Package 'swt'

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

Type Package

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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 3

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/

4 exam.sumstats

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 5

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

6 get_days_in_year

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 7

HLA_mismatch

 ${\it The function \ calculates \ HLA \ mismatches}.$

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.B2 R.DR1	Recipient HLA Antigen on allele 2 locus B Recipient HLA Antigen on allele 1 locus DR
	1

Value

data frame with mismatch information.

8 kidmo_hr2rank

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 9

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 frame or matrix with temperature or perfusion data

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

Value

vector with D-squares

10 lifeport_process

lifeport_d2toRank

 ${\it Returns the percentile rank of the temperature or perfusion D-squared}.$

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

Value

a list with LifePort data

lifeport_read 11

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

12 median_iqr

mean	SO
IIICali	- 50

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

 $\mbox{compact} \qquad \mbox{use en dash instead of "from X to Y"}$

Value

character object

miss_perc 13

 ${\tt miss_perc}$

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

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 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

SWT colors

Description

Easy access to official SWT color scheme.

Usage

```
swt_colors()
```

Value

a SWT color object

swt_style 15

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()
```

16 tidy_pvalues

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 17

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

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