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, rms

LazyData true

License file LICENSE

Encoding UTF-8

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Depends R (>= 3.5.0)

Contents

`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
systolicPressure.mean 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
D2perf self explaining
Pperf self explaining
D2temp self explaining
Ptemp 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 *KIDMO Score*

Description

Calculates the KIDMO Score.

Usage

```
kidmo(
  D_age = 55,
  D_deathcause = "cerebral hemorrhage",
  D_diabetes = FALSE,
  D_hypertension = FALSE,
  R_age = 57,
  R_retpx = FALSE,
  R_tpxyear = 2026,
  times = c(2, 5),
  newdata = NULL
)
```

Arguments

D_age	donor age in years
D_deathcause	donor cause of death (cerebral hemorrhage, anoxia, or others)
D_diabetes	donor history of diabetes (binary)
D_hypertension	donor history of hypertension (binary)
R_age	recipient age in years
R_retpx	recipient listed for retransplant (binary)
R_tpxyear	recipient year of transplant (continuous)
times	time points for predictions, in years
newdata	data frame with variables (requires correct variable names)

Value

KIDMO Score

kidmo_hr2rank *KIDMO rank*

Description

Conversion of (unscaled) hazard ratio into percentile rank.

Usage

```
kidmo_hr2rank(hr)
```

Arguments

hr	hazard ratio

Value

percentile

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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

data frame with D-squared and 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 = 3, 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/kdpi-calculator/.

Value

KDRI hazard ratio

print.kidmo *Print method for kidmo objects*

Description

Print method for kidmo objects

Usage

```
## S3 method for class 'kidmo'
print(x, ...)
```

Arguments

x	An object of class kidmo.
...	Additional arguments (ignored).

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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