

Package ‘swt’

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Type Package

Title Swisstransplant R Package

Version 0.1

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

License file LICENSE

Encoding UTF-8

RoxygenNote 7.2.3

Depends R (>= 3.5.0)

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d2prc_temp_lifeport	<i>Returns the percentile rank of the distance D-squared for the temperature.</i>
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Description

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

Usage

```
d2prc_temp_lifeport(d2)
```

Arguments

d2	D-squared
----	-----------

Value

percentile rank

d2_temp_lifeport	<i>Calculate Mahalanobis distance D-square for LifePort temperature data.</i>
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Description

Calculate Mahalanobis distance D-square for LifePort temperature data.

Usage

```
d2_temp_lifeport(data)
```

Arguments

data	data frame or matrix with temperature data
------	--

Value

vector with D-square for temperature

fmt_hla	<i>Helper function to format strings for broads, e.g. A(10) becomes A10 and A becomes NA</i>
---------	--

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
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Value

formatted character vector

get_kidmo_model	<i>KIDMO prediction model fit.</i>
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Description

KIDMO prediction model fit.

Usage

```
get_kidmo_model()
```

Value

Model fit

`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	<i>Parser for the unstructured SOAS HLA information into structured data.</i>
-----------	---

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.

nearest	<i>Nearest element in vector for a given set of values.</i>
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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.

process_lifeport	<i>Process LifePort data. Adds runtime, clock time vectors, and filtered time series.</i>
------------------	---

Description

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

Usage

```
process_lifeport(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

read_lifeport	<i>Read LifePort data</i>
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Description

Read LifePort data

Usage

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

Arguments

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

Value

a list with LifePort data

sumstats_lifeport	<i>Summary statistics for LifePort data.</i>
-------------------	--

Description

Summary statistics for LifePort data.

Usage

```
sumstats_lifeport(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

swt_colors	<i>SWT colors</i>
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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

<code>data.file</code>	Lifeport data file
<code>output.file</code>	target file docx
<code>template.file</code>	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

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

Examples

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

tidy_pvalues	<i>Formats p-values.</i>
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Description

Formats p-values.

Usage

```
tidy_pvalues(x)
```

Arguments

x	numerical vector with p-values
---	--------------------------------

Value

formatted p-values as character vector

tidy_rmsfit	<i>Tidy rms model fit results.</i>
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Description

Tidy rms model fit results.

Usage

```
tidy_rmsfit(fit)
```

Arguments

fit	model fit from rms
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Value

formatted data.frame

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