

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, testit, segmented, lubridate

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date2num	<i>Convert POSIXct data type (date/time) to Excel days since origin</i>
----------	---

Description

Convert POSIXct data type (date/time) to Excel days since origin

Usage

```
date2num(dates)
```

Arguments

dates	character string in the form of YYYY-mm-dd
-------	--

Value

number of days

egfr_ckd_epi	<i>CKD-EPI Creatinine Equation for eGFR (2021) see https://www.kidney.org/content/ckd-epi-creatinine-equation-2021</i>
--------------	--

Description

CKD-EPI Creatinine Equation for eGFR (2021) see <https://www.kidney.org/content/ckd-epi-creatinine-equation-2021>

Usage

```
egfr_ckd_epi(SCr, age, sex, units = "SI")
```

Arguments

SCr	Serum creatinine in mg/dL (US) or umol/L (S)
age	age in years
sex	either "F" for female, or "M" for male
units	unit for SCr, either "SI" (umol/L; default) or "US" (mg/dL)

Value

eGFR mL/min/1.73m²

egfr_schwartz	<i>Revised Schwartz Equation for eGFR (2009) see https://www.mdcalc.com/calc/10008/revised-schwartz-equation-glomerular-filtration-rate-gfr-2009#evidence</i>
---------------	--

Description

Revised Schwartz Equation for eGFR (2009) see <https://www.mdcalc.com/calc/10008/revised-schwartz-equation-glomerular-filtration-rate-gfr-2009#evidence>

Usage

```
egfr_schwartz(SCr, height, units = "SI")
```

Arguments

SCr	Serum creatinine in mg/dL (US) or umol/L (S)
height	in cm
units	unit for SCr, either "SI" (umol/L; default) or "US" (mg/dL)

Value

eGFR mL/min/1.73m²

exam.device	<i>EXAM device data</i>
-------------	-------------------------

Description

Example data form the LifePort kidney transporter.

Usage

```
exam.device
```

Format

'exam.device' A data frame with self explaining variable names:

SerialNumber serial number of the device

UnitID name given to the device ...

Source

<<https://data.swisstransplant.org/>>

exam.organ

EXAM organ data

Description

Example data form the LifePort kidney transporter.

Usage

exam.organ

Format

'exam.organ' A data frame with self explaining variable names:

OrganID identifier entered into the machine

KidneySide left or right kidney ...

Source

<<https://data.swisstransplant.org/>>

exam.sumstats

EXAM summary statistics

Description

Example data form the LifePort kidney transporter.

Usage

exam.sumstats

Format

'exam.sumstats' A data frame with self explaining variable names:

perfusion.dur perfusion duration in minutes

perfusion.dur.str perfusion duration in HH:MM:SS ...

Source

<<https://data.swisstransplant.org/>>

exam.timeseries	<i>EXAM time series data</i>
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Description

Example data form the LifePort kidney transporter.

Usage

```
exam.timeseries
```

Format

'exam.timeseries' A list of data frames with time series data:

SerialNumber serial number of the device

FlowRate flow rate ...

Source

<<https://data.swisstransplant.org/>>

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

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

get_days_in_year	Get the number of days in a year. Used in survival analysis to convert event times.
------------------	---

Description

Get the number of days in a year. Used in survival analysis to convert event times.

Usage

```
get_days_in_year()
```

Value

number of days

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.

kidmo_hr2rank	<i>KIDMO conversion of hazard ratio to percentile rank.</i>
---------------	---

Description

KIDMO conversion of hazard ratio to percentile rank.

Usage

```
kidmo_hr2rank(hr)
```

Arguments

hr	hazard ratio
----	--------------

Value

percentile

kidmo_model	<i>Gets KIDMO prediction model fit.</i>
-------------	---

Description

Gets KIDMO prediction model fit.

Usage

```
kidmo_model()
```

Value

Model fit

lifeport_d2	<i>Calculate Mahalanobis distance D-square for LifePort temperature and perfusion data.</i>
-------------	---

Description

Calculate Mahalanobis distance D-square for LifePort temperature and perfusion data.

Usage

```
lifeport_d2(data, type)
```

Arguments

data	data frame or matrix with temperature or perfusion data
type	string, type of D-square either "temp" or "perf"

Value

vector with D-squares

lifeport_d2toRank	Returns the percentile rank of the temperature or perfusion D-squared.
-------------------	--

Description

Returns the percentile rank of the temperature or perfusion D-squared.

Usage

```
lifeport_d2toRank(d2, type)
```

Arguments

d2	D-squared
type	string, type of D-square either "temp" or "perf"

Value

percentile rank

lifeport_process	Process LifePort data. Adds runtime, clock time, and smoothed time series.
------------------	--

Description

Process LifePort data. Adds runtime, clock time, and smoothed time series.

Usage

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

Arguments

lpdat	a list with data from lifeport_read()
window_size	rolling window size for filtering

Value

a list with LifePort data

lifeport_read	<i>Read LifePort raw data</i>
---------------	-------------------------------

Description

Read LifePort raw data

Usage

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

Arguments

file	data file with path
format	guess (default), binary or plaintxt

Value

a list with LifePort data

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

Description

Summary statistics for LifePort data.

Usage

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

Arguments

lpdat	a list with data from lifeport_process()
ice_threshold	threshold for ice temperature in degrees Celsius
infuse_threshold	threshold for infuse temperature in degrees Celsius

Value

a list with LifePort data

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, compact = FALSE)
```

Arguments

x	a numeric vector
d1	number of digits
d2	number of digits
d3	number of digits
compact	use en dash instead of "from X to Y"

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

<code>x</code>	a vector
<code>d2</code>	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

<code>y</code>	vector to be searched
<code>q</code>	vector of values of interest

Value

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

num2date	<i>Convert Excel days since origin to POSIXct data type (date/time)</i>
----------	---

Description

Convert Excel days since origin to POSIXct data type (date/time)

Usage

```
num2date(
  days,
  origin = "1899-12-30",
  tz = "CET",
  filter = TRUE,
  pattern = "[0-9]{2}\\.[0-9]{2}\\.[0-9]{4}",
  format = "%d.%m.%Y",
  round = TRUE
)
```

Arguments

days	days since origin as numeric or string
origin	origin, default in excel is 1899-12-30
tz	time zone to be forced upon
filter	a fix for dates not recognized (default is TRUE)
pattern	the pattern to find dates not recognized
format	format to convert dates not recognized, e.g. %d.%m.%Y %H:%M:%OS
round	recommended when format has no time, only date information

Value

date of the type POSIXct

swt_colors	<i>SWT colors</i>
------------	-------------------

Description

Easy access to official SWT color scheme.

Usage

```
swt_colors()
```

Value

a SWT color object

Examples

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

swt_style	<i>SWT theme for ggplot</i>
-----------	-----------------------------

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	<i>Tidy missing data summary from data frame.</i>
--------------	---

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

Description

Formats p-values.

Usage

```
tidy_pvalues(x, compact = FALSE)
```

Arguments

x	numerical vector with p-values
compact	logical, no asterisks when TRUE

Value

formatted p-values as character vector

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

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

UK_DCD_Score	<i>UK DCD Risk Score by Schlegel et al.</i>
--------------	---

Description

UK DCD Risk Score by Schlegel et al.

Usage

```
UK_DCD_Score(D_age, D_BMI, fWIT, CIT, R_age, R_MELD, retpx)
```

Arguments

D_age	donor age in years
D_BMI	donor BMI in kg/m^2
fWIT	functional warm ischemia time in minutes
CIT	cold ischemia time in hours
R_age	recipient age in years
R_MELD	recipient lab MELD score
retpx	whether the aim is a retransplant

Value

UK DCD Risk Score

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