Package bengaltiger

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Title bengaltiger

Version 1.1.0

Description Streamlines data analysis and manuscript writing for medical research, primarily on the Towards Improved Trauma Care Outcomes (TITCO) in India cohort.

Depends R (>= 3.3.0)

Imports RMySQL,
rmarkdown,
DBI,
tableone,
knitr,
rowr

License LICENCE.md

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

R topics documented:

Add24HourInHospitalMortality

Add 24-hour in hospital mortality

Description

Adds the variable 24-hour in hospital mortality to the study sample

Usage

```
Add24HourInHospitalMortality(study.sample, from.date = "doar",
  from.time = "toar", to.date = "dodd", to.time = "todd",
  date.format = "%Y-%m-%d", time.format = "%H:%M",
  died.variable = "died", died.value = "Yes", levels = c("Yes",
  "No"), variable.name = "m24h", add.as.factor = TRUE,
  drop.used.variables = TRUE)
```

Arguments

study.sample   Data frame. The study sample. No default.

from.date   Character or POSIXt vector of length 1. The name of the variable with the date
                 from which to start counting. Defaults to "doar".

from.time   Character or POSIXt vector of length 1. The name of the variable with the time
                 from which to start counting. Defaults to "toar".

to.date	Character or POSIXt vector of length 1. The name of the variable with the date from which to start counting. Defaults to "dodd".
to.time	Character or POSIXt vector of length 1. The name of the variable with the time from which to start counting. Defaults to "todd".
date.format	Character vector of length 1. The date format. Defaults to "%Y-%m-%d".
time.format	Character vector of length 1. The date format. Defaults to "%H:%M".
died.variable	Character vector of length 1. The name of the variable indicating whether the patient was dead at the end of follow up. Defaults to "died".
died.value	Character vector of length 1. The value or level of the died variable that means that the patients died. Defaults to "Yes".
levels	Character vector of length 2. The levels to use to encode the resulting 24-hour in hospital mortality variable. The first item in the vector should be the level to be used to represent a death. Defaults to c("Yes", "No").
variable.name	Character vector of length 1. The name of the 24-hour in hospital mortality variable. Defaults to "m24h".
add.as.factor	Logical vector of length 1. If TRUE the 24-hour in hospital mortality variables is added to the study sample as a factor. If FALSE it is added as character. Defaults to TRUE.
drop.used.variables	
	Logical vector of length 1. If TRUE the date and time variables used to calculate 24-hour in hospital mortality is dropped from the sample. Defaults to TRUE.

Add30DayInHospitalMortality

Add 30-day in hospital mortality

Description

Adds the variable 30-day in hospital mortality to the study sample

Usage

```
Add30DayInHospitalMortality(study.sample, from.date = "doar",
  from.time = "toar", to.date = "dodd", to.time = "todd",
  date.format = "%Y-%m-%d", time.format = "%H:%M",
  died.variable = "died", died.value = "Yes", levels = c("Yes",
  "No"), variable.name = "m30d", add.as.factor = TRUE,
  drop.used.variables = TRUE)
```

Arguments

study.sample	Data frame. The study sample. No default.
from.date	Character or POSIXt vector of length 1. The name of the variable with the date from which to start counting. Defaults to "doar".
from.time	Character or POSIXt vector of length 1. The name of the variable with the time from which to start counting. Defaults to "toar".
to.date	Character or POSIXt vector of length 1. The name of the variable with the date from which to start counting. Defaults to "dodd".

to.time	Character or POSIXt vector of length 1. The name of the variable with the time from which to start counting. Defaults to "todd".
date.format	Character vector of length 1. The date format. Defaults to "%Y-%m-%d".
time.format	Character vector of length 1. The date format. Defaults to "%H:%M".
died.variable	Character vector of length 1. The name of the variable indicating whether the patient was dead at the end of follow up. Defaults to "died".
died.value	Character vector of length 1. The value or level of the died variable that means that the patients died. Defaults to "Yes".
levels	Character vector of length 2. The levels to use to encode the resulting 30-day in hospital mortality variable. The first item in the vector should be the level to be used to represent a death. Defaults to c("Yes", "No").
variable.name	Character vector of length 1. The name of the 30-day in hospital mortality variable. Defaults to "m30d".
add.as.factor	Logical vector of length 1. If TRUE the 30-day in hospital mortality variables is added to the study sample as a factor. If FALSE it is added as character. Defaults to TRUE.
drop.used.variables	
	Logical vector of length 1. If TRUE the date and time variables used to calculate 30-day in hospital mortality is dropped from the sample. Defaults to TRUE.

AddAISSeverityIndicator

Add AIS severity indicator

Description

Adds a variable to the data that indicates if a patient has an abbreviated injury scale (AIS) severity above or equal to a certain cutoff in a certain body region.

Usage

```
AddAISSeverityIndicator(study.sample,
  severity.variable.name = "head_and_neck", cutoff = 2,
  levels = c("Yes", "No"),
  variable.name = paste0(severity.variable.name, "geq", cutoff),
  add.as.factor = TRUE, drop.used.variables = FALSE)
```

Arguments

study.sample	Data frame. The study sample. No default.
severity.variable.name	
	Character vector of length 1. The name of the variable with AIS severity data. Defaults to "head_and_neck".
cutoff	Numeric vector of length 1. The AIS severity cutoff. Has to be between 1 and 6. Defaults to 2.
levels	Character vector of length 2. The levels to use to encode the resulting indicator variable. The first item in the vector should be the level to be used to indicate that the patient had an injury of the specified severity. Defaults to c("Yes", "No").

variable.name	Character vector of length 1. The name of the resulting variable. Defaults to paste0(severity.variable.name, "geq", cutoff), where geq refers to the Latex command greater than or equal to.
add.as.factor	Logical vector of length 1. If TRUE the indicator variable is added to the study sample as a factor. If FALSE it is added as character. Defaults to TRUE.
drop.used.variables	
	Logical vector of length 1. If TRUE variables used to calculate the variable is dropped from the sample. Defaults to FALSE.

AddSpecificInjuryVariable

Add specific injury variable

Description

Adds a new indicator variable to the study sample, defining what patients had the specific injury or injury pattern provided.

Usage

```
AddSpecificInjuryVariable(study.sample, injury.codes, variable.name,
  injury.variables = c("e_1_icd", "e_2_icd", "e_3_icd", "e_4_icd",
  "e_5_icd", "e_6_icd", "e_7_icd", "e_8_icd", "e_9_icd", "e_10_icd",
  "e_11_icd", "e_12_icd", "xray_1_icd", "xray_2_icd", "xray_3_icd",
  "xray_4_icd", "xray_5_icd", "xray_6_icd", "xray_7_icd", "xray_8_icd",
  "xray_9_icd", "xray_10_icd", "xray_11_icd", "fast_1_icd", "fast_2_icd",
  "fast_3_icd", "fast_4_icd", "fast_5_icd", "fast_6_icd", "fast_7_icd",
  "fast_8_icd", "fast_9_icd", "fast_10_icd", "fast_11_icd", "ct_1_icd",
  "ct_2_icd", "ct_3_icd", "ct_4_icd", "ct_5_icd",         "ct_6_icd",
  "ct_7_icd", "ct_8_icd", "ct_9_icd", "ct_10_icd", "ct_11_icd",
  "ct_12_icd", "ct_13_icd", "op_1_icd", "op_2_icd", "op_3_icd", "op_4_icd",
  "op_5_icd", "op_6_icd", "op_7_icd", "op_8_icd", "op_9_icd", "op_10_icd",
  "op_11_icd"), levels = c("Yes", "No"), add.as.factor = TRUE,
  drop.used.variables = FALSE)
```

Arguments

study.sample	Data frame. The study sample. No default.
injury.codes	Character vector. The patterns to be used to define the specific injury or injury pattern. If any of the codes is present in any of the variables listen in injury.variables an observation will be classified as having the injury. No default.
variable.name	Character vector of length 1. The name of the variable. No default.
injury.variables	
	Character vector. The names of the variables with injudy data. Defaults to c("e_1_icd", "e_2_icd", "e_3_icd", "e_4_icd", "e_5_icd", "e_6_icd", "e_7_icd", "e_8_icd", "e_9_icd", "e_10_icd", "e_11_icd", "e_12_icd", "xray_1_icd", "xray_2_icd", "xray_3_icd", "xray_4_icd", "xray_5_icd", "xray_6_icd", "xray_7_icd", "xray_8_icd", "xray_9_icd", "xray_10_icd", "xray_11_icd", "fast_1_icd", "fast_2_icd", "fast_3_icd", "fast_4_icd", "fast_5_icd", "fast_6_icd", "fast_7_icd", "fast_8_icd", "fast_9_icd", "fast_10_icd", "fast_11_icd", "ct_1_icd", "ct_2_icd", "ct_3_icd", "ct_4_icd",

> "ct_5_icd", "ct_6_icd", "ct_7_icd", "ct_8_icd", "ct_9_icd", "ct_10_icd", "ct_11_icd",
> "ct_12_icd", "ct_13_icd", "op_1_icd", "op_2_icd", "op_3_icd", "op_4_icd", "op_5_icd",
> "op_6_icd", "op_7_icd", "op_8_icd", "op_9_icd", "op_10_icd", "op_11_icd").

levels	Character vector of length 2. The levels to use to encode the resulting injury variable. The first item in the vector should be the level to be used to represent having the injury. Defaults to c("Yes", "No").
add.as.factor	Logical vector of length 1. If TRUE the variable is added to the study sample as a factor. If FALSE it is added as character. Defaults to TRUE.
drop.used.variables	
	Logical vector of length 1. If TRUE the injury variables used to calculate the injury variable are dropped from the sample. Defaults to FALSE.

AddTimeBetweenArrivalAndDishcarge

Add time between arrival and discharge

Description

Adds the variable time between arrival to and discharge from participating centre.

Usage

```
AddTimeBetweenArrivalAndDishcarge(study.sample, from.date = "doar",
  from.time = "toar", to.date = "dodd", to.time = "todd",
  date.format = "%Y-%m-%d", time.format = "%H:%M",
  units = "days", variable.name = "tadd", drop.used.variables = TRUE)
```

Arguments

study.sample	Data frame. The study sample. No default.
from.date	Character or POSIXt vector of length 1. The name of the variable with the date from which to start counting. Defaults to "doar".
from.time	Character or POSIXt vector of length 1. The name of the variable with the time from which to start counting. Defaults to "toar".
to.date	Character or POSIXt vector of length 1. The name of the variable with the date from which to start counting. Defaults to "dodd".
to.time	Character or POSIXt vector of length 1. The name of the variable with the time from which to start counting. Defaults to "todd".
date.format	Character vector of length 1. The date format. Defaults to "%Y-%m-%d".
time.format	Character vector of length 1. The date format. Defaults to "%H:%M".
units	Character vector of length 1. Should be one of "days", "hours", "minutes", or "seconds". Defaults to "days".
variable.name	Character vector of length 1. The name of the time between injury and arrival variable. Defaults to "tadd".
drop.used.variables	
	Logical vector of length 1. If TRUE the date and time variables used to calculate time between injury and arrival are dropped from the sample. Defaults to TRUE.

```
AddTimeBetweenInjuryAndArrival
```
Add time between injury and arrival

Description

Adds the variable time between injury and arrival to participating centre.

Usage

```
AddTimeBetweenInjuryAndArrival(study.sample, from.date = ”doi”,
  from.time = ”toi”, to.date = ”doar”, to.time = ”toar”,
  date.format = ”%Y-%m-%d”, time.format = ”%H:%M”,
  units = ”hours”, variable.name = ”tbia”,
  drop.used.variables = TRUE)
```

Arguments

study.sample	Data frame. The study sample. No default.
from.date	Character or POSIXt vector of length 1. The name of the variable with the date from which to start counting. Defaults to "doi".
from.time	Character or POSIXt vector of length 1. The name of the variable with the time from which to start counting. Defaults to "toi".
to.date	Character or POSIXt vector of length 1. The name of the variable with the date from which to start counting. Defaults to "doar".
to.time	Character or POSIXt vector of length 1. The name of the variable with the time from which to start counting. Defaults to "toar".
date.format	Character vector of length 1. The date format. Defaults to "%Y-%m-%d".
time.format	Character vector of length 1. The date format. Defaults to "%H:%M".
units	Character vector of length 1. Should be one of "days", "hours", "minutes", or "seconds". Defaults to "hours".
variable.name	Character vector of length 1. The name of the time between injury and arrival variable. Defaults to "tbia".
drop.used.variables	
	Logical vector of length 1. If TRUE the date and time variables used to calculate time between injury and arrival are dropped from the sample. Defaults to TRUE.

```
AddTimeToFirstVitals
```
Add time to first vitals

Description

Adds the variable time to first vitals, defined as the difference in time between arrival to participating centre and time when first set of vitals was recorded.

Usage

```
AddTimeToFirstVitals(study.sample, from.date = "doar",
  from.time = "toar", to.date = "dom_1", to.time = "tom_1",
  date.format = "%Y-%m-%d", time.format = "%H:%M",
  units = "hours", variable.name = "tt1v",
  drop.used.variables = TRUE)
```

Arguments

study.sample	Data frame. The study sample. No default.
from.date	Character or POSIXt vector of length 1. The name of the variable with the date from which to start counting. Defaults to "doar".
from.time	Character or POSIXt vector of length 1. The name of the variable with the time from which to start counting. Defaults to "toar".
to.date	Character or POSIXt vector of length 1. The name of the variable with the date from which to start counting. Defaults to "dom_1".
to.time	Character or POSIXt vector of length 1. The name of the variable with the time from which to start counting. Defaults to "tom_1".
date.format	Character vector of length 1. The date format. Defaults to "%Y-%m-%d".
time.format	Character vector of length 1. The date format. Defaults to "%H:%M".
units	Character vector of length 1. Should be one of "days", "hours", "minutes", or "seconds". Defaults to "hours".
variable.name	Character vector of length 1. The name of the time between injury and arrival variable. Defaults to "tt1v".
drop.used.variables	
	Logical vector of length 1. If TRUE the date and time variables used to calculate time between injury and arrival are dropped from the sample. Defaults to TRUE.

AddTraumaticBrainInjury

Add traumatic brain injury

Description

Adds a new indicator variable to the study sample, defining what patients had a traumatic brain injury (TBI).

Usage

```
AddTraumaticBrainInjury(study.sample, icd.codes = c("s02.0", "s02.1",
  "s02.7", "s02.8", "s02.9", "s04.0", "s04.1", "s04.2", "s04.3", "s04.4",
  "s04.5", "s04.6", "s04.7", "s04.8", "s04.9", "s06.0", "s06.1", "s06.2",
  "s06.3", "s06.4", "s06.5", "s06.6", "s06.7", "s06.8", "s06.9", "s07.0",
  "s07.1", "s07.8", "s07.9", "s09.7", "s09.8", "s09.9", "t02.0", "t04.0",
  "t06.0"), icd.variables = c("e_1_icd", "e_2_icd", "e_3_icd", "e_4_icd",
  "e_5_icd", "e_6_icd", "e_7_icd", "e_8_icd", "e_9_icd", "e_10_icd",
  "e_11_icd", "e_12_icd", "xray_1_icd", "xray_2_icd", "xray_3_icd",
  "xray_4_icd", "xray_5_icd", "xray_6_icd", "xray_7_icd", "xray_8_icd",
```

```
"xray_9_icd", "xray_10_icd", "xray_11_icd", "fast_1_icd", "fast_2_icd",
"fast_3_icd", "fast_4_icd", "fast_5_icd", "fast_6_icd", "fast_7_icd",
"fast_8_icd", "fast_9_icd", "fast_10_icd", "fast_11_icd", "ct_1_icd",
"ct_2_icd", "ct_3_icd", "ct_4_icd", "ct_5_icd",      "ct_6_icd",
"ct_7_icd", "ct_8_icd", "ct_9_icd", "ct_10_icd", "ct_11_icd",
"ct_12_icd", "ct_13_icd", "op_1_icd", "op_2_icd", "op_3_icd", "op_4_icd",
"op_5_icd", "op_6_icd", "op_7_icd", "op_8_icd", "op_9_icd", "op_10_icd",
"op_11_icd"), levels = c("Yes", "No"), variable.name = "tbi",
add.as.factor = TRUE, drop.used.variables = TRUE)
```

Arguments

study.sample	Data frame. The study sample. No default.
icd.codes	Character vector. The codes to be used to define a TBI. If any of the codes is present in any of the variables listen in icd.variables an observation will be classified as having a TBI. Defaults to c("s02.0", "s02.1", "s02.7", "s02.8", "s02.9", "s04.0", "s04.1", "s04.2", "s04.3", "s04.4", "s04.5", "s04.6", "s04.7", "s04.8", "s04.9", "s06.0", "s06.1", "s06.2", "s06.3", "s06.4", "s06.5", "s06.6", "s06.7", "s06.8", "s06.9", "s07.0", "s07.1", "s07.8", "s07.9", "s09.7", "s09.8", "s09.9", "t02.0", "t04.0", "t06.0").
icd.variables	Character vector. The names of the variables with international classification of disease (ICD) codes. Defaults to c("e_1_icd", "e_2_icd", "e_3_icd", "e_4_icd", "e_5_icd", "e_6_icd", "e_7_icd", "e_8_icd", "e_9_icd", "e_10_icd", "e_11_icd", "e_12_icd", "xray_1_icd", "xray_2_icd", "xray_3_icd", "xray_4_icd", "xray_5_icd", "xray_6_icd", "xray_7_icd", "xray_8_icd", "xray_9_icd", "xray_10_icd", "xray_11_icd", "fast_1_icd", "fast_2_icd", "fast_3_icd", "fast_4_icd", "fast_5_icd", "fast_6_icd", "fast_7_icd", "fast_8_icd", "fast_9_icd", "fast_10_icd", "fast_11_icd", "ct_1_icd", "ct_2_icd", "ct_3_icd", "ct_4_icd", "ct_5_icd", "ct_6_icd", "ct_7_icd", "ct_8_icd", "ct_9_icd", "ct_10_icd", "ct_11_icd", "ct_12_icd", "ct_13_icd", "op_1_icd", "op_2_icd", "op_3_icd", "op_4_icd", "op_5_icd", "op_6_icd", "op_7_icd", "op_8_icd", "op_9_icd", "op_10_icd", "op_11_icd").
levels	Character vector of length 2. The levels to use to encode the resulting TBI variable. The first item in the vector should be the level to be used to represent a TBI. Defaults to c("Yes", "No").
variable.name	Character vector of length 1. The name of the TBI. Defaults to "tbi".
add.as.factor	Logical vector of length 1. If TRUE the TBI is added to the study sample as a factor. If FALSE it is added as character. Defaults to TRUE.
drop.used.variables	
	Logical vector of length 1. If TRUE the ICD variables used to calculate TBI is dropped from the sample. Defaults to TRUE.

AddTriageRevisedTraumaScore

Add Triage Revised Trauma Score

Description

Add the Triage Revised Trauma Score to the sample

Usage

```
AddTriageRevisedTraumaScore(study.sample, gcs.name = "gcs_t_1",
  sbp.name = "sbp_1", rr.name = "rr_1", variable.name = "trts",
  drop.used.variables = FALSE)
```

Arguments

`study.sample`	Data frame. The study sample. No default.
`gcs.name`	Character vector of length 1. The name of the Glasgow coma scale variable. Defaults to "gcs_t_1".
`sbp.name`	Character vector of length 1. The name of the systolic blood pressure variable. Defaults to "sbp_1".
`rr.name`	Character vector of length 1. The name of the respiratory rate variable. Defaults to "rr_1".
`variable.name`	Character vector of length 1. The name of the triage revised trauma score variable. Defaults to "trts".
`drop.used.variables`	
	Logical vector of length 1. If TRUE the date and time variables used to calculate time between injury and arrival are dropped from the sample. Defaults to FALSE.

`AISVariables`	*AIS variables*

Description

Returns the names of all AIS variables in the TITCO dataset

Usage

```
AISVariables()
```

Examples

```
AISVariables()
```

`CompileResults`	*Compile results*

Description

Compiles the results saved to the results.Rds file and saves it to disk in the format of your choice.

Usage

```
CompileResults(file.format = "docx", delete.results.file = TRUE)
```

Arguments

file.format   Character vector of length 1. The file format in which to save the results. Must be one of "md", "pdf", or "docx". Defaults to "docx".

delete.results.file

     Logical vector of length 1. If TRUE the results.Rds file is deleted once its content has been compiled and saved. Defaults to TRUE.

CreateBootstrapSamples

Create bootstrap samples

Description

Creates bootstrap samples and save them to disk, to use in functions that rely on bootstraping to estimate uncertainty intervals or to come up with other estimators, for example a linear shrinkage factor.

Usage

```
CreateBootstrapSamples(study.sample, random.seed.already.set = FALSE,
  random.seed = NULL, number.of.bootstrap.samples = 1000,
  strata = NULL, create.as.list = TRUE, return.samples = FALSE,
  save.to.disk = TRUE)
```

Arguments

study.sample   Data frame. The study sample. No default.

random.seed.already.set

     Logical vector of length 1. If TRUE random.seed does not need to be set within this function as it indicates that this has been done (which is good practice) earlier in the code. Defaults to FALSE.

random.seed   Numeric vector of length 1. Has to be an integer. The seed to use for random number generation. Only used if random.seed.already.set is FALSE. Defaults to NULL.

number.of.bootstrap.samples

     Numeric vector of length 1. Has to be a positive integer. The number of bootstrap samples to create. Only used it bootstrap.confidence.interval is TRUE. Defaults to 1000.

strata   Character vector of length 1 or NULL. The name of the variable on which to stratify the bootstrap, i.e. do the bootstrap separately in each level of the strata variable and then combine the results. If NULL the bootstrap is not stratified. Defaults to NULL.

create.as.list   Logical vector of length 1. If TRUE the bootstrap samples are returned or saved as a list. If FALSE the samples are returned as a data.frame. Defaults to TRUE.

return.samples   Logical vector of length 1. If TRUE, the function returns bootstrap.samples to parent enviroment. Defaults to FALSE.

save.to.disk   Logical vector of length 1. If TRUE, bootstrap.samples are saved to disk in RDS format. Defaults to TRUE.

CreateFlowchart   *Create flowchart*

Description

Generates flowchart using TikZ. Requires the xstring and tikz packages. Compiled with knitr or pdflatex depending on file extension in flowchart.file.path. However, if non-default font is used, flowchart is compiled using xelatex and the mathspec package is required.

Usage

```
CreateFlowchart(flowchart.elements = NULL, flowchart.font = NULL,
  flowchart.file.path = "./flowchart.tex", print.tikz = TRUE,
  save.tikz = TRUE, compile.flowchart = TRUE,
  train.test.split = FALSE, prettify = FALSE,
  read.from.results = TRUE, ...)
```

Arguments

flowchart.elements
:   Character vector. Content for nodes. Length must be > 1. Defaults to NULL.

flowchart.font Character vector of length 1. The font for flowchart nodes, e.g. LiberationSerif. Uses the mathspec package. Flowchart is compiled with XeLaTex or knitr depending on file extension in flowchart.file.path. Defaults to NULL.

flowchart.file.path
:   Character vector of length 1. The flowchart file path. Defaults to "./flowchart.tex".

print.tikz Logical. If TRUE TikZ code is printed to console. Defaults to TRUE.

save.tikz Logical. If TRUE TikZ code for flowchart is saved to disk. Defaults to TRUE.

compile.flowchart
:   Logical. If TRUE the flowchart is compiled using knitr or pdflatex, depending on the file format. Defaults to TRUE

train.test.split
:   Logical. If TRUE last two elements of flowchart list are interpreted as "train" and "test" texts, i.e. text explaining how many patients are grouped in train and test samples. Second to last element is displayed to the left and last element is displayed to the right. Defaults to FALSE.

prettify Logical. If TRUE shadows are used for flowchart nodes. Requires TikZ package shadows.blur. Defaults to FALSE.

read.from.results
:   Logical. If TRUE flowchart.elements is read from results.Rds. Defaults to TRUE.

...   Additional arguments for system function.

CreateLogisticRegressionSubTable
Create logistic regression subtable

Description

Creates a subtable for reporting logistic regression results.

Usage

```
CreateLogisticRegressionSubTable(model.object, odds.ratio = TRUE,
  confidence.interval = 0.95, include.intercept = FALSE,
  include.p.value = FALSE, digits = 2, verbose = FALSE)
```

Arguments

model.object   List of class glm. The model object on which to base the table. No default.

odds.ratio   Logical vector of length 1. If TRUE odds ratios are reported in the table instead
                 of coefficients. Defaults to TRUE.

confidence.interval
                 Numeric vector of length 1. Has to be greater than 0 and less than 1. The width
                 of the confidence interval. Defaults to 0.95.

include.intercept
                 Logical vector of length 1. If TRUE the model intercept is reported. Defaults to
                 FALSE.

include.p.value
                 Logical vector of length 1. If TRUE the p-value is reported. Defaults to FALSE.

digits   Numerical vector of length 1. Has to be an integer greater than 0. The number
                 of digits when reporting results. Defaults to 2.

verbose   Logical vector of length 1. If TRUE progress is printed as the function runs.
                 Useful for debugging. Defaults to FALSE.

save.table   Logical vector of length 1. If TRUE the table is saved to the results file. Defaults
                 to TRUE.

table.name   Character vector of length 1 or NULL. The name of the table when saved. Only
                 used if save.table is TRUE, in which case table.name cannot be NULL. Defaults
                 to NULL.

CreateLogisticRegressionTable
Create logistic regression table

Description

Creates a table for reporting logistic regression results.

Usage

```
CreateLogisticRegressionTable(model.list, odds.ratio = TRUE,
  confidence.interval = 0.95, include.intercept = FALSE,
  include.p.value = FALSE, digits = 2, save.table = TRUE,
  table.name = NULL, verbose = FALSE)
```

Arguments

`model.list`	List. The model objects on which to base the table. No default.
`odds.ratio`	Logical vector of length 1. If TRUE odds ratios are reported in the table instead of coefficients. Defaults to TRUE.
`confidence.interval`	
	Numeric vector of length 1. Has to be greater than 0 and less than 1. The width of the confidence interval. Defaults to 0.95.
`include.intercept`	
	Logical vector of length 1. If TRUE the model intercept is reported. Defaults to FALSE.
`include.p.value`	
	Logical vector of length 1. If TRUE the p-value is reported. Defaults to FALSE.
`digits`	Numerical vector of length 1. Has to be an integer greater than 0. The number of digits when reporting results. Defaults to 2.
`save.table`	Logical vector of length 1. If TRUE the table is saved to the results file. Defaults to TRUE.
`table.name`	Character vector of length 1 or NULL. The name of the table when saved. Only used if save.table is TRUE, in which case table.name cannot be NULL. Defaults to NULL.
`verbose`	Logical vector of length 1. If TRUE progress is printed as the function runs. Useful for debugging. Defaults to FALSE.

CreateSampleCharacteristicsTable

Create sample characteristics table

Description

Creates the sample characteristics table. Wrapper of TableOne.

Usage

```
CreateSampleCharacteristicsTable(study.sample, group = NULL,
  variables = NULL, exclude.variables = NULL, include.overall = TRUE,
  include.missing = TRUE, include.complete.data = FALSE, digits = 1,
  codebook = NULL, only.codebook.variables = TRUE,
  codebook.options = list(full.label.entry = "full.label",
  abbreviated.label.entry = "abbreviated.label"), return.pretty = FALSE,
  return.as.data.frame = TRUE, save.to.results = TRUE,
  table.name = "sample.characteristics.table",
  table.caption = "Sample characteristics", save.to.disk = FALSE,
  file.format = "docx")
```

Arguments

study.sample	Data frame. The study sample. No default.
group	Character vector of length 1. The grouping variable. If NULL the table is not grouped. Defaults to NULL.
variables	Character vector. The names of variables to include in the table. If NULL all variables in study.sample are included. Defaults to NULL.
exclude.variables	
	Character vector. The names of variables to exclude from the table. If NULL no variables are excluded. Defaults to NULL.
include.overall	
	Logical vector of length 1. If TRUE an overall column is included in the tables. Used only if group is not NULL. Defaults to TRUE.
include.missing	
	Not currently used. Logical vector of length 1. If TRUE a column with the number (included. Defaults to TRUE.
include.complete.data	
	Logical vector of length 1. If TRUE the final table has two columns, one with complete cases only and one with multiple imputed data. Only used if the data is detected as multiple imputed, i.e. includes the variables ".imp" AND ".id". Overrides group and include.overall.
digits	Numeric vector of length 1 greater than or equal to 0. Number of digits to use when rounding table entries. Defaults to 1.
codebook	A list or NULL. If a list is provided this list will be assumed to be a codebook, in the sense that it is a collection of variable descriptions. In other words, each entry is a description of a variable. The names of the first level entries of the list are assumed to be variable names. Must include at least two entries that define the full and abbreviated label of each variable respectively. Defaults to NULL.
only.codebook.variables	
	A logical vector of length 1. If TRUE only the variables defined in codebook are included in the table. The rows of the table are also in the same order as in the codebook. Only used if codebook is not NULL. Defaults to TRUE.
codebook.options	
	A list. The list can only include the entries full.label.entry and abbreviated.label.entry, which in turn should should be character vectors of length 1 specifying the names of the full and abbreviated label entries in the codebook. Defaults to list(full.label.entry = "full.label", abbreviated.label.entry = "abbreviated.label"). If codebook is NULL this option is ignored.
return.pretty	Logical vector of length 1. If TRUE the returned table object is made pretty by adding the caption and abbreviations. Defaults to FALSE.
return.as.data.frame	
	Logical vector of length 1. If TRUE the table is returned as a data.frame instad of a matrix. Defaults to TRUE.
save.to.results	
	Logical vector of length 1. If TRUE the table object is saved to a results file on disk using SaveToResults. Defaults to TRUE.
table.name	Character vector of length 1. The name of the table when passed to SaveToResults and saved to disk.. Deafults to "sample.characteristics.table".
table.caption	Character vector of length 1. The table caption. Deafults to "Sample characteristics".

save.to.disk	Logical vector of length 1. If TRUE the table object is saved to disk. Defaults to FALSE.
file.format	Character vector of length 1. The format in which to save the table to disk. Has to be one of c("pdf", "rmd", "docx"). Defaults to "docx".

CreateStudySample　　　　　　　*Create study sample*

Description

Creates the study sample using a list of inclusion criteria. Note that the selection process is stepwise in the order given by the inclusion criteria.

Usage

```
CreateStudySample(study.data, inclusion.criteria, complete.cases = TRUE,
  return.incomplete.cases = FALSE, relevant.variables = c("hos", "sex",
  "tran", "doi", "toi", "doar", "toar", "dodd", "todd", "moi", "age",
  "sbp_1", "hr_1", "rr_1", "gcs_t_1", "iss", "died", "head_and_neck",
  "face", "chest", "extremities", "external", "e_1_icd", "e_2_icd",
  "e_3_icd", "e_4_icd", "e_5_icd", "e_6_icd", "e_7_icd", "e_8_icd",
  "e_9_icd", "e_10_icd", "e_11_icd", "e_12_icd", "xray_1_icd",
  "xray_2_icd", "xray_3_icd", "xray_4_icd", "xray_5_icd", "xray_6_icd",
  "xray_7_icd", "xray_8_icd", "xray_9_icd", "xray_10_icd", "xray_11_icd",
  "fast_1_icd",     "fast_2_icd", "fast_3_icd", "fast_4_icd",
  "fast_5_icd", "fast_6_icd", "fast_7_icd", "fast_8_icd", "fast_9_icd",
  "fast_10_icd", "fast_11_icd", "ct_1_icd", "ct_2_icd", "ct_3_icd",
  "ct_4_icd", "ct_5_icd", "ct_6_icd", "ct_7_icd", "ct_8_icd", "ct_9_icd",
  "ct_10_icd", "ct_11_icd", "ct_12_icd", "ct_13_icd", "op_1_icd",
  "op_2_icd", "op_3_icd", "op_4_icd", "op_5_icd", "op_6_icd", "op_7_icd",
  "op_8_icd", "op_9_icd", "op_10_icd", "op_11_icd"),
  add.to.relevant.variables = NULL,
  remove.from.relevant.variables = NULL,
  ignore.variables = c("head_and_neck", "face", "chest", "extremities",
  "external", "e_1_icd", "e_2_icd", "e_3_icd", "e_4_icd", "e_5_icd",
  "e_6_icd", "e_7_icd", "e_8_icd", "e_9_icd", "e_10_icd", "e_11_icd",
  "e_12_icd", "xray_1_icd", "xray_2_icd", "xray_3_icd", "xray_4_icd",
  "xray_5_icd", "xray_6_icd", "xray_7_icd", "xray_8_icd", "xray_9_icd",
  "xray_10_icd", "xray_11_icd", "fast_1_icd", "fast_2_icd", "fast_3_icd",
  "fast_4_icd", "fast_5_icd", "fast_6_icd", "fast_7_icd", "fast_8_icd",
  "fast_9_icd", "fast_10_icd", "fast_11_icd",     "ct_1_icd", "ct_2_icd",
  "ct_3_icd", "ct_4_icd", "ct_5_icd", "ct_6_icd", "ct_7_icd", "ct_8_icd",
  "ct_9_icd", "ct_10_icd", "ct_11_icd", "ct_12_icd", "ct_13_icd",
  "op_1_icd", "op_2_icd", "op_3_icd", "op_4_icd", "op_5_icd", "op_6_icd",
  "op_7_icd", "op_8_icd", "op_9_icd", "op_10_icd", "op_11_icd"),
  save.to.results = TRUE, results.name = "inclusions.and.exclusions",
  save.to.disk = FALSE, file.format = "docx", override = TRUE)
```

Arguments

study.data   Data frame. The study data. No defaults.

inclusion.criteria

A list of functions. Each function should represent an inclusion criterion. No default.

complete.cases   Logical vector of length 1. If TRUE only complete cases will be returned. If FALSE all cases are returned. Defaults to TRUE.

return.incomplete.cases

Logical vector of length 1. Ignored if complete.cases is FALSE. If complete.cases is TRUE and this is TRUE a list is returned instead of a data.frame. The list has two entries. The first is a data.frame with only complete cases, called complete.sample. The second is a data.frame with only incomplete cases, called incomplete.sample. Defaults to FALSE.

relevant.variables

Character vector. The names of variables to keep in the study sample. Defaults to c("hos", "sex", "tran", "doi", "toi", "doar", "toar", "dodd", "todd", "moi", "age", "sbp_1", "hr_1", "rr_1", "gcs_t_1", "iss", "died", "head_and_neck", "face", "chest", "extremities", "external", "e_1_icd", "e_2_icd", "e_3_icd", "e_4_icd", "e_5_icd", "e_6_icd", "e_7_icd", "e_8_icd", "e_9_icd", "e_10_icd", "e_11_icd", "e_12_icd", "xray_1_icd", "xray_2_icd", "xray_3_icd", "xray_4_icd", "xray_5_icd", "xray_6_icd", "xray_7_icd", "xray_8_icd", "xray_9_icd", "xray_10_icd", "xray_11_icd", "fast_1_icd", "fast_2_icd", "fast_3_icd", "fast_4_icd", "fast_5_icd", "fast_6_icd", "fast_7_icd", "fast_8_icd", "fast_9_icd", "fast_10_icd", "fast_11_icd", "ct_1_icd", "ct_2_icd", "ct_3_icd", "ct_4_icd", "ct_5_icd", "ct_6_icd", "ct_7_icd", "ct_8_icd", "ct_9_icd", "ct_10_icd", "ct_11_icd", "ct_12_icd", "ct_13_icd", "op_1_icd", "op_2_icd", "op_3_icd", "op_4_icd", "op_5_icd", "op_6_icd", "op_7_icd", "op_8_icd", "op_9_icd", "op_10_icd", "op_11_icd").

add.to.relevant.variables

Character vector. The names of variables to add to the default variables in relevant.variables. If NULL no variables are added. Defaults to NULL.

remove.from.relevant.variables

Character vector. The names of variables to remove from the default variables in relevant.variables. If NULL no variables are removed. Defaults to NULL.

ignore.variables

Character vector. The names of variables to ignore when complete cases are determined. The variables included in this vector must also be in relevant.variables. If NULL no variables are ignored. Defaults to c("head_and_neck", "face", "chest", "extremities", "external", "e_1_icd", "e_2_icd", "e_3_icd", "e_4_icd", "e_5_icd", "e_6_icd", "e_7_icd", "e_8_icd", "e_9_icd", "e_10_icd", "e_11_icd", "e_12_icd", "xray_1_icd", "xray_2_icd", "xray_3_icd", "xray_4_icd", "xray_5_icd", "xray_6_icd", "xray_7_icd", "xray_8_icd", "xray_9_icd", "xray_10_icd", "xray_11_icd", "fast_1_icd", "fast_2_icd", "fast_3_icd", "fast_4_icd", "fast_5_icd", "fast_6_icd", "fast_7_icd", "fast_8_icd", "fast_9_icd", "fast_10_icd", "fast_11_icd", "ct_1_icd", "ct_2_icd", "ct_3_icd", "ct_4_icd", "ct_5_icd", "ct_6_icd", "ct_7_icd", "ct_8_icd", "ct_9_icd", "ct_10_icd", "ct_11_icd", "ct_12_icd", "ct_13_icd", "op_1_icd", "op_2_icd", "op_3_icd", "op_4_icd", "op_5_icd", "op_6_icd", "op_7_icd", "op_8_icd", "op_9_icd", "op_10_icd", "op_11_icd").

save.to.results

Logical vector of length 1. If TRUE the output is saved to a results file on disk. Defaults to TRUE.

results.name	Character vector of length 1. The name of the analysis of missingness and exclusions saved to results. Defaults to "inclusions.and.exclusions".
save.to.disk	Logical vector of length 1. If TRUE a file named "exclusions_and_missingness" is saved to disk where the exclusions and missingness are described. Defaults to FALSE.
file.format	Character vector of length 1. Has to be either "docx" or "rmd". The format in which the file detailing the exclusions and missingness is saved. Defaults to "docx".
override	Logical vector of length 1. If TRUE the file "exclusions_and_missingness" is replaced if it exists. If FALSE the function aborts if the file exists. Defaults to TRUE.

CreateStudyTemplate   *Create study template*

Description

Creates a .R file with a custom name where all study steps are documented and run.

Usage

```
CreateStudyTemplate(study.name = "My bengaltiger study",
  authors = "Firstname Lastname",
  description = "This is a bengaltiger study.", file.name = "RunStudy",
  path = ".", create.directory = FALSE,
  functions.to.include = c("ImportStudyData"), save.as.function = TRUE,
  function.name = file.name, open = TRUE)
```

Arguments

study.name	Character vector of length 1. The name of the study. Defaults to "My bengaltiger study".
authors	Character vector. The names of the study authors. Defaults to c("Firstname Lastname").
description	Character vector of length 1. Short description of the study. Defaults to "This is a bengaltiger study.".
file.name	Character vector of length 1. The file name. Defaults to "RunStudy".
path	Character vector of length 1. The path where the study template is saved. Defaults to ".", i.e. the current working directory.
create.directory	
	Logical vector of length 1. If TRUE the directory to which path is pointing is created using dir.create(path) if it does not already exist. Defaults to FALSE.
functions.to.include	
	Character vector. The names of the functions to include in the template. Defaults to c("ImportsStudyData").
save.as.function	
	Logical vector of length 1. If TRUE the study template is structured as a R function. Defaults to TRUE.

function.name	Character vector of length 1. The name of the study function. Is used only if as.functions = TRUE. Defaults to file.name.
open	Logical vector of length 1. If TRUE the study template file is opened using R's file.edit(). Defaults to TRUE.

EstimateInHospitalMortality

Estimate in hospital mortality

Description

Estimates the proportion of patients who died in hospital with a bootstrap confidence interval if requested.

Usage

```
EstimateInHospitalMortality(study.sample, variable.name = "m24h",
  died.level = "Yes", digits = 3,
  bootstrap.confidence.interval = TRUE,
  bootstrap.samples.exist = FALSE, random.seed.already.set = FALSE,
  random.seed = NULL, number.of.bootstrap.samples = 1000,
  save.to.results = TRUE, print.result = TRUE, return.result = FALSE)
```

Arguments

study.sample	Data frame. The study sample. No default.
variable.name	Character vector of length 1. The name of the in hospital mortality variable. Defaults to "m24h".
died.level	Character vector of length 1. The level of the in hospital mortality variable that indicates in hospital mortality. Defaults to "Yes".
digits	Numeric vector of length 1. Must be a positive integer. The number of digits to use when rounding the proportion, and if applicable, the lower and upper bounds of the confidence interval. Defaults to 3.
bootstrap.confidence.interval	
	Logical vector of length 1. If TRUE a confidence interval is estimated using an emperical bootstrap. Deafults to TRUE.
bootstrap.samples.exist	
	Logical vector of length 1. If TRUE bootstrap samples are assumed to have been created using CreateBootstrapSamples, and are therefore read from the file bootstrap.samples.Rds. Defaults to FALSE.
random.seed.already.set	
	Logical vector of length 1. If TRUE random.seed does not need to be set within this function as it indicates that this has been done (which is good practice) earlier in the code. Defaults to FALSE.
random.seed	Numeric vector of length 1. Has to be an integer. The seed to use for random number generation. Only used if bootstrap.conficence.interval is TRUE and random.seed.already.set is FALSE. Defaults to NULL.

number.of.bootstrap.samples

> Numeric vector of length 1. Has to be a positive integer. The number of boot-strap samples to use. Only used it bootstrap.confidence.interval is TRUE. Defaults to 1000.

save.to.results

> Logical vector of length 1. If TRUE the table object is saved to a results file on disk using SaveToResults. Defaults to TRUE.

print.result   Logical vector of length 1. If TRUE the result is printed so that you see what is saved to results. Defaults to TRUE.

return.result   Logical vector of length 1. If TRUE the result is returned to the parent environment. Default to FALSE.

EstimateTraumaticBrainInjuryProportion

Estimate traumatic brain injury proportion

Description

Estimates the proportion of patients with traumatic brain injury.

Usage

```
EstimateTraumaticBrainInjuryProportion(study.sample,
  variable.name = "tbi", tbi.level = "Yes", digits = 3,
  bootstrap.confidence.interval = TRUE, random.seed = NULL,
  number.of.bootstrap.samples = 1000, save.to.disk = TRUE,
  return.result = FALSE)
```

Arguments

study.sample   Data frame. The study sample. No default.

variable.name   Character vector of length 1. The name of the traumatic brain injury variable. Defaults to "tbi".

tbi.level   Character vector of length 1. The level of the traumatic brain injury variable that indicates a traumatic brain injury. Defaults to "Yes".

digits   Numeric vector of length 1. Must be a positive integer. The number of digits to use when rounding the proportion, and if applicable, the lower and upper bounds of the confidence interval. Defaults to 3.

bootstrap.confidence.interval

> Logical vector of length 1. If TRUE a confidence interval is estimated using an emperical bootstrap. Deafults to TRUE.

random.seed   Numeric vector of length 1. Has to be an integer. The seed to use for random number generation. Only used if bootstrap.conficence.interval is TRUE. Defaults to NULL.

number.of.bootstrap.samples

> Numeric vector of length 1. Has to be a positive integer. The number of boot-strap samples to use. Only used it bootstrap.confidence.interval is TRUE. Defaults to 1000.

save.to.disk	Logical vector of length 1. If TRUE the result is saved to disk in "results.rmd". Defaults to TRUE.
return.result	Logical vector of length 1. If TRUE the result is returned to the parent environment. Default to FALSE.

GetRevisedTraumaScoreComponents

Get revised trauma score components

Description

Gets revised trauma score components

Usage

```
GetRevisedTraumaScoreComponents(study.sample, gcs.name = "gcs_t_1",
  sbp.name = "sbp_1", rr.name = "rr_1", return.labels = FALSE)
```

Arguments

study.sample	Data frame. The study sample. No default.
gcs.name	Character vector of length 1. The name of the Glasgow coma scale variable. Defaults to "gcs_t_1".
sbp.name	Character vector of length 1. The name of the systolic blood pressure variable. Defaults to "sbp_1".
rr.name	Character vector of length 1. The name of the respiratory rate variable. Defaults to "rr_1".
return.labels	Logical vector of length 1. If TRUE the labels rather than the values are returned. Defaults to FALSE.

GetSampleIndex *GetSampleIndex*

Description

Internal function to get an index of observations to include in each sample

Usage

```
GetSampleIndex(n.obs)
```

Arguments

n.obs	A named numeric vector. The number of observations that should be included in each sample. No default.

ICDVariables   *ICD variables*

Description

Returns the names of ICD 10 variables in the TITCO dataset

Usage

```
ICDVariables(subset = "all")
```

Arguments

subset   Character vector. Must be one or more of "all", "external", "xray", "fast", "ct", "intraoperative". Defaults "all", which is equal to c("external", "xray", "fast", "ct", "intraoperative").

Examples

```
ICDVariables()
ICDVariables("external")
ICDVariables(c("xray", "ct"))
```

ImportStudyData   *Import study data*

Description

Imports the study data from a csv file.

Usage

```
ImportStudyData(data.file.name = NULL, data.path = "./data/")
```

Arguments

data.file.name Character vector of length 1. The name of the study data file. Defaults to NULL.

data.path   Character vector of length 1. The path to the data directory. Defaults to "./data/"

ImportTitcoMySQL   *Import titco study data from mysql server*

Description

Imports the titco study data from a mysql server, if no arguments are set, defaults to mangrove SSH tunnel-configuration.

Usage

```
ImportTitcoMySQL(mysql.server.name = "127.0.0.1",
  mysql.server.port = 3307, mysql.database = "TITCO",
  mysql.username = "titco", mysql.password = "mangrovetitco",
  mysql.titco.table = "titco")
```

Arguments

mysql.server.name
:   Character vector of length 1. The hostname or IP of the mysql-server, defaults to 127.0.0.1.

mysql.server.port
:   Integer. The port of mysql-server, defaults is 3307.

mysql.database   Character vector of length 1. The name of the database, defaults to TITCO

mysql.username   Character vector of length 1. The username for the database, defaults to titco.

mysql.password   Character vector of length 1. Password for db access, defaults to mangrovetitco

mysql.titco.table
:   Character vector of length 1. The mysql table name, defaults to titco. To use the smaller sample data set, set this to titco_sample

---

Init   *Initiate a bengaltiger study*

Description

Initiates a bengeltiger study by creating a standard directory structure and study template.

Usage

```
Init(create.study.template = TRUE, study.name = "My bengaltiger study",
  authors = "Firstname Lastname",
  description = "This is a bengaltiger study.", file.name = "RunStudy",
  path = ".", create.directory = FALSE,
  functions.to.include = c("ImportStudyData"), save.as.function = TRUE,
  function.name = file.name, open = TRUE)
```

Arguments

create.study.template

Logical vector of length 1. If TRUE a study template will be created in the current working directory. Defaults to TRUE.

study.name
Character vector of length 1. The name of the study. Defaults to "My bengaltiger study".

authors
Character vector. The names of the study authors. Defaults to c("Firstname Lastname").

description
Character vector of length 1. Short description of the study. Defaults to "This is a bengaltiger study.".

file.name
Character vector of length 1. The file name. Defaults to "RunStudy".

path
Character vector of length 1. The path where the study template is saved. Defaults to ".", i.e. the current working directory.

create.directory

Logical vector of length 1. If TRUE the directory to which path is pointing is created using dir.create(path) if it does not already exist. Defaults to FALSE.

functions.to.include

Character vector. The names of the functions to include in the template. Defaults to c("ImportsStudyData").

save.as.function

Logical vector of length 1. If TRUE the study template is structured as a R function. Defaults to TRUE.

function.name
Character vector of length 1. The name of the study function. Is used only if as.functions = TRUE. Defaults to file.name.

open
Logical vector of length 1. If TRUE the study template file is opened using R's file.edit(). Defaults to TRUE.

IsLength1   *Is length 1*

Description

Checks if a given object is a non-list vector of length 1

Usage

```
IsLength1(x)
```

Arguments

x   A vector. The object to be checked. No default.

LogisticRegression   *Logistic regression*

Description

Runs a logistic regression.

Usage

```
LogisticRegression(study.sample, outcome.name, covariate.names,
  run.bivariable.analyses = FALSE, stop.if.missing = TRUE,
  create.table = TRUE, table.options = list(odds.ratio = TRUE,
  confidence.interval = 0.95, include.p.value = FALSE, digits = 2,
  save.table = TRUE, table.name = NULL, verbose = FALSE),
  verbose = FALSE)
```

Arguments

`study.sample`	Data frame. The study sample. No default.
`outcome.name`	Character vector of length 1. The name of the outcome variable. No default.
`covariate.names`	
	Character vector. The names of the covariates. No default.
`run.bivariable.analyses`	
	Logical vector of length 1. If TRUE bivariable analyses are run before the full model is run and these results are included in the final table as unadjusted estimates. Defaults to FALSE.
`stop.if.missing`	
	Logical vector of length 1. If TRUE the execution stops if there is missing data in the outcome or covariates. Defaults to TRUE.
`create.table`	Logical vector of length 1. If TRUE a table with the regression results is created and returned. The apperance of this table can be modified using table.options. If FALSE the model object is returned. Defaults to TRUE.
`table.options`	List. Can only include "odds.ratio", "confidence.interval", "include.intercept", "include.p.value", "digits", "save.table", "table.name", and "verbose". See ?CreateLogisticRegressionTable for details.
`verbose`	Logical vector of length 1. If TRUE progress is printed as the function runs. Useful for debugging. Defaults to FALSE.

MergeRoadTrafficInjuryCategories
    Merge road traffic injury categories

Description

Merges road traffic injury categories into one

Usage

```
MergeRoadTrafficInjuryCategories(study.sample, variable.name = "moi")
```

Arguments

study.sample   Data frame. The study sample. No default.

variable.name   Character vector of length 1. The name of the mechanism of injury variable.
                Defaults to "moi".

OnlyAdolescentsAndYoungAdults

Only adolescents and young adults

Description

Keeps only the adolescents and young adults.

Usage

```
OnlyAdolescentsAndYoungAdults(study.sample, age.variable.name = "age",
  lower.age.cutoff = 10, upper.age.cutoff = 24,
  remove.missing = TRUE)
```

Arguments

study.sample   Data frame. The study sample. No default.

age.variable.name

                Character vector of length 1. The name of the age variable. Defaults to "age".

lower.age.cutoff

                Numeric vector of length 1. The lower age cutoff. Defaults to 10, i.e. only
                observations with an age of at least ten and at most upper.age.cutoff are kept in
                the sample.

upper.age.cutoff

                Numeric vector of length 1. The upper age cutoff. Defaults to 24, i.e. only
                observations with an age of at least lower.age.cutoff and at most 24 are kept in
                the sample.

remove.missing Logical vector of length 1. If TRUE all observations with missing age, as de-
                tected by is.na, are removed from the sample. Defaults to TRUE.

OnlyAdults   *Only adults*

Description

Keeps only the adult patients in the sample.

Usage

```
OnlyAdults(study.sample, age.variable.name = "age", age.cutoff = 18,
  remove.missing = TRUE)
```

Arguments

study.sample Data frame. The study sample. No default.

age.variable.name

Character vector of length 1. The name of the age variable. Defaults to "age".

age.cutoff Numeric vector of length 1. The age cutoff. Defaults to 18, i.e. only observations with an age less than 18 are kept in the sample.

remove.missing Logical vector of length 1. If TRUE all observations with missing age, as detected by is.na, are removed from the sample. Defaults to TRUE.

OnlyBluntTraumaPatients

Only patients with blunt trauma

Description

Keeps only patients with blunt trauma in the sample.

Usage

```
OnlyBluntTraumaPatients(study.sample, injury.type.variable.name = "ti",
  blunt.value = "Blunt", remove.missing = TRUE)
```

Arguments

study.sample Data frame. The study sample. No default.

injury.type.variable.name

Character vector of length 1. The name of the age variable. Defaults to "ti".

blunt.value Character or numeric vector of length 1. The value of the injury type variable that indicates that a patients had blunt trauma. Defaults to "Blunt".

remove.missing Logical vector of length 1. If TRUE all observations with missing injury type, as detected by is.na, are removed from the sample. Defaults to TRUE.

OnlyEmergencyAdmissions

Only emergency admissions

Description

Keeps only emergency admissions in the sample

Usage

```
OnlyEmergencyAdmissions(study.sample,
  admission.type.variable.name = "ad_type",
  emergency.value = "Emergency", remove.missing = TRUE)
```

Arguments

study.sample   Data frame. The study sample. No default.

admission.type.variable.name
                Character vector of length 1. The name of the admission type variable. Defaults
                to "ad_type".

emergency.value
                Character or numeric vector of length 1. The value of the admission type vari-
                able that indicates that an admission is an emergency admission. Defaults to
                "Emergency".

remove.missing Logical vector of length 1. If TRUE all observations with missing admission
                type, as detected by is.na, are removed from the sample. Defaults to TRUE.

OnlyHemothoraxPatients

Only patients with hemothorax

Description

Keeps only patients with hemothorax.

Usage

```
OnlyHemothoraxPatients(study.sample, hemothorax.value = "s27.1",
  remove.missing = TRUE)
```

Arguments

study.sample   Data frame. The study sample. No default.

hemothorax.value
                Character or numeric vector of length 1. The patterns to be used to define that a
                patient had a hemothorax. Defaults to "s27.1".

remove.missing Logical vector of length 1. If TRUE all observations with data on hemothorax
                diagnosis, as detected by is.na, are removed from the sample. Defaults to TRUE.

OnlyIsolatedTraumaticBrainInjuryPatients

Only isolated traumatic brain injury patients

Description

Keeps only the isolated traumatic brain injury (TBI) patients. Isolated traumatic brain injury is
here defined as having any of the international classification of disease (ICD) codes listed in the
parameter icd.codes below and no abbreviated injury scale (AIS) score >1 in any other body region.

Usage

```
OnlyIsolatedTraumaticBrainInjuryPatients(study.sample,
  icd.codes = c("s02.0", "s02.1", "s02.7", "s02.8", "s02.9", "s04.0",
  "s04.1", "s04.2", "s04.3", "s04.4", "s04.5", "s04.6", "s04.7", "s04.8",
  "s04.9", "s06.0", "s06.1", "s06.2", "s06.3", "s06.4", "s06.5", "s06.6",
  "s06.7", "s06.8", "s06.9", "s07.0", "s07.1", "s07.8", "s07.9", "s09.7",
  "s09.8", "s09.9", "t02.0", "t04.0", "t06.0"),
  icd.variables = c("e_1_icd", "e_2_icd", "e_3_icd", "e_4_icd",
  "e_5_icd", "e_6_icd", "e_7_icd", "e_8_icd", "e_9_icd", "e_10_icd",
  "e_11_icd", "e_12_icd", "xray_1_icd", "xray_2_icd", "xray_3_icd",
  "xray_4_icd", "xray_5_icd", "xray_6_icd", "xray_7_icd", "xray_8_icd",
  "xray_9_icd", "xray_10_icd", "xray_11_icd", "fast_1_icd", "fast_2_icd",
  "fast_3_icd", "fast_4_icd", "fast_5_icd", "fast_6_icd", "fast_7_icd",
  "fast_8_icd", "fast_9_icd", "fast_10_icd", "fast_11_icd", "ct_1_icd",
  "ct_2_icd", "ct_3_icd", "ct_4_icd", "ct_5_icd",      "ct_6_icd",
  "ct_7_icd", "ct_8_icd", "ct_9_icd", "ct_10_icd", "ct_11_icd",
  "ct_12_icd", "ct_13_icd", "op_1_icd", "op_2_icd", "op_3_icd", "op_4_icd",
  "op_5_icd", "op_6_icd", "op_7_icd", "op_8_icd", "op_9_icd", "op_10_icd",
  "op_11_icd"), ais.variables = c("face", "chest", "extremities",
  "external"), ais.cutoff = 1, remove.missing = FALSE)
```

Arguments

study.sample	Data frame. The study sample. No default.
icd.codes	Character vector. The codes to be used to define a TBI. If any of the codes is present in any of the variables listen in icd.variables an observation will be classified as having a TBI. Defaults to c("s02.0", "s02.1", "s02.7", "s02.8", "s02.9", "s04.0", "s04.1", "s04.2", "s04.3", "s04.4", "s04.5", "s04.6", "s04.7", "s04.8", "s04.9", "s06.0", "s06.1", "s06.2", "s06.3", "s06.4", "s06.5", "s06.6", "s06.7", "s06.8", "s06.9", "s07.0", "s07.1", "s07.8", "s07.9", "s09.7", "s09.8", "s09.9", "t02.0", "t04.0", "t06.0").
icd.variables	Character vector. The names of the variables with international classification of disease (ICD) codes. Defaults to c("e_1_icd", "e_2_icd", "e_3_icd", "e_4_icd", "e_5_icd", "e_6_icd", "e_7_icd", "e_8_icd", "e_9_icd", "e_10_icd", "e_11_icd", "e_12_icd", "xray_1_icd", "xray_2_icd", "xray_3_icd", "xray_4_icd", "xray_5_icd", "xray_6_icd", "xray_7_icd", "xray_8_icd", "xray_9_icd", "xray_10_icd", "xray_11_icd", "fast_1_icd", "fast_2_icd", "fast_3_icd", "fast_4_icd", "fast_5_icd", "fast_6_icd", "fast_7_icd", "fast_8_icd", "fast_9_icd", "fast_10_icd", "fast_11_icd", "ct_1_icd", "ct_2_icd", "ct_3_icd", "ct_4_icd", "ct_5_icd", "ct_6_icd", "ct_7_icd", "ct_8_icd", "ct_9_icd", "ct_10_icd", "ct_11_icd", "ct_12_icd", "ct_13_icd", "op_1_icd", "op_2_icd", "op_3_icd", "op_4_icd", "op_5_icd", "op_6_icd", "op_7_icd", "op_8_icd", "op_9_icd", "op_10_icd", "op_11_icd").
ais.variables	Character vector. The names of the variables with AIS scores for each body region. Defaults to c("head_and_neck", "face", "chest", "extremities", "external").
ais.cutoff	Integer vector of length 1 between 1 and 6. The cutoff above which an injury should not be included as isolated TBI. Defaults to 1.
remove.missing	Logical vector of length 1. If TRUE all observations with missing AIS, as detected by is.na, are removed from the sample. Defaults to FALSE.

`OnlyPatientsPresentingAfter`
                    Only patients presenting later than a specific delay

---

Description

Keeps only the patients whom presented later than a specific delay, where delay refers to the time between injury and arrival to hospital.

Usage

```
OnlyPatientsPresentingAfter(study.sample, delay.variable.name = "delay",
  delay.cutoff = 6, remove.missing = TRUE)
```

Arguments

`study.sample`	Data frame. The study sample. No default.
`delay.variable.name`	
	Character vector of length 1. The name of the delay variable. Defaults to "delay".
`delay.cutoff`	Numeric vector of length 1. The delay cutoff in hours. Defaults to 6, i.e. only observations with an delay equal to or more than 6 hours are kept in the sample.
`remove.missing`	Logical vector of length 1. If TRUE all observations with missing delay, as detected by is.na, are removed from the sample. Defaults to TRUE.

`OnlyPatientsPresentingBefore`
                    Only patients presenting within a specific delay

---

Description

Keeps only the patients whom presented within a specific delay, where delay refers to the time between injury and arrival to hospital.

Usage

```
OnlyPatientsPresentingBefore(study.sample, delay.variable.name = "delay",
  delay.cutoff = 6, remove.missing = TRUE)
```

Arguments

`study.sample`	Data frame. The study sample. No default.
`delay.variable.name`	
	Character vector of length 1. The name of the delay variable. Defaults to "delay".
`delay.cutoff`	Numeric vector of length 1. The delay cutoff in hours. Defaults to 6, i.e. only observations with an delay less than 6 hours are kept in the sample.
`remove.missing`	Logical vector of length 1. If TRUE all observations with missing delay, as detected by is.na, are removed from the sample. Defaults to TRUE.

OnlyPediatricPatients *Only pediatric patients*

Description

Keeps only the pediatric patients in the sample.

Usage

```
OnlyPediatricPatients(study.sample, age.variable.name = "age",
  age.cutoff = 18, remove.missing = TRUE)
```

Arguments

study.sample	Data frame. The study sample. No default.
age.variable.name	
	Character vector of length 1. The name of the age variable. Defaults to "age".
age.cutoff	Numeric vector of length 1. The age cutoff. Defaults to 18, i.e. only observations with an age less than 18 are kept in the sample.
remove.missing	Logical vector of length 1. If TRUE all observations with missing age, as detected by is.na, are removed from the sample. Defaults to TRUE.

OnlyPolytraumaPatients

Only polytrauma patients

Description

Keeps only the polytrauma patients. Polytrauma is here defined as at least two injuries scored above a certain abbreviated injury scale (AIS) score cutoff in at least two different body regions.

Usage

```
OnlyPolytraumaPatients(sample, ais.variables = c("head_and_neck", "face",
  "chest", "extremities", "external"), ais.cutoff = 2,
  remove.missing = FALSE)
```

Arguments

sample	Data frame. The study sample. No default.
ais.variables	Character vector. The names of the variables with AIS scores for each body region. Defaults to c("head_and_neck", "face", "chest", "extremities", "external").
ais.cutoff	Integer vector of length 1 between 1 and 6. The cutoff above which an injury is counted for polytrauma. Defaults to 2.
remove.missing	Logical vector of length 1. If TRUE all observations with missing AIS, as detected by is.na, are removed from the sample. Defaults to FALSE.

```
OnlyTransferredPatients
```
Only transferred patients

Description

Keeps only patients who were transferred from another health facility in the sample.

Usage

```
OnlyTransferredPatients(study.sample, transfer.variable.name = "tran",
  transfer.value = "Yes", remove.missing = TRUE)
```

Arguments

study.sample   Data frame. The study sample. No default.

transfer.variable.name
                Character vector of length 1. The name of the transfer variable. Defaults to
                "tran".

transfer.value Character or numeric vector of length 1. The value of the transfer variable that
                indicates that a patients was transferred. Defaults to "Yes".

remove.missing Logical vector of length 1. If TRUE all observations with missing transfer, as
                detected by is.na, are removed from the sample. Defaults to TRUE.

```
SaveToResults
```
Save to results

Description

Saves the desired output to a results file in the current working directory. Output saved in this file
can later be compiled as a document.

Usage

```
SaveToResults(output.object, object.name, overwrite = TRUE)
```

Arguments

output.object   Any object. The output to be saved. Most often you want this to be a character
                vector of length 1, why you will see a warning if it is something else. No default.

object.name   Character vector of length 1. The name of the output object in the results object.
                No default.

overwrite   Logical vector of length 1. If TRUE any entry in the results object with the same
                name as object.name is overwritten. Defaults to TRUE.

SourceAdditionalFunctions
Source additional functions

Description

Sources additional functions for use within the project. These functions may be user written and intended only for this specific projects, or they may be functions that are yet to be added to the package.

Usage

```
SourceAdditionalFunctions(path = "./misc/R/")
```

Arguments

path
: Character vector of length 1. The path to the directory that holds the additional functions. Defaults to "./misc/R/".

SplitDataset
SplitDataset

Description

Splits the dataset into training, validation, and test samples, although they can be given different names.

Usage

```
SplitDataset(study.sample, events = NULL, event.variable.name = NULL,
  event.level = NULL, split.proportions = NULL,
  temporal.split = NULL, remove.missing = FALSE, random.seed = NULL,
  sample.names = NULL, return.data.frame = FALSE)
```

Arguments

study.sample
: A data.frame. The study sample. No default.

events
: A numeric vector of the same length as the number of splits or NULL. Each item should indicate the number of events to be included in the resulting sample. If NULL split.proportions is used instead. Defaults to NULL.

event.variable.name
: A character vector of length 1 or NULL. The name of the variable that defines an event. Defaults to NULL.

event.level
: A character or numeric vector of length 1 or NULL. The level of event.variable that defines an event. Default to NULL.

split.proportions
: A numeric vector of the same length as the number of splits or NULL. Each item should indicate the proportion of the dataset that should be included in the resulting sample. If NULL events is used instead. Defaults to NULL.

temporal.split Not yet implemented.

remove.missing A logical vector of length 1. If TRUE observations with missing event data, as detected by is.na(), are removed from the sample and a warning is issued. If FALSE execution stops if there is missing event data. Defaults to FALSE.

random.seed A numeric vector of length 1 or NULL. The random seed to be used when creating splits. Remember to set the seed outside this function if you are running other tasks that perform random operations. Defaults to NULL.

sample.names A character vector of the same length as events or split.proportions, depending on which is used, or NULL. If NULL the samples will be called "training" and "test" if two samples are to created, or "training", "validation", and "test" if three samples are to be created. Defaults to NULL.

return.data.frame

A A logical vector of length 1. If TRUE a single data.frame is returned. This data.frame includes a new column called .sample which indicates what sample observations belong to. Defaults to FALSE.

Value

A named list with three data frames or a single data frame with an added column indicating what sample observations belong to.

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