

# Package ‘tiefightR’

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**Title** Calculate Preference Positions

**Version** 0.0.0.9000

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**Description** The tiefightR package is for preference testing. Its goal is to rank commodity positions obtained from preference test experiments. Special attention is laid to intransitivities in the data and tie evaluation.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Suggests** knitr,  
rmarkdown

**VignetteBuilder** knitr

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.0

**URL** <https://github.com/mytalbot/tiefightR>

**BugReports** <https://github.com/mytalbot/tiefightR/issues>

**Imports** magrittr,  
tibble,  
dplyr,  
reshape2,  
prefmod,  
gnm,  
ggplot2,  
ggpubr,  
parallel,  
doParallel,  
foreach,  
viridis,  
ggsci,  
Rmisc

**Depends** R (>= 2.10)

R topics documented:

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|       |                               |
|-------|-------------------------------|
| human | <i>tiefightR - human data</i> |
|-------|-------------------------------|

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Description

Two sets of seven pictures each were taken for preference ranking. The subjects for the first set were 32 (16 male, 16 female) persons aged between 19 and 46 years (average: 25.5 years). The second set of pictures was ranked by 63 persons (33 male, 29female, 1 other) with an average age of 29.1 years (ranging from 19-70). 73 of the probands were recruited at the campus of the University of Göttingen, Germany and conducted the test in a controlled laboratory environment. The other 22 persons conducted the internet-based test somewhere else. The first set of pictures was tested a second time during the course of a graduate spring school by 16 participants (age range from 26 to 40 years, mean 31.1 years; 12 female, 4 male).

Usage

data(human)

Format

A 2331 x 7 data frame with binary response data (pref\_img1).

Examples

data(human)  
head(human)

---

|       |                               |
|-------|-------------------------------|
| mouse | <i>tiefightR - mouse data</i> |
|-------|-------------------------------|

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**Description**

Eleven female C57BL/6J mice were tested. The mice were purchased from Charles River Sulzfeld, Germany and arrived at the institute at the age of 21 days. All mice were implanted with an RFID chip (Planet ID, FDX-B transponder according to ISO 11784/85) holding a unique ID for individual differentiation at an age of 33 or 56 days, a procedure performed under anesthesia (Isofluran). Two hours before the transplantation, all mice were given an analgesic (Meloxicam). At the start of the first run, the mice were seven months old and weighed between 25.0 and 29.0 g. At the start of the second run, the mice were 14 month old and weighed between 25.5 and 37.0 g.

**Usage**

```
data(mouse)
```

**Format**

A 880 x 10 data frame with continuous response data (numOF\_visits\_with\_Licks).

**Examples**

```
data(mouse)
head(mouse)
```

---

|        |                                |
|--------|--------------------------------|
| rhesus | <i>tiefightR - rhesus data</i> |
|--------|--------------------------------|

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**Description**

Six male rhesus macaques (*Macaca mulatta*) at an age range of 6-19 years (mean = 13.09) living in same-sexual groups of 2 - 4 at the Cognitive Neuroscience Laboratory, German Primate Centre, took part in this study. Monkeys were housed in indoor rooms equipped with a multitude of toys and wooden structures as well as natural and artificial light. The space per monkey exceeded all applicable German and European regulations (Berger et al. 2018). Indoor rooms were temperature-controlled and connected by a tunnel with rooms at ambient outdoor temperature and lighting, but protected from precipitation. On test days, monkeys had free access to water for at least 4 hours (typically much more: for definitions of access to water see (Pfefferle et al. 2018)) and received monkey chow ad libitum. On non-test days, the monkeys had free access to water and received monkey chow ad libitum, supplemented with dried fruits, fresh fruits and vegetables. The health of the monkeys was monitored daily by the animal care staff, veterinarians, and the laboratory researchers who were all highly experienced with these animals.

**Usage**

```
data(rhesus)
```

**Format**

A 240 x 7 data frame with continuous response data (amountDrank).

**Examples**

```
data(rhesus)
head(rhesus)
```

---

|              |                                |
|--------------|--------------------------------|
| tie_binarize | <i>Binarize continous data</i> |
|--------------|--------------------------------|

---

**Description**

Uses tie\_import output as input.

**Usage**

```
tie_binarize(
  xdata = NULL,
  SV = "side",
  RF = "fluidType",
  CF = "combinationWith",
  id = "animalID",
  RV = "numOF_visits_with_Licks",
  datalabel = "binarized",
  compiled_studies = 1,
  setseed = TRUE,
  prefLimit = 50,
  sidevar = "side",
  refval = "refValue",
  oval = "otherValue",
  aid = "animalID",
  fldrnk = "fluid_drunk"
)
```

**Arguments**

|                  |   |
|------------------|---|
| xdata            | imported (binarized) data frame                                   |
| SV               | name of the side variable   |
| RF               | name of the reference fluid variable                              |
| CF               | name of the combination fluid variable                            |
| id               | subject IDs   |
| RV               | name of the response variable                                     |
| datalabel        | universal study label for the binarized data                      |
| compiled_studies | label of the compiled sub study (used for filtering)              |
| setseed          | TRUE/FALSE for seeding  |
| prefLimit        | preference limit for binarization threshold                       |
| sidevar          | the name of the standardized side variable in the org data        |
| refval           | the name of the standardized reference variable in the org data   |
| oval             | the name of the standardized combination variable in the org data |
| aid              | the name of the standardized animal id column in the org data     |
| fldrnk           | the name of the standardizedresponse variable in the org data     |

**Value**

tada

---

tie\_cores

*CPU Core Detection*

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**Description**

The tie\_cores detects the number of available CPUs for parallel computing. Don't overdo it!

**Usage**

```
tie_cores()
```

**Value**

No of CPUs on your machine

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tie\_import

*Import Function*

---

**Description**

The tie\_import function loads the raw data

**Usage**

```
tie_import(path = NULL, valenceset = NULL)
```

**Arguments**

|            |                           |
|------------|---------------------------|
| path       | path to the raw data      |
| valenceset | subset filtering argument |

**Value**

data.frame with the filtered subset

---

|             |                                 |
|-------------|---------------------------------|
| tie_intrans | <i>Calculate Intransitivity</i> |
|-------------|---------------------------------|

---

### Description

The tie\_intrans function loads the raw data

### Usage

```
tie_intrans(
  mydata = NULL,
  idcolumn = "ID",
  I1 = "img1",
  I2 = "img2",
  response = "pref_img1"
)
```

### Arguments

|          |   |
|----------|---|
| mydata   | input data frame  |
| idcolumn | name of the ID column in the input data                   |
| I1       | name of the test image column in the input data           |
| I2       | name of the other (tested) items column in the input data |
| response | name of the response variable                             |

### Value

intranscount intransitivity counts

---

|           |                                 |
|-----------|---------------------------------|
| tie_rwalk | <i>Tie random walk function</i> |
|-----------|---------------------------------|

---

### Description

The tie\_rwalk function prepares binary and continuous data form import into the tiefightR analysis.

### Usage

```
tie_rwalk(
  dat = NULL,
  SV = NULL,
  RF = NULL,
  CF = NULL,
  id = NULL,
  RV = NULL,
  ord = NULL,
  prefLimit = 50,
```

```

    setseed = FALSE,
    compstudy = NULL,
    default = NULL,
    R = NULL
  )

```

### Arguments

|           |   |
|-----------|---|
| dat       | imported (binarized) data frame   |
| SV        | name of the side variable   |
| RF        | name of the reference fluid variable                                    |
| CF        | name of the combination fluid variable                                  |
| id        | subject IDs   |
| RV        | name of the response variable   |
| ord       | item category order   |
| prefLimit | preference limit for binarization threshold                             |
| setseed   | BOOLEAN; set a random seed TRUE/FALSE?                                  |
| compstudy | label of the compiled sub study (used for filtering)                    |
| default   | default item in worth value estimation (usually the lowest worth value) |
| R         | number of randomizations  |

### Value

Exports random binarize response for distance cutoff selection

---

|           |  |
|-----------|--|
| tie_rwrap | <i>Tie random wrapper for the rwalk function</i> |
|-----------|--|

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### Description

The tie\_rwrap is a wrapper function for tie\_rwalk and uses a number of R randomization steps to calculate the mean Euclidean distance between worth values. The resulting curve will tell something about tie stability in the data and can be used for the definition of a randomization step cut-off value.

### Usage

```

tie_rwrap(
  dat = NULL,
  SV = NULL,
  RF = NULL,
  CF = NULL,
  id = NULL,
  RV = NULL,
  ord = NULL,
  default = NULL,
  prefLimit = 50,
  setseed = FALSE,
  compstudy = NULL,
  R = 2
)

```

**Arguments**

|           |   |
|-----------|---|
| dat       | imported raw data (should be binary, if not, will be binarized automatically) |
| SV        | name of the side variable   |
| RF        | name of the reference fluid variable  |
| CF        | name of the combination fluid variable  |
| id        | subject IDs   |
| RV        | name of the response variable   |
| ord       | item category order   |
| default   | default item in worth value estimation (usually the lowest worth value)       |
| prefLimit | preference limit for binarization threshold                                   |
| setseed   | TRUE/FALSE for seeding  |
| compstudy | label of the compiled sub study (used for filtering)                          |
| R         | number of maximum randomization steps   |

**Value**

Exports random binarize response for distance cutoff selection

---

|         |                                |
|---------|--------------------------------|
| tie_sim | <i>Tie Simulation Function</i> |
|---------|--------------------------------|

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**Description**

The `tie_sim` function starts a simulation of item pairings and introduces random pairs for the remaining combinations. In parallel, the intransitivity of triple pairings can be calculated to estimate the quality of the pairings. Good transitiviy and massed localization in a position will improve the likelihood of a good fit for the item.

**Usage**

```
tie_sim(
  xdata = NULL,
  R = 2,
  SV = "side_img1",
  RF = "img1",
  CF = "img2",
  id = "ID",
  RV = "pref_img1",
  intrans = TRUE,
  compstudy = "LagreValenceRange_SpringSchool",
  default = "War",
  cpus = 2,
  ord = NULL,
  v1 = NULL
)
```



**Arguments**

|           |   |
|-----------|---|
| xdata     | imported (binarized) data frame   |
| R         | No. of randomization steps  |
| SV        | name of the side variable   |
| RF        | name of the reference fluid variable  |
| CF        | name of the combination fluid variable                                      |
| id        | subject IDs   |
| RV        | name of the response variable   |
| intrans   | calculate intransitivities (calculation intense!)                           |
| compstudy | label of the compiled sub study (used for filtering)                        |
| default   | default item in worth value estimation (usually the lowest worth value)     |
| cpus      | No. of used local CPUs for parallel computing (you should have more than 2) |
| ord       | item category order   |
| v1        | testing variable (can be one item from the item list)                       |

**Value**

data.frame with the simulation results

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|            |                          |
|------------|--------------------------|
| tie_simrep | <i>Simulation report</i> |
|------------|--------------------------|

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**Description**

The tie\_simrep function prepares some tables and plots for analysing the simulation output.

**Usage**

```
tie_simrep(res = NULL, v1 = NULL, path = NULL)
```

**Arguments**

|      |  |
|------|--|
| res  | result or output from the simulation                       |
| v1   | test variable  |
| path | path to where the report shall be stored (including plots) |

**Value**

A frequency table for item positions during the simulation; Tukey's HSD Test for positions; Position Bubble Plot

---

|          |                      |
|----------|----------------------|
| tie_test | <i>Test Function</i> |
|----------|----------------------|

---

## Description

The tie\_test function can be used for individual item testing.

## Usage

```
tie_test(
  xdata = NULL,
  R = NULL,
  intrans = TRUE,
  compstudy = NULL,
  default = NULL,
  ord = NULL,
  seed = TRUE,
  testme = NULL,
  against = NULL
)
```

## Arguments

|            |  |
|------------|--|
| xdata      | imported (binarized) data frame  |
| R          | number of randomizations   |
| intrans    | calculate intransitivities (calculation intense!)  |
| compsstudy | label of the compiled sub study (used for filtering)   |
| default    | default item in worth value estimation (usually the lowest worth value)  |
| ord        | item category order  |
| seed       | BOOLEAN; set a random seed TRUE/FALSE?   |
| testme     | test this variable against...  |
| against    | any other single variable from the commodity list (or combinations); vectorize if necessary c("item1","item2") |

## Value

A frequency table for item positions during the simulation; Tukey's HSD Test for positions; Position Bubble Plot

tie\_worth

*Main preference function***Description**

The `tie_import` function prepares binary and continuous data form import into the `tiefightR` analysis.

**Usage**

```
tie_worth(
  xdata = NULL,
  esti = "worth",
  SV = "side_img1",
  RF = "img1",
  CF = "img2",
  id = "ID",
  RV = "pref_img1",
  default = NULL,
  showplot = FALSE,
  intrans = FALSE,
  compstudy = NULL,
  ordn = NULL,
  r1 = NULL,
  r2 = NULL,
  ymin = 0,
  ymax = 0.5
)
```

**Arguments**

|                        |   |
|------------------------|---|
| <code>xdata</code>     | imported (binarized) data frame   |
| <code>esti</code>      | worth estimator (default, "worth", alt: "estimator")                    |
| <code>SV</code>        | name of the side variable   |
| <code>RF</code>        | name of the reference fluid variable                                    |
| <code>CF</code>        | name of the combination fluid variable                                  |
| <code>id</code>        | subject IDs   |
| <code>RV</code>        | name of the response variable   |
| <code>default</code>   | default item in worth value estimation (usually the lowest worth value) |
| <code>showplot</code>  | show worth plot TRUE/FALSE  |
| <code>intrans</code>   | calculate intransitivities (calculation intense!)                       |
| <code>compstudy</code> | label of the compiled sub study (used for filtering)                    |
| <code>ordn</code>      | item category order   |
| <code>r1</code>        | label of the test item (e.g., "Lake")                                   |
| <code>r2</code>        | label(s) of the remaining item(s)                                       |
| <code>ymin</code>      | minimum y-scale of the worth plot                                       |
| <code>ymax</code>      | maximum y-scale of the worth plot                                       |

**Value**

Exports the results of the worth value calculation, including the GNM analysis.

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