

Package bengaltiger

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Title bengaltiger

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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,
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DBI,
tableone,
knitr

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R topics documented:

Add30DayInHospitalMortality	2
AddTraumaticBrainInjury	3
CompileResults	4
CreateLogisticRegressionTable	4
CreateSampleCharacteristicsTable	5
CreateStudySample	6
CreateStudyTemplate	8
EstimateTraumaticBrainInjuryProportion	9
ImportStudyData	10
ImportTitcoMySQL	10
Init	11
IsLength1	12
LogisticRegression	12
MergeRoadTrafficInjuryCategories	13
OnlyIsolatedTraumaticBrainInjuryPatients	13
OnlyPediatricPatients	14
OnlyPolytraumaPatients	15
SaveToResults	15
SourceAdditionalFunctions	16

Index**17**

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.

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

<code>study.sample</code>	Data frame. The study sample. No default.
<code>icd.codes</code>	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 <code>icd.variables</code> an observation will be classified as having a TBI. Defaults to <code>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")</code> .
<code>icd.variables</code>	Character vector. The names of the variables with international classification of disease (ICD) codes. Defaults to <code>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")</code> .

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.

 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.

 CreateLogisticRegressionTable

Create logistic regression table

Description

Creates a table for reporting logistic regression results.

Usage

```
CreateLogisticRegressionTable(model.object, 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

<code>model.object</code>	List of class <code>glm</code> . The model object on which to base the table. No default.
<code>odds.ratio</code>	Logical vector of length 1. If TRUE odds ratios are reported in the table instead of coefficients. Defaults to TRUE.
<code>confidence.interval</code>	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.
<code>include.intercept</code>	Logical vector of length 1. If TRUE the model intercept is reported. Defaults to FALSE.
<code>include.p.value</code>	Logical vector of length 1. If TRUE the p-value is reported. Defaults to FALSE.
<code>digits</code>	Numerical vector of length 1. Has to be an integer greater than 0. The number of digits when reporting results. Defaults to 2.
<code>save.table</code>	Logical vector of length 1. If TRUE the table is saved to the results file. Defaults to TRUE.
<code>table.name</code>	Character vector of length 1 or NULL. The name of the table when saved. Only used if <code>save.table</code> is TRUE, in which case <code>table.name</code> cannot be NULL. Defaults to NULL.
<code>verbose</code>	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, data.dictionary = NULL,
  group = NULL, variables = NULL, exclude.variables = NULL,
  include.overall = TRUE, include.missing = TRUE, digits = 1,
  save.to.results = TRUE, save.to.disk = FALSE, file.format = "docx")
```

Arguments

<code>study.sample</code>	Data frame. The study sample. No default.
<code>data.dictionary</code>	Not currently used.
<code>group</code>	Character vector of length 1. The grouping variable. If NULL the table is not grouped. Defaults to NULL.
<code>variables</code>	Character vector. The names of variables to include in the table. If NULL all variables in <code>data.dictionary</code> is included. Defaults to NULL.

<code>exclude.variables</code>	Character vector. The names of variables to exclude from the table. If NULL no variables are excluded. Defaults to NULL.
<code>include.overall</code>	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.
<code>include.missing</code>	Not currently used. Logical vector of length 1. If TRUE a column with the number (included. Defaults to TRUE.
<code>digits</code>	Numeric vector of length 1 greater than or equal to 0. Number of digits to use when rounding table entries. Defaults to 1.
<code>save.to.results</code>	Logical vector of length 1. If TRUE the table object is saved to a results file on disk using SaveToResults. Defaults to TRUE.
<code>save.to.disk</code>	Logical vector of length 1. If TRUE the table object is saved to disk. Defaults to FALSE.
<code>file.format</code>	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,
  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, 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.

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.
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	<i>Create study template</i>
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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.

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 empirical bootstrap. Defaults 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.confidence.interval is TRUE. Defaults to NULL.
number.of.bootstrap.samples	Numeric vector of length 1. Has to be a positive integer. The number of bootstrap samples to use. Only used if 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.

ImportStudyData	<i>Import study data</i>
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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	<i>Import titco study data from mysql server</i>
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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 bengaltiger 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

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

IsLength1	<i>Is length 1</i>
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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.
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LogisticRegression	<i>Logistic regression</i>
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Description

Runs a logistic regression.

Usage

```
LogisticRegression(study.sample, outcome.name, covariate.names,
  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.
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 appearance 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".

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

<code>study.sample</code>	Data frame. The study sample. No default.
<code>icd.codes</code>	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 <code>icd.variables</code> an observation will be classified as having a TBI. Defaults to <code>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")</code> .
<code>icd.variables</code>	Character vector. The names of the variables with international classification of disease (ICD) codes. Defaults to <code>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")</code> .
<code>ais.variables</code>	Character vector. The names of the variables with AIS scores for each body region. Defaults to <code>c("head_and_neck", "face", "chest", "extremities", "external")</code> .
<code>ais.cutoff</code>	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.
<code>remove.missing</code>	Logical vector of length 1. If TRUE all observations with missing AIS, as detected by <code>is.na</code> , are removed from the sample. Defaults to FALSE.

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

<code>study.sample</code>	Data frame. The study sample. No default.
<code>age.variable.name</code>	Character vector of length 1. The name of the age variable. Defaults to "age".
<code>age.cutoff</code>	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.
<code>remove.missing</code>	Logical vector of length 1. If TRUE all observations with missing age, as detected by <code>is.na</code> , 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.

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/".
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Index

Add30DayInHospitalMortality, [2](#)
AddTraumaticBrainInjury, [3](#)

CompileResults, [4](#)
CreateLogisticRegressionTable, [4](#)
CreateSampleCharacteristicsTable, [5](#)
CreateStudySample, [6](#)
CreateStudyTemplate, [8](#)

EstimateTraumaticBrainInjuryProportion,
[9](#)

ImportStudyData, [10](#)
ImportTitcoMySQL, [10](#)
Init, [11](#)
IsLength1, [12](#)

LogisticRegression, [12](#)

MergeRoadTrafficInjuryCategories, [13](#)

OnlyIsolatedTraumaticBrainInjuryPatients,
[13](#)
OnlyPediatricPatients, [14](#)
OnlyPolytraumaPatients, [15](#)

SaveToResults, [15](#)
SourceAdditionalFunctions, [16](#)