konfound

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Abstract An abstract of less than 150 words.

Introduction

In social science (and educational) research, we often wish to understand how robust inferences about effects are to unobserved (or controlled for) covariates, possible problems with measurement, and other sources of bias. The goal of konfound is to carry out sensitivity analysis to help analysts to *quantify how robust inferences are to potential sources of bias*. This package provides functions based on developments in sensitivity analysis by Frank and colleagues, which previously have been implemented in Stata and through an Excel spreadsheet, in R through the konfound package.

Background on sensitivity analysis

Impact threshold of a confounding variable

Percent bias to invalidate an inference

Tutorial

You can install konfound with the following:

```
install.packages("konfound")
```

You can then load konfound with the library() function:

library(konfound)

#> Sensitivity analysis as described in Frank, Maroulis, Duong, and Kelcey (2013) and in Frank (2000).
#> For more information visit https://jmichaelrosenberg.shinyapps.io/shinykonfound/.

Use of pkonfound() for values from an already-conducted analysis

pkonfound() is used when we have values from an already-conducted analysis (like a regression analysis), such as one in an already-published study or from an analysis carried out using other software.

In the case of a regression analysis, values from the analysis would simply be used as the inputs to the pkonfound() function. For example, in the use below, we simply enter the values for the estimated effect (an unstandardardized beta coefficient) (2), its standard error (.4), the sample size (100), and the number of covariates (3):

```
pkonfound(2, .4, 100, 3)

#> Replacement of Cases Approach:
#> To invalidate an inference, 60.3% of the estimate would have to be due to bias. This is based on a threshold of 0.794 for statistical significance (alpha = 0.05).
#> To invalidate an inference, 60 observations would have to be replaced with cases for which the effect is 0.
#>
#> Correlation-based Approach:
#> An omitted variable would have to be correlated at 0.568 with the outcome and at 0.568 with the predictor of interest (conditioning on observed covariates) to invalidate an inference based on a threshold of 0.201 for statistical significance (alpha = 0.05).
#> Correspondingly the impact of an omitted variable (as defined in Frank 2000) must be 0.568 X 0.568 = 0.323 to invalidate an inference.
#> For other forms of output, change `to_return` to table, raw_output, thres_plot, or corr_plot.
```

pkonfound(.4, 2, 100, 3)

#> For models fit in R, consider use of konfound().

For this set of values, around 60% would need to be false due to a source of bias for the inference to be invalidated (based on statistical significance and a p-value (or alpha) of .05), possible a very robust effect. An omitted, confounding variable (sometimes referred to as a covariate) would need to have an impact (defined as the product of the confounding variable's correlation with both the predictor of interest and the outcome) of 0.323, presenting a different interpretation of how robust this (hypothetical) effect is to a variable which is important but not included in the analysis.

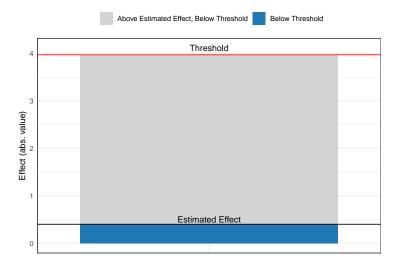
Here is another example, but one in which the unstandardized beta coefficient is smaller than its standard error:

```
#> Replacement of Cases Approach:
#> To sustain an inference, 89.924% of the estimate would have to be due to
bias. This is based on a threshold of 3.97 for statistical significance (alpha
#> To sustain an inference, 90 of the cases with 0 effect would have to be
replaced with cases at the threshold of inference.
#>
#> Correlation-based Approach:
#> An omitted variable would have to be correlated at 0.387 with the outcome
and at 0.387 with the predictor of interest (conditioning on observed
covariates) to sustain an inference based on a threshold of 3.97 for
statistical significance (alpha = 0.05).
#> Correspondingly the impact of an omitted variable (as defined in Frank 2000)
must be 0.387 \times 0.387 = 0.15 to sustain an inference.
#> For other forms of output, change `to_return` to table, raw_output, thres_plot, or corr_plot.
#> For models fit in R, consider use of konfound().
   Note that this use of pkonfound() is equivalent to naming the arguments, i.e. for a different set of
values:
pkonfound(est_eff = -2.2,
          std_err = .65,
          n_{obs} = 200,
          n_{covariates} = 3)
#> Replacement of Cases Approach:
#> To invalidate an inference, 41.732% of the estimate would have to be due to
bias. This is based on a threshold of -1.282 for statistical significance
(alpha = 0.05).
#> To invalidate an inference, 83 observations would have to be replaced with
cases for which the effect is 0.
#>
#> Correlation-based Approach:
#> An omitted variable would have to be correlated at 0.334 with the outcome
and at 0.334 with the predictor of interest (conditioning on observed
covariates) to invalidate an inference based on a threshold of -0.14 for
statistical significance (alpha = 0.05).
#> Correspondingly the impact of an omitted variable (as defined in Frank 2000)
must be 0.334 \times 0.334 = 0.112 to invalidate an inference.
#> For other forms of output, change `to_return` to table, raw_output, thres_plot, or corr_plot.
#> For models fit in R, consider use of konfound().
```

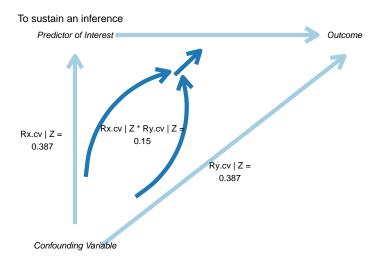
We notice that the output includes a message that says we can view other forms of output by changing the to_return argument. Here are the two plots - for the bias necessary to alter an inference (thresh_plot) and for the robustness of an inference in terms of the impact of a confounding variable

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

(corr_plot) that can be returned:



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



You can also specify multiple forms of output at once.

```
#> Replacement of Cases Approach:
#> To invalidate an inference, 60.557% of the estimate would have to be due to bias. This is based on a three
#> To invalidate an inference, 121 observations would have to be replaced with cases for which the effect is
#>
#> Correlation-based Approach:
```

model_output <- pkonfound(2, .4, 200, 3, to_return = c("raw_output", "thresh_plot", "corr_plot"))</pre>

#> An omitted variable would have to be correlated at 0.479 with the outcome and at 0.479 with the predictor #> Correspondingly the impact of an omitted variable (as defined in Frank 2000) must be 0.479 X 0.479 = 0.229

#> Print output created by default. Created 3 other forms of output. Use list indexing or run summary() on to

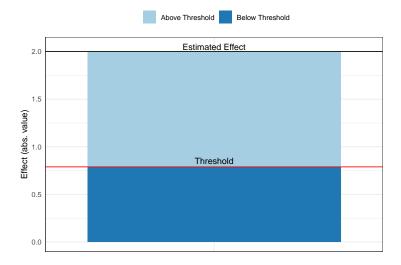
summary(model_output)

#> Created 3 forms of output. To access type:
#>

#> model_output\$raw_output
#> model_output\$thresh_plot
#> model_output\$corr_plot

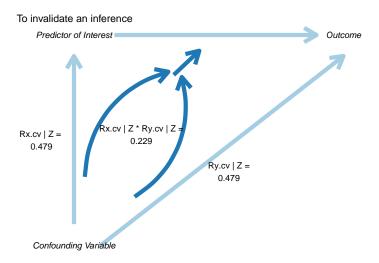
When we type the name of the object, we see that we created three types of output that we can access as follows:

model_output\$raw_output



model_output\$corr_plot

model_output\$thresh_plot



Finally, you can return the raw output, for use in other analyses.

```
pkonfound(.4, 2, 100, 3, to_return = "raw_output")
#> # A tibble: 1 x 8
#> action inference percent_bias_to~ replace_null_ca~ unstd_beta
#> <chr> <chr> <dbl> <dbl> <dbl> <dbl> <dbl> #> 1 to_su~ fail_to_~ 89.9 90 0.4
#> # ... with 3 more variables: beta_threshhold <dbl>,
#> # omitted_variable_corr <dbl>, itcv <dbl>
```

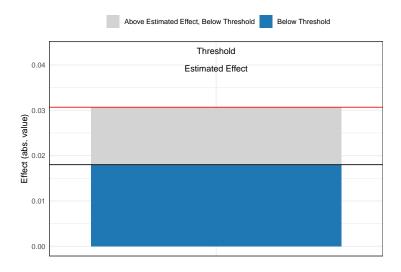
Use of konfound() for models fit in R

Where pkonfound() can be used with values from already-conducted analyses, konfound() can be used with models (lm(), glm(), and lme4::lmer()) fit in R.

For linear models fit with lm()

```
m1 <- lm(mpg ~ wt + hp + qsec, data = mtcars)
m1
#>
#> Call:
#> lm(formula = mpg ~ wt + hp + qsec, data = mtcars)
#> Coefficients:
#> (Intercept)
                                      hp
                         wt.
                                                  gsec
      27.61053
                   -4.35880
                                -0.01782
                                              0.51083
konfound(m1, hp)
#> Note that this output is calculated based on the correlation-based approach used in mkonfound()
#> Replacement of Cases Approach:
#> To sustain an inference, 41.327% of the estimate would have to be due to bias. This is based on a threshold
#> To sustain an inference, 13 of the cases with 0 effect would have to be replaced with cases at the thresho
#> Correlation-based Approach:
#> An omitted variable would have to be correlated at 0.322 with the outcome and at 0.322 with the predictor
#> Correspondingly the impact of an omitted variable (as defined in Frank 2000) must be 0.322 X 0.322 = 0.10
#> For more detailed output, consider setting `to_return` to table
#> To consider other predictors of interest, consider setting `test_all` to TRUE.
   Like with pkonfound(), we can also output multiple forms of output at once with konfound():
konfound_output <- konfound(m1, hp, to_return = c("raw_output", "thresh_plot", "corr_plot"))</pre>
#> Note that this output is calculated based on the correlation-based approach used in mkonfound()
#> Replacement of Cases Approach:
#> To sustain an inference, 41.327% of the estimate would have to be due to bias. This is based on a thresho.
#> To sustain an inference, 13 of the cases with 0 effect would have to be replaced with cases at the thresho
#> Correlation-based Approach:
#> An omitted variable would have to be correlated at 0.322 with the outcome and at 0.322 with the predictor
#> Correspondingly the impact of an omitted variable (as defined in Frank 2000) must be 0.322 X 0.322 = 0.10
#> Print output created by default. Created 3 other forms of output. Use list indexing or run summary() on the
summary(konfound_output)
#> Created 3 forms of output. To access type:
#> konfound_output$raw_output
#> konfound_output$thresh_plot
#> konfound_output$corr_plot
   Again, we can type each of those, i.e.:
konfound_output$raw_output
#> # A tibble: 1 x 8
   action inference percent_bias_to~ replace_null_ca~ unstd_beta
                                                  <dbl>
                                                             <dbl>
    <chr> <chr>
                                 <dbl>
#> 1 to_su~ fail_to_~
                                  41.3
                                                     13
                                                             -0.018
#> # ... with 3 more variables: beta_threshhold <dbl>,
#> # omitted_variable_corr <dbl>, itcv <dbl>
```

konfound_output\$thresh_plot



We can also test all of the variables as predictors of interest:

konfound(m1, wt, test_all = TRUE)

```
#> # A tibble: 3 x 8
#>
                       df action
    var_name
                                   inference pct_bias_to_chang~
                t
                                                                    itcv r_con
#>
              <dbl> <dbl> <chr>
                                                           <fdb> <fdb> <fdb>
     <chr>
                                   <chr>
                       29 to_inva~ reject_nu~
#> 1 wt
              -5.79
                                                            51.5 0.585 0.765
#> 2 hp
              -1.2
                       29 to_sust~ fail_to_r~
                                                             38.7 -0.102 0.319
                       29 to_sust~ fail_to_r~
#> 3 qsec
              1.16
                                                             40.5 -0.106 0.326
```

Whereas this cannot be carried out with pkonfound(), with konfound() you can also return a table with some key output from the correlation-based approach.

```
konfound(m1, wt, to_return = "table")
```

- #> Note that this output is calculated based on the correlation-based approach used in mkonfound()
- #> Dependent variable is mpg
- #> Warning: Unknown or uninitialised column: 'itcv'.
- #> Warning: Unknown or uninitialised column: 'impact'.

```
#> # A tibble: 4 x 7
#>
    term
                 estimate std.error statistic p.value
                                                         itcv impact
#>
    <chr>
                    <fdb1>
                              <dbl>
                                         <dbl>
                                                 <dbl> <dbl> <dbl>
#> 1 (Intercept)
                   27.6
                              8.42
                                          3.28
                                                 0.003 NA
                                                              NA
#> 2 wt
                   -4.36
                              0.753
                                         -5.79
                                                 0
                                                        0.243 NA
#> 3 hp
                   -0.018
                              0.015
                                         -1.19
                                                 0.244 NA
                                                               0.511
#> 4 qsec
                    0.511
                              0.439
                                                 0.255 NA
                                                               0.073
                                          1.16
```

If the impact threshhold is greater than the impacts of the Zs (the other covariates) then an omitted variable would have to have a greater impact than any of the observed covariates to change the inference. Note that in fields in which there is a lot known about covariates given the outcome of interest, then the omitted ones are likely less important than those that are known an included (i.e., we have a good sense of the factors that matter in terms of educational achievement).

For generalized linear models fit with glm()

Effects for these models are interpreted on the basis of average partial (or marginal) effects (calculated using the margins package).

```
# if forcats is not installed, this install it first using install.packages("forcats") for this to run
if (requireNamespace("forcats")) {
    d <- forcats::gss_cat

    d$married <- ifelse(d$marital == "Married", 1, 0)</pre>
```

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

#> Replacement of Cases Approach:
#> To sustain an inference, 80.978% of the estimate would have to be due to bias. This is based on a threshold
#> To sustain an inference, 17334 of the cases with 0 effect would have to be replaced with cases at the three
#> Correlation-based Approach:
#> An omitted variable would have to be correlated at 5.535 with the outcome and at 5.535 with the predictor
#> Correspondingly the impact of an omitted variable (as defined in Frank 2000) must be 5.535 X 5.535 = 30.63
#> NULL
```

As with models fit with lm() (and use of pkonfound()), multiple forms of output can be specified with the to_return argument to konfound(), i.e. konfound(m2, age, to_return = c("raw_output", "corr_plot", "thresh_plot")).

For mixed effects (or multi-level) models fit with the lmer() function from the lme4 package

konfound also works with models fit with the lmer() function from the package lme4, for mixed-effects or multi-level models. One challenge with carrying out sensitivity analysis for fixed effects in mixed effects models is calculating the correct denominator degrees of freedom for the t-test associated with the coefficients. This is not unique to sensitivity analysis, as, for example, lmer() does not report degrees of freedom (or p-values) for fixed effects predictors (see this information in the lme4 FAQ here). While it may be possible to determine the correct degrees of freedom for some models (i.e., models with relatively simple random effects structures), it is difficult to generalize this approach, and so in this package the Kenward-Roger approximation for the denominator degrees of freedom as implemented in the pbkrtest package (described in Halekoh and Højsgaard, 2014).

Here is an example of the use of konfound() with a model fit with lmer():

```
library(lme4)
    m3 <- fm1 <- lmer(Reaction ~ Days + (1 | Subject), sleepstudy)
    konfound(m3, Days)
}
#> Loading required namespace: lme4
#> Loading required package: Matrix
#> Warning in bind_rows_(x, .id): binding factor and character vector,
#> coercing into character vector
#> Warning in bind_rows_(x, .id): binding character and factor vector,
#> coercing into character vector
#> Replacement of Cases Approach:
#> To invalidate an inference, 84.83% of the estimate would have to be due to bias. This is based on a thresl
#> To invalidate an inference, 137 observations would have to be replaced with cases for which the effect is
#>
#> Correlation-based Approach:
#> An omitted variable would have to be correlated at 0.817 with the outcome and at 0.817 with the predictor
#> Correspondingly the impact of an omitted variable (as defined in Frank 2000) must be 0.817 X 0.817 = 0.66
#> Note that the Kenward-Roger approximation is used to estimate degrees of freedom for the predictor(s) of
```

Use of mkonfound() for meta-analyses that include sensitivity analysis

We can also use konfound to carry out sensitivity analysis as part of meta-analyses. For example, here, d represents output from a number (30 in this case) of past studies, read in a CSV file from a website:

```
d <- read.csv("https://msu.edu/~kenfrank/example%20dataset%20for%20mkonfound.csv")
head(d)</pre>
```

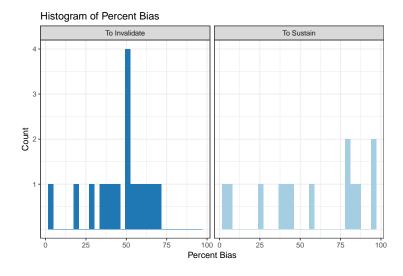
#> NULL

if (requireNamespace("lme4")) {

```
#>
            t df
#> 1 7.076763 178
#> 2 4.127893 193
#> 3 1.893137 47
#> 4 -4.166395 138
#> 5 -1.187599 97
#> 6 3.585478 87
mkonfound(d, t, df)
#> # A tibble: 30 x 7
#>
          t
               df action
                            inference
                                           pct_bias_to_change_~
                                                                  itcv r_con
#>
       <dbl> <int> <chr>
                            <chr>
                                                          <dbl> <dbl> <dbl>
#>
   1
      7.08
             178 to_inval~ reject_null
                                                          68.8
                                                                0.378 0.614
#>
                                                          50.6
                                                                0.168 0.41
   2 4.13
              193 to_inval~ reject_null
#>
   3 1.89
              47 to_susta~ fail_to_rejec~
                                                           5.47 -0.012 0.11
#>
   4 -4.17
              138 to_inval~ reject_null
                                                          50.3
                                                                0.202 0.449
#>
   5 -1.19
                                                          39.4
              97 to_susta~ fail_to_rejec~
                                                                -0.065 0.255
#>
   6
      3.59
               87 to_inval~ reject_null
                                                          41.9
                                                                 0.19 0.436
#>
      0.282
              117 to_susta~ fail_to_rejec~
                                                          85.5
                                                                -0.131 0.361
               75 to_inval~ reject_null
#>
                                                          20.6
                                                                 0.075 0.274
      2.55
              137 to_inval~ reject_null
#>
   9 -4.44
                                                          53.0
                                                                 0.225 0.475
#> 10 -2.05
              195 to_inval~ reject_null
                                                           3.51 0.006 0.077
#> # ... with 20 more rows
```

We can also return a plot summarizing the percent bias needed to sustan or invalidate an inference across all of the past studies:

```
mkonfound(d, t, df, return_plot = T)
#> `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



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