

# Package ‘tiefightR’

July 14, 2020

**Title** Calculate Preference Positions

**Version** 0.0.0.9000

**Year** 2020

**Maintainer** Steven R. Talbot <talbot.steven@mh-hannover.de>

**Description** The tiefightR package is for preference test evaluation and simulation. Its goal is to rank commodity positions obtained from preference test experiments. Special attention goes into the analysis of intransitivities in the data and resulting tie evaluation after data binarization.

**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,  
doRNG

**Depends** R (>= 2.10)

R topics documented:

human . . . . .	2
mouse . . . . .	3
rhesus . . . . .	3
tie_binarize . . . . .	4
tie_cicheck . . . . .	5
tie_cores . . . . .	6
tie_cutoff . . . . .	6
tie_import . . . . .	7
tie_intrans . . . . .	8
tie_rwalk . . . . .	8
tie_sim . . . . .	9
tie_simrep . . . . .	10
tie_test . . . . .	11
tie_worth . . . . .	11
<b>Index</b>	<b>13</b>

---

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

---

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>
-------	-------------------------------

---

**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>
--------	--------------------------------

---

**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 non-binary outcome data as input. The outcome variable is randomized for ties in the continous data.

**Usage**

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

**Arguments**

xdata	imported (binarized) data frame
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
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**

binarized data in the default format (column headers)

---

tie_cicheck	<i>Commodity position and confidence interval check for a discrete number of randomizations</i>
-------------	---

---

## Description

The `tie_cicheck` is a wrapper for checking the confidence intervals for data with ties. The function calculates the worth values for a specific number of randomizations and reports the confidence intervals for the commodity means.

## Usage

```
tie_cicheck(
  data = tiefightR::mouse,
  R = NULL,
  ciLvl = 0.95,
  seed = TRUE,
  RF = NULL,
  CF = NULL,
  id = NULL,
  RV = NULL,
  ord = NULL,
  prefLimit = 50,
  compstudy = NULL,
  default = NULL,
  showplot = TRUE,
  showstats = FALSE,
  ylim = c(0.1, 0.35)
)
```

## Arguments

<code>R</code>	number of maximum randomization steps
<code>ciLvl</code>	Level of confidence (default: 0.95)
<code>seed</code>	TRUE/FALSE for constant seeding
<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>ord</code>	item category order
<code>prefLimit</code>	preference limit for binarization threshold
<code>compsstudy</code>	label of the compiled sub study (used for filtering)
<code>default</code>	default item in worth value estimation (usually the lowest worth value)
<code>showplot</code>	show the errorplot with confidence intervals
<code>showstats</code>	calculate ANOVA1 and Tukey's test for the commodities
<code>dat</code>	imported raw data (should be binary, if not, will be binarized automatically)

**Value**

Exports random binarize response for distance cutoff selection

---

tie_cores	<i>CPU Core Detection</i>
-----------	---------------------------

---

**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

---

tie_cutoff	<i>Cutoff determination for increasing number of randomizations</i>
------------	---

---

**Description**

The tie\_cutoff function calculates the mean Euclidean distance between commodity worth values. This becomes relevant when ties are present in the data. Depending on how ties are resolved (see prefLimit argument in the function), the items' position will change a lot. Since their relative positions are a function of the number of ties, more randomizations will stabilize their means and thus commodity positions. Increasing the number of randomizations usually leads not only to a stabilized mean but also to smaller confidence intervals. By defining a relative cutoff (e.g., 5 or 10%) for the range of the CIs regarding the maximum range in the data, a cutoff for the number of randomizations can be found.

**Usage**

```
tie_cutoff(
  data = tiefightR::mouse,
  R = 50,
  ciLvl = 0.95,
  cutoff = 0.1,
  cpus = 2,
  RF = NULL,
  CF = NULL,
  id = NULL,
  RV = NULL,
  ord = NULL,
  prefLimit = 50,
  compstudy = NULL,
  default = NULL,
  showplot = FALSE,
  showCutoff = FALSE
)
```

**Arguments**

R	number of maximum randomization steps
cutoff	Percent cutoff level (default: 0.10) - means CI range < than cutoff value
cpus	No. of used local CPUs for parallel computing (you should have more than 2)
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
compstudy	label of the compiled sub study (used for filtering)
default	default item in worth value estimation (usually the lowest worth value)
showplot	show the plot for randomization cutoff determination
showCutoff	show vertical line of the cutoff
dat	imported raw data (should be binary, if not, will be binarized automatically)
standardize	standardize on the maximum CI value?

**Value**

Exports cutoff value and plots

---

tie_import	<i>Import Function</i>
------------	------------------------

---

**Description**

The `tie_import` function loads the raw data as a data frame. This function can be skipped when one of the three internal data sets (human, mouse, rhesus) are used. For a user who wants to import own data this function is a good start. Make sure that the imported data has at least the following information: data, subset (even if none is there), SV (side variable, left/right), RF (reference fluid/item), CF (combination fluid), id (animal id), RV (response variable)).

**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 for tiefightR analysis.

**Usage**

```
tie_rwalk(
  dat = 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
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_sim	<i>Tie Simulation Function</i>
---------	--------------------------------

---

**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 their position quality. Good transitivity and massed localization in a position will improve the Likelihood of a good fit for the item.

**Usage**

```
tie_sim(
  xdata = NULL,
  R = 2,
  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
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

---

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

---

**Description**

The tie\_simrep function prepares a frequency table and plots for analysing the simulation output. Can also be used for saving the output to file when a path is provided.

**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; Position Bubble Plot

---

tie_worth	<i>Main preference function</i>
-----------	---------------------------------

---

### Description

The tie\_import function prepares binary and continuous data form import into the tiefightR analysis. The user has to specify the names of the input columns (if they deviate from the default values in the function argument list). The function randomizes the response variable for any non chosen item test combination and reports the worth values.

**Usage**

```

tie_worth(
  xdata = NULL,
  esti = "worth",
  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**

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

**Value**

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

# Index

## \*Topic **datasets**

human, [2](#)

mouse, [3](#)

rhesus, [3](#)

human, [2](#)

mouse, [3](#)

rhesus, [3](#)

tie\_binarize, [4](#)

tie\_cicheck, [5](#)

tie\_cores, [6](#)

tie\_cutoff, [6](#)

tie\_import, [7](#)

tie\_intrans, [8](#)

tie\_rwalk, [8](#)

tie\_sim, [9](#)

tie\_simrep, [10](#)

tie\_test, [11](#)

tie\_worth, [11](#)