Package 'swt'

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Type Package

Title Swisstransplant R Package

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Description This R package provides tools for data analysis and visualization by Swisstransplant--the national organisation for organ donation and transplantation in Switzerland.

Imports ggplot2, grDevices, utils, hms, data.table, rlang, officer, cowplot, utf8, testit

LazyData true

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Encoding UTF-8

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`fmt_hla` *Helper function to format strings for broads, e.g. A(10) becomes A10 and A becomes NA*

Description

Helper function to format strings for broads, e.g. A(10) becomes A10 and A becomes NA

Usage

```
fmt_hla(v_char)
```

Arguments

`v_char`	character vector

Value

formatted character vector

`freq_perc` *Returns frequency count and percentage.*

Description

Returns frequency count and percentage.

Usage

```
freq_perc(x, count.na = TRUE, d2 = 1)
```

Arguments

`x`	a logical vector
`count.na`	count NAs in denominator
`d2`	number of digits

Value

character object

HLA_mismatch *The function calculates HLA mismatches.*

Description

The function calculates HLA mismatches.

Usage

```
HLA_mismatch(
  D.A1,
  D.A2,
  D.B1,
  D.B2,
  D.DR1,
  D.DR2,
  R.A1,
  R.A2,
  R.B1,
  R.B2,
  R.DR1,
  R.DR2
)
```

Arguments

D.A1	Donor HLA Antigen on allele 1 locus A
D.A2	Donor HLA Antigen on allele 2 locus A
D.B1	Donor HLA Antigen on allele 1 locus B
D.B2	Donor HLA Antigen on allele 2 locus B
D.DR1	Donor HLA Antigen on allele 1 locus DR
D.DR2	Donor HLA Antigen on allele 2 locus DR
R.A1	Recipient HLA Antigen on allele 1 locus A
R.A2	Recipient HLA Antigen on allele 2 locus A
R.B1	Recipient HLA Antigen on allele 1 locus B
R.B2	Recipient HLA Antigen on allele 2 locus B
R.DR1	Recipient HLA Antigen on allele 1 locus DR
R.DR2	Recipient HLA Antigen on allele 2 locus DR

Value

data frame with mismatch information.

HLA_parse — *Parser for the unstructured SOAS HLA information into structured data.*

Description

Parser for the unstructured SOAS HLA information into structured data.

Usage

```
HLA_parse(D_HLA, R_HLA)
```

Arguments

D_HLA	Donor HLA antigens. Character string from SOAS variable D HLA Ag.
R_HLA	Recipient HLA antigens. Character string from SOAS variable R HLA Ag.

Value

a data frame with structured HLA information.

kidmo_hr2rank — *KIDMO conversion of hazard ratio to percentile rank.*

Description

KIDMO conversion of hazard ratio to percentile rank.

Usage

```
kidmo_hr2rank(hr)
```

Arguments

hr	hazard ratio

Value

percentile

kidmo_model — *Gets KIDMO prediction model fit.*

Description

Gets KIDMO prediction model fit.

Usage

```
kidmo_model()
```

Value

Model fit

kidmo_scaling — *Get KIDMO scaling factor.*

Description

Get KIDMO scaling factor.

Usage

```
kidmo_scaling()
```

Value

scaling factor

lifeport_d2prc_temp — *Returns the percentile rank of the distance D-squared for the temperature.*

Description

Returns the percentile rank of the distance D-squared for the temperature.

Usage

```
lifeport_d2prc_temp(d2)
```

Arguments

d2	D-squared

Value

percentile rank

`lifeport_d2_temp` *Calculate Mahalanobis distance D-square for LifePort temperature data.*

Description

Calculate Mahalanobis distance D-square for LifePort temperature data.

Usage

```
lifeport_d2_temp(data)
```

Arguments

`data`	data frame or matrix with temperature data

Value

vector with D-square for temperature

`lifeport_process` *Process LifePort data. Adds runtime, clock time vectors, and filtered time series.*

Description

Process LifePort data. Adds runtime, clock time vectors, and filtered time series.

Usage

```
lifeport_process(lpdat, window_size = 15)
```

Arguments

`lpdat`	A list with data from read.lifeport()
`window_size`	rolling window size for filtering

Value

a list with additional processed data tables

lifeport_read *Read LifePort data*

Description

Read LifePort data

Usage

```
lifeport_read(file, format = "guess")
```

Arguments

file	The data file
format	guess, binary or plaintxt (default guess)

Value

a list with LifePort data

lifeport_sumstats *Summary statistics for LifePort data.*

Description

Summary statistics for LifePort data.

Usage

```
lifeport_sumstats(lpdat, ice_threshold = 2.5, infuse_threshold = 10)
```

Arguments

lpdat	A list with data from read.lifeport()
ice_threshold	Threshold for ice temperature in degrees Celsius
infuse_threshold	Threshold for infuse temperature in degrees Celsius

Value

a list with additional summary statistics

mean_sd *Returns mean and SD.*

Description

Returns mean and SD.

Usage

```
mean_sd(x, d1 = 1, d2 = 1)
```

Arguments

x	a numeric vector
d1	number of digits
d2	number of digits

Value

character object

median_iqr *Returns median and interquartile range IQR.*

Description

Returns median and interquartile range IQR.

Usage

```
median_iqr(x, d1 = 1, d2 = 1, d3 = 1)
```

Arguments

x	a numeric vector
d1	number of digits
d2	number of digits
d3	number of digits

Value

character object

miss_perc *Returns frequency count and percentage of missing data.*

Description

Returns frequency count and percentage of missing data.

Usage

```
miss_perc(x, d2 = 1)
```

Arguments

x	a vector
d2	number of digits

Value

character object

nearest *Nearest element in vector for a given set of values.*

Description

Nearest element in vector for a given set of values.

Usage

```
nearest(y, q)
```

Arguments

y	vector to be searched
q	vector of values of interest

Value

indices of the nearest elements in y for a set of values in q.

swt_colors *SWT colors*

Description

Easy access to official SWT color scheme.

Usage

```
swt_colors()
```

Value

a SWT color object

Examples

```
mycolors = swt_colors()
mycolors$red.liver
```

swt_LifePortCaseReport *Create SWT LifePort Case Report in MS Word.*

Description

Create SWT LifePort Case Report in MS Word.

Usage

```
swt_LifePortCaseReport(data.file, output.file, template.file)
```

Arguments

data.file	Lifeport data file
output.file	target file docx
template.file	template file docx

swt_style *SWT theme for ggplot*

Description

This function allows you to add the SWT theme to your ggplot graphics.

Usage

```
swt_style(
  title_size = 14,
  subtitle_size = 14,
  font_size = 10,
  grey_theme = FALSE,
  legend_position = "top"
)
```

Arguments

title_size	The font size of the title
subtitle_size	The font size of the subtitle
font_size	The font font size of the legend, axis text, and axis titles
grey_theme	Whether to use the grey theme instead (TRUE or FALSE)
legend_position	Position of the legend (top, bottom, left or right)

Examples

```
library(ggplot2)
ggplot(mtcars, aes(wt, mpg)) +
   geom_point() +
   swt_style()
```

tidy_missing *Tidy missing data summary from data frame.*

Description

Tidy missing data summary from data frame.

Usage

```
tidy_missing(df)
```

Arguments

df	data frame with raw data

Value

data frame with summary data

`tidy_pvalues` *Formats p-values.*

Description

Formats p-values.

Usage

```
tidy_pvalues(x)
```

Arguments

`x`	numerical vector with p-values

Value

formatted p-values as character vector

`tidy_rmsfit` *Tidy rms model fit results.*

Description

Tidy rms model fit results.

Usage

```
tidy_rmsfit(fit, ...)
```

Arguments

`fit`	model fit from rms
`...`	optional arguments to summary of the rms fit object.

Value

formatted data.frame

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