

# Package ‘catfun’

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**Type** Package

**Title** Categorical Data Analysis

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**Description** Includes wrapper functions around existing functions for the analysis of categorical data and introduces functions for calculating risk differences and matched odds ratios. R currently supports a wide variety of tools for the analysis of categorical data. However, many functions are spread across a variety of packages with differing syntax and poor compatibility with each another. `prop_test()` combines the functions `binom.test()`, `prop.test()` and `BinomCI()` into one output. `prop_power()` allows for power and sample size calculations for both balanced and unbalanced designs. `riskdiff()` is used for calculating risk differences and `matched_or()` is used for calculating matched odds ratios. For further information on methods used that are not documented in other packages see Nathan Mantel and William Haenszel (1959) <[doi:10.1093/jnci/22.4.719](https://doi.org/10.1093/jnci/22.4.719)> and Alan Agresti (2002) <ISBN:0-471-36093-7>.

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matched_or	<i>Matched pairs odds ratio and confidence interval</i>
------------	---

---

## Description

Create odds ratio and confidence interval from matched pairs data.

## Usage

```
matched_or(df, ...)
```

## Arguments

df	a dataframe with binary variables x and y or a 2 x 2 frequency table/matrix. If a table or matrix, x and y must be NULL. Used to select method.
...	further arguments passed to or from other methods.

## Details

The matched pairs odds ratio and confidence interval is the equivalent of calculating a Cochran-Mantel-Haenszel odds ratio where each pair is treated as a stratum.

## Value

a list with class "matched\_or" with the following components:

tab	2x2 table using for calculating risk difference
or	dataframe with columns corresponding to matched-pairs OR, lower bound, and upper bound of CI
conf.level	specified confidence level

**Examples**

```
set.seed(1)
gene <- data.frame(pair = seq(1:35),
                  ulcer = rbinom(35, 1, .7),
                  healthy = rbinom(35, 1, .4))

matched_or(gene, ulcer, healthy)
```

---

matched\_or.data.frame *Matched pairs odds ratio from a data frame*

---

**Description**

Create odds ratio and confidence interval from matched pairs data.

**Usage**

```
## S3 method for class 'data.frame'
matched_or(df, x, y, weight = NULL, alpha = 0.05,
           rev = c("neither", "rows", "columns", "both"), ...)
```

**Arguments**

df	a dataframe with binary variables x and y.
x	binary vector, used as rows for frequency table and calculations.
y	binary vector, used as columns for frequency table and calculations.
weight	an optional vector of count weights.
alpha	level of significance for confidence interval.
rev	reverse order of cells. Options are "row", "columns", "both", and "neither" (default).
...	further arguments passed to or from other methods.

**Value**

a list with class "matched\_or" with the following components:

tab	2x2 table using for calculating risk difference
or	dataframe with columns corresponding to matched-pairs OR, lower bound, and upper bound of CI
conf.level	specified confidence level

**Examples**

```
gene <- data.frame(pair = seq(1:35),
                  ulcer = rbinom(35, 1, .7),
                  healthy = rbinom(35, 1, .4))

matched_or(gene, ulcer, healthy)
```

---

matched_or.table	<i>Matched pairs odds ratio from a table</i>
------------------	--

---

**Description**

Create odds ratio and confidence interval from matched pairs data.

**Usage**

```
## S3 method for class 'table'
matched_or(df, alpha = 0.05, rev = c("neither", "rows",
  "columns", "both"), ...)
```

**Arguments**

df	a dataframe with binary variables x and y or a 2 x 2 frequency table/matrix.
alpha	level of significance for confidence interval.
rev	reverse order of cells. Options are "row", "columns", "both", and "neither" (default).
...	further arguments passed to or from other methods.

**Value**

a list with class "matched\_or" with the following components:

tab	2x2 table using for calculating risk difference
or	dataframe with columns corresponding to matched-pairs OR, lower bound, and upper bound of CI
conf.level	specified confidence level

**Examples**

```
gene <- data.frame(pair = seq(1:35),
                  ulcer = rbinom(35, 1, .7),
                  healthy = rbinom(35, 1, .4))

gene_tab <- xtabs(~ ulcer + healthy, data = gene)

gene_tab %>% matched_or()
```

---

prop_power	<i>Power and sample size for 2 proportions</i>
------------	--

---

**Description**

Calculate power and sample size for comparison of 2 proportions for both balanced and unbalanced designs.

**Usage**

```
prop_power(n, n1, n2, p1, p2, fraction = 0.5, alpha = 0.05,
           power = NULL, alternative = c("two.sided", "one.sided"), odds.ratio,
           percent.reduction, ...)
```

**Arguments**

n	total sample size.
n1	sample size in group 1.
n2	sample size in group 2.
p1	group 1 proportion.
p2	group 2 proportion.
fraction	fraction of total observations that are in group 1.
alpha	significance level/type 1 error rate.
power	desired power, between 0 and 1.
alternative	alternative hypothesis, one- or two-sided test.
odds.ratio	odds ratio comparing p2 to p1.
percent.reduction	percent reduction of p1 to p2.
...	further arguments passed to or from other methods.

**Details**

Power calculations are done using the methods described in 'stats::power.prop.test', 'Hmisc::bsamsize', and 'Hmisc::bpower'.

**Value**

a list with class "prop\_power" containing the following components:

n	the total sample size
n1	the sample size in group 1
n2	the sample size in group 2
p1	the proportion in group 1
p2	the proportion in group 2
power	calculated or desired power
sig.level	level of significance

**See Also**

[stats::power.prop.test], [Hmisc::bsamsize], [Hmisc::bpower]

**Examples**

```
prop_power(n = 220, p1 = 0.35, p2 = 0.2)
prop_power(p1 = 0.35, p2 = 0.2, fraction = 2/3, power = 0.85)
prop_power(p1 = 0.35, n = 220, percent.reduction = 42.857)
prop_power(p1 = 0.35, n = 220, odds.ratio = 0.4642857)
```

---

prop_test	<i>Tests for equality of proportions</i>
-----------	--

---

**Description**

Conduct 1-sample tests of proportions and tests for equality of k proportions.

**Usage**

```
prop_test(x, ...)
```

**Arguments**

x	a vector of counts, a one-dimensional table with two entries, or a two-dimensional table with 2 columns. Used to select method.
...	further arguments passed to or from other methods.

**Details**

Calculations are done using the methods described in ‘stats::binom.test()’ and ‘stats::prop.test()’

**Value**

a list with class "prop\_test" containing the following components:

x	number of successes
n	number of trials
p	null proportion
statistic	the value of Pearson’s chi-squared test statistic
p_value	p-value corresponding to chi-squared test statistic
df	degrees of freedom
method	the method used to calculate the confidence interval
method_ci	confidence interval calculated using specified method
exact_ci	exact confidence interval
exact_p	p-value from exact test

**See Also**

[stats::binom.test()], [stats::prop.test()]

**Examples**

```
prop_test(7, 50, method = "wald", p = 0.2)
prop_test(7, 50, method = "wald", p = 0.2, exact = TRUE)
prop_test(c(23, 24), c(50, 55))

vietnam <- data.frame(
  service = c(rep("yes", 2), rep("no", 2)),
  sleep = c(rep(c("yes", "no"), 2)),
  count = c(173, 160, 599, 851)
)

sleep <- xtabs(count ~ service + sleep, data = vietnam)
prop_test(sleep)

prop_test(vietnam, service, sleep, count)
```

---

prop\_test.data.frame *Tests for equality of proportions*

---

**Description**

Conduct 1-sample tests of proportions and tests for equality of k proportions.

**Usage**

```
## S3 method for class 'data.frame'
prop_test(x, pred, out, weight = NULL,
  rev = c("neither", "rows", "columns", "both"), method = c("wald",
  "wilson", "agresti-couli", "jeffreys", "modified wilson", "wilsoncc",
  "modified jeffreys", "clopper-pearson", "arcsine", "logit", "witting",
  "pratt"), alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95, correct = FALSE, exact = FALSE, ...)
```

**Arguments**

x	a dataframe with categorical variable pred and binary outcome out.
pred	predictor/exposure, vector.
out	outcome, vector.
weight	an optional vector of count weights.
rev	reverse order of cells. Options are "row", "columns", "both", and "neither" (default).

<code>method</code>	a character string indicating method for calculating confidence interval, default is "wald". Options include, wald, wilson, agresti-couli, jeffreys, modified wilson, wilsoncc modified jeffreys, clopper-pearson, arcsine, logit, witting, and pratt.
<code>alternative</code>	character string specifying the alternative hypothesis. Possible options are "two.sided" (default), "greater", or "less".
<code>conf.level</code>	confidence level for confidence interval, default is 0.95.
<code>correct</code>	a logical indicating whether Yate's continuity correction should be applied.
<code>exact</code>	a logical indicating whether to output exact p-value, ignored if k-sample test.
<code>...</code>	further arguments passed to or from other methods.

**Value**

a list with class "prop\_test" containing the following components:

<code>x</code>	number of successes
<code>n</code>	number of trials
<code>p</code>	null proportion
<code>statistic</code>	the value of Pearson's chi-squared test statistic
<code>p_value</code>	p-value corresponding to chi-squared test statistic
<code>df</code>	degrees of freedom
<code>method</code>	the method used to calculate the confidence interval
<code>method_ci</code>	confidence interval calculated using specified method
<code>exact_ci</code>	exact confidence interval
<code>exact_p</code>	p-value from exact test

**Examples**

```

vietnam <- data.frame(
  service = c(rep("yes", 2), rep("no", 2)),
  sleep = c(rep(c("yes", "no"), 2)),
  count = c(173, 160, 599, 851)
)

prop_test(vietnam, service, sleep, count)

```



---

prop\_test.matrix      *Tests for equality of proportions*

---

### Description

Conduct 1-sample tests of proportions and tests for equality of k proportions.

### Usage

```
## S3 method for class 'matrix'
prop_test(x, method = c("wald", "wilson",
  "agresti-couli", "jeffreys", "modified wilson", "wilsoncc",
  "modified jeffreys", "clopper-pearson", "arcsine", "logit", "witting",
  "pratt"), alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95, correct = FALSE, exact = FALSE, ...)
```

### Arguments

x	a 2 x k matrix.
method	a character string indicating method for calculating confidence interval, default is "wald". Options include, wald, wilson, agresti-couli, jeffreys, modified wilson, wilsoncc modified jeffreys, clopper-pearson, arcsine, logit, witting, and pratt.
alternative	character string specifying the alternative hypothesis. Possible options are "two.sided" (default), "greater", or "less".
conf.level	confidence level for confidence interval, default is 0.95.
correct	a logical indicating whether Yate's continuity correction should be applied.
exact	a logical indicating whether to output exact p-value, ignored if k-sample test.
...	further arguments passed to or from other methods.

### Value

a list with class "prop\_test" containing the following components:

x	number of successes
n	number of trials
p	null proportion
statistic	the value of Pearson's chi-squared test statistic
p_value	p-value corresponding to chi-squared test statistic
df	degrees of freedom
method	the method used to calculate the confidence interval
method_ci	confidence interval calculated using specified method
exact_ci	exact confidence interval
exact_p	p-value from exact test

**Examples**

```
matrix(c(23, 48, 76, 88), nrow = 2, ncol = 2) %>% prop_test()
```

---

```
prop_test.numeric      Tests for equality of proportions
```

---

**Description**

Conduct 1-sample tests of proportions and tests for equality of k proportions.

**Usage**

```
## S3 method for class 'numeric'
prop_test(x, n, p = 0.5, method = c("wald", "wilson",
  "agresti-couli", "jeffreys", "modified wilson", "wilsoncc",
  "modified jeffreys", "clopper-pearson", "arcsine", "logit", "witting",
  "pratt"), alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95, correct = FALSE, exact = FALSE, ...)
```

**Arguments**

x	a vector of counts.
n	a vector of counts of trials
p	a probability for the null hypothesis when testing a single proportion; ignored if comparing multiple proportions.
method	a character string indicating method for calculating confidence interval, default is "wald". Options include, wald, wilson, agresti-couli, jeffreys, modified wilson, wilsoncc modified jeffreys, clopper-pearson, arcsine, logit, witting, and pratt.
alternative	character string specifying the alternative hypothesis. Possible options are "two.sided" (default), "greater", or "less".
conf.level	confidence level for confidence interval, default is 0.95.
correct	a logical indicating whether Yate's continuity correction should be applied.
exact	a logical indicating whether to output exact p-value, ignored if k-sample test.
...	further arguments passed to or from other methods.

**Value**

a list with class "prop\_test" containing the following components:

x	number of successes
n	number of trials
p	null proportion
statistic	the value of Pearson's chi-squared test statistic

p_value	p-value corresponding to chi-squared test statistic
df	degrees of freedom
method	the method used to calculate the confidence interval
method_ci	confidence interval calculated using specified method
exact_ci	exact confidence interval
exact_p	p-value from exact test

### Examples

```
prop_test(7, 50, method = "wald", p = 0.2)
prop_test(7, 50, method = "wald", p = 0.2, exact = TRUE)
```

---

prop_test.table	<i>Tests for equality of proportions</i>
-----------------	--

---

### Description

Conduct 1-sample tests of proportions and tests for equality of k proportions.

### Usage

```
## S3 method for class 'table'
prop_test(x, method = c("wald", "wilson",
  "agresti-couli", "jeffreys", "modified wilson", "wilsoncc",
  "modified jeffreys", "clopper-pearson", "arcsine", "logit", "witting",
  "pratt"), alternative = c("two.sided", "less", "greater"),
  conf.level = 0.95, correct = FALSE, exact = FALSE, ...)
```

### Arguments

x	a 2 x k table.
method	a character string indicating method for calculating confidence interval, default is "wald". Options include, wald, wilson, agresti-couli, jeffreys, modified wilson, wilsoncc modified jeffreys, clopper-pearson, arcsine, logit, witting, and pratt.
alternative	character string specifying the alternative hypothesis. Possible options are "two.sided" (default), "greater", or "less".
conf.level	confidence level for confidence interval, default is 0.95.
correct	a logical indicating whether Yate's continuity correction should be applied.
exact	a logical indicating whether to output exact p-value, ignored if k-sample test.
...	further arguments passed to or from other methods.

**Value**

a list with class "prop\_test" containing the following components:

x	number of successes
n	number of trials
p	null proportion
statistic	the value of Pearson's chi-squared test statistic
p_value	p-value corresponding to chi-squared test statistic
df	degrees of freedom
method	the method used to calculate the confidence interval
method_ci	confidence interval calculated using specified method
exact_ci	exact confidence interval
exact_p	p-value from exact test

**Examples**

```
vietnam <- data.frame(
  service = c(rep("yes", 2), rep("no", 2), rep("maybe", 2)),
  sleep = rep(c("yes", "no"), 3),
  count = c(173, 160, 599, 851, 400, 212)
)

xtabs(count ~ service + sleep, data = vietnam) %>% prop_test()
```

---

riskdiff	<i>Risk difference</i>
----------	------------------------

---

**Description**

Calculate risk difference and 95 percent confidence interval using Wald method.

**Usage**

```
riskdiff(df, ...)
```

**Arguments**

df	a dataframe with binary variables x and y or a 2 x 2 frequency table/matrix. If a table or matrix, x and y must be NULL. Used to select method.
...	further arguments passed to or from other methods.

**Value**

a list with class "rdiff" containing the following components:

rd	risk difference
conf.level	specified confidence level
ci	calculated confidence interval
p1	proportion one
p2	proportion two
tab	2x2 table using for calculating risk difference

**Examples**

```
trial <- data.frame(
  disease = c(rep("yes", 2), rep("no", 2)),
  treatment = c(rep(c("estrogen", "placebo"), 2)),
  count = c(751, 623, 7755, 7479))

riskdiff(trial, treatment, disease, count, rev = "columns")
```

---

riskdiff.data.frame    *Risk difference*

---

**Description**

Calculate risk difference and 95 percent confidence interval using Wald method.

**Usage**

```
## S3 method for class 'data.frame'
riskdiff(df, x = NULL, y = NULL, weight = NULL,
  conf.level = 0.95, rev = c("neither", "rows", "columns", "both"),
  ...)
```

**Arguments**

df	a dataframe with binary variables x and y.
x	binary predictor/exposure, vector.
y	binary outcome, vector.
weight	an optional vector of count weights.
conf.level	confidence level for confidence interval, default is 0.95.
rev	reverse order of cells. Options are "row", "columns", "both", and "neither" (default).
...	further arguments passed to or from other methods.

**Value**

a list with class "rdiff" containing the following components:

rd	risk difference
conf.level	specified confidence level
ci	calculated confidence interval
p1	proportion one
p2	proportion two
tab	2x2 table using for calculating risk difference

**Examples**

```
trial <- data.frame(
  disease = c(rep("yes", 2), rep("no", 2)),
  treatment = c(rep(c("estrogen", "placebo"), 2)),
  count = c(751, 623, 7755, 7479))

riskdiff(trial, treatment, disease, count, rev = "columns")
```

---

riskdiff.matrix	<i>Risk difference</i>
-----------------	------------------------

---

**Description**

Calculate risk difference and 95 percent confidence interval using Wald method.

**Usage**

```
## S3 method for class 'matrix'
riskdiff(df, conf.level = 0.95, dnn = NULL,
  rev = c("neither", "rows", "columns", "both"), ...)
```

**Arguments**

df	a 2 x 2 frequency matrix.
conf.level	confidence level for confidence interval, default is 0.95.
dnn	optional character vector of dimension names.
rev	reverse order of cells. Options are "row", "columns", "both", and "neither" (default).
...	further arguments passed to or from other methods.

**Value**

a list with class "rdiff" containing the following components:

rd	risk difference
conf.level	specified confidence level
ci	calculated confidence interval
p1	proportion one
p2	proportion two
tab	2x2 table using for calculating risk difference

**Examples**

```
matrix(c(12, 45, 69, 15), nrow = 2, ncol = 2) %>%
  riskdiff(dnn = c("New Drug", "Adverse Outcome"))
```

---

riskdiff.table	<i>Risk difference</i>
----------------	------------------------

---

**Description**

Calculate risk difference and 95 percent confidence interval using Wald method.

**Usage**

```
## S3 method for class 'table'
riskdiff(df, conf.level = 0.95, rev = c("neither",
  "rows", "columns", "both"), ...)
```

**Arguments**

df	a 2 x 2 frequency table.
conf.level	confidence level for confidence interval, default is 0.95.
rev	reverse order of cells. Options are "row", "columns", "both", and "neither" (default).
...	further arguments passed to or from other methods.

**Value**

a list with class "rdiff" containing the following components:

rd	risk difference
conf.level	specified confidence level
ci	calculated confidence interval
p1	proportion one
p2	proportion two
tab	2x2 table using for calculating risk difference

**Examples**

```
trial <- data.frame(
  disease = c(rep("yes", 2), rep("no", 2)),
  treatment = c(rep(c("estrogen", "placebo"), 2)),
  count = c(751, 623, 7755, 7479))

xtabs(count ~ treatment + disease, data = trial) %>% riskdiff()
```

---

tavolo	<i>Create 2 x k frequency tables</i>
--------	--------------------------------------

---

**Description**

Helper function for creating 2 x k frequency tables.

**Usage**

```
tavolo(df, ...)
```

**Arguments**

df	a dataframe with binary variable y and categorical variable x or a 2 x k frequency table/matrix. If a table or matrix, x and y must be NULL. Used to select method.
...	further arguments passed to or from other methods.

**Value**

tab	2 x k frequency table
-----	-----------------------

**Examples**

```
trial <- data.frame(disease = c(rep("yes", 2), rep("no", 2)),
  treatment = c(rep(c("estrogen", "placebo"), 2)),
  count = c(751, 623, 7755, 7479))

tavolo(trial, treatment, disease, count)
```



---

tavolo.data.frame	<i>Create 2 x k frequency tables</i>
-------------------	--------------------------------------

---

**Description**

Helper function for creating 2 x k frequency tables.

**Usage**

```
## S3 method for class 'data.frame'  
tavolo(df, x, y, weight = NULL, rev = c("neither",  
    "rows", "columns", "both"), ...)
```

**Arguments**

df	a dataframe with binary variable y and categorical variable x.
x	categorical predictor/exposure, vector.
y	binary outcome, vector.
weight	an optional vector of count weights.
rev	character string indicating whether to switch row or column order, possible options are "neither", "rows", "columns", or "both". The default is "neither".
...	further arguments passed to or from other methods.

**Value**

tab	2 x k frequency table
-----	-----------------------

**Examples**

```
trial <- data.frame(disease = c(rep("yes", 2), rep("no", 2)),  
    treatment = c(rep(c("estrogen", "placebo"), 2)),  
    count = c(751, 623, 7755, 7479))  
  
tavolo(trial, treatment, disease, count)
```

---

tavolo.matrix	<i>Create 2 x k frequency tables</i>
---------------	--------------------------------------

---

**Description**

Helper function for creating 2 x k frequency tables.

**Usage**

```
## S3 method for class 'matrix'
tavolo(df, dnn = NULL, rev = c("neither", "rows",
  "columns", "both"), ...)
```

**Arguments**

df                    a 2 x k frequency matrix.

dnn                   optional character vector of dimension names.

rev                   character string indicating whether to switch row or column order, possible options are "neither", "rows", "columns", or "both". The default is "neither".

...                   further arguments passed to or from other methods.

**Value**

tab                   2 x k frequency table

**Examples**

```
tavolo(matrix(c(23, 45, 67, 12), nrow = 2, ncol = 2), rev = "both")
```

---

tavolo.table	<i>Create 2 x k frequency tables</i>
--------------	--------------------------------------

---

**Description**

Helper function for creating 2 x k frequency tables.

**Usage**

```
## S3 method for class 'table'
tavolo(df, rev = c("neither", "rows", "columns", "both"),
  ...)
```

**Arguments**

df                    a 2 x k frequency table.

rev                   character string indicating whether to switch row or column order, possible options are "neither", "rows", "columns", or "both". The default is "neither".

...                   further arguments passed to or from other methods.

**Value**

tab                   2 x k frequency table

**Examples**

```
trial <- data.frame(disease = c(rep("yes", 3), rep("no", 3)),
                  treatment = rep(c("estrogen", "placebo", "other"), 2),
                  count = c(751, 623, 7755, 7479, 9000, 456))

xtabs(count ~ treatment + disease, data = trial) %>% tavolo(rev = "columns")
```

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