Package ‘BiostatsUHNplus’

December 4, 2023

Title Nested Data Summary and Adverse Events

Version 0.0.9

Description Miscellaneous code snippets and functions with pipes and multiple package dependencies used for summarizing nested data and adverse events.

License MIT + file LICENSE

Depends R (>= 4.2)

Imports afex, coda, cowplot, dplyr, forcats, ggh4x, ggplot2, ggstance, lifecycle, MCMCglmm, modeest, openxlsx, plyr, purrr, reportRmd, rlang, rstatix, stats, stringr, tibble, utils

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Collate 'data.R' 'globals.R' 'as_numeric_parse.R' 'covsum_nested.R'
'dsmb_ccru.R' 'nice_mcmcglm.R' 'nice_mcmcglm_icc.R'
'ae_timeline_plot.R' 'caterpillar_plot.R'

NeedsCompilation no

Author Lisa Avery [aut] (<https://orcid.org/0000-0002-8431-5143>), Zeynep Baskurt [aut], Osvaldo Espin-Garcia [aut], Katrina Hueniken [aut], Katherine Lajkosz [aut] (<https://orcid.org/0000-0003-3760-5401>), Xuan Li [aut], Tyler Pittman [cre, aut] (<https://orcid.org/0000-0002-5013-6980>), Anna Santiago [aut] (<https://orcid.org/0000-0002-0932-2386>), Jessica Weiss [aut], Wei Xu [aut]

Maintainer Tyler Pittman <tyler.pittman@uhn.ca>

Repository CRAN

Date/Publication 2023-12-04 14:50:02 UTC
R topics documented:

ae ................................................................. 2
ae_timeline_plot ........................................... 3
as_numeric_parse .................................. 5
caterpillar_plot ...................................... 6
covsum_nested ................................ 8
demography ........................................ 10
drug1_admin .................................... 10
drug2_admin .................................... 11
dsmc_ccru ....................................... 11
enrollment ...................................... 13
ineligibility ..................................... 14
nice_mcmcglmm .................................. 14
nice_mcmcglmm_icc ................................ 15
rm_covsum_nested ...................................... 16

Index 20

---

ae Simulated adverse events for patients receiving two study agents.

Description

Simulated adverse events for patients receiving two study agents.

Usage

ae

Format

A data frame with 394 rows and 9 variables:

Subject  Patient ID

ae_detail  Adverse event detail, also known as lowest level term

ae_category  Adverse event category, also known as system organ class

CTCAE5_LLT_NM  Common Terminology Criteria for Adverse Events (CTCAE) version 5

AE_VERBATIM_TRM_TXT  Adverse event verbatim text entered by clinical registered nurse, for "Other, specify"

AE_SEV_GD  Adverse event severity grade, scale from 1 to 5

AE_ONSET_DT_INT  Adverse event onset date

CTC_AE_ATTR_SCALE  Attribution scale of adverse event to first study agent

CTC_AE_ATTR_SCALE_1  Attribution scale of adverse event to second study agent
Description

Outputs related adverse event timeline plots including just system organ class (AE category), or system organ class and lowest level term (AE detail). This function can fit up to 5 different attributions. Modify width, height and scale parameters in ggsave() to customize fit for large plot.

Usage

```r
ae_timeline_plot(
  subjID,
  subjID_ineligText = NULL,
  baseline_datasets,
  ae_dataset,
  ae_attribVars,
  ae_attribVarsName = NULL,
  ae_attribVarText = NULL,
  startDtVars,
  ae_detailVar,
  ae_categoryVar,
  ae_severityVar,
  ae_onsetDtVar,
  time_unit = c("day", "week", "month", "year"),
  include_ae_detail = TRUE,
  legendPerSpace = NULL,
  fonts = NULL,
  fontColours = NULL,
  panelColours = NULL,
  attribColours = NULL,
  attribSymbols = NULL,
  columnWidths = NULL
)
```

Arguments

- `subjID` key identifier field for participant ID in data sets
- `subjID_ineligText` character text that denotes participant IDs to exclude, for example, c("New Subject") (if provided)
baseline_datasets
list of data frames that contain baseline participant characteristics, for example,
list(enrollment_DF,demography_DF,ineligibility_DF)

ae_dataset
data frame that contains subject AEs

ae_attribVars
field(s) that denotes attribution to intervention under study, for example, c("CTC_AE_ATTR_SCALE","CTC_AE_ATTR_SCALE_1")
(if provided)

ae_attribVarsName
character text that denotes name of interventions under study, for example, c("Drug 1","Drug 2") (if provided)

ae_attribVarText
character text that denotes related attribution, for example c("Definite","Probable","Possible")
(if provided)

startDtVars
field(s) that denotes participant start date (i.e. 10MAY2021). For example, it could be enrollment date or screening date. If more than one field given (unique names are required), each field is assumed to be specific start date for attribution in corresponding field order

ae_detailVar
field that denotes participant AE detail (lowest level term)

ae_categoryVar
field that denotes participant AE category (system organ class)

ae_severityVar
field that denotes participant AE severity grade (numeric)

ae_onsetDtVar
field that denotes participant AE onset date

time_unit
character text that denotes time unit for desired timeline, for example, could be one of c("day","week","month","year")
(if provided)

include_ae_detail
boolean that denotes if AE detail should be included in timeline plot. Default is True

legendPerSpace
parameter that denotes proportion of vertical image space dedicated to legend at bottom. Default is 0.05 for AE detail and 0.1 for AE Category

fonts
character text that denotes font for AE category, AE detail, axis, legend and plot labels (if provided)

fontColours
character text that denotes system font colours for AE category and AE detail (if provided)

panelColours
character text that denotes panel background colours for AE category, AE detail and plot area (if provided)

attribColours
character text that denotes colours for attributions, supports up to 10 distinct colours (if provided)

attribSymbols
text that denotes median plot symbols for attributions, supports up to 10 distinct symbols (if provided)

columnWidths
text that denotes character columns widths for AE category and AE detail columns (if provided)

Value
ggplot object of AE timeline plot
Examples

data("drug1_admin", "drug2_admin", "ae");
p <- ae_timeline_plot(subjID="Subject", subjID_ineligText=c("01","11"),
baseline_datasets=list(drug1_admin, drug2_admin),
ae_dataset=ae,
ae_attribVars=c("CTC_AE_ATTR_SCALE","CTC_AE_ATTR_SCALE_1"),
ae_attribVarsName=c("Drug 1","Drug 2"),
ae_attribVarText=c("Definite", "Probable", "Possible"),
startDtVars=c("TX1_DATE_INT","TX2_DATE_INT"),
ae_detailVar="ae_detail",
ae_categoryVar="ae_category",ae_severityVar="AE_SEV_GD",
ae_onsetDtVar="AE_ONSET_DT_INT",time_unit="month",
include_ae_detail=FALSE,
fonts=c("Calibri","Albany AMT","Gadugi","French Script MT","Forte"),
fontColours=c("#FFE135"),
panelColours=c("#E52B50",NA,"#FFE4C4"),
attribColours=c("#9AB973","#01796F","#FFA343","#CC7722"),
attribSymbols=c(7,8,5,6),
columnWidths=c(23))

as_numeric_parse
Modification of the as.numeric function that prints entries that fail to
parse as a message

Description

Modification of the as.numeric function that prints entries that fail to parse as a message

Usage

as_numeric_parse(x)

Arguments

x string or vector to coerce to numeric

Value

No return value, called for side effects

Examples

z <- as_numeric_parse(c(1:5, "String1", 6:10,"String2"))
z
caterpillar_plot  

Caterpillar plot. Useful for plotting random effects from hierarchical models, such as MCMCglmm::MCMCglmm() object, that have binary outcome.

Description

Caterpillar plot. Useful for plotting random effects from hierarchical models, such as MCMCglmm::MCMCglmm() object, that have binary outcome.

Usage

caterpillar_plot(
  subjID,
  remove.text.subjID = FALSE,
  mcmcglmm_object,
  orig_dataset,
  binaryOutcomeVar,
  prob = NULL,
  title = NULL,
  no.title = FALSE,
  subtitle = NULL,
  ncol = NULL,
  fonts = NULL,
  columnTextWidth = NULL,
  break.label.summary = FALSE
)

Arguments

subjID  key identifier field for participant ID in data sets
remove.text.subjID  boolean indicating if non-numeric text should be removed from subjID in plot label. Note that this can only be used if there are non-duplicate participant IDs when non-numeric text is removed. Default is FALSE (if provided)
mcmcglmm_object  MCMCglmm model output
orig_dataset  data frame supplied to MCMCglmm function
binaryOutcomeVar  name of binary variable (0,1) that denotes outcome in MCMCglmm model
prob  probability for highest posterior density interval, similar to a confidence interval. Default is 0.95 (if provided)
title  title of the plot. Overrides default title (if provided)
no.title  boolean that denotes if title should be outputted in plot. Default is TRUE (if provided)
caterpillar_plot

subtitle
subtitle of the plot. Overrides default subtitle (if provided)

ncol
number of columns in plot. Default is 2 (if provided)

fonts
character text that denotes font for title, subtitle, category labels, x-axis plot
labels (if provided)

columnTextWidth
numeric that denotes character width for label text before breaking to start new
line. Default is 20 characters (if provided)

break.label.summary
boolean to indicate if new line should start in label before (n, event) summary.
Default is FALSE

Value
ggplot object of caterpillar plot

Examples
data("ae");

ae$G3Plus <- 0;
ae$G3Plus[ae$AE_SEV_GD %in% c("3", "4", "5")] <- 1;

ae$Drug_1_Attribution <- 0;

ae$Drug_1_Attribution[ae$CTC_AE_ATTR_SCALE %in% c("Definite", "Probable", "Possible")]
<- 1;

ae$Drug_2_Attribution <- 0;

ae$Drug_2_Attribution[ae$CTC_AE_ATTR_SCALE_1 %in% c("Definite", "Probable", "Possible")]
<- 1;

prior2RE <- list(R = list(V = diag(1), fix = 1),
G=list(G1=list(V=1, nu=0.02), G2=list(V=1, nu=0.02)));

model1 <- MCMCglmm::MCMCglmm(G3Plus ~ Drug_1_Attribution + Drug_2_Attribution,
random=Subject + ae_category, family="categorical", data=ae, saveX=TRUE,
verbose=FALSE, burnin=2000, nitt=10000, thin=10, pr=TRUE, prior=prior2RE);

p <- caterpillar_plot(subjID = "Subject",
mcmcglmm_object = model1,
prob = 0.99,
orig_dataset = ae,
binaryOutcomeVar = "G3Plus")

p <- caterpillar_plot(subjID = "ae_category",
mcmcglmm_object = model1,
prob = 0.95,
orig_dataset = ae,
remove.text.subjID = FALSE,
ncol = 4,
binaryOutcomeVar = "G3Plus",
subtitle = "System organ class (n, event)",
title = "Odds Ratio for G3+ Severity with 95% Highest Posterior Density Interval",
fonts = c("Arial", "Arial", "Arial", "Arial"),
break.label.summary = TRUE)
Description

Nested version of reportRmd covsum()

Usage

covsum_nested(
data,
covs,
maincov = NULL,
id = NULL,
digits = 1,
umobs = NULL,
markup = TRUE,
sanitize = TRUE,
nicenames = TRUE,
IQR = FALSE,
all.stats = FALSE,
pvalue = TRUE,
effSize = TRUE,
show.tests = TRUE,
nCores = NULL,
nested.test = NULL,
nsim = NULL,
excludeLevels = NULL,
dropLevels = TRUE,
full = TRUE,
digits.cat = 0,
testcont = c("rank-sum test", "ANOVA"),
testcat = c("Chi-squared", "Fisher"),
include_missing = FALSE,
percentage = c("column", "row")
)

Arguments

data       dataframe containing data

covs       character vector with the names of columns to include in table

maincov    covariate to stratify table by

id         covariates to nest summary by

digits     number of digits for summarizing mean data, does not affect p-values

numobs     named list overriding the number of people you expect to have the covariate
markup  boolean indicating if you want latex markup
sanitize  boolean indicating if you want to sanitize all strings to not break LaTeX
nicenames  boolean indicating if you want to replace . and _ in strings with a space
IQR  boolean indicating if you want to display the inter quantile range (Q1,Q3) as opposed to (min,max) in the summary for continuous variables
all.stats  boolean indicating if all summary statistics (Q1,Q3 + min,max on a separate line) should be displayed. Overrides IQR.
pvalue  boolean indicating if you want p-values included in the table
effSize  boolean indicating if you want effect sizes included in the table. Can only be obtained if pvalue is also requested.
show.tests  boolean indicating if the type of statistical used should be shown in a column beside the p-values. Ignored if pvalue=FALSE.
nCores  if > 1, specifies number of cores to use for parallel processing for calculating the nested p-value (default: 1).
nested.test  specifies test used for calculating nested p-value from afex::mixed function. Either parametric bootstrap method or likelihood ratio test method (default: "LRT"). Parametric bootstrap takes longer.
nsim  specifies number of simulations to use for calculating nested p-value with parametric bootstrap method used for nested.test (default: 1000).
excludeLevels  a named list of covariate levels to exclude from statistical tests in the form list(varname =c('level1','level2')). These levels will be excluded from association tests, but not the table. This can be useful for levels where there is a logical skip (i.e. not missing, but not presented). Ignored if pvalue=FALSE.
dropLevels  logical, indicating if empty factor levels be dropped from the output, default is TRUE.
full  boolean indicating if you want the full sample included in the table, ignored if maincov is NULL
digits.cat  number of digits for the proportions when summarizing categorical data (default: 0)
testcont  test of choice for continuous variables, one of rank-sum (default) or ANOVA
testcat  test of choice for categorical variables, one of Chi-squared (default) or Fisher
include_missing  Option to include NA values of maincov. NAs will not be included in statistical tests
percentage  choice of how percentages are presented, one of column (default) or row

See Also
fisher.test, chisq.test, wilcox.test, kruskal.test, anova and mixed
**demography**

*Simulated demography for patients.*

**Description**

Simulated demography for patients.

**Usage**

demography

**Format**

A data frame with 12 rows and 2 variables:

- **Subject**  Patient ID
- **GENDER_CODE**  Patient gender

---

**drug1_admin**

*Simulated study agent 1 for patients.*

**Description**

Simulated study agent 1 for patients.

**Usage**

drug1_admin

**Format**

A data frame with 12 rows and 2 variables:

- **Subject**  Patient ID
- **TX1_DATE_INT**  Study agent 1 start date of patient on study
**drug2_admin**

*Simulated study agent 2 for patients.*

**Description**

Simulated study agent 2 for patients.

**Usage**

```
drug2_admin
```

**Format**

A data frame with 12 rows and 2 variables:

- **Subject** Patient ID
- **TX2_DATE_INT** Study agent 2 start date of patient on study

**dsmb_ccru**

*Outputs the three DSMB-CCRU AE summary tables in Excel format per UHN template*

**Description**

Outputs the three DSMB-CCRU AE summary tables in Excel format per UHN template

**Usage**

```
dsmb_ccru(
    protocol,
    setwd,
    title,
    comp = NULL,
    pi,
    presDate,
    cutDate,
    boundDate = NULL,
    subjID,
    subjID_ineligText = NULL,
    baseline_datasets,
    ae_dataset,
    ineligibleVar,
    ineligibleVarText = NULL,
    genderVar,
    enrolDtVar,
)```
ae_detailVar,
ae_categoryVar,
ae_severityVar,
ae_onsetDtVar,
ae_detailOtherText = NULL,
ae_detailOtherVar = NULL,
ae_verbatimVar = NULL,
numSubj = NULL,
fileNameUnderscore = TRUE
}

Arguments

protocol  study protocol name (uppercase, no spaces permitted)
setwd  directory to write Excel summary files to
title  full character vector with name of study
comp  baseline comparison group, for example, cohort (if provided)
pi  character vector name of study principal investigator
presDate  presentation date (i.e. 17NOV2023) for DSMB
cutDate  recent cutoff date for AEs (i.e. 31AUG2023)
boundDate  lower bound cutoff date for AEs (if provided)
subjID  key identifier field for participant ID in data sets
subjID_ineligText  character text that denotes participant IDs to exclude, for example, c("New Subject") (if provided)
baseline_datasets  list of data frames that contain baseline participant characteristics, for example, list(enrollment_DF,demography_DF,ineligibility_DF)
ae_dataset  data frame that contains subject AEs
ineligVar  field that denotes participant ineligibility
ineligVarText  character text that denotes participant ineligibility, for example, c("Yes", "Y") (if provided)
genderVar  field that denotes participant gender
enrolDtVar  field that denotes participant enrollment date (i.e. 10MAY2021)
ae_detailVar  field that denotes participant AE detail (lowest level term)
ae_categoryVar  field that denotes participant AE category (system organ class)
ae_severityVar  field that denotes participant AE severity grade (numeric)
ae_onsetDtVar  field that denotes participant AE onset date
ae_detailOtherText  character text that denotes referencing verbatim AE field, for example, c("Other, specify", "OTHER") (if provided)
ae_detailOtherVar  field that denotes participant AE detail other (if provided)
ae_verbatimVar field that denotes participant AE detail verbatim (if provided)
numSubj vector to override value for number of participants in summary (if provided)
fileNameUnderscore boolean that denotes if spaces should be underscore in filename

Value
three Excel files containing DSMB-CCRU AE summary tables

Examples

data("enrollment", "demography", "ineligibility", "ae");
dsmb_ccru(protocol="EXAMPLE_STUDY", setwd="./man/tables/",
title="Phase X Study to Evaluate Treatments A-D",
comp="COHORT", pi="Dr. Principal Investigator",
presDate="30OCT2020", cutDate="31AUG2020",
boundDate=NULL, subjID="Subject", subjID_ineligText=c("New Subject","Test"),
baseline_datasets=list(enrollment, demography, ineligible),
ae_dataset=ae, ineligibleVar="INELIGIBILITY_STATUS", ineligibleVarText=c("Yes","Y"),
genderVar="GENDER_CODE", enrolDtVar="ENROL_DATE_INT", ae_detailVar="ae_detail",
ae_categoryVar="ae_category", ae_severityVar="AE_SEV_GD",
ae_onsetDtVar="AE_ONSET_DT_INT", ae_detailOtherText="Other, specify",
ae_detailOtherVar="CTCAE5_LLT_NM", ae_verbatimVar="AE_VERBATIM_TRM_TXT",
numSubj=c(2,4,5,6))

<table>
<thead>
<tr>
<th>enrollment</th>
<th>Enrollment data Simulated enrollment for patients.</th>
</tr>
</thead>
</table>

Description
Enrollment data
Simulated enrollment for patients.

Usage
enrollment

Format
A data frame with 12 rows and 3 variables:

- **Subject**: Patient ID
- **COHORT**: Study cohort for patient
- **ENROL_DATE_INT**: Enrollment date of patient to study
### ineligibility

*Simulated ineligibility for patients.*

**Description**

Simulated ineligibility for patients.

**Usage**

ineligibility

**Format**

A data frame with 11 rows and 2 variables:

- **Subject** Patient ID
- **INELIGIBILITY_STATUS** Recorded ineligibility status of patient to study

### nice_mcmcglmm

*Nice table of model output from MCMCglmm::MCMCglmm()*

**Description**

Nice table of model output from MCMCglmm::MCMCglmm()

**Usage**

nice_mcmcglmm(mcmcglmm_object, dataset)

**Arguments**

- `mcmcglmm_object` returned output from MCMCglmm()
- `dataset` dataframe containing data

**Value**

grouped_df
### Examples

```r
## Not run:
data(ae)

ae$AE_SEV_GD <- as.numeric(ae$AE_SEV_GD);
ae$Drug_1_Attribution <- "No";
ae$Drug_1_Attribution[ae$CTC_AE_ATTR_SCALE %in% c("Definite", "Probable", "Possible")]
  <- "Yes";
ae$Drug_1_Attribution <- as.factor(ae$Drug_1_Attribution);
ae$Drug_2_Attribution <- "No";
ae$Drug_2_Attribution[ae$CTC_AE_ATTR_SCALE_1 %in% c("Definite", "Probable", "Possible")]
  <- "Yes";
ae$Drug_2_Attribution <- as.factor(ae$Drug_2_Attribution);

prior2RE <- list(R = list(V = diag(1), fix = 1),
  G=list(G1=list(V=1, nu=0.02),
    G2=list(V=1, nu=0.02)));

model1 <- MCMCglmm::MCMCglmm(Drug_1_Attribution ~ AE_SEV_GD + Drug_2_Attribution,
  random=~ae_detail + Subject, family="categorical", data=ae, saveX=TRUE,
  verbose=FALSE, burnin=2000, nitt=10000, thin=10, pr=TRUE, prior=prior2RE);
mcmcglmm_mva <- nice_mcmcglmm(model1, ae);

## End(Not run)
```

---

nice_mcmcglmm_icc

Nice table of intraclass correlation coefficients from MCMCglmm::MCMCglmm() model output

---

### Description

Nice table of intraclass correlation coefficients from MCMCglmm::MCMCglmm() model output

### Usage

```r
nice_mcmcglmm_icc(mcmcglmm_object, prob = NULL, decimals = NULL)
```

### Arguments

- `mcmcglmm_object`: returned output from MCMCglmm()
- `prob`: probability for highest posterior density interval, similar to a confidence interval. Default is 0.95 (if provided)
- `decimals`: number of decimal places to use in estimates

### Value

- `grouped_df`
Examples

```r
## Not run:
data(ae)
ae$AE_SEV_GD <- as.numeric(ae$AE_SEV_GD);
ae$Drug_1_Attribution <- 0;
ae$Drug_1_Attribution[ae$CTC_AE_ATTR_SCALE %in% c("Definite", "Probable", "Possible")]<- 1;
ae$Drug_2_Attribution <- 0;
ae$Drug_2_Attribution[ae$CTC_AE_ATTR_SCALE_1 %in% c("Definite", "Probable", "Possible")]<- 1;
prior2RE <- list(R = list(V = diag(1), fix = 1), G=list(G1=list(V=1, nu=0.02),
G2=list(V=1, nu=0.02)));
model1 <- MCMCglmm::MCMCglmm(Drug_1_Attribution ~ AE_SEV_GD + Drug_2_Attribution,
random=~ae_detail + Subject, family="categorical", data=ae, saveX=TRUE,
verbose=FALSE, burnin=2000, nitt=10000, thin=10, pr=TRUE, prior=prior2RE);
mcmcglmm_icc <- nice_mcmcglmm_icc(model1);
## End(Not run)
```

rm_covsum_nested  Outputs a nested version of reportRmd::rm_covsum()

Description

Outputs a nested version of reportRmd::rm_covsum()

Usage

```r
rm_covsum_nested(
data, 
covs, 
maincov = NULL, 
id = NULL, 
caption = NULL, 
tableOnly = FALSE, 
covTitle = "", 
digits = 1, 
digits.cat = 0, 
nicenames = TRUE, 
IQR = FALSE, 
all.stats = FALSE, 
pvalue = TRUE, 
effSize = TRUE, 
p.adjust = "none", 
unformattedp = FALSE, 
show.tests = TRUE, 
just.nested.pvalue = FALSE, 
nCores = NULL, 
nested.test = NULL, 
nsim = NULL,
```

## Not run:
testcont = c("rank-sum test", "ANOVA"),
testcat = c("Chi-squared", "Fisher"),
full = TRUE,
include_missing = FALSE,
percentage = c("column", "row"),
dropLevels = TRUE,
excludeLevels = NULL,
numobs = NULL,
markup = TRUE,
sanitize = TRUE,
chunk_label
)

**Arguments**

data: dataframe containing data
covs: character vector with the names of columns to include in table
maincov: covariate to stratify table by
id: covariates to nest summary by
caption: character containing table caption (default is no caption)
tableOnly: Logical, if TRUE then a dataframe is returned, otherwise a formatted printed object is returned (default).
covTitle: character with the names of the covariate (predictor) column. The default is to leave this empty for output or, for table only output to use the column name 'Covariate'.
digits: number of digits for summarizing mean data
digits.cat: number of digits for the proportions when summarizing categorical data (default: 0)
nicenames: boolean indicating if you want to replace . and _ in strings with a space
IQR: boolean indicating if you want to display the inter quantile range (Q1,Q3) as opposed to (min,max) in the summary for continuous variables
all.stats: boolean indicating if all summary statistics (Q1,Q3 + min,max on a separate line) should be displayed. Overrides IQR.
pvalue: boolean indicating if you want p-values included in the table
effSize: boolean indicating if you want effect sizes included in the table. Can only be obtained if pvalue is also requested.
p.adjust: p-adjustments to be performed
unformattedp: boolean indicating if you would like the p-value to be returned unformatted (ie not rounded or prefixed with '〈'). Best used with tableOnly = T and outTable function.
show.tests: boolean indicating if the type of statistical used should be shown in a column beside the p-values. Ignored if pvalue=FALSE.
just.nested.pvalue
boolean indicating if the just the nested p-value should be shown in a column, and not unnested p-value, unnested statistical tests and effect size. Overrides effSize and show.tests arguments.
nCores
number of cores to use for parallel processing if calculating the nested p-value (if provided).
nested.test
specifies test used for calculating nested p-value from afex::mixed function. Either parametric bootstrap method or likelihood ratio test method (default: "LRT"). Parametric bootstrap takes longer.
nsim
specifies number of simulations to use for calculating nested p-value with parametric bootstrap method used for nested.test (default: 1000).
testcont
test of choice for continuous variables, one of rank-sum (default) or ANOVA
testcat
test of choice for categorical variables, one of Chi-squared (default) or Fisher
full
boolean indicating if you want the full sample included in the table, ignored if maincov is NULL
include_missing
Option to include NA values of maincov. NAs will not be included in statistical tests
percentage
choice of how percentages are presented, one of column (default) or row
dropLevels
logical, indicating if empty factor levels be dropped from the output, default is TRUE.
excludeLevels
a named list of covariate levels to exclude from statistical tests in the form list(varname =c(‘level1’,’level2’)). These levels will be excluded from association tests, but not the table. This can be useful for levels where there is a logical skip (ie not missing, but not presented). Ignored if pvalue=FALSE.
numobs
named list overriding the number of people you expect to have the covariate
markup
boolean indicating if you want latex markup
sanitize
boolean indicating if you want to sanitize all strings to not break LaTeX
chunk_label
only used if output is to Word to allow cross-referencing

Value
A character vector of the table source code, unless tableOnly=TRUE in which case a data frame is returned

See Also
covsum,fisher.test,chisq.test,wilcox.test,kruskal.test,anova,mixed and outTable

Examples
## Not run:
# Example 1
data(ae)
rm_covsum_nested(data = ae, id = c("ae_detail", "Subject"), covs = c("AE_SEV_GD", "AE_ONSET_DT_INT"), maincov = "CTC_AE_ATTR_SCALE")
# Example 2: set variable labels and other options, save output with markup
data("ae")
lbls <- data.frame(c1=c("AE_SEV_GD","AE_ONSET_DT_INT"),
c2=c("Adverse event severity grade","Adverse event onset date"))
ae$AE_SEV_GD <- as.numeric(ae$AE_SEV_GD)
ae <- reportRmd::set_labels(ae, lbls)
output_tab <- rm_covsum_nested(data = ae, id = c("ae_detail", "Subject"),
covs = c("AE_SEV_GD", "AE_ONSET_DT_INT"), maincov = "CTC_AE_ATTR_SCALE",
testcat = "Fisher", percentage = c("col"), show.tests = FALSE, pvalue = TRUE,
effSize = FALSE, full = TRUE, IQR = FALSE, nicenames = TRUE, sanitize = TRUE,
markup = TRUE, include_missing = TRUE, just.nested.pvalue = TRUE,
tableOnly = TRUE)
cat(reportRmd::outTable(tab=output_tab))
cat(reportRmd::outTable(output_tab, format="html"), file = paste("./man/tables/",
"output_tab.html", sep=""))
cat(reportRmd::outTable(output_tab, format="latex"), file = paste("./man/tables/",
"output_tab.tex", sep=""))

## End(Not run)
Index

* as.numeric
  `as_numeric_parse`, 5
* dataframe
  `dsmb_ccru`, 11
  `nice_mcmcglmm`, 14
  `nice_mcmcglmm_icc`, 15
  `rm_covsum_nested`, 16
* datasets
  `ae`, 2
  `demography`, 10
  `drug1_admin`, 10
  `drug2_admin`, 11
  `enrollment`, 13
  `ineligibility`, 14
* plot
  `ae_timeline_plot`, 3
  `caterpillar_plot`, 6

  `ae`, 2
  `ae_timeline_plot`, 3
  `anova`, 9, 18
  `as_numeric_parse`, 5
  `caterpillar_plot`, 6
  `chisq.test`, 9, 18
  `covsum`, 18
  `covsum_nested`, 8
  `demography`, 10
  `drug1_admin`, 10
  `drug2_admin`, 11
  `dsmb_ccru`, 11
  `enrollment`, 13
  `fisher.test`, 9, 18
  `ineligibility`, 14
  `kruskal.test`, 9, 18
  `mixed`, 9, 18
  `nice_mcmcglmm`, 14
  `nice_mcmcglmm_icc`, 15
  `outTable`, 18
  `rm_covsum_nested`, 16
  `wilcox.test`, 9, 18