

# Package bengaltiger

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**Title** bengaltiger

**Version** 0.0.29.9000

**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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**LazyData** true

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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 = "toddd",
  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 "toddd".
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.

---

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 = "ttl1v",
  drop.used.variables = TRUE)
```

### Arguments

<code>study.sample</code>	Data frame. The study sample. No default.
<code>from.date</code>	Character or POSIXt vector of length 1. The name of the variable with the date from which to start counting. Defaults to "doar".
<code>from.time</code>	Character or POSIXt vector of length 1. The name of the variable with the time from which to start counting. Defaults to "toar".
<code>to.date</code>	Character or POSIXt vector of length 1. The name of the variable with the date from which to start counting. Defaults to "dom_1".
<code>to.time</code>	Character or POSIXt vector of length 1. The name of the variable with the time from which to start counting. Defaults to "tom_1".
<code>date.format</code>	Character vector of length 1. The date format. Defaults to "%Y-%m-%d".
<code>time.format</code>	Character vector of length 1. The date format. Defaults to "%H:%M".
<code>units</code>	Character vector of length 1. Should be one of "days", "hours", "minutes", or "seconds". Defaults to "hours".
<code>variable.name</code>	Character vector of length 1. The name of the time between injury and arrival variable. Defaults to "ttl1v".
<code>drop.used.variables</code>	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

<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>levels</code>	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 <code>c("Yes", "No")</code> .
<code>variable.name</code>	Character vector of length 1. The name of the TBI. Defaults to <code>"tbi"</code> .
<code>add.as.factor</code>	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.
<code>drop.used.variables</code>	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**

<code>study.sample</code>	Data frame. The study sample. No default.
<code>gcs.name</code>	Character vector of length 1. The name of the Glasgow coma scale variable. Defaults to "gcs_t_1".
<code>sbp.name</code>	Character vector of length 1. The name of the systolic blood pressure variable. Defaults to "sbp_1".
<code>rr.name</code>	Character vector of length 1. The name of the respiratory rate variable. Defaults to "rr_1".
<code>variable.name</code>	Character vector of length 1. The name of the triage revised trauma score variable. Defaults to "trts".
<code>drop.used.variables</code>	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	<i>Compile results</i>
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---

**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 bootstrapping 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)
```

**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 if bootstrap.confidence.interval is TRUE. Defaults to 1000.



---

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

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

---

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**

<code>model.list</code>	List. The model objects 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,
  include.complete.data = FALSE, digits = 1, save.to.results = TRUE,
  table.name = "sample.characteristics.table",
  table.caption = "Sample characteristics", 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 <code>group</code> 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>include.complete.data</code>	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 <code>group</code> and <code>include.overall</code> .
<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 <code>SaveToResults</code> . Defaults to TRUE.
<code>table.name</code>	Character vector of length 1. The name of the table when passed to <code>SaveToResults</code> and saved to disk.. Defaults to "sample.characteristics.table".
<code>table.caption</code>	Character vector of length 1. The table caption. Defaults to "Sample characteristics".
<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 <code>c("pdf", "rmd", "docx")</code> . 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",

	<code>"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>add.to.relevant.variables</code>	Character vector. The names of variables to add to the default variables in <code>relevant.variables</code> . If NULL no variables are added. Defaults to NULL.
<code>remove.from.relevant.variables</code>	Character vector. The names of variables to remove from the default variables in <code>relevant.variables</code> . If NULL no variables are removed. Defaults to NULL.
<code>ignore.variables</code>	Character vector. The names of variables to ignore when complete cases are determined. The variables included in this vector must also be in <code>relevant.variables</code> . If NULL no variables are ignored. Defaults to <code>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").</code>
<code>save.to.results</code>	Logical vector of length 1. If TRUE the output is saved to a results file on disk. Defaults to TRUE.
<code>save.to.disk</code>	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.
<code>file.format</code>	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".
<code>override</code>	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**

<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 <code>c("Firstname Lastname")</code> .
<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 <code>c("ImportsStudyData")</code> .
<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.

---

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**

<code>study.sample</code>	Data frame. The study sample. No default.
<code>variable.name</code>	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 empirical bootstrap. Defaults 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.confidence.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 bootstrap samples to use. Only used if 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**

<code>study.sample</code>	Data frame. The study sample. No default.
<code>variable.name</code>	Character vector of length 1. The name of the traumatic brain injury variable. Defaults to "tbi".
<code>tbi.level</code>	Character vector of length 1. The level of the traumatic brain injury variable that indicates a traumatic brain injury. Defaults to "Yes".
<code>digits</code>	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.
<code>bootstrap.confidence.interval</code>	Logical vector of length 1. If TRUE a confidence interval is estimated using an empirical bootstrap. Defaults to TRUE.
<code>random.seed</code>	Numeric vector of length 1. Has to be an integer. The seed to use for random number generation. Only used if <code>bootstrap.confidence.interval</code> is TRUE. Defaults to NULL.
<code>number.of.bootstrap.samples</code>	Numeric vector of length 1. Has to be a positive integer. The number of bootstrap samples to use. Only used if <code>bootstrap.confidence.interval</code> is TRUE. Defaults to 1000.
<code>save.to.disk</code>	Logical vector of length 1. If TRUE the result is saved to disk in "results.rmd". Defaults to TRUE.
<code>return.result</code>	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")
```

**Arguments**

<code>study.sample</code>	Data frame. The study sample. No default.
<code>gcs.name</code>	Character vector of length 1. The name of the Glasgow coma scale variable. Defaults to "gcs_t_1".
<code>sbp.name</code>	Character vector of length 1. The name of the systolic blood pressure variable. Defaults to "sbp_1".
<code>rr.name</code>	Character vector of length 1. The name of the respiratory rate variable. Defaults to "rr_1".



---

ICDVariables	<i>ICD variables</i>
--------------	----------------------

---

**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	<i>Import study data</i>
-----------------	--------------------------

---

**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 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 <code>c("Firstname Lastname")</code> .
<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 <code>c("ImportsStudyData")</code> .
<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

*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	<i>Logistic regression</i>
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---

### 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 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	<i>Merge road traffic injury categories</i>
----------------------------------	---

---

### Description

Merges road traffic injury categories into one

### Usage

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

**Arguments**

<code>study.sample</code>	Data frame. The study sample. No default.
<code>variable.name</code>	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**

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

---

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

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.

---

SaveToResults	<i>Save to results</i>
---------------	------------------------

---

**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	<i>Source additional functions</i>
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---

**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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