Package 'swt'

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Type Package

Title Swisstransplant R Package

Version 0.3

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

LazyData true

License file LICENSE

Encoding UTF-8

RoxygenNote 7.3.2

Depends R (>= 3.5.0)

Contents

---

date2num   *Convert POSIXct data type (date/time) to Excel days since origin*

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

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

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	*EXAM device data*

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   *EXAM time series data*

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   *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

---

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   *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

---

lifeport_d2 *Calculate Mahalanobis distance D-square for LifePort temperature and perfusion data.*

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 *Read LifePort raw data*

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 *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 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

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.

---

num2date   *Convert Excel days since origin to POSIXct data type (date/time)*

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

---

optn_kdri   *OPTN KDRI*

Description

OPTN KDRI

Usage

```
optn_kdri(
  D_age,
  D_height,
  D_weight,
  D_hypertension,
  D_diabetes,
  D_CVA,
  D_SCr,
  D_DCD,
  scaling = 1.40436817065005
)
```

Arguments

D_age	donor age in years
D_height	donor height in cm
D_weight	donor weight in kg
D_hypertension	donor hypertension
D_diabetes	donor diabetes
D_CVA	donor cause of death is cardiovascular accident
D_SCr	serum creatinine in mg/dL
D_DCD	donation after cardiac death
scaling	scaling factor that is published every year by the OPTN

Value

KDRI hazard ratio

---

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_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, compact = FALSE)
```

Arguments

x   numerical vector with p-values

compact   logical, no asterisks when TRUE

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

---

uk_dcd_score *UK DCD Risk Score by Schlegel et al.*

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

Index