

# Package ‘subscreen’

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**Type** Package

**Title** Systematic Screening of Study Data for Subgroup Effects

**Version** 3.0.7

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**Description** Identifying outcome relevant subgroups has now become as simple as possible! The formerly lengthy and tedious search for the needle in a haystack will be replaced by a single, comprehensive and coherent presentation.

The central result of a subgroup screening is a diagram in which each single dot stands for a subgroup.

The diagram may show thousands of them. The position of the dot in the diagram is determined by the

sample size of the subgroup and the statistical measure of the treatment effect in that subgroup. The

sample size is shown on the horizontal axis while the treatment effect is displayed on the vertical axis. Furthermore,

the diagram shows the line of no effect and the overall study results. For small subgroups, which are found on the left side of the plot, larger random deviations from the mean study effect are expected,

while for larger subgroups only small deviations from the study mean can be expected to be chance findings.

So for a study with no conspicuous subgroup effects, the dots in the figure are expected to form a kind of funnel. Any deviations from this funnel shape hint to conspicuous subgroups.

This approach was presented in Muysers (2020) <[doi:10.1007/s43441-019-00082-6](https://doi.org/10.1007/s43441-019-00082-6)> and referenced in Ballarini (2020) <[doi:10.1002/pst.2012](https://doi.org/10.1002/pst.2012)>.

New to version 3 is the Automatic Screening of one- or Multi-factorial Subgroups (ASMUS) for documentation of the structured review of subgroup findings.

**License** GPL-3

**Encoding** UTF-8

**Imports** utils, plyr, data.table, grDevices, graphics, shiny, DT, stats, shinyjs, bsplus, jsonlite, colourpicker, dplyr, ranger, purrr, shinyWidgets

**Suggests** parallel, survival, knitr, rmarkdown

**NeedsCompilation** no**RoxygenNote** 7.1.2**VignetteBuilder** knitr**Repository** CRAN**Date/Publication** 2022-05-12 22:00:03 UTC

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subscreenalc	<i>(i) Calculation of the results for the subgroups</i>
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## Description

This function systematically calculates the defined outcome for every combination of subgroups up to the given level (`max_comb`), i.e. the number of maximum combinations of subgroup defining factors. If, e.g., in a study sex, age group ( $\leq 60$ ,  $> 60$ ), BMI group ( $\leq 25$ ,  $> 25$ ) are of interest, subgroups of level 2 would be, e.g. male subjects with BMI  $> 25$  or young females, while subgroups of level 3 would be any combination of all three variables.

## Usage

```
subscreenalc(
  data,
  eval_function,
  endpoints,
  treat = "trtp",
  subjectid = "subjid",
  factors = NULL,
  min_comb = 1,
  max_comb = 3,
  nkernel = 1,
  par_functions = "",
  verbose = TRUE,
  factorial = FALSE,
  use_complement = FALSE
)
```

**Arguments**

<code>data</code>	dataframe with study data
<code>eval_function</code>	name of the function for data analysis
<code>endpoints</code>	vector containing the names of the endpoint variables in data
<code>treat</code>	name of variable in data that contains the treatment identifier, defaults to <code>trtp</code>
<code>subjectid</code>	name of variable in data that contains the subject identifier, defaults to <code>subjid</code>
<code>factors</code>	vector containing the names of variables that define the subgroups, defaults to <code>NULL</code> . If set to <code>NULL</code> , all variables in data are used that are not included in <code>subjectid</code> , <code>treat</code> , and <code>endpoints</code>
<code>min_comb</code>	minimum number of factor combination levels to define subgroups, defaults to 1
<code>max_comb</code>	maximum number of factor combination levels to define subgroups, defaults to 3
<code>nkernel</code>	number of kernels for parallelization (defaults to 1)
<code>par_functions</code>	vector of names of functions used in <code>eval_function</code> to be exported to cluster (needed only if <code>nkernel &gt; 1</code> )
<code>verbose</code>	switch on/off output of computational information
<code>factorial</code>	switch on/off calculation of factorial contexts
<code>use_complement</code>	switch on/off calculation of complement subgroups

**Details**

The evaluation function (`eval_function`) has to be defined by the user. The result needs to be a vector of numerical values, e.g., outcome variable(s) and number of observations/subjects. The input of `eval_function` is a data frame with the same structure as the input data frame (`data`) used in the `subscreencalc` call. See example below. Potential errors occurring due to small subgroups should be caught and handled within `eval_function`. As the `eval_function` will be called with every subgroup it may happen that there is only one observation or only one treatment arm or only observations with missing data going into the `eval_function`. There should always be a valid result vector returned (NAs allowed) and no error causing program abort. For a better display the results may be cut-off to a reasonable range. For example: If my endpoint is a hazard ratio that is expected to be between 0.5 and 2 I would set all values smaller than 0.01 to 0.01 and values above 100 to 100.

**Value**

an object of type `SubScreenResult` of the form `list(sge=H, max_comb=max_comb, min_comb=min_comb, subjectid=subjectid, endpoints=endpoints, treat=treat, factors=factors, results_total=eval_function(cbind(F,T)))`

**Examples**

```
# get the pbc data from the survival package
require(survival)
data(pbc, package="survival")
# generate categorical versions of some of the baseline covariates
pbc$ageg[!is.na(pbc$age)] <-
```

```

  ifelse(pbc$age[!is.na(pbc$age)]      <= median(pbc$age,   na.rm=TRUE), "Low", "High")
pbc$albuming[!is.na(pbc$albumin)]<-
  ifelse(pbc$albumin[!is.na(pbc$albumin)] <= median(pbc$albumin, na.rm=TRUE), "Low", "High")
pbc$phosg[!is.na(pbc$alk.phos)] <-
  ifelse(pbc$alk.phos[!is.na(pbc$alk.phos)]<= median(pbc$alk.phos,na.rm=TRUE), "Low", "High")
pbc$astg[!is.na(pbc$ast)]      <-
  ifelse(pbc$ast[!is.na(pbc$ast)]      <= median(pbc$ast,   na.rm=TRUE), "Low", "High")
pbc$bilig[!is.na(pbc$bili)]    <-
  ifelse(pbc$bili[!is.na(pbc$bili)]    <= median(pbc$bili,   na.rm=TRUE), "Low", "High")
pbc$cholg[!is.na(pbc$chol)]    <-
  ifelse(pbc$chol[!is.na(pbc$chol)]    <= median(pbc$chol,   na.rm=TRUE), "Low", "High")
pbc$copperg[!is.na(pbc$copper)] <-
  ifelse(pbc$copper[!is.na(pbc$copper)] <= median(pbc$copper, na.rm=TRUE), "Low", "High")
pbc$ageg[is.na(pbc$age)]      <- "No Data"
pbc$albuming[is.na(pbc$albumin)] <- "No Data"
pbc$phosg[is.na(pbc$alk.phos)] <- "No Data"
pbc$astg[is.na(pbc$ast)]      <- "No Data"
pbc$bilig[is.na(pbc$bili)]    <- "No Data"
pbc$cholg[is.na(pbc$chol)]    <- "No Data"
pbc$copperg[is.na(pbc$copper)] <- "No Data"
#eliminate treatment NAs
pbcdat <- pbc[!is.na(pbc$strtr), ]
# PFS and OS endpoints
set.seed(2006)
pbcdat$'event.pfs' <- sample(c(0,1),dim(pbcdat)[1],replace=TRUE)
pbcdat$'timepfs' <- sample(1:5000,dim(pbcdat)[1],replace=TRUE)
pbcdat$'event.os' <- pbcdat$event
pbcdat$'timeos' <- pbcdat$time
#variable importance for OS for the created categorical variables
#(higher is more important, also works for numeric variables)
varnames <- c('ageg', 'sex', 'bilig', 'cholg', 'astg', 'albuming', 'phosg')
# define function the eval_function()
# Attention: The eval_function ALWAYS needs to return a dataframe with one row.
#           Include exception handling, like if(N1>0 && N2>0) hr <- exp(coxph(...))
#           to avoid program abort due to errors
hazardratio <- function(D) {

  HRpfs <- tryCatch(exp(coxph(Surv(D$timepfs, D$event.pfs) ~ D$strtr )$coefficients[[1]]),
    warning=function(w) {NA})
  HRpfs <- 1/HRpfs
  HR.pfs <- round(HRpfs, 2)
  HR.pfs[HR.pfs > 10] <- 10
  HR.pfs[HR.pfs < 0.00001] <- 0.00001
  HRos <- tryCatch(exp(coxph(Surv(D$timeos, D$event.os) ~ D$strtr )$coefficients[[1]]),
    warning=function(w) {NA})
  HRos <- 1/HRos
  HR.os <- round(HRos, 2)
  HR.os[HR.os > 10] <- 10
  HR.os[HR.os < 0.00001] <- 0.00001
  data.frame( HR.pfs, HR.os#, N.of.subjects,N1 ,N2
  )
}

```

```

# run subscreen

## Not run:
results <- subscreencalc(data=pbcdat,
                        eval_function=hazardratio,
                        endpoints = c("timepfs" , "event.pfs", "timeos", "event.os"),
                        treat="trt",
                        subjectid = "id",
                        factors=c("ageg", "sex", "bilig", "cholg", "copperg"),
                        use_complement = FALSE,
                        factorial = FALSE)

# visualize the results of the subgroup screening with a Shiny app
subscreenshow(results)
## End(Not run)

```

---

subscreenshow

*(ii) Visualization*


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## Description

Start the Shiny based interactive visualization tool to show the subgroup results generated by subscreencalc. See and explore all subgroup results at one glance. Pick and chose a specific subgroup, the level of combinations or a certain factor with its combinations. Switch easily between different endpoint/target variables.

## Usage

```

subscreenshow(
  sresults,
  variable_importance = NULL,
  host = NULL,
  port = NULL,
  NiceNumbers = c(1, 1.5, 2, 4, 5, 6, 8, 10)
)

```

## Arguments

sresults	SubScreenResult object with results from a subscreencalc call
variable_importance	add description
host	host name or IP address for Shiny display
port	port number for Shiny display
NiceNumbers	list of numbers used for a 'nice' scale

subscreenvi

*(iii) Determine variable importance***Description**

Determine variable importance for continuous, categorical or right-censored survival endpoints (overall and per treatment group) using random forests

**Usage**

```
subscreenvi(data, y, cens = NULL, x = NULL, trt = NULL, ...)
```

**Arguments**

<code>data</code>	The data frame containing the dependent and independent variables.
<code>y</code>	The name of the column in <code>data</code> that contains the dependent variable.
<code>cens</code>	The name of the column in <code>data</code> that contains the censoring variable, if <code>y</code> is an event time (default=NULL).
<code>x</code>	Vector that contains the names of the columns in <code>data</code> with the independent variables (default=NULL, i.e. all remaining variables)
<code>trt</code>	The name of the column in <code>data</code> that contains the treatment variable (default=NULL).
<code>...</code>	additional arguments to be passed to function <code>rfsrc</code>

**Value**

A list containing ordered data frames with the variable importances (one for each treatment level, one with the ranking variability between the treatment levels and one with the total results)

**Examples**

```
## Not run:
require(survival)
data(pbc, package="survival")
# generate categorical versions of some of the baseline covariates
pbc$ageg[!is.na(pbc$age)] <-
  ifelse(pbc$age[!is.na(pbc$age)] <= median(pbc$age, na.rm=TRUE), "Low", "High")
pbc$albuming[!is.na(pbc$albumin)] <-
  ifelse(pbc$albumin[!is.na(pbc$albumin)] <= median(pbc$albumin, na.rm=TRUE), "Low", "High")
pbc$phosg[!is.na(pbc$alk.phos)] <-
  ifelse(pbc$alk.phos[!is.na(pbc$alk.phos)] <= median(pbc$alk.phos, na.rm=TRUE), "Low", "High")
pbc$astg[!is.na(pbc$ast)] <-
  ifelse(pbc$ast[!is.na(pbc$ast)] <= median(pbc$ast, na.rm=TRUE), "Low", "High")
pbc$bilig[!is.na(pbc$bili)] <-
  ifelse(pbc$bili[!is.na(pbc$bili)] <= median(pbc$bili, na.rm=TRUE), "Low", "High")
pbc$cholg[!is.na(pbc$chol)] <-
  ifelse(pbc$chol[!is.na(pbc$chol)] <= median(pbc$chol, na.rm=TRUE), "Low", "High")
pbc$copperg[!is.na(pbc$copper)] <-
```

```
  ifelse(pbc$copper[!is.na(pbc$copper)] <= median(pbc$copper, na.rm=TRUE), "Low", "High")
pbc$ageg[is.na(pbc$age)] <- "No Data"
pbc$albuming[is.na(pbc$albumin)] <- "No Data"
pbc$phosg[is.na(pbc$alk.phos)] <- "No Data"
pbc$astg[is.na(pbc$ast)] <- "No Data"
pbc$bilig[is.na(pbc$bili)] <- "No Data"
pbc$cholg[is.na(pbc$chol)] <- "No Data"
pbc$copperg[is.na(pbc$copper)] <- "No Data"
#eliminate treatment NAs
pbcdat <- pbc[!is.na(pbc$trt), ]
pbcdat$status <- ifelse(pbcdat$status==0,0,1)
importance <- subscreenvi(data=pbcdat, y='time', cens='status',
  trt='trt', x=c("ageg", "sex", "bilig", "cholg", "copperg"))

## End(Not run)
```

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