

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, rms

LazyData true

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count_perc	<i>Returns count and percentage</i>
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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	<i>Convert date to Excel numeric days</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 *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-fraction-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 gaps

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

CassetteExpirationDate 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 from 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)
)
```

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

Value

KIDMO Score

<code>kidmo_hr2rank</code>	<i>KIDMO rank</i>
----------------------------	-------------------

Description

Conversion of (unscaled) hazard ratio into percentile rank.

Usage

`kidmo_hr2rank(hr)`

Arguments

<code>hr</code>	hazard ratio
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Value

percentile

<code>kidmo_model</code>	<i>KIDMO prediction model</i>
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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

<code>file</code>	data file with path
<code>format</code>	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

<code>lpdat</code>	list with data from <code>lifeport_process()</code>
<code>ice_threshold</code>	threshold for ice temperature in degrees Celsius
<code>infuse_threshold</code>	threshold for infuse temperature in degrees Celsius

Value

list with LifePort data

mean_sd	<i>Returns mean and SD as string</i>
---------	--------------------------------------

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	<i>Returns median and interquartile range IQR</i>
------------	---

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

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

<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 numeric days to date</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	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	<i>OPTN KDRI</i>
-----------	------------------

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

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

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

Description

Shows tidy regression table with results as data frame.

Usage

```
tidy_rmsfit(fit, ...)
```

Arguments

<code>fit</code>	model fit from rms
<code>...</code>	optional arguments to summary of the rms fit object.

Value

formatted data.frame

<code>uk_dcd_score</code>	<i>UK DCD Risk Score</i>
---------------------------	--------------------------

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

<code>D_age</code>	donor age in years
<code>D_BMI</code>	donor BMI in kg/m ²
<code>fWIT</code>	functional warm ischemia time in minutes
<code>CIT</code>	cold ischemia time in hours
<code>R_age</code>	recipient age in years
<code>R_MELD</code>	recipient lab MELD score
<code>retpx</code>	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/1.73m ²
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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