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

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count_perc *Returns count and percentage*

Description

Helper function for tidy formatting.

Usage

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

Arguments

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

Value

character object

---

date2num *Convert date to Excel numeric days*

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 (2021)*

Description

Calculates eGFR according to the 2021 formula.

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)

Details

See equation and references at <https://www.kidney.org/ckd-epi-creatinine-equation-2021>.

Value

eGFR in mL/min/1.73m2

---

egfr_schwartz   *Revised Schwartz Equation (2009)*

Description

Calculates eGFR for pediatric patients.

Usage

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

Arguments

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

Details

See equation and examples at <https://www.mdcalc.com/calc/10008/revised-schwartz-equation-glomerular-f>
evidence.

Value

eGFR in mL/min/1.73m2

---

exam.device	*EXAM device data*

Description

Example data form the LifePort kidney transporter.

Usage

```
exam.device
```

Format

A data frame with self explaining variable names:

SerialNumber serial number of the device

Type type note

SubType subtype note

UnitID name given to the device

FirmwareVersion firmware version

FileID file id

StartTime start date and time of machine

DataState data state, if it is complete

HasGaps whether data has haps

Runtime run time of the machine

StopTime time and date of machine stop

Filename file name#'

Source

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

---

exam.organ	*EXAM organ data*

Description

Example data form the LifePort kidney transporter.

Usage

```
exam.organ
```

Format

A data frame with self explaining variable names:

OrganID identifier entered into the machine

KidneySide left or right kidney

BloodType self explaining

CrossClampTime.Date self explaining

CrossClampTimezone self explaining

TotalIschemicTime self explaining

PerfusateLot self explaining

PerfusateExpirationDate self explaining

PerfusateUsed self explaining

Cannula self explaining

CannulaExpirationDate self explaining

CassetteLot. self explaining

CasetteExpirationDate self explaining

ID self explaining

DonorID self explaining

Source

https://data.swisstransplant.org/

---

exam.sumstats   *EXAM summary statistics*

Description

Example data form the LifePort kidney transporter.

Usage

```
exam.sumstats
```

Format

A data frame with self explaining variable names:

perfusion.dur perfusion duration in minutes

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

systolicPressure.md self explaining

diastolicPressure.mean self explaining

flowRate.mean self explaining

organResistance.mean self explaining

organResistance.sd self explaining

organResistance.x1 self explaining

organResistance.y1 self explaining

organResistance.x2 self explaining

organResistance.y2 self explaining

organResistance.delta self explaining

organResistance.slope self explaining

iceContainerTemperature.mean self explaining

iceContainerTemperature.sd self explaining

iceContainerTemperature.minAbove self explaining

iceContainerTemperature.minAbove.str self explaining

infuseTemperature.mean self explaining

infuseTemperature.sd self explaining

infuseTemperature.start self explaining

infuseTemperature.minAbove self explaining

infuseTemperature.minAbove.str self explaining

D2temp self explaining

Ptemp self explaining

D2perf self explaining

Pperf self explaining

Source

https://data.swisstransplant.org/

---

exam.timeseries	*EXAM time series data*

Description

Example data form the LifePort kidney transporter.

Usage

```
exam.timeseries
```

Format

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 *Format HLA*

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

---

get_days_in_year *Get the number of days in a year*

Description

Helper function useful in survival analysis to convert event times.

Usage

```
get_days_in_year()
```

Value

number of days

---

hla_mismatch *Calculates HLA mismatches.*

Description

The function calculates HLA mismatches for SOAS data.

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

Details

The serological nomenclature in SOAS as follows: L[p, q] with L is the locus A B or DR, p and q are the two alleles of the locus L, and the convention is p <= q. The case p != q is known as heterozygote, A[2, 25]. Homozygote, if p = q, such as in DR[11,11].

The HLA-matching process has to handle broad and splits. Two alleles p and r on the same locus L match if they are equal or if one of the allele is the broad of the other allele. Two different splits of same broad do not match. To calculate mismatch, we look up donor antigens and match them in the recipient. In other words, how many unknown antigens are transferred to the donor?

Value

data frame with mismatch information

---

hla_parse   *Parse HLA data*

Description

Parser to convert 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

data frame with structured HLA information

---

kidmo_hr2rank   *KIDMO rank*

Description

Conversion of hazard ratio into percentile rank.

Usage

```
kidmo_hr2rank(hr)
```

Arguments

hr   hazard ratio

Value

percentile

---

kidmo_model	*KIDMO prediction model*

Description

Returns KIDMO prediction model fit.

Usage

```
kidmo_model()
```

Value

model fit

---

lifeport_d2	*D-squared for LifePort data*

Description

Calculate Mahalanobis distance D-squared 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-squared

lifeport_d2toRank *Rank of D-squared for LifePort data*

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*

Description

Processing of LifPort data adds runtime, clock time, and smoothed time series.

Usage

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

Arguments

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

Value

list with LifePort data

---

lifeport_read   *Read LifePort raw data*

Description

Function to read LifePort binary as well as ASCII raw data files.

Usage

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

Arguments

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

Value

list with LifePort data

---

lifeport_sumstats   *Summary statistics for LifePort data*

Description

Adds summary statistics for pressure, flow, resistance, and temperature time series.

Usage

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

Arguments

lpdat	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

list with LifePort data

mean_sd *Returns mean and SD as string*

Description

Helper function for tidy formatting.

Usage

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

Arguments

x	numeric vector
d1	number of digits
d2	number of digits

Value

character object

median_iqr *Returns median and interquartile range IQR*

Description

Helper function for tidy formatting.

Usage

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

Arguments

x	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 count and percentage of missing data.*

Description

Helper function for tidy formatting.

Usage

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

Arguments

x	vector
d2	number of digits

Value

character object

---

nearest	*Nearest element*

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 numeric days to date*

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	apply 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

Calculates the OPTN KDRI according to the 2024 version.

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

Details

See details under "Learn about KDPI" at [https://optn.transplant.hrsa.gov/data/allocation-calculators/](https://optn.transplant.hrsa.gov/data/allocation-calculators/kdpi-calculator/)[kdpi-calculator/](https://optn.transplant.hrsa.gov/data/allocation-calculators/kdpi-calculator/).

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_skeleton	*SWT skeleton*

Description

This internal function enables a Swisstransplant Document in Quarto for RStudio projects.

Usage

```
swt_skeleton(path)
```

Arguments

path   project path

---

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   font size of the title

subtitle_size   font size of the subtitle

font_size   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*

Description

Calculates missing data for each variable in 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

Helper function for tidy formatting.

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

Shows tidy regression table with results as data frame.

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*

Description

Calculates the UK DCD Risk Score that can range between 0 and 27.

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

Details

Reference: Schlegel A, Kalisvaart M, Scalera I, et al. The UK DCD Risk Score: A new proposal to define futility in donation-after-circulatory-death liver transplantation. J Hepatol. 2018;68(3):456-464. doi:10.1016/j.jhep.2017.10.034

Value

UK DCD Risk Score

uk_kdri   *UK KDRI 2019*

Description

Calculates the UK KDRI version from 2019.

Usage

```
uk_kdri(D_age, D_height, D_hypertension, D_female, D_CMV, D_eGFR, D_days_hosp)
```

Arguments

D_age	donor age in years
D_height	donor height in cm
D_hypertension	donor hypertension
D_female	donor is female
D_CMV	donor cytomegalovirus positive
D_eGFR	estimated glomerular filtration rate (eGFR) in mL/min/1.73m2
D_days_hosp	days in hospital

Details

Reference: Kim JJ, Curtis RMK, Reynolds B, et al. The UK kidney donor risk index poorly predicts long-term transplant survival in paediatric kidney transplant recipients. Front Immunol. 2023;14:1207145. doi:10.3389/fimmu.2023.1207145

Calculator at <https://www.glasgowtransplant.com/tools/ukkdri.html>.

Value

UK KDRI 2019 hazard ratio

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