

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

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|------------|-------------------------------------|
| count_perc | <i>Returns count and percentage</i> |
|------------|-------------------------------------|

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 | <i>CKD-EPI Creatinine Equation (2021)</i> |
|--------------|---|

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 | <i>Revised Schwartz Equation (2009)</i> |
|---------------|---|

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-filtration-rate-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 | <i>EXAM summary statistics</i> |
|---------------|--------------------------------|

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 $p \leq q$. The case $p \neq q$ 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 | <i>Parse HLA data</i> |
|-----------|-----------------------|

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 | <i>KIDMO Score</i> |
|-------|--------------------|

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

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

Description

Conversion of (unscaled) hazard ratio into percentile rank.

Usage

kidmo_hr2rank(hr)

Arguments

hr hazard ratio

Value

percentile

| | |
|-------------|-------------------------------|
| kidmo_model | <i>KIDMO prediction model</i> |
|-------------|-------------------------------|

Description

Returns KIDMO prediction model fit.

Usage

kidmo_model()

Value

model fit

| | |
|-------------|------------------------------------|
| lifeport_d2 | <i>D-squared for LifePort data</i> |
|-------------|------------------------------------|

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 | <i>Process LifePort data</i> |
|------------------|------------------------------|

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 | <i>Read LifePort raw data</i> |
|---------------|-------------------------------|

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 plaintext |

Value

list with LifePort data

| | |
|-------------------|---|
| lifeport_sumstats | <i>Summary statistics for LifePort data</i> |
|-------------------|---|

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 <i>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 | <i>Returns count and percentage of missing data.</i> |
|-----------|--|

Description

Helper function for tidy formatting.

Usage

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

Arguments

| | |
|----|------------------|
| x | vector |
| d2 | number of digits |

Value

character object

| | |
|---------|------------------------|
| nearest | <i>Nearest element</i> |
|---------|------------------------|

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 | <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 | <i>SWT colors</i> |
|------------|-------------------|

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 | <i>SWT skeleton</i> |
|--------------|---------------------|

Description

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

Usage

```
swt_skeleton(path)
```

Arguments

| | |
|------|--------------|
| path | project path |
|------|--------------|

| | |
|-----------|-----------------------------|
| swt_style | <i>SWT theme for ggplot</i> |
|-----------|-----------------------------|

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 | <i>Tidy missing data summary</i> |
|--------------|----------------------------------|

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 | <i>Formats p-values.</i> |
|--------------|--------------------------|

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 | <i>Tidy rms model fit results</i> |
|-------------|-----------------------------------|

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 | <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

| | |
|--------|--|
| 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

| | |
|-----------------------------|--|
| <code>D_age</code> | donor age in years |
| <code>D_height</code> | donor height in cm |
| <code>D_hypertension</code> | donor hypertension |
| <code>D_female</code> | donor is female |
| <code>D_CMV</code> | donor cytomegalovirus positive |
| <code>D_eGFR</code> | estimated glomerular filtration rate (eGFR) in mL/min/1.73m ² |
| <code>D_days_hosp</code> | 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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