

# Package ‘litteR’

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**Title** Litter Analysis

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**Description** Data sets on various litter types like beach litter, riverain litter, floating litter, and seafloor litter are rapidly growing. This package offers a simple user interface to analyse these litter data in a consistent and reproducible way. It also provides functions to facilitate several kinds of litter analysis, e.g., trend analysis, power analysis, and baseline analysis. Under the hood, these functions are also used by the user interface. See Schulz et al. (2019) <[doi:10.1016/j.envpol.2019.02.030](https://doi.org/10.1016/j.envpol.2019.02.030)> for details. MS-Windows users are advised to run 'litteR' in 'RStudio'. See our vignette: Installation manual for 'RStudio' and 'litteR'.

**Depends** R (>= 4.0.0)

**Imports** readr (>= 1.3.1), stringr (>= 1.4.0), dplyr (>= 1.0.0), tidyselect (>= 1.1.0), tidyr (>= 1.1.0), fs (>= 1.4.1), ggplot2 (>= 3.3.1), purrr (>= 0.3.4), rlang (>= 0.4.6), yaml (>= 2.2.1), rmarkdown (>= 2.2), tcltk

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## Description

A tool for the analysis of various litter types, e.g., beach litter, riverain litter, floating litter, and seafloor litter.

## Details



The easiest way to get convenient with **litteR** is to create an empty project directory and fill it with example files by calling the function `create_litter_project`. The workhorse function in **litteR** is called `litter`. This function will start a simple user interface and lets you select an input file (\*.csv) and a settings file (\*.yaml). It will produce an HTML-report with litter analysis results according to the selected options in the settings file. See the package vignette for more details.

## Author(s)

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## References

Schulz, Marcus, Dennis J.J. Walvoort, Jon Barry, David M. Fleet & Willem M.G.M. van Loon, 2019. Baseline and power analyses for the assessment of beach litter reductions in the European OSPAR region. Environmental Pollution 248:555-564 <doi:10.1016/j.envpol.2019.02.030>

---

adj\_boxplot\_stats      *Adjusted Boxplot Statistics*

---

### Description

Adjusted boxplot statistics according to Hubert & Vandervieren (2008). The upper whisker extends from the hinge to the largest value no further than the upper fence. Similarly, the lower whisker extends from the hinge to the smallest value no further than the lower fence. See Hubert & Vandervieren (2008, p.5191, Eq.5).

### Usage

```
adj_boxplot_stats(x, ...)
```

```
## Default S3 method:  
adj_boxplot_stats(x, ...)
```

### Arguments

x	numeric vector
...	further arguments passed to or from other methods.

### Value

Numeric vector consisting of respectively the lower whisker/fence, the first quartile/hinge, the median, the third quartile/hinge, and the upper whisker/fence.

### Methods (by class)

- `adj_boxplot_stats(default)`: Adjusted Boxplot Statistics

### References

Hubert, M., and E. Vandervieren, 2008. An adjusted boxplot for skewed distributions. *Computational Statistics and Data Analysis* 52:5186-5201 [doi:10.1016/j.csda.2007.11.008](https://doi.org/10.1016/j.csda.2007.11.008)

### See Also

[stat\\_adj\\_boxplot](#)

### Examples

```
adj_boxplot_stats(rlnorm(100))
```

---

create\_litter\_project *Create Project Directory*

---

### Description

Fills an empty directory (path) with example files. If the path' argument is missing or NULL, a Tcl/Tk dialogue will be started.

### Usage

```
create_litter_project(path = NULL)
```

### Arguments

path                   (Existing) directory name

---

create\_logger           *Simple Logger*

---

### Description

Logger, in the spirit of loggers like log4j. Implemented logging levels are DEBUG, INFO, WARN, ERROR (in increasing order of specificity. Logging events can be filtered to show only events with a minimum specificity.

### Usage

```
create_logger(con = stdout(), level = c("DEBUG", "INFO", "WARN", "ERROR"))
```

### Arguments

con                    [connection](#) to write logging data to  
level                  log only events of this level and those that are more specific (see details)

### Value

Anonymous logging functions

### Examples

```
logger <- create_logger(level = "INFO")  
logger$info("starting specific computation")  
logger$info("Today is {Sys.Date()}")
```

---

cv	<i>Coefficient of Variation</i>
----	---------------------------------

---

**Description**

Coefficient of Variation

**Usage**

```
cv(x, na.rm = FALSE)
```

**Arguments**

x	a numeric vector
na.rm	logical. Should missing values be removed?

**Value**

coefficient of variation (numeric vector of length 1).

**References**

[https://en.wikipedia.org/wiki/Coefficient\\_of\\_variation](https://en.wikipedia.org/wiki/Coefficient_of_variation)

---

enumerate	<i>Enumerate Objects</i>
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---

**Description**

Generic function for enumerating objects

**Usage**

```
enumerate(x, ...)  
  
## S3 method for class 'numeric'  
enumerate(x, ...)
```

**Arguments**

x	object to enumerate
...	further arguments passed to or from other methods.

**Methods (by class)**

- `enumerate(numeric)`: enumerate numeric vector.

**See Also**[enumerate.character](#)


---

 enumerate.character    *Enumerate Character Vector*


---

**Description**

Collapsing a character vector of length n, to a character vector of length 1.

**Usage**

```
## S3 method for class 'character'
enumerate(x, ...)
```

**Arguments**

x                    character vector  
 ...                  further arguments passed to or from other methods.

**Value**

character vector of length 1, with elements separated by a comma except for the last element which is prepended by "and".

**Examples**

```
enumerate("apples")
enumerate(c("apples", "oranges"))
enumerate(c("apples", "oranges", "pears"))
```

---

 enumerate.sequenzied    *Convert Sequenzied Output to Character String*


---

**Description**

Convert Sequenzied Output to Character String

**Usage**

```
## S3 method for class 'sequenzied'
enumerate(x, ...)
```

**Arguments**

x                    object of class sequenzied.  
 ...                  further arguments passed to or from other methods.

**Value**

string representation (character vector of length 1) of a sequenized object

**See Also**

[sequenize.integer](#)

---

has_write_access	<i>Check Write Permission</i>
------------------	-------------------------------

---

**Description**

Simple wrapper for [file.access](#) with mode=2

**Usage**

```
has_write_access(path)
```

**Arguments**

path	filename
------	----------

**Value**

TRUE if write access, FALSE if not

---

intercept	<i>Intercept</i>
-----------	------------------

---

**Description**

Extract the intercept from object x.

**Usage**

```
intercept(x, ...)
```

**Arguments**

x	object
...	further arguments passed to or from other methods.

**Value**

estimate of the intercept (numeric vector of length 1).

---

iod	<i>Index of Dispersion</i>
-----	----------------------------

---

**Description**

A normalized measure of the dispersion of a probability distribution.

**Usage**

```
iod(x, na.rm = FALSE)
```

**Arguments**

x	a numeric vector
na.rm	logical. Should missing values be removed?

**Value**

index of dispersion (numeric vector of length 1).

**References**

[https://en.wikipedia.org/wiki/Index\\_of\\_dispersion](https://en.wikipedia.org/wiki/Index_of_dispersion)

---

is_date_format	<i>Check Date Format</i>
----------------	--------------------------

---

**Description**

Checks if the data format x complies with format.

**Usage**

```
is_date_format(x, format = "%Y-%m-%d")
```

**Arguments**

x	object of class character or Date
format	required date format (see <a href="#">strptime</a> )

**Value**

TRUE if x complies with format, and FALSE otherwise.

**Examples**

```
is_date_format("2019-05-14", "%Y-%m-%d")
```

---

is_natural_number	<i>Test for Natural Numbers</i>
-------------------	---------------------------------

---

**Description**

Test for natural numbers according to ISO 80000-2, that is the set {0, 1, 2, ...}

**Usage**

```
is_natural_number(x)
```

**Arguments**

x	numeric vector
---	----------------

**Value**

TRUE in case x is a natural number, FALSE otherwise.

**Examples**

```
stopifnot(!is_natural_number(3.1))
stopifnot(!is_natural_number(2.99))
stopifnot(is_natural_number(3))
stopifnot(all(is_natural_number(0:9)))
stopifnot(sum(is_natural_number(c(1, 2.5, 3))) == 2)
```

---

kendall_s	<i>Mann-Kendall S Statistic</i>
-----------	---------------------------------

---

**Description**

Mann-Kendall S Statistic

**Usage**

```
kendall_s(x, t = seq_along(x))
```

**Arguments**

x	observations
t	time index

**References**

Gilbert, R.O., 1987. Statistical methods for environmental pollution monitoring.

**See Also**[kendall\\_var\\_s](#)


---

kendall_var_s	<i>Mann-Kendall Variance of S Statistic</i>
---------------	---

---

**Description**

Mann-Kendall Variance of S Statistic

**Usage**

```
kendall_var_s(x, t = seq_along(x))
```

**Arguments**

x	observations
t	time index

**References**

Gilbert, R.O., 1987. Statistical Methods for Environmental Pollution Monitoring.

Van Belle and Hughes, 1984, Nonparametric Tests for Trend in Water Quality. Water Resources Research 20:127-136

---

list_duplicates	<i>List Duplicates</i>
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---

**Description**

Lists all duplicates as a list of tuples.

**Usage**

```
list_duplicates(x, ...)

## S3 method for class 'character'
list_duplicates(x, ...)

## S3 method for class 'tbl'
list_duplicates(x, ...)

## S3 method for class 'data.frame'
list_duplicates(x, ...)
```

**Arguments**

x                    object of class `character`, `tibble` or `data.frame`.  
...                    further arguments passed to or from other methods.

**Value**

`list` of row numbers with duplicates

**Methods (by class)**

- `list_duplicates(character)`: list duplicates for a `character` vector.
- `list_duplicates(tbl)`: lists duplicates for a `tibble`.
- `list_duplicates(data.frame)`: lists duplicates for a `data.frame`.

**Examples**

```
list_duplicates(c("a", "b", "c")) # list()
list_duplicates(c("a", "b", "a", "c")) # list(c(1, 3))
```

---

litter

*Graphical User Interface to the litterR-package*

---

**Description**

Starts a graphical user interface for analysing litter data. A Tcl/Tk-dialogue will be started if one or more arguments are missing.

**Usage**

```
litter(filename = NULL)
```

**Arguments**

filename            name of file containing settings (see vignette for details)

**Details**

For details, see our vignette by typing: `vignette("litter-manual")`

**Value**

directory name (invisibly) where all results are stored.

---

mann_kendall	<i>Mann Kendall</i>
--------------	---------------------

---

## Description

Performs Mann-Kendall non-parametric test for trend.

## Usage

```
mann_kendall(x, t = seq_along(x), type = c("both", "increasing", "decreasing"))

## S3 method for class 'mann_kendall'
test_statistic(x, ...)

## S3 method for class 'mann_kendall'
p_value(x, ...)
```

## Arguments

x	numeric vector representing a time-series.
t	time index (a numeric vector, or a vector of class <a href="#">Date</a> ).
type	direction to test (both, increasing, or decreasing).
...	further arguments passed to or from other methods.

## Value

object of class Mann-Kendall.

## Methods (by generic)

- `test_statistic(mann_kendall)`: Extracts Mann Kendall tau
- `p_value(mann_kendall)`: Extract p-value

## See Also

[test\\_statistic](#), [p\\_value](#), [cor.test](#), [regional\\_kendall](#)

## Examples

```
# create mann_kendall object
mk <- mann_kendall(c(9, 4, 7, 5, 3), type = "decreasing")
mk <- mann_kendall(
  x = c(9, 4, 7, 5, 3),
  t = c(1, 3, 2, 5, 9),
  type = "decreasing")

# get test statistic tau
```

```
test_statistic(mk)

# get p-value
p_value(mk)
```

---

medcouple

*Medcouple*

---

## Description

Robust statistic that quantifies the skewness of univariate distributions.

## Usage

```
medcouple(x, ...)
```

## Default S3 method:  
medcouple(x, ...)

## Arguments

x                    numeric vector  
...                   further arguments passed to or from other methods.

## Value

medcouple (numeric vector of length 1).

## Methods (by class)

- medcouple(default): default method

## Note

This is a naive, but robust en simple implementation. For a more efficient implementation see package [robustbase](#) and the references section below.

## References

Brys, G., M. Hubert, A. Struyf, 2004. A Robust Measure of Skewness. *Journal of Computational and Graphical Statistics* 13: 996-1017. doi:[10.1198/106186004X12632](https://doi.org/10.1198/106186004X12632).

---

p_value	<i>p-value</i>
---------	----------------

---

**Description**

Extract p-value.

**Usage**

```
p_value(x, ...)
```

**Arguments**

x	object
...	further arguments passed to or from other methods.

**Value**

p-value of a test (numeric vector of length 1).

---

read_litter	<i>Read Litter Data</i>
-------------	-------------------------

---

**Description**

Reads litter data from various formats. Currently only the OSPAR data snapshot format, and a wide format are supported. See the package vignette for more details.

**Usage**

```
read_litter(filename, logger = create_logger(level = "INFO"), type_names)
```

**Arguments**

filename	name of litter file
logger	optional logger object (see <a href="#">create_logger</a> )
type_names	character vector of allowed type_names

**Value**

tibble with litter data in long format

---

read_litter_types	<i>Read Type Names</i>
-------------------	------------------------

---

**Description**

Read the file that links type names to group codes See the package vignette for more details.

**Usage**

```
read_litter_types(filename, logger = create_logger(level = "INFO"))
```

**Arguments**

filename	name of type file
logger	optional logger object (see <a href="#">create_logger</a> )

**Value**

tibble with look-up-table of type names and group codes

---

read_settings	<i>Read Settings File</i>
---------------	---------------------------

---

**Description**

Reads settings file. See tutorial for its format.

**Usage**

```
read_settings(filename, logger = create_logger(level = "INFO"))
```

**Arguments**

filename	name of litter file
logger	optional logger object (see <a href="#">create_logger</a> )

**Value**

validated settings file

---

recdf	<i>Sample From an ECDF</i>
-------	----------------------------

---

**Description**

Type stable implementation of an Empirical Cumulative Distribution Function (ECDF) sampler.

**Usage**

```
recdf(x, n)
```

**Arguments**

x	numeric vector
n	number of draws

**Value**

vector of n elements of the same type as x

**See Also**

[ecdf](#)

**Examples**

```
recdf(1:5, 10)
```

---

regional_kendall	<i>Regional Kendall Test for Trend</i>
------------------	--

---

**Description**

Performs Regional Kendall non-parametric test for trend.

**Usage**

```
regional_kendall(  
  x,  
  t = seq_along(x),  
  r = rep.int(1, length(x)),  
  type = c("both", "increasing", "decreasing")  
)  
  
## S3 method for class 'regional_kendall'  
test_statistic(x, ...)
```

```
## S3 method for class 'regional_kendall'
p_value(x, ...)
```

### Arguments

x	observations
t	time index
r	region index
type	direction to test (both, increasing, or decreasing).
...	further arguments passed to or from other methods.

### Methods (by generic)

- `test_statistic(regional_kendall)`: Extracts Regional Kendall Z
- `p_value(regional_kendall)`: Extract Regional Kendall p-value

### References

Gilbert, R.O., 1987. Statistical methods for environmental pollution monitoring.

### See Also

[mann\\_kendall](#)

---

rma

*Relative Median Absolute Deviation*

---

### Description

This is the Median Absolute Deviation divided by the median and is similar to the coefficient of variation.

### Usage

```
rma(x, na.rm = FALSE)
```

### Arguments

x	a numeric vector
na.rm	logical. Should missing values be removed?

### Value

Relative median absolute deviation (numeric vector of length 1).

### References

[https://en.wikipedia.org/wiki/Median\\_absolute\\_deviation](https://en.wikipedia.org/wiki/Median_absolute_deviation)

---

roll	<i>Rolling Statistics</i>
------	---------------------------

---

**Description**

Applies function fun within a rolling (moving) window of size w to vector numeric vector x.

**Usage**

```
roll(x, w = 3, fun = mean)
```

**Arguments**

x	numeric vector (time-series)
w	width of moving window
fun	function to be applied

**Value**

vector of length length(x)-w

---

sequenize	<i>Sequenize Objects</i>
-----------	--------------------------

---

**Description**

Generic function for sequenizing objects

**Usage**

```
sequenize(x, ...)
```

**Arguments**

x	object to sequenize
...	further arguments passed to or from other methods.

**See Also**

[sequenize.integer](#)

---

sequenize.integer	<i>Sequenize Integer Sequence</i>
-------------------	-----------------------------------

---

**Description**

Compression of integer sequences to 'start-end' notation. For instance `c(1:5, 8:9)` becomes "1-5, 8-9".

**Usage**

```
## S3 method for class 'integer'
sequenize(x, ...)
```

**Arguments**

<code>x</code>	vector of integers.
<code>...</code>	further arguments passed to or from other methods.

**Value**

object of class `sequenized`

**Note**

The elements of `x` should be unique and in ascending order.

**Examples**

```
sequenize(c(1:4, 8:9))
```

---

slope	<i>Slope</i>
-------	--------------

---

**Description**

Extract slope.

**Usage**

```
slope(x, ...)
```

**Arguments**

<code>x</code>	object
<code>...</code>	further arguments passed to or from other methods.

**Value**

estimate of the slope (numeric vector of length 1).

---

stat_adj_boxplot	<i>Adjusted Boxplot Statistics for ggplot2</i>
------------------	--

---

**Description**

Computes adjusted boxplot statistics to be used by ggplot2. See Hubert & Vandervieren (2008, p.5191, Eq.5).

**Usage**

```
stat_adj_boxplot()
stat_adj_boxplot_outlier()
```

**Functions**

- `stat_adj_boxplot_outlier()`: add outliers to adjusted boxplot

**References**

Hubert, M., and E. Vandervieren, 2008. An adjusted boxplot for skewed distributions. Computational Statistics and Data Analysis 52:5186-5201 [doi:10.1016/j.csda.2007.11.008](https://doi.org/10.1016/j.csda.2007.11.008)

**See Also**

[adj\\_boxplot\\_stats](#), [stat\\_adj\\_boxplot\\_outlier](#)

**Examples**

```
library(ggplot2)

d <- data.frame(x = gl(2, 50), y = rnorm(100))
ggplot(data = d, mapping = aes(x = x, y = y)) +
  stat_adj_boxplot()
```

---

test_statistic	<i>Test Statistic</i>
----------------	-----------------------

---

**Description**

Extract test\_statistic.

**Usage**

```
test_statistic(x, ...)
```

**Arguments**

x	object
...	further arguments passed to or from other methods.

**Value**

test statistic of a test (numeric vector of length 1).

**See Also**

[test\\_statistic.wilcoxon](#), [test\\_statistic.mann\\_kendall](#)

---

theil_sen	<i>Theil Sen Slope Estimator</i>
-----------	----------------------------------

---

**Description**

Theil Sen Slope Estimator

**Usage**

```
theil_sen(x, y, ...)

## S3 method for class 'theil_sen'
slope(x, ...)

## S3 method for class 'theil_sen'
intercept(x, ...)
```

**Arguments**

x	time vector (numeric, or Date).
y	numeric value.
...	further arguments passed to or from other methods.

**Value**

object of class Theil\_Sen.

**Methods (by generic)**

- `slope(theil_sen)`: Extract slope.
- `intercept(theil_sen)`: Extract intercept.

**References**

[https://en.wikipedia.org/wiki/Theil-Sen\\_estimator](https://en.wikipedia.org/wiki/Theil-Sen_estimator)

**Examples**

```
# create theil_sen object
ts <- theil_sen(1:5, c(1, 2, 3, 5, 9))

# get slope
slope(ts)

# get intercept
intercept(ts)
```

---

trimean

*Tukey's Trimean*

---

**Description**

Robust centrality measure estimated as the weighted average of the three quartiles:  $(Q_1 + 2Q_2 + Q_3)/4$ , where  $Q_1, Q_2$  and  $Q_3$  are the first, second and third quartiles respectively.

**Usage**

```
trimean(x, ...)
```

```
## Default S3 method:
trimean(x, ...)
```

**Arguments**

`x` numeric vector  
`...` further arguments passed to or from other methods.

**Value**

trimean (numeric value of length 1).

**Methods (by class)**

- `trimean(default)`: Tukey's trimean

**References**

<https://en.wikipedia.org/wiki/Trimean>

**Examples**

```
stopifnot(trimean(0:100) == mean(0:100))
stopifnot(trimean(0:100) == median(0:100))
```

---

validate

*Validation of Litter File Formats*

---

**Description**

Generic function for validation of file formats.

**Usage**

```
validate(x, ...)
```

```
## S3 method for class 'litter'
validate(x, type_names, logger = create_logger(level = "INFO"), ...)
```

```
## S3 method for class 'litter_types'
validate(x, logger = create_logger(level = "INFO"), ...)
```

```
## S3 method for class 'settings'
validate(x, logger = create_logger(level = "INFO"), ...)
```

**Arguments**

<code>x</code>	object to validate
<code>...</code>	further arguments passed to or from other methods.
<code>type_names</code>	character vector of permissible types
<code>logger</code>	optional logger object (see <a href="#">create_logger</a> )

**Value**

validated object of class wide  
validated object of class `litter_types`  
validated settings (list)

**Methods (by class)**

- `validate(litter)`: validate litter data.
- `validate(litter_types)`: validate litter\_types file
- `validate(settings)`: validate settings file

---

 wilcoxon

*Wilcoxon Test*


---

**Description**

Constructor for a Wilcoxon test (simple wrapper for `wilcox.test`).

**Usage**

```
wilcoxon(x, type = c("both", "greater", "less"), mu = 0)
```

```
## S3 method for class 'wilcoxon'
test_statistic(x, ...)
```

```
## S3 method for class 'wilcoxon'
p_value(x, ...)
```

**Arguments**

<code>x</code>	numeric vector representing a time-series.
<code>type</code>	direction to test (both, increasing, or decreasing).
<code>mu</code>	baseline value (null hypothesis)
<code>...</code>	further arguments passed to or from other methods.

**Value**

object of class `wilcoxon`.

**Methods (by generic)**

- `test_statistic(wilcoxon)`: Extract test statistic V
- `p_value(wilcoxon)`: Extract p-value

**See Also**

[wilcox.test](#), [p\\_value](#), [test\\_statistic](#)

**Examples**

```
# create wilcoxon object
w <- wilcoxon(c(9, 4, 7, 5, 3), type = "less")

# get test statistic V
test_statistic(w)

# get p-value
p_value(w)
```

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