

# Package ‘swt’

November 22, 2023

**Type** Package

**Title** Swisstransplant R Package

**Version** 0.1

**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, rlang, officer, cowplot, utf8, testit

**LazyData** true

**License** file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.2.3

**Depends** R (>= 3.5.0)

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fmt_hla	<i>Helper function to format strings for broads, e.g. A(10) becomes A10 and A becomes NA</i>
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**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
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**Value**

formatted character vector

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HLA_mismatch	<i>The function calculates HLA mismatches.</i>
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**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.DR1	Recipient HLA Antigen on allele 1 locus DR
R.DR2	Recipient HLA Antigen on allele 2 locus DR

**Value**

data frame with mismatch information.

---

HLA_parse	<i>Parser for the unstructured SOAS HLA information into structured data.</i>
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---

**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	<i>KIDMO conversion of hazard ratio to percentile rank.</i>
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**Description**

KIDMO conversion of hazard ratio to percentile rank.

**Usage**

```
kidmo_hr2rank(hr)
```

**Arguments**

hr	hazard ratio
----	--------------

**Value**

percentile

---

kidmo_model	<i>Gets KIDMO prediction model fit.</i>
-------------	---

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**Description**

Gets KIDMO prediction model fit.

**Usage**

```
kidmo_model()
```

**Value**

Model fit

---

kidmo_scaling	<i>Get KIDMO scaling factor.</i>
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**Description**

Get KIDMO scaling factor.

**Usage**

```
kidmo_scaling()
```

**Value**

scaling factor

---

lifeport_d2prc_temp	<i>Returns the percentile rank of the distance D-squared for the temperature.</i>
---------------------	---

---

**Description**

Returns the percentile rank of the distance D-squared for the temperature.

**Usage**

```
lifeport_d2prc_temp(d2)
```

**Arguments**

d2	D-squared
----	-----------

**Value**

percentile rank

---

lifeport_d2_temp	<i>Calculate Mahalanobis distance D-square for LifePort temperature data.</i>
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---

**Description**

Calculate Mahalanobis distance D-square for LifePort temperature data.

**Usage**

```
lifeport_d2_temp(data)
```

**Arguments**

data	data frame or matrix with temperature data
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**Value**

vector with D-square for temperature

---

lifeport_process	<i>Process LifePort data. Adds runtime, clock time vectors, and filtered time series.</i>
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**Description**

Process LifePort data. Adds runtime, clock time vectors, and filtered time series.

**Usage**

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

**Arguments**

lpdat	A list with data from read.lifeport()
window_size	rolling window size for filtering

**Value**

a list with additional processed data tables

---

lifeport_read	<i>Read LifePort data</i>
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---

**Description**

Read LifePort data

**Usage**

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

**Arguments**

file	The data file
format	guess, binary or plaintext (default guess)

**Value**

a list with LifePort data

---

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

---

**Description**

Summary statistics for LifePort data.

**Usage**

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

**Arguments**

lpdat	A list with data from read.lifeport()
ice_threshold	Threshold for ice temperature in degrees Celsius
infuse_threshold	Threshold for infuse temperature in degrees Celsius

**Value**

a list with additional summary statistics

---

mean_sd	<i>Returns mean and SD.</i>
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**Description**

Returns mean and SD.

Returns frequency count and percentage.

**Usage**

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

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

**Arguments**

x	a logical vector
d1	number of digits
d2	number of digits

**Value**

character object  
character object

---

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

**Description**

Returns median and interquartile range *IQR*.

**Usage**

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

**Arguments**

x	a numeric vector
d1	number of digits
d2	number of digits
d3	number of digits

**Value**

character object

---

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	<i>Nearest element in vector for a given set of values.</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.

---

swt_colors	<i>SWT colors</i>
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**Description**

Easy access to official SWT color scheme.

**Usage**

```
swt_colors()
```

**Value**

a SWT color object

**Examples**

```
mycolors = swt_colors()
mycolors$red.liver
```

---

```
swt_LifePortCaseReport
```

*Create SWT LifePort Case Report in MS Word.*

---

### Description

Create SWT LifePort Case Report in MS Word.

### Usage

```
swt_LifePortCaseReport(data.file, output.file, template.file)
```

### Arguments

<code>data.file</code>	Lifeport data file
<code>output.file</code>	target file docx
<code>template.file</code>	template file docx

---

```
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

<code>title_size</code>	The font size of the title
<code>subtitle_size</code>	The font size of the subtitle
<code>font_size</code>	The font font size of the legend, axis text, and axis titles
<code>grey_theme</code>	Whether to use the grey theme instead (TRUE or FALSE)
<code>legend_position</code>	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 from data frame.</i>
--------------	---

---

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

**Description**

Formats p-values.

**Usage**

```
tidy_pvalues(x)
```

**Arguments**

x                      numerical vector with p-values

**Value**

formatted p-values as character vector

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

**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

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