

Package ‘konfound’

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Type Package

Title Quantify the Robustness of Causal Inferences

Version 0.2.2

Description Statistical methods that quantify the conditions necessary to alter inferences, also known as sensitivity analysis, are becoming increasingly important to a variety of quantitative sciences. A series of recent works, including Frank (2000) <doi:10.1177/0049124100029002001> and Frank et al. (2013) <doi:10.3102/0162373713493129> extend previous sensitivity analyses by considering the characteristics of omitted variables or unobserved cases that would change an inference if such variables or cases were observed. These analyses generate statements such as “an omitted variable would have to be correlated at xx with the predictor of interest (e.g., treatment) and outcome to invalidate an inference of a treatment effect”. Or “one would have to replace pp percent of the observed data with null hypothesis cases to invalidate the inference”. We implement these recent developments of sensitivity analysis and provide modules to calculate these two robustness indices and generate such statements in R. In particular, the functions `konfound()`, `pkonfound()` and `mkonfound()` allow users to calculate the robustness of inferences for a user's own model, a single published study and multiple studies respectively.

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Imports broom, broom.mixed, crayon, dplyr, ggplot2, mice, purrr, rlang, tidyr

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VignetteBuilder knitr

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URL <https://github.com/jrosen48/konfound>

BugReports <https://github.com/jrosen48/konfound/issues>

NeedsCompilation no

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getswitch_chisq	<i>Get switch result for tkonfound based on chi-square tests</i>
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Description

This function serves for tkonfound

Usage

getswitch_chisq(a, b, c, d, thr_p = 0.05, switch_trm = T)

Arguments

- a cell is the number of cases in the control group showing unsuccessful results
- b cell is the number of cases in the control group showing successful results
- c cell is the number of cases in the treatment group showing unsuccessful results
- d cell is the number of cases in the treatment group showing successful results
- thr_p the p-value threshold used to evaluate statistical significance, with the default of 0.05
- switch_trm whether switching the two cells in the treatment row or the two cells in the control row, with the default of the treatment row

Value

prints the results that are needed for tkonfound

Examples

```
# using getswitch_chisq for a 2x2 table
getswitch_chisq(35, 17, 17, 38)
getswitch_chisq(35, 17, 17, 38, thr_p = 0.01)
getswitch_chisq(35, 17, 17, 38, thr_p = 0.01, switch_trm = FALSE)
```

konfound

Perform sensitivity analysis on fitted models

Description

For fitted models, this command calculates (1) how much bias there must be in an estimate to invalidate/sustain an inference; (2) the impact of an omitted variable necessary to invalidate/sustain an inference for a regression coefficient. Currently works for: models created with `lm()` (linear models).

Usage

```
konfound(
  model_object,
  tested_variable,
  alpha = 0.05,
  tails = 2,
  to_return = "print",
  test_all = FALSE
)
```

Arguments

<code>model_object</code>	output from a model (currently works for: <code>lm</code>)
<code>tested_variable</code>	Variable associated with the unstandardized beta coefficient to be tested
<code>alpha</code>	probability of rejecting the null hypothesis (defaults to 0.05)
<code>tails</code>	integer whether hypothesis testing is one-tailed (1) or two-tailed (2; defaults to 2)
<code>to_return</code>	whether to return a data.frame (by specifying this argument to equal "raw_output" for use in other analyses) or a plot ("plot"); default is to print ("print") the output to the console; can specify a vector of output to return
<code>test_all</code>	whether to carry out the sensitivity test for all of the coefficients (defaults to FALSE)

Value

prints the bias and the number of cases that would have to be replaced with cases for which there is no effect to invalidate the inference

Examples

```
# using lm() for linear models
m1 <- lm(mpg ~ wt + hp, data = mtcars)
konfound(m1, wt)
konfound(m1, wt, test_all = TRUE)
konfound(m1, wt, to_return = "table")

# using glm() for non-linear models
if (requireNamespace("forcats")) {
  d <- forcats::gss_cat

  d$married <- ifelse(d$marital == "Married", 1, 0)

  m2 <- glm(married ~ age, data = d, family = binomial(link = "logit"))
  konfound(m2, age)
}

# using lme4 for mixed effects (or multi-level) models
if (requireNamespace("lme4")) {
  library(lme4)
  m3 <- fm1 <- lme4::lmer(Reaction ~ Days + (1 | Subject), sleepstudy)
  konfound(m3, Days)
}
```

launch_shiny

Open interactive web application for konfound

Description

Open interactive web application for konfound

Usage

```
launch_shiny()
```

Details

Open the Shiny interactive web application in a browser

Value

Launches a web browser

mkonfound

Perform meta-analyses including sensitivity analysis

Description

For fitted models, this command carries out sensitivity analysis for a number of models, when their parameters stored in a data.frame.

Usage

```
mkonfound(d, t, df, alpha = 0.05, tails = 2, return_plot = FALSE)
```

Arguments

d	data.frame or tibble with the t-statistics and associated degrees of freedom
t	t-statistic or vector of t-statistics
df	degrees of freedom or vector of degrees of freedom associated with the t-statistics in the t argument
alpha	probability of rejecting the null hypothesis (defaults to 0.05)
tails	integer whether hypothesis testing is one-tailed (1) or two-tailed (2; defaults to 2)
return_plot	whether to return a plot of the percent bias; defaults to FALSE

Value

prints the bias and the number of cases that would have to be replaced with cases for which there is no effect to invalidate the inference for each of the cases in the data.frame

Examples

```
d <- read.csv("https://msu.edu/~kenfrank/example%20dataset%20for%20mkonfound.csv")
d <- d[1:3, ] # this is only so that the example runs more quickly
str(d)
mkonfound(d, t, df)
```

pkonfound

Perform sensitivity analysis for published studies

Description

For published studies, this command calculates (1) how much bias there must be in an estimate to invalidate/sustain an inference; (2) the impact of an omitted variable necessary to invalidate/sustain an inference for a regression coefficient.

Usage

```
pkonfound(
  est_eff,
  std_err,
  n_obs,
  n_covariates = 1,
  alpha = 0.05,
  tails = 2,
  nu = 0,
  n_trm = NULL,
  switch_trm = TRUE,
  non_linear = FALSE,
  to_return = "print"
)
```

Arguments

<code>est_eff</code>	the estimated effect (such as an unstandardized beta coefficient or a group mean difference)
<code>std_err</code>	the standard error of the estimate of the unstandardized regression coefficient
<code>n_obs</code>	the number of observations in the sample
<code>n_covariates</code>	the number of covariates in the regression model
<code>alpha</code>	probability of rejecting the null hypothesis (defaults to 0.05)
<code>tails</code>	integer whether hypothesis testing is one-tailed (1) or two-tailed (2; defaults to 2)
<code>nu</code>	what hypothesis to be tested; defaults to testing whether <code>est_eff</code> is significantly different from 0
<code>n_trm</code>	the number of cases associated with the treatment condition; applicable only when <code>non_linear = TRUE</code>
<code>switch_trm</code>	whether to switch the treatment and control cases; defaults to FALSE; applicable only when <code>non_linear = TRUE</code>
<code>non_linear</code>	whether the model is a non-linear model; defaults to FALSE
<code>to_return</code>	whether to return a data.frame (by specifying this argument to equal "raw_output" for use in other analyses) or a plot ("plot"); default is to print ("print") the output to the console; can specify a vector of output to return

Value

prints the bias and the number of cases that would have to be replaced with cases for which there is no effect to invalidate the inference

Examples

```
pkonfound(2, .4, 100, 3)
pkonfound(-2.2, .65, 200, 3)
pkonfound(.5, 3, 200, 3)
```

```

pkonfound(-0.2, 0.103, 20888, 3, n_trm = 17888, non_linear = TRUE)

pkonfound(2, .4, 100, 3, to_return = "thresh_plot")
pkonfound(2, .4, 100, 3, to_return = "corr_plot")

pkonfound_output <- pkonfound(2, .4, 200, 3,
  to_return = c("raw_output", "thresh_plot", "corr_plot")
)
summary(pkonfound_output)
pkonfound_output$raw_output
pkonfound_output$thresh_plot
pkonfound_output$corr_plot

```

summary.konfound	<i>Concise summary of konfound output</i>
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Description

Concise summary of konfound output

Usage

```

## S3 method for class 'konfound'
summary(object, ...)

```

Arguments

object	A 'konfound' object
...	Additional arguments

Details

Prints a concise summary of konfound output with multiple types of data specified in the to_return argument

tkonfound	<i>Perform sensitivity analysis for a 2x2 table</i>
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Description

This function calculates the number of cases (RIS) that would have to be switched from one cell to another of a 2x2 table to invalidate an inference made about the association between the rows and columns. This can be applied to treatment vs control with successful vs unsuccessful outcomes.

Usage

```
tkonfound(a, b, c, d, thr_p = 0.05, switch_trm = T)
```

Arguments

a	cell is the number of cases in the control group showing unsuccessful results
b	cell is the number of cases in the control group showing successful results
c	cell is the number of cases in the treatment group showing unsuccessful results
d	cell is the number of cases in the treatment group showing successful results
thr_p	the p-value threshold used to evaluate statistical significance, with the default of 0.05
switch_trm	whether switching the two cells in the treatment row or the two cells in the control row, with the default of the treatment row

Value

prints a 2x2 table after switching cases from one cell to another so that the inference is invalidated about the association between the rows and columns

Examples

```
# using tkonfound for a 2x2 table
tkonfound(35, 17, 17, 38)
tkonfound(35, 17, 17, 38, thr_p = 0.01)
tkonfound(35, 17, 17, 38, thr_p = 0.01, switch_trm = FALSE)
```

tkonfound_fig	<i>Draw figures for change in effect size as a function of switching outcomes</i>
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Description

This function returns two plots for change in effect size as a function of switching outcomes (RIS), one for all possibilities, another zoomed in the area around the two thresholds

Usage

```
tkonfound_fig(a, b, c, d, thr_p = 0.05, switch_trm = T)
```

Arguments

a	cell is the number of cases in the control group showing unsuccessful results
b	cell is the number of cases in the control group showing successful results
c	cell is the number of cases in the treatment group showing unsuccessful results
d	cell is the number of cases in the treatment group showing successful results
thr_p	the p-value threshold used to evaluate statistical significance, with the default of 0.05
switch_trm	whether switching the two cells in the treatment row or the two cells in the control row, with the default of the treatment row

Value

prints 2 figures for how number of hypothetical cases switched changes the effect size

Examples

```
# using tkonfound_fig for a study where 2 by 2 table is (35, 17, 17, 38)
tkonfound_fig(35, 17, 17, 38)
tkonfound_fig(35, 17, 17, 38, thr_p = 0.01)
tkonfound_fig(35, 17, 17, 38, thr_p = 0.01, switch_trm = FALSE)
```

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