Package 'subgroup'

July 23, 2025

Type Package

Title Methods for exploring treatment effect heterogeneity in subgroup analysis of clinical trials

Version 1.1

Date 2014-07-31

Author I. Manjula Schou

Maintainer I. Manjula Schou <im.schou@yahoo.com.au>

Description Produces various measures of expected treatment effect heterogeneity under an assumption of homogeneity across subgroups. Graphical presentations are created to compare these expected differences with the observed differences.

License GPL-2 | GPL-3

Depends graphics, grDevices, utils, stats, R (>= 3.1)

NeedsCompilation no

Repository CRAN

Date/Publication 2014-08-01 12:37:02

Contents

subgroup	*Compute measures for assessing treatment effect heterogeneity across subgroups in clinical trials and produce graphical presentations*

Description

This function produces various measures of expected treatment effect heterogeneity and allows graphical comparisons with the observed counterparts. The resulting measures can also be saved for creation of user-specified graphics.

Usage

```
subgroup(data, overall.diff = NA, force.theoretical = FALSE,
force.simulation = FALSE, design = FALSE, plots = TRUE)
```

Arguments

data   A matrix of 2 columns containing the subgroup treatment effects and their asso-
                    ciated standard errors. The treatment effects must be measured on a scale where
                    0 means no effect. For example, a mean difference, a log relative risk, log odds
                    ratio, or log hazard ratio. Column 2 must contain the standard errors associ-
                    ated with the subgroup treatment effects in Column 1. Furthermore, a treatment
                    effect that is > 0 is considered to favour the control.

overall.diff   The overall treatment effect, provided optionally by the user. If not specified
                    this is calculated within the `subgroup` routine as a reciprocal variance weighted
                    mean.

force.theoretical
                    The default value for this argument is FALSE. If TRUE, theoretical computations
                    are conducted regardless of the number of subgroups, R. If the standard errors of
                    the subgroup treatment effects is heterogeneous and R > 20, a warning is given
                    to advise the user that the processing time may be significant. An error message
                    is given if both `force.theoretical` and `force.simulation` are set to TRUE,
                    and the routine will stop execution.

force.simulation
                    The default value for this argument is FALSE. If TRUE, simulation based computa-
                    tions are conducted regardless of the number of subgroups, R. An error message
                    is given if both `force.theoretical` and `force.simulation` are set to TRUE,
                    and the routine will stop execution.

design   The default value for this argument is FALSE. If TRUE, the plots will not include
                    any observed measures.

plots   The default value for this argument is TRUE. If FALSE, no plots will be displayed.

Details

Subgroup analysis principles require a significant test of interaction in order to claim heterogeneity
of treatment effect. As clinical trials are typically underpowered for tests of interaction, overly op-
timistic expectations of treatment effect homogeneity can make interpretation difficult when treat-
ment effects seemingly differ between subgroups. In addition to extending the ideas proposed by
Marschner (2010), the package **subgroup** also implements some new measures, and provides a
suite of graphical tools that allow visual comparison of the magnitude and nature of the observed
and expected subgroup differences that can arise as an artefact of chance. These tools are intended
to supplement a formal test of interaction in subgroup analyses, and are described in the manuscript
Schou and Marschner (2014).

Three outputs are computed by the package. These include the following: the expectations of the
ordered treatment effects, the probability density of the range, and the probability distribution of the
number of subgroups favouring the control treatment. The user has the option to have the in-built
plot suppressed. The content of the default plot produced will depend on the user choice of an

analysis stage evaluation or a design stage evaluation; if it is the former, the observed counterparts of the measures produced will be included in the plots.

Value

The following list of components is returned by the routine `subgroup`:

expectations   A matrix of dimension R x 4, where R is the number of subgroups. The first two columns present the treatment differences and the standard errors contained in the dataset `data` as submitted by the user. The third column contains the expected ordered treatment differences, and the fourth column the order number.

favourcontrol   A matrix of dimension (R+1) x 2, where R is the number of subgroups. The first column contains the number of subgroups favouring control. The second contains the probability of that event. Here, a treatment effect that is > 0 is considered to favour the control.

rangedensity   A matrix with 2 columns. The first column contains the sample space for the range which takes on values > 0. The second column contains the probability density.

overalldiff   A numeric variable which returns the input argument `overall.diff` if specified by the user or the reciprocal variance weighted mean treatment difference as calculated within the routine `subgroup`.

Author(s)

I. Manjula Schou

References

Marschner IC. Regional differences in multinational clinical trials: anticipating change variation. Clinical Trials 2010; 7:147-156.

Schou IM and Marschner IC. Methods for exploring treatment effect heterogeneity in subgroup analysis: an application to global clinical trials. COBRA Preprint Series. Working Paper 108. http://biostats.bepress.com/cobra/art108/.

Examples

```
# Create dataset containing treatment differences and standard errors. ------------
difference<-c(-0.163, -0.083, -0.030, 0.095)
se<-c(0.48, 0.27, 0.19, 0.39)
mydata<-cbind(difference, se)

# Example code to produce the expected measures together with the plot created ----
# by the subgroup routine for comparison against the observed differences. --------
# NOTE: The execution time increases as the number of subgroups increases. --------
test1<-subgroup(data=mydata)

# Expected measures produced by the subgroup routine that the user ---------------
# can manipulate to produce own graphics. ----------------------------------------
test1$overalldiff        # Overall difference between treatment groups.
test1$expectations       # Expectations of the ordered treatment differences.
```

```
test1$rangedensity[1:15,] # Sample of the probability density of the range.
test1$favourcontrol   # Prob dist of subgroups favouring the control treatment.

# Example code for evaluation of chance heterogeneity at the design stage. --------
test2<-subgroup(data=mydata, design=TRUE)

# Example code for simulation based evaluation of chance heterogeneity. ----------
test3<-subgroup(data=mydata, force.simulation=TRUE)
```

Index