorithms for the IAT. All the algorithms are identified by their corresponding label (such as "dscore_d1"). This data set is used for testing the replicability of the results of the `compute_iat()` function over time.

**Usage**

```r
data("iatdscres")
```

**Format**

A dataframe with 7 variables, the first one contains the respondents' id, the other 6 columns contain a specific D-score algorithm.

---

**IAT_rel**

**IAT reliability**

**Description**

Compute the practice – test IAT reliability.

**Usage**

```r
IAT_rel(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")
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 <- compute_iat(iat_data, 
Dscore = "d2")

IAT_rel(iat_dscore)
```

---

**multi_dsciat**

*Plot SC-IATs scores*

**Description**

Plot the scores from two different SC-IATs.

**Usage**

```r
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.
**multi_dscore**

Compute and plot multiple D-scores

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>x_values</td>
<td>Logical. Shows the values for x-axis (default = TRUE). Only for the point graph.</td>
</tr>
<tr>
<td>gcolors</td>
<td>String. Colors palette for plotting the results. Default is dark.</td>
</tr>
<tr>
<td>label_sc1</td>
<td>String. Label to display in the graph for the first SC-IAT. Default is SC-IAT1.</td>
</tr>
<tr>
<td>label_sc2</td>
<td>String. Label to display in the graph for the first SC-IAT. Default is SC-IAT2.</td>
</tr>
<tr>
<td>label_y</td>
<td>String. Label to plot on the y-axis.</td>
</tr>
<tr>
<td>dens_mean</td>
<td>Logical. Whether to include the mean in the density plot. Default is TRUE.</td>
</tr>
</tbody>
</table>

**Value**

A ggplot object

**Examples**

```r
# 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 <- compute_sciat(sciat1,
                           mappingA = "test.sc_dark.Darkbad",
                           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 <- compute_sciat(sciat2,
                           mappingA = "test.sc_milk.Milkbad",
                           mappingB = "test.sc_milk.Milkgood",
                           non_response = "alert") # dataframe with the first D SC-IAT

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

**Description**

Compute and plot multiple D-scores.
multi_dscore

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 D-scores. The second object is a ggplot object, depicting the distribution of the D-scores through violin plots.

Examples
# Compute multiple IAT D-scores
data("raw_data") # import data
iaat_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")
iaat_data <- iat_cleandata[[1]]

# compute the multiple scores and prepare the graphs for the built-in # strategies
multiple_scores <- multi_dscore(iat_data, ds = "built-in")
data_multiple <- multiple_scores$dscores # store the D-score in a dataframe

# plot the results
multiple_scores$graph
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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