

# Package ‘lidR’

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**Type** Package

**Title** Airborne LiDAR Data Manipulation and Visualization for Forestry Applications

**Version** 3.2.2

**Description** Airborne LiDAR (Light Detection and Ranging) interface for data manipulation and visualization. Read/write 'las' and 'laz' files, computation of metrics in area based approach, point filtering, artificial point reduction, classification from geographic data, normalization, individual tree segmentation and other manipulations.

**URL** <https://github.com/Jean-Romain/lidR>

**BugReports** <https://github.com/Jean-Romain/lidR/issues>

**License** GPL-3

**Depends** R (>= 3.4.0), methods, raster, sp (>= 1.4.2)

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'Class-LAScluster.R' 'RcppExports.R' 'add\_attribute.R'  
'algorithm-dec.R' 'algorithm-dsm.R' 'algorithm-gnd.R'  
'algorithm-itd.R' 'algorithm-its.R' 'algorithm-noi.R'  
'algorithm-out.R' 'algorithm-shp.R' 'algorithm-snag.R'  
'algorithm-spi.R' 'algorithm-trk.R' 'catalog\_apply.R'

'catalog\_boundaries.R' 'catalog\_fakerun.R' 'catalog\_index.R'  
 'catalog\_intersect.R' 'catalog\_laxindex.R'  
 'catalog\_makecluster.R' 'catalog\_merge\_results.R'  
 'catalog\_overlaps.R' 'catalog\_retile.R' 'catalog\_select.R'  
 'classify\_ground.R' 'classify\_noise.R' 'classify\_poi.R'  
 'clip\_roi.R' 'cloud\_metrics.R' 'clusters\_apply.R'  
 'concaveman.R' 'decimate\_points.R' 'delineate\_crowns.R'  
 'deprecated.R' 'doc-drivers.R' 'doc-lidR.R' 'doc-parallelism.R'  
 'filter\_duplicates.R' 'filter\_poi.R' 'filter\_roi.R'  
 'filter\_surfacepoints.R' 'find\_localmaxima.R' 'find\_trees.R'  
 'fullwaveform.R' 'generate\_las.R' 'grid\_canopy.R'  
 'grid\_density.R' 'grid\_metrics.R' 'grid\_terrain.R'  
 'io\_readLAS.R' 'io\_readLAScatalog.R' 'io\_readXLAS.R'  
 'io\_writeANY.R' 'io\_writeLAS.R' 'las\_check.R' 'las\_tools.R'  
 'merge\_las.R' 'merge\_spatial.R' 'methods-LAS.R'  
 'methods-LAScatalog.R' 'methods-LAScluster.R'  
 'methods-LASheader.R' 'normalize\_height.R'  
 'normalize\_intensity.R' 'plot.R' 'plot.s3.R' 'plot\_metrics.R'  
 'point\_metrics.R' 'print.R' 'projection.R' 'retrieve\_info.R'  
 'segment\_shapes.R' 'segment\_snags.R' 'segment\_trees.R'  
 'sensor\_tracking.R' 'smooth\_height.R' 'tree\_metrics.R'  
 'utils\_assertive.R' 'utils\_catalog\_options.R' 'utils\_colors.R'  
 'utils\_define\_constant.R' 'utils\_delaunay.R' 'utils\_geometry.R'  
 'utils\_is.R' 'utils\_metrics.R' 'utils\_misc.R' 'utils\_raster.R'  
 'utils\_spatial\_index.R' 'utils\_threads.R' 'utils\_typecast.R'  
 'voxel\_metrics.R' 'voxelize\_points.R' 'zzz.R'

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lidR-package	<i>lidR: airborne LiDAR for forestry applications</i>
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## Description

lidR provides a set of tools to manipulate airborne LiDAR data in forestry contexts. The package works essentially with .las or .laz files. The toolbox includes algorithms for DSM, CHM, DTM, ABA, normalisation, tree detection, tree segmentation and other tools, as well as an engine to process wide LiDAR coverages split into many files.

## Details

To learn more about lidR, start with the vignettes: `browseVignettes(package = "lidR")`. Users can also find unofficial supplementary documentation in the [lidR book](#). To ask "how to" questions please ask on [gis.stackexchange.com](https://gis.stackexchange.com) with the tag `lidr`.

## Package options

- `lidR.progress` Several functions have a progress bar for long operations (but not all). Should lengthy operations show a progress bar? Default: TRUE
- `lidR.progress.delay` The progress bar appears only for long operations. After how many seconds of computation does the progress bar appear? Default: 2
- `lidR.verbose` Make the package verbose. Default: FALSE
- `lidR.buildVRT` The functions `grid_*` can write the rasters sequentially on the disk and load back a virtual raster mosaic (VRT) instead of the list of written files. Should a VRT be built? Default: TRUE
- `lidR.check.nested.parallelism` The catalog processing engine ([catalog\\_apply](#)) checks the parallel strategy chosen by the user and verify if C++ parallelization with OpenMP should be disabled to avoid nested parallel loops. Default: TRUE. If FALSE the catalog processing engine will not check for nested parallelism and will respect the settings of [set\\_lidr\\_threads](#).

## Author(s)

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- Florian De Boissieu (Fixed bugs and improved catalog features) [contributor]
- Andrew Sánchez Meador (Implemented wing2015() for segment\_snags()) [contributor]
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- Gatzolis Demetrios (Implemented Gatzolis2019() for track\_sensor()) [contributor]
- Leon Steinmeier (Contributed to parallelization management) [contributor]
- Stanislaw Adaszewski (Author of the C++ concaveman code) [copyright holder]

### See Also

Useful links:

- <https://github.com/Jean-Romain/lidR>
- Report bugs at <https://github.com/Jean-Romain/lidR/issues>

---

add\_attribute

*Add attributes into a LAS object*

---

### Description

A **LAS** object represents a las file in R. According to the **LAS specifications** a las file contains a core of defined attributes, such as XYZ coordinates, intensity, return number, and so on, for each point. It is possible to add supplementary attributes.

### Usage

```
add_attribute(las, x, name)
```

```
add_lasattribute(las, x, name, desc)
```

```
add_lasattribute_manual(  
  las,  
  x,  
  name,  
  desc,  
  type,  
  offset = NULL,  
  scale = NULL,  
  NA_value = NULL  
)
```

```
add_lasrgb(las, R, G, B)
```

```
remove_lasattribute(las, name)
```

**Arguments**

las	An object of class <a href="#">LAS</a>
x	a vector that needs to be added in the LAS object. For <code>add_lasattribute*</code> it can be missing (see details).
name	character. The name of the extra bytes attribute to add in the file.
desc	character. A short description of the extra bytes attribute to add in the file (32 characters).
type	character. The data type of the extra bytes attribute. Can be "uchar", "char", "ushort", "short", "uint"
scale, offset	numeric. The scale and offset of the data. NULL if not relevant.
NA_value	numeric or integer. NA is not a valid value in a las file. At time of writing it will be replaced by this value that will be considered as NA. NULL if not relevant.
R, G, B	integer. RGB values

**Details**

Users cannot assign names that are the same as the names of the core attributes. These functions are dedicated to adding data that are not part of the LAS specification. For example, `add_lasattribute(las, x, "R")` will fail because R is a name reserved for the red channel of a .las file that contains RGB attributes. Use `add_lasrgb` instead.

`add_attribute` Simply adds a new column in the data but does not update the header. Thus the LAS object is not strictly valid. These data will be temporarily usable at the R level but will not be written in a las file with [writeLAS](#).

`add_lasattribute` Does the same as `add_attribute` but automatically updates the header of the LAS object. Thus, the LAS object is valid and the new data is considered as "extra bytes". This new data will be written in a las file with [writeLAS](#).

`add_lasattribute_manual` Allows the user to manually write all the extra bytes metadata. This function is reserved for experienced users with a good knowledge of the LAS specifications. The function does not perform tests to check the validity of the information. When using `add_lasattribute` and `add_lasattribute_manual`, x can only be of type numeric, (integer or double). It cannot be of type character or logical as these are not supported by the LAS specifications. The types that are supported in lidR are types 0 to 10 (Table 24 on page 25 of the specification). Types greater than 10 are not supported.

`add_lasrgb` Adds 3 columns named RGB and updates the point format of the LAS object for a format that supports RGB attributes. If the RGB values are ranging from 0 to 255 they are automatically scaled on 16 bits.

**Value**

An object of class [LAS](#)

**Examples**

```
LASfile <- system.file("extdata", "example.laz", package="rlas")
las <- readLAS(LASfile, select = "xyz")
```

```

print(las)
print(las@header)

x <- 1:30

las <- add_attribute(las, x, "mydata")
print(las)      # The las object has a new attribute called "mydata"
print(las@header) # But the header has not been updated. This new data will not be written

las <- add_lasattribute(las, x, "mydata2", "A new data")
print(las)      # The las object has a new attribute called "mydata2"
print(las@header) # The header has been updated. This new data will be written

# Optionally if the data is already in the LAS object you can update the header skipping the
# parameter x
las <- add_lasattribute(las, name = "mydata", desc = "Amplitude")
print(las@header)

# Remove an extra bytes attribute
las <- remove_lasattribute(las, "mydata2")
print(las)
print(las@header)

las <- remove_lasattribute(las, "mydata")
print(las)
print(las@header)

```

---

area

*Surface covered by a LAS\* object*

---

## Description

Surface covered by a LAS\* object. For LAS point clouds it is computed based on the convex hull of the points. For a LAScatalog it is computed as the sum of the bounding boxes of the files. For overlapping tiles the value may be larger than the total covered area because some regions are sampled twice. For a LASheader it is computed with the bounding box. The function `npoints` does what the user may expect it to do and the function `density` is equivalent to `npoints(x)/area(x)`. As a consequence for the same file `area` applied on a `LASheader` or on a `LAS` can return slightly different values.

## Usage

```

area(x, ...)

## S4 method for signature 'LAS'
area(x, ...)

## S4 method for signature 'LASheader'
area(x, ...)

```



```
## S4 method for signature 'LAScatalog'  
area(x, ...)  
  
npoints(x, ...)  
  
## S4 method for signature 'LAS'  
npoints(x, ...)  
  
## S4 method for signature 'LASheader'  
npoints(x, ...)  
  
## S4 method for signature 'LAScatalog'  
npoints(x, ...)  
  
density(x, ...)  
  
## S4 method for signature 'LAS'  
density(x, ...)  
  
## S4 method for signature 'LASheader'  
density(x, ...)  
  
## S4 method for signature 'LAScatalog'  
density(x, ...)
```

### Arguments

x	An object of the class LAS*.
...	unused.

### Value

numeric. A number. Notice that for area the measure is in the same units as the coordinate reference system.

---

as.list.LASheader	<i>Transform to a list</i>
-------------------	----------------------------

---

### Description

Functions to construct, coerce and check for both kinds of R lists.

### Usage

```
## S3 method for class 'LASheader'  
as.list(x, ...)
```

**Arguments**

x                    A LASheader object  
 ...                   unused

---

as.spatial                    *Transform a LAS\* object into an sp object*

---

**Description**

LAS and LAScatalog objects are transformed into SpatialPointsDataFrame and SpatialPolygons-DataFrame objects, respectively.

**Usage**

as.spatial(x)

**Arguments**

x                    an object from the lidR package

**Value**

An object from sp

---

asprs                    *ASPRS LAS Classification*

---

**Description**

A set of global variables corresponding to the point classification defined by the ASPRS for the LAS format. Instead of remembering the classification table of the specification it is possible to use one of these global variables.

**Usage**

LASNONCLASSIFIED

LASUNCLASSIFIED

LASGROUND

LASLOWVEGETATION

LASMEDIUMVEGETATION

LASHIGHVEGETATION

LASBUILDING

LASLOWPOINT

LASKEYPOINT

LASWATER

LASRAIL

LASROADSURFACE

LASWIREGUARD

LASWIRECONDUCTOR

LASTRANSMISSIONTOWER

LASBRIGDE

LASNOISE

**Format**

An object of class integer of length 1.

An object of class integer of length 1.

An object of class integer of length 1.

An object of class integer of length 1.

An object of class integer of length 1.

An object of class integer of length 1.

An object of class integer of length 1.

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An object of class integer of length 1.

An object of class integer of length 1.

An object of class integer of length 1.

An object of class integer of length 1.

An object of class integer of length 1.

An object of class integer of length 1.

An object of class integer of length 1.

## Examples

```
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las = readLAS(LASfile)
las2 = filter_poi(las, Classification %in% c(LASGROUND, LASWATER))

print(LASGROUND)
```

---

catalog\_apply

*LAScatalog processing engine*

---

## Description

This function gives users access to the [LAScatalog](#) processing engine. It allows the application of a user-defined routine over an entire catalog. The LAScatalog processing engine tool is explained in the [LAScatalog class](#)

catalog\_apply() is the core of the lidR package. It drives every single function that can process a LAScatalog. It is flexible and powerful but also complex. catalog\_sapply is the same with the option automerge = TRUE enforced to simplify the output.

**Warning:** the LAScatalog processing engine has a mechanism to load buffered data 'on-the-fly' to avoid edge artifacts, but no mechanism to remove the buffer after applying user-defined functions, since this task is specific to each process. In other lidR functions this task is performed specifically for each function. In catalog\_apply() the user's function can return any output, thus users must take care of this task themselves (See section "Edge artifacts")

## Usage

```
catalog_apply(ctg, FUN, ..., .options = NULL)
```

```
catalog_sapply(ctg, FUN, ..., .options = NULL)
```

## Arguments

ctg	A <a href="#">LAScatalog</a> object.
FUN	A user-defined function that respects a given template (see section function template)
...	Optional arguments to FUN.
.options	See dedicated section and examples.

## Edge artifacts

It is important to take precautions to avoid 'edge artifacts' when processing wall-to-wall tiles. If the points from neighboring tiles are not included during certain processes, this could create 'edge artifacts' at the tile boundaries. For example, empty or incomplete pixels in a rasterization process, or dummy elevations in a ground interpolation. The LAScatalog processing engine provides internal

tools to load buffered data 'on-the-fly'. However, there is no mechanism to remove the results computed in the buffered area since this task depends on the output of the user-defined function. The user must take care of this task (see examples) to prevent unexpected output with duplicated entries or conflict between values computed twice.

### Buffered data

The LAS objects read by the user function have a special attribute called 'buffer' that indicates, for each point, if it comes from a buffered area or not. Points from non-buffered areas have a 'buffer' value of 0, while points from buffered areas have a 'buffer' value of 1, 2, 3 or 4, where 1 is the bottom buffer and 2, 3 and 4 are the left, top and right buffers, respectively. This allows for filtering of buffer points if required.

### Function template

The parameter FUN expects a function with a first argument that will be supplied automatically by the LAScatalog processing engine. This first argument is a LAScluster. A LAScluster is an internal undocumented class but the user needs to know only three things about this class:

- It represents a chunk of the catalog
- The function [readLAS](#) can be used with a LAScluster
- The function [extent](#) or [bbox](#) can be used with a LAScluster and it returns the bounding box of the cluster without the buffer. It can be used to clip the output and remove the buffered region (see examples).

A user-defined function must be templated like this:

```
myfun <- function(cluster, ...) {
  las <- readLAS(cluster)
  if (is.empty(las)) return(NULL)
  # do something
  # remove the buffer of the output
  return(something)
}
```

The line `if(is.empty(las)) return(NULL)` is important because some clusters (chunks) may contain 0 points (we can't know this before reading the file). In this case an empty point cloud with 0 points is returned by `readLAS()` and this may fail in subsequent code. Thus, exiting early from the user-defined function by returning NULL indicates to the internal engine that the cluster was empty.

From v3.0.0 if `autoread = TRUE` the following template is accepted because the engine takes care of the above mentioned steps:

```
myfun <- function(las, bbox ...) {
  # do something
}
```

**.options**

Users may have noticed that some lidR functions throw an error when the processing options are inappropriate. For example, some functions need a buffer and thus `buffer = 0` is forbidden. Users can add the same constraints to protect against inappropriate options. The `.options` argument is a `list` that allows users to tune the behavior of the processing engine.

- `drop_null = FALSE` Not intended to be used by regular users. The engine does not remove NULL outputs
- `need_buffer = TRUE` the function complains if the buffer is 0.
- `need_output_file = TRUE` the function complains if no output file template is provided.
- `raster_alignment = ...` the function checks the alignment of the chunks. This option is important if the output is a raster. See below for more details.
- `automerge = TRUE` by default the engine returns a `list` with one item per chunk. If `automerge = TRUE`, it tries to merge the outputs into a single object: a `Raster*`, a `Spatial*`, a `LAS*` similar to other functions of the package. This is a fail-safe option so in the worst case, if the merge fails, the `list` is returned.
- `autoread = TRUE`. Introduced in v3.0.0 this option enables to get rid of the first steps of the function i.e `readLAS()` and `if(is.empty())`. In this case the function must take two objects as input, first a `LAS` object and second a `Extent` from raster.

When the function FUN returns a raster it is important to ensure that the chunks are aligned with the raster to avoid edge artifacts. Indeed, if the edge of a chunk does not correspond to the edge of the pixels, the output will not be strictly continuous and will have edge artifacts (that might not be visible). Users can check this with the options `raster_alignment`, that can take the resolution of the raster as input, as well as the starting point if needed. The following are accepted:

```
# check if chunks are aligned with a raster of resolution 20
raster_alignment = 20
raster_alignment = list(res = 20)

# check if chunks are aligned with a raster of resolution 20
# that starts at (0,10)
raster_alignment = list(res = 20, start = c(0,10))
```

See also [grid\\_metrics](#) for more details.

**Supported processing options**

Supported processing options for a `LAScatalog` (in bold). For more details see the [LAScatalog engine documentation](#):

- ***chunk\_size***: How much data is loaded at once.
- ***chunk\_buffer***: Load chunks with a buffer.
- ***chunk\_alignment***: Align the chunks.
- ***progress***: Displays a progress estimate.
- ***output\_files***: The user-defined function outputs will be written to files instead of being returned into R.

- *laz\_compression*: write las or laz files only if the user-defined function returns a 'LAS' object.
- *select*: Select only the data of interest to save processing memory.
- *filter*: Read only the points of interest.

## Examples

```
# More examples might be available in the official lidR vignettes or
# on the github book <https://jean-romain.github.io/lidRbook/>

## =====
## Example 1: detect all the tree tops over an entire catalog
## (this is basically a reproduction of the existing lidR function 'tree_detection')
## =====

# 1. Build the user-defined function that analyzes each chunk of the catalog.
# The function's first argument is a LAScluster object. The other arguments can be freely
# chosen by the user.
my_tree_detection_method <- function(cluster, ws)
{
  # The cluster argument is a LAScluster object. The user does not need to know how it works.
  # readLAS will load the region of interest (chunk) with a buffer around it, taking advantage of
  # point cloud indexing if possible. The filter and select options are propagated automatically
  las <- readLAS(cluster)
  if (is.empty(las)) return(NULL)

  # Find the tree tops using a user-developed method (here simply a LMF).
  ttops <- find_trees(las, lmf(ws))

  # ttops is a SpatialPointsDataFrame that contains the tree tops in our region of interest
  # plus the trees tops in the buffered area. We need to remove the buffer otherwise we will get
  # some trees more than once.
  bbox <- raster::extent(cluster)
  ttops <- raster::crop(ttops, bbox)

  return(ttops)
}

# 2. Build a project (here, a single file catalog for the purposes of this dummy example).
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
prj <- readLAScatalog(LASfile)
plot(prj)

# 3. Set some processing options.
# For this dummy example, the chunk size is 100 m and the buffer is 10 m
opt_chunk_buffer(prj) <- 10
opt_chunk_size(prj) <- 100 # small because this is a dummy example.
opt_chunk_alignment(prj) <- c(-50, -35) # Align such as it creates 2 chunks only.
opt_select(prj) <- "xyz" # Read only the coordinates.
opt_filter(prj) <- "-keep_first" # Read only first returns.

# 4. Apply a user-defined function to take advantage of the internal engine
```

```

opt  <- list(need_buffer = TRUE, # catalog_apply will throw an error if buffer = 0
            automerge   = TRUE) # catalog_apply will merge the outputs into a single object
output <- catalog_apply(prj, my_tree_detection_method, ws = 5, .options = opt)

splot(output)

## Not run:

## =====
## Example 2: compute a rumple index on surface points
## =====

rumple_index_surface = function(cluster, res)
{
  las = readLAS(cluster)
  if (is.empty(las)) return(NULL)

  las  <- filter_surfacepoints(las, 1)
  rumple <- grid_metrics(las, ~rumple_index(X,Y,Z), res)
  bbox  <- raster::extent(cluster)
  rumple <- raster::crop(rumple, bbox)

  return(rumple)
}

LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
prj <- readLAScatalog(LASfile)

opt_chunk_buffer(prj) <- 1
opt_chunk_size(prj)   <- 140 # small because this is a dummy example.
opt_select(prj)       <- "xyz" # read only the coordinates.

opt  <- list(raster_alignment = 20, # catalog_apply will adjust the chunks if required
            automerge = TRUE) # catalog_apply will merge the outputs into a single raster
output <- catalog_apply(prj, rumple_index_surface, res = 20, .options = opt)

plot(output, col = height.colors(50))

## End(Not run)

```

---

catalog\_boundaries      *Computes the polygon that encloses the points*

---

### Description

Computes the polygon that encloses the points. It reads all the files one by one and computes a concave hull using the [concaveman](#) function. When all the hulls are computed it updates the LAScatalog to set the true polygons instead of the bounding boxes.



## Usage

```
catalog_boundaries(ctg, concavity = 5, length_threshold = 5)
```

## Arguments

ctg	A LAScatalog
concavity	numeric. A relative measure of concavity. 1 results in a relatively detailed shape, Infinity results in a convex hull. You can use values lower than 1, but they can produce pretty crazy shapes.
length_threshold	numeric. When a segment length is under this threshold, it stops being considered for further detailed processing. Higher values result in simpler shapes.

## Value

A LAScatalog with true boundaries

## Supported processing options

Supported processing options for more details see the [LAScatalog engine documentation](#):

- chunk size: Not supported, it processes by file.
- chunk buffer: Not supported, it processes by file with no buffer.
- chunk alignment: Not supported, it processes by file.
- **progress**: Displays a progress estimate.
- output files: Not supported, it returns an R object.
- select: Not supported, it loads XYZ only.
- **filter**: Read only the points of interest.

## Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
ctg <- readLAScatalog(LASfile, filter = "-drop_z_below 0.5")
ctg2 <- catalog_boundaries(ctg, 1, 15)
plot(ctg)
plot(ctg2, add = TRUE)
```

---

catalog\_intersect      *Subset a LAScatalog with a spatial object*

---

### Description

Subset a LAScatalog with a spatial object to keep only the tiles of interest. It can be used to select tiles of interest that encompass spatial objects such as Spatial\* objects, Raster\* objects or sf and sfc objects

### Usage

```
catalog_intersect(ctg, y)
```

### Arguments

ctg	A <a href="#">LAScatalog</a> object
y	Extent, Raster*, Spatial*, sf, sfc, Extent or bbox objects

### Value

A LAScatalog

---

catalog\_makechunks      *Subdivide a LAScatalog into chunks*

---

### Description

Virtually subdivide a LAScatalog into chunks. This function is an internal function exported to users in version 3.0.0 because it might be useful for some debugging purposes. It might also be useful for some advanced developers. Regular users are not expected to use this function. The chunks are made according to the [catalog processing options](#).

### Usage

```
catalog_makechunks(ctg, realignment = FALSE, plot = opt_progress(ctg))
```

### Arguments

ctg	an object of class LAScatalog
realignment	FALSE or list(res = x, start = c(y, z)). Sometimes the chunk must be aligned with a raster, for example to ensure the continuity of the output. If the chunk size is 800 and the expected product is a raster with a resolution of 35, 800 and 35 are not compatible and will create 2 different partial pixels on the edges. The realignment option forces the chunk to fit the grid alignment.
plot	logical. Displays the chunk pattern.

**Value**

A list containing objects of class LAScluster.

---

catalog\_options\_tools *Get or set LAScatalog processing engine options*

---

**Description**

The names of the options and their roles are documented in [LAScatalog](#). The options are used by all the functions that support a LAScatalog as input. Most options are easy to understand and to link to the documentation of [LAScatalog](#) but some need more details. See section 'Details'.

**Usage**

```
opt_chunk_buffer(ctg)
opt_chunk_buffer(ctg) <- value
opt_chunk_size(ctg)
opt_chunk_size(ctg) <- value
opt_chunk_alignment(ctg)
opt_chunk_alignment(ctg) <- value
opt_restart(ctg) <- value
opt_progress(ctg)
opt_progress(ctg) <- value
opt_stop_early(ctg)
opt_stop_early(ctg) <- value
opt_wall_to_wall(ctg)
opt_wall_to_wall(ctg) <- value
opt_independent_files(ctg)
opt_independent_files(ctg) <- value
opt_output_files(ctg)
```

```
opt_output_files(ctg) <- value
opt_laz_compression(ctg)
opt_laz_compression(ctg) <- value
opt_merge(ctg)
opt_merge(ctg) <- value
opt_select(ctg)
opt_select(ctg) <- value
opt_filter(ctg)
opt_filter(ctg) <- value
```

### Arguments

ctg	An object of class <a href="#">LAScatalog</a>
value	An appropriate value depending on the expected input.

### Details

- **opt\_restart()** automatically sets the chunk option named "drop" in such a way that the engine will restart at a given chunk and skip all previous chunks. Useful for restarting after a crash.
- **opt\_independent\_file()** automatically sets the chunk size, chunk buffer and wall-to-wall options to process files that are not spatially related to each other, such as plot inventories.
- **opt\_laz\_compression()** automatically modifies the drivers to write LAZ files instead of LAS files.

### Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
ctg = readLAScatalog(LASfile)

plot(ctg, chunk_pattern = TRUE)

opt_chunk_size(ctg) <- 150
plot(ctg, chunk_pattern = TRUE)

opt_chunk_buffer(ctg) <- 10
plot(ctg, chunk_pattern = TRUE)

opt_chunk_alignment(ctg) <- c(270,250)
plot(ctg, chunk_pattern = TRUE)

summary(ctg)
```

```
opt_output_files(ctg) <- "/path/to/folder/templated_filename_{XBOTTOM}_{ID}"  
summary(ctg)
```

---

catalog_retile	<i>Retile a LAScatalog</i>
----------------	----------------------------

---

## Description

Splits or merges files to reshape the original catalog files (.las or .laz) into smaller or larger files. It also enables the addition or removal of a buffer around the tiles. The function first displays the layout of the new tiling pattern and then asks the user to validate the command.

Internally, the function reads and writes the clusters defined by the internal processing options of a [LAScatalog](#) processing engine. Thus, the function is flexible and enables the user to retile the dataset, retile while adding or removing a buffer (negative buffers are allowed), or optionally to compress the data by retiling without changing the pattern but by changing the format (las/laz).

Note that this function is not actually very useful since `lidR` manages everything (clipping, processing, buffering, ...) internally using the proper options. Thus, retiling may be useful for working in other software, for example, but not in `lidR`.

## Usage

```
catalog_retile(ctg)
```

## Arguments

ctg                    A [LAScatalog](#) object

## Value

A new [LAScatalog](#) object

## Working with a LAScatalog

This section appears in each function that supports a [LAScatalog](#) as input.

In `lidR` when the input of a function is a [LAScatalog](#) the function uses the [LAScatalog](#) processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing [LAScatalogs](#). Each `lidR` function should come with a section that documents the supported engine options.

The [LAScatalog](#) engine supports `.lax` files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a `.lax` files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk\_size**: Size of the new tiles.
- **buffer**: Load new tiles with a buffer. The expected value is usually 0.
- **alignment**: Alignment of the new tiles.
- **cores**: The number of cores used. catalog\_retile streams the data (nothing is loaded at the R level). The maximum number of cores can be safely used.
- **progress**: Displays a progress estimation.
- **output\_files\***: Mandatory. The new tiles will be written in new files.
- **laz\_compression**: save las or laz files.
- **select**: catalog\_retile preserve the file format anyway.
- **filter**: Retile and save only the points of interest.

### Examples

```
## Not run:
ctg = readLAScatalog("path/to/catalog")

# Create a new set of .las files 500 x 500 wide in the folder
# path/to/new/catalog/ and iteratively named Forest_1.las, Forest_2.las
# Forest_3.las, and so on.

opt_chunk_buffer(ctg) <- 0
opt_chunk_size(ctg) <- 500
opt_output_files(ctg) <- "path/to/new/catalog/Forest_{ID}"
newctg = catalog_retile(ctg)

# Create a new set of .las files equivalent to the original,
# but extended with a 50 m buffer in the folder path/to/new/catalog/
# and iteratively named named after the original files.

opt_chunk_buffer(ctg) <- 50
opt_chunk_size(ctg) <- 0
opt_output_files(ctg) <- "path/to/new/catalog/{ORIGINALFILENAME}_buffered"
newctg = catalog_retile(ctg)

# Create a new set of compressed .laz file equivalent to the original, keeping only
# first returns above 2 m

opt_chunk_buffer(ctg) <- 0
opt_chunk_size(ctg) <- 0
opt_laz_compression(ctg) <- TRUE
opt_filter(ctg) <- "-keep_first -drop_z_below 2"
newctg = catalog_retile(ctg)

## End(Not run)
```

---

catalog_select	Select LAS files manually from a LAScatalog
----------------	---

---

## Description

Select a set of LAS tiles from a LAScatalog interactively using the mouse. This function allows users to subset a LAScatalog by clicking on a map of the file.

## Usage

```
catalog_select(  
  ctg,  
  mapview = TRUE,  
  method = c("subset", "flag_unprocessed", "flag_processed")  
)
```

## Arguments

ctg	A <a href="#">LAScatalog</a> object
mapview	logical. If FALSE, use R base plot instead of mapview (no pan, no zoom, see also <a href="#">plot</a> )
method	character. By default selecting tiles that are a subset of the catalog. It is also possible to flag the files to maintain the catalog as a whole but process only a subset of its content. <code>flag_unprocessed</code> enables users to point and click on files that will not be processed. <code>flag_processed</code> enables users to point and click on files that will be processed.

## Value

A LAScatalog object

## Examples

```
## Not run:  
ctg = readLAScatalog("<Path to a folder containing a set of .las files>")  
new_ctg = catalog_select(ctg)  
  
## End(Not run)
```

---

classify_ground	<i>Classify points as 'ground'</i>
-----------------	------------------------------------

---

### Description

Classify points as 'ground' with several possible algorithms. The function updates the attribute Classification of the LAS object. The points classified as 'ground' are assigned a value of 2 according to [las specifications](#).

### Usage

```
classify_ground(las, algorithm, last_returns = TRUE)
```

### Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
algorithm	a ground-segmentation function. lidR has: <a href="#">pmf</a> and <a href="#">csf</a> . The <a href="#">lidRplugins</a> package has 'mcc'.
last_returns	logical. The algorithm will use only the last returns (including the first returns in cases of a single return) to run the algorithm. If FALSE all the returns are used. If the attribute 'ReturnNumber' or 'NumberOfReturns' are absent, 'last_returns' is turned to FALSE automatically.

### Value

If the input is a LAS object, return a LAS object. If the input is a LAScatalog, returns a LAScatalog.

### Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.



- **chunk buffer\***: Mandatory to get a continuous output without edge effects. The buffer is always removed once processed and will never be returned either in R or in files.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files\***: Mandatory because the output is likely to be too big to be returned in R and needs to be written in las/laz files. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The function will write files equivalent to the original ones. Thus select = "\*" and cannot be changed.
- **filter**: Read only points of interest.

### Examples

```

LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las <- readLAS(LASfile, select = "xyzrn", filter = "-inside 273450 5274350 273550 5274450")

# Using the Progressive Morphological Filter
# -----

# (Parameters chosen mainly for speed)
ws <- seq(3,12, 4)
th <- seq(0.1, 1.5, length.out = length(ws))

las <- classify_ground(las, pmf(ws, th))
#plot(las, color = "Classification")

#' # Using the Cloth Simulation Filter
# -----

# (Parameters chosen mainly for speed)
mycsf <- csf(TRUE, 1, 1, time_step = 1)
las <- classify_ground(las, mycsf)
#plot(las, color = "Classification")

```

---

classify_noise	<i>Classify points as 'noise'</i>
----------------	-----------------------------------

---

### Description

Classify points as 'noise' (outliers) with several possible algorithms. The function updates the attribute Classification of the LAS object. The points classified as 'noise' are assigned a value of 18 according to [las specifications](#).

### Usage

```
classify_noise(las, algorithm)
```

**Arguments**

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
algorithm	a noise-segmentation function. lidR has: <a href="#">sor</a> , <a href="#">ivf</a> .

**Value**

If the input is a LAS object, return a LAS object. If the input is a LAScatalog, returns a LAScatalog.

**Working with a LAScatalog**

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

**Supported processing options**

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- **chunk buffer\***: Mandatory to get a continuous output without edge effects. The buffer is always removed once processed and will never be returned either in R or in files.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files\***: Mandatory because the output is likely to be too big to be returned in R and needs to be written in las/laz files. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The function will write files equivalent to the original ones. Thus select = "\*" and cannot be changed.
- **filter**: Read only points of interest.

**Examples**

```
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las <- readLAS(LASfile, filter = "-inside 273450 5274350 273550 5274450")

# Add 20 artificial outliers
set.seed(314)
```

```

id = round(runif(20, 0, npoints(las)))
set.seed(42)
err = runif(20, -50, 50)
las$Z[id] = las$Z[id] + err

# Using SOR
las <- classify_noise(las, sor(15,7))
#plot(las, color = "Classification")

# Using IVF
las <- classify_noise(las, ivf(5,2))

# Remove outliers using filter_poi()
las_denoise <- filter_poi(las, Classification != LASNOISE)

```

---

classify\_poi

*Classify points of interest*


---

### Description

Classify points that meet some logical criterion and/or that belong in a region of interest. The function updates the attribute Classification of the LAS object.

### Usage

```

classify_poi(
  las,
  class,
  poi = NULL,
  roi = NULL,
  inverse_roi = FALSE,
  by_reference = FALSE,
  ...
)

```

### Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
class	The ASPRS class to attribute to the points that meet the criterion.
poi	a formula of logical predicates. The points that are TRUE will be classified class.
roi	A SpatialPolygons, SpatialPolygonDataFrame from <a href="#">sp</a> or a POLYGON from <a href="#">sf</a> . The points that are in the region of interest delimited by the polygon(s) are classified class.
inverse_roi	bool. Inverses the roi. The points that are outside the polygon(s) are classified class
by_reference	bool. Updates the classification in place (LAS only).
...	Unused

**Value**

If the input is a LAS object, return a LAS object. If the input is a LAScatalog, returns a LAScatalog.

**Working with a LAScatalog**

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

**Supported processing options**

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- chunk buffer: A buffer is not need for this function to works thus `buffer = 0` and cannot be changed.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files\***: Mandatory because the output is likely to be too big to be returned in R and needs to be written in las/laz files. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The function will write files equivalent to the original ones. Thus `select = "*"`  and cannot be changed.
- **filter**: Read only points of interest.

**Examples**

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
shp      <- system.file("extdata", "lake_polygons_UTM17.shp", package = "lidR")

las <- readLAS(LASfile, filter = "-keep_random_fraction 0.1")
lake <- sf::st_read(shp, quiet = TRUE)

# Classifies the points that are NOT in the lake and that are NOT ground points as class 5
poi <- ~Classification != LASGROUND
las <- classify_poi(las, LASHIGHVEGETATION, poi = poi, roi = lake, inverse = TRUE)
```

```
# Classifies the points that are in the lake as class 9
las <- classify_poi(las, LASWATER, roi = lake, inverse = FALSE)

#plot(las, color = "Classification")
```

---

clip

*Clip points in regions of interest*


---

## Description

Clip points within a given region of interest (ROI) from a point cloud (LAS object) or a catalog (LAScatalog object). With a LAS object, the user first reads and loads a point cloud into memory and then can clip it to get a subset within a region of interest. With a LAScatalog object, the user can extract any arbitrary ROI for a set of las/laz files, loading only the points of interest. This is faster, easier and much more memory-efficient for extracting ROIs.

## Usage

```
clip_roi(las, geometry, ...)

clip_rectangle(las, xleft, ybottom, xright, ytop, ...)

clip_polygon(las, xpoly, ypoly, ...)

clip_circle(las, xcenter, ycenter, radius, ...)

clip_transect(las, p1, p2, width, xz = FALSE, ...)
```

## Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
geometry	a geometric object. Many types are supported, see section 'supported geometries'.
...	in clip_roi: optional supplementary options (see supported geometries). Unused in other functions
xleft	numeric. left x coordinates of rectangles.
ybottom	numeric. bottom y coordinates of rectangles.
xright	numeric. right x coordinates of rectangles.
ytop	numeric. top y coordinates of rectangles.
xpoly	numeric. x coordinates of a polygon.
ypoly	numeric. y coordinates of a polygon.
xcenter	numeric. x coordinates of disc centers.
ycenter	numeric. y coordinates of disc centers.
radius	numeric. disc radius or radii.

p1, p2	numeric vectors of length 2 that gives the coordinates of two points that define a transect
width	numeric. width of the transect.
xz	bool. If TRUE the point cloud is reoriented to fit on XZ coordinates

### Value

If the input is a LAS object: an object of class LAS, or a list of LAS objects if the query implies several regions of interest will be returned.

If the input is a LAScatalog object: an object of class LAS, or a list of LAS objects if the query implies several regions of interest will be returned, or a LAScatalog if the queries are immediately written into files without loading anything in R.

### Supported geometries

- **WKT string**: describing a POINT, a POLYGON or a MULTIPOLYGON. If points, a parameter 'radius' must be passed in . . .
- **Polygon, SpatialPolygons, SpatialPolygonsDataFrame, SpatialPoints or SpatialPointsDataFrame** in that case a parameter 'radius' must be passed in . . .
- **SimpleFeature** from sf that consistently contains POINT or POLYGON/MULTIPOLYGON. In case of POINT a parameter 'radius' must be passed in . . .
- **Extent** from package raster
- **bbox** from package sf
- **matrix** 2 x 2 describing a bounding box following this order:

```

      min      max
x 684816 684943
y 5017823 5017957

```

### Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

## Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- `chunk_size`: Does not make sense here.
- `buffer`: Not supported yet.
- `alignment`: Does not makes sense here.
- **`progress`**: Displays a progress estimation.
- **`output_files`**: If 'output\_files' is set in the catalog, the ROIs will not be returned in R. They will be written immediately in files. See [LAScatalog-class](#) and examples. The allowed templates in `clip_*` are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {ID}, {XCENTER}, {YCENTER}. In addition `clip_roi` supports any names from the table of attributes of a spatial object given as input such as {PLOTID}, {YEAR}, {SPECIES}, for examples, if these attributes exist. If empty everything is returned into R.
- **`laz_compression`**: write las or laz files
- `select`: The function will write files equivalent to the originals. This option is not respected.
- **`filter`**: Read only the points of interest.

## Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")

# Load the file and clip the region of interest
las = readLAS(LASfile, select = "xyz", filter = "-keep_first")
subset1 = clip_rectangle(las, 684850, 5017850, 684900, 5017900)

# Do not load the file(s), extract only the region of interest
# from a bigger dataset
ctg = readLAScatalog(LASfile, progress = FALSE, filter = "-keep_first")
subset2 = clip_rectangle(ctg, 684850, 5017850, 684900, 5017900)

# Extract all the polygons from a shapefile
f <- system.file("extdata", "lake_polygons_UTM17.shp", package = "lidR")
lakes <- sf::st_read(f, quiet = TRUE)
subset3 <- clip_roi(las, lakes)

# Extract the polygons for a catalog, write them in files named
# after the lake names, do not load anything in R
opt_output_files(ctg) <- paste0(tempfile(), "_{LAKENAME_1}")
new_ctg = clip_roi(ctg, lakes)
plot(new_ctg)

# Extract a transect
p1 <- c(684800, y = 5017800)
p2 <- c(684900, y = 5017900)
tr1 <- clip_transect(las, p1, p2, width = 4)

## Not run:
plot(subset1)
```

```
plot(subset2)
plot(subset3)

plot(tr1, axis = TRUE, clear_artifacts = FALSE)

## End(Not run)
```

---

cloud\_metrics

*Compute metrics for a cloud of points*

---

## Description

cloud\_metrics computes a series of user-defined descriptive statistics for a LiDAR dataset. See [grid\\_metrics](#) to compute metrics on a grid. Basically there are no predefined metrics. Users must write their own functions to create metrics (see example). The following existing functions can serve as a guide to help users compute their own metrics:

- [stdmetrics](#)
- [entropy](#)
- [VCI](#)
- [LAD](#)

## Usage

```
cloud_metrics(las, func)
```

## Arguments

las	An object of class LAS
func	formula. An expression to be applied to the point cloud (see example)

## Value

It returns a list containing the metrics

## See Also

[grid\\_metrics](#) [stdmetrics](#) [entropy](#) [VCI](#) [LAD](#)

Other metrics: [grid\\_metrics\(\)](#), [plot\\_metrics\(\)](#), [point\\_metrics\(\)](#), [tree\\_metrics\(\)](#), [voxel\\_metrics\(\)](#)



**Examples**

```

LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
lidar = readLAS(LASfile)

cloud_metrics(lidar, ~max(Z))
cloud_metrics(lidar, ~mean(Intensity))

# Define your own new metrics
myMetrics = function(z, i)
{
  metrics = list(
    zwimean = sum(z*i)/sum(i), # Mean elevation weighted by intensities
    zimean = mean(z*i), # Mean products of z by intensity
    zsqmean = sqrt(mean(z^2)) # Quadratic mean
  )

  return(metrics)
}

metrics = cloud_metrics(lidar, ~myMetrics(Z, Intensity))

# Predefined metrics
cloud_metrics(lidar, .stdmetrics)

```

---

 concaveman

*A very fast 2D concave hull algorithm*


---

**Description**

A very fast 2D concave hull algorithm for a set of points

**Usage**

```
concaveman(x, y = NULL, concavity = 2, length_threshold = 0)
```

**Arguments**

<code>x, y</code>	coordinate vectors of points. This can be specified as two vectors <code>x</code> and <code>y</code> , a 2-column matrix <code>x</code> , a list with two components, etc.
<code>concavity</code>	numeric a relative measure of concavity. 1 results in a relatively detailed shape, Infinity results in a convex hull. You can use values lower than 1, but they can produce pretty crazy shapes.
<code>length_threshold</code>	numeric. When a segment length is under this threshold, it stops being considered for further detailed processing. Higher values result in simpler shapes.

## Details

The algorithm is based on ideas from Park and Oh (2012). A first implementation in JavaScript was proposed by Vladimir Agafonkin in [mapbox](#). This implementation dramatically improved performance over the one stated in the paper using a spatial index. The algorithm was then ported to R by Joël Gombin in the R package [concaveman](#) that runs the JavaScript implementation proposed by Vladimir Agafonkin. Later a C++ version of Vladimir Agafonkin's JavaScript implementation was proposed by Stanislaw Adaszewski in [concaveman-cpp](#). This concaveman function uses Stanislaw Adaszewski's C++ code making the concaveman algorithm an order of magnitude (up to 50 times) faster than the Javascript version.

## References

Park, J.-S & Oh, S.-J. (2013). A New Concave Hull Algorithm and Concaveness Measure for n-dimensional Datasets. *Journal of Information Science and Engineering*. 29. 379-392.

## Examples

```
x = runif(35)
y = runif(35)
hull <- concaveman(x,y)
plot(x,y, asp = 1)
lines(hull, lwd = 3, col = "red")
```

---

csf

*Ground Segmentation Algorithm*

---

## Description

This function is made to be used in [classify\\_ground](#). It implements an algorithm for segmentation of ground points base on a Cloth Simulation Filter. This method is a strict implementation of the CSF algorithm made by Zhang et al. (2016) (see references) that relies on the authors' original source code written and exposed to R via the the RCSF package.

## Usage

```
csf(
  sloop_smooth = FALSE,
  class_threshold = 0.5,
  cloth_resolution = 0.5,
  rigidness = 1L,
  iterations = 500L,
  time_step = 0.65
)
```

## Arguments

<code>sloop_smooth</code>	logical. When steep slopes exist, set this parameter to TRUE to reduce errors during post-processing.
<code>class_threshold</code>	scalar. The distance to the simulated cloth to classify a point cloud into ground and non-ground. The default is 0.5.
<code>cloth_resolution</code>	scalar. The distance between particles in the cloth. This is usually set to the average distance of the points in the point cloud. The default value is 0.5.
<code>rigidness</code>	integer. The rigidness of the cloth. 1 stands for very soft (to fit rugged terrain), 2 stands for medium, and 3 stands for hard cloth (for flat terrain). The default is 1.
<code>iterations</code>	integer. Maximum iterations for simulating cloth. The default value is 500. Usually, there is no need to change this value.
<code>time_step</code>	scalar. Time step when simulating the cloth under gravity. The default value is 0.65. Usually, there is no need to change this value. It is suitable for most cases.

## References

W. Zhang, J. Qi\*, P. Wan, H. Wang, D. Xie, X. Wang, and G. Yan, “An Easy-to-Use Airborne LiDAR Data Filtering Method Based on Cloth Simulation,” *Remote Sens.*, vol. 8, no. 6, p. 501, 2016. (<http://www.mdpi.com/2072-4292/8/6/501/htm>)

## See Also

Other ground segmentation algorithms: [pmf\(\)](#)

## Examples

```
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las <- readLAS(LASfile, select = "xyzrn")

mycsf <- csf(TRUE, 1, 1, time_step = 1)
las <- classify_ground(las, mycsf)
#plot(las, color = "Classification")
```

## Description

This function is made to be used in [segment\\_trees](#). It implements an algorithm for tree segmentation based on the Dalponte and Coomes (2016) algorithm (see reference). This is a seeds + growing region algorithm. This algorithm exists in the package `itcSegment`. This version has been written from the paper in C++. Consequently it is hundreds to millions times faster than the original version. Note that this algorithm strictly performs a segmentation, while the original method as implemented in `itcSegment` and described in the manuscript also performs pre- and post-processing tasks. Here these tasks are expected to be done by the user in separate functions.

**Usage**

```
dalponte2016(
  chm,
  treetops,
  th_tree = 2,
  th_seed = 0.45,
  th_cr = 0.55,
  max_cr = 10,
  ID = "treeID"
)
```

**Arguments**

chm	RasterLayer. Image of the canopy. Can be computed with <a href="#">grid_canopy</a> or read from an external file.
treetops	SpatialPointsDataFrame. Can be computed with <a href="#">find_trees</a> or read from an external shapefile.
th_tree	numeric. Threshold below which a pixel cannot be a tree. Default is 2.
th_seed	numeric. Growing threshold 1. See reference in Dalponte et al. 2016. A pixel is added to a region if its height is greater than the tree height multiplied by this value. It should be between 0 and 1. Default is 0.45.
th_cr	numeric. Growing threshold 2. See reference in Dalponte et al. 2016. A pixel is added to a region if its height is greater than the current mean height of the region multiplied by this value. It should be between 0 and 1. Default is 0.55.
max_cr	numeric. Maximum value of the crown diameter of a detected tree (in pixels). Default is 10.
ID	character. If the SpatialPointsDataFrame contains an attribute with the ID for each tree, the name of this attribute. This way, original IDs will be preserved. If there is no such data trees will be numbered sequentially.

**Details**

Because this algorithm works on a CHM only there is no actual need for a point cloud. Sometimes the user does not even have the point cloud that generated the CHM. `lidR` is a point cloud-oriented library, which is why this algorithm must be used in [segment\\_trees](#) to merge the result with the point cloud. However the user can use this as a stand-alone function like this:

```
chm = raster("file/to/a/chm/")
ttops = find_trees(chm, lmf(3))
crowns = dalponte2016(chm, ttops)()
```

**References**

Dalponte, M. and Coomes, D. A. (2016), Tree-centric mapping of forest carbon density from airborne laser scanning and hyperspectral data. *Methods Ecol Evol*, 7: 1236–1245. doi:10.1111/2041-210X.12575.

**See Also**

Other individual tree segmentation algorithms: [li2012\(\)](#), [silva2016\(\)](#), [watershed\(\)](#)

Other raster based tree segmentation algorithms: [silva2016\(\)](#), [watershed\(\)](#)

**Examples**

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile, select = "xyz", filter = "-drop_z_below 0")
col <- pastel.colors(200)

chm <- grid_canopy(las, 0.5, p2r(0.3))
ker <- matrix(1,3,3)
chm <- raster::focal(chm, w = ker, fun = mean, na.rm = TRUE)

ttops <- find_trees(chm, lmf(4, 2))
las <- segment_trees(las, dalponte2016(chm, ttops))
#plot(las, color = "treeID", colorPalette = col)
```

---

decimate_points	<i>Decimate a LAS object</i>
-----------------	------------------------------

---

**Description**

Reduce the number of points using several possible algorithms.

**Usage**

```
decimate_points(las, algorithm)
```

**Arguments**

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
algorithm	function. An algorithm of point decimation. lidR have: <a href="#">random</a> , <a href="#">homogenize</a> , <a href="#">highest</a> , <a href="#">lowest</a> and <a href="#">random_per_voxel</a> .

**Value**

If the input is a LAS object, returns a LAS object. If the input is a LAScatalog, returns a LAScatalog.

**Working with a LAScatalog**

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function

should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- **chunk buffer**: This function guarantee a strict wall-to-wall continuous output. The buffer option is not considered.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files\***: Mandatory because the output is likely to be too big to be returned in R and needs to be written in las/laz files. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The function will write files equivalent to the original ones. Thus select = "\*" and cannot be changed.
- **filter**: Read only points of interest.

### Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las = readLAS(LASfile, select = "xyz")

# Select points randomly to reach an overall density of 1
thinned1 = decimate_points(las, random(1))
#plot(grid_density(las))
#plot(grid_density(thinned1))

# Select points randomly to reach an homogeneous density of 1
thinned2 = decimate_points(las, homogenize(1,5))
#plot(grid_density(thinned2))

# Select the highest point within each pixel of an overlaid grid
thinned3 = decimate_points(las, highest(5))
#plot(thinned3)
```

---

delineate\_crowns      *Compute the hull of each tree.*

---

### Description

Compute the hull of each segmented tree. The hull can be convex, concave or a bounding box (see details and references).

### Usage

```
delineate_crowns(
  las,
  type = c("convex", "concave", "bbox"),
  concavity = 3,
  length_threshold = 0,
  func = NULL,
  attribute = "treeID"
)
```

### Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
type	character. Hull type. Can be 'convex', 'concave' or 'bbox'.
concavity	numeric. If type = "concave", a relative measure of concavity. 1 results in a relatively detailed shape, Infinity results in a convex hull.
length_threshold	numeric. If type = "concave", when a segment length is below this threshold, no further detail is added. Higher values result in simpler shapes.
func	formula. An expression to be applied to each tree. It works like in <a href="#">grid_metrics</a> , <a href="#">voxel_metrics</a> or <a href="#">tree_metrics</a> and computes, in addition to the hulls a set of metrics for each tree.
attribute	character. The attribute where the ID of each tree is stored. In lidR, the default is "treeID".

### Details

The concave hull method under the hood is described in Park & Oh (2012). The function relies on the [concaveman](#) function.

### Value

A SpatialPolygonsDataFrame. If a tree has less than 4 points it is not considered.

## Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

## Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- **chunk buffer\***: Mandatory to get a continuous output without edge effects. The buffer is always removed once processed and will never be returned either in R or in files.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files**: Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: Load only attributes of interest.
- **filter**: Read only points of interest.

## References

Park, J. S., & Oh, S. J. (2012). A new concave hull algorithm and concaveness measure for n-dimensional datasets. *Journal of Information science and engineering*, 28(3), 587-600.

## Examples

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
poi = "-drop_z_below 0 -inside 481280 3812940 481320 3812980"
las = readLAS(LASfile, select = "xyz0", filter = poi)

# NOTE: This dataset is already segmented

#plot(las, color = "treeID", colorPalette = pastel.colors(200))

# Only the hulls
convex_hulls = delineate_crowns(las)
plot(convex_hulls)
```



```

# The hulls + some user-defined metrics
convex_hulls = delineate_crowns(las, func = ~list(Zmean = mean(Z)))
convex_hulls

# The bounding box
bbox_hulls = delineate_crowns(las, "bbox")
plot(bbox_hulls)

# With concave hull
concave_hulls = delineate_crowns(las, "concave")
plot(concave_hulls)

spplot(convex_hulls, "ZTOP")
spplot(convex_hulls, "Zmean")

```

---

 deprecated

*Deprecated functions in lidR*


---

## Description

These functions are provided for compatibility with older versions of lidR but are deprecated since lidR version 3. They will progressively print a message, throw a warning and eventually be removed. The links below point to the documentation of the new names

[lasadd](#) [lascheck](#) [lasclip](#) [lasdetectshape](#) [lasfilter](#) [lasfiltersurfacepoints](#) [lasflightline](#) [lasground](#) [lasmergespatial](#) [lasnormalize](#) [laspulse](#) [lasrange correction](#) [lasflightline](#) [lasreoffset](#) [lasrescale](#) [lasscanlines](#) [lassmooth](#) [lassnags](#) [lastrees](#) [lasvoxelize](#) [sensor\\_tracking](#) [tree\\_detection](#) [tree\\_hull](#)

## Usage

```

lascheck(las)

lasclip(las, geometry, ...)

lasclipRectangle(las, xleft, ybottom, xright, ytop, ...)

lasclipPolygon(las, xpoly, ypoly, ...)

lasclipCircle(las, xcenter, ycenter, radius, ...)

lasdetectshape(las, algorithm, attribute = "Shape", filter = NULL)

lasfilter(las, ...)

lasfilterfirst(las)

lasfilterfirstlast(las)

```

```
lasfilterfirstofmany(las)
lasfilterground(las)
lasfilterlast(las)
lasfilternth(las, n)
lasfiltersingle(las)
lasfilterdecimate(las, algorithm)
lasfilterduplicates(las)
lasfiltersurfacepoints(las, res)
lasground(las, algorithm, last_returns = TRUE)
laspulse(las)
lasflightline(las, dt = 30)
lasscanline(las)
lasmergespatial(las, source, attribute = NULL)
lasnormalize(
  las,
  algorithm,
  na.rm = FALSE,
  use_class = c(2L, 9L),
  ...,
  add_lasattribute = FALSE
)
lasunnormalize(las)
lasrange correction(
  las,
  sensor,
  Rs,
  f = 2.3,
  gpstime = "gpstime",
  elevation = "Z"
)
lasrescale(las, xscale, yscale, zscale)
```

```
lasreoffset(las, xoffset, yoffset, zoffset)

lassmooth(
  las,
  size,
  method = c("average", "gaussian"),
  shape = c("circle", "square"),
  sigma = size/6
)

lasunsmooth(las)

lassnags(las, algorithm, attribute = "snagCls")

lastransform(las, CRSobj)

lastrees(las, algorithm, attribute = "treeID", uniqueness = "incremental")

lasadddata(las, x, name)

lasaddextrabytes(las, x, name, desc)

lasaddextrabytes_manual(
  las,
  x,
  name,
  desc,
  type,
  offset = NULL,
  scale = NULL,
  NA_value = NULL
)

lasremoveextrabytes(las, name)

lasvoxelize(las, res)

sensor_tracking(
  las,
  interval = 0.5,
  pmin = 50,
  extra_check = TRUE,
  thin_pulse_with_time = 0.001
)

tree_detection(las, algorithm)

tree_hulls(
```

```

las,
type = c("convex", "concave", "bbox"),
concavity = 3,
length_threshold = 0,
func = NULL,
attribute = "treeID"
)

hexbin_metrics(...)

```

### Arguments

las	See the new functions that replace the old ones
geometry	See the new functions that replace the old ones
...	See the new functions that replace the old ones
xleft, ybottom, xright, ytop	See the new functions that replace the old ones
xpoly, ypoly	See the new functions that replace the old ones
xcenter, ycenter, radius	See the new functions that replace the old ones
algorithm	See the new functions that replace the old ones
attribute	See the new functions that replace the old ones
filter	See the new functions that replace the old ones
n, res, dt	See the new functions that replace the old ones
last_returns	See the new functions that replace the old ones
source	See the new functions that replace the old ones
na.rm, use_class, add_lasattribute	See the new functions that replace the old ones
sensor, Rs, f, gpstime, elevation	See the new functions that replace the old ones
xscale, yscale, zscale, xoffset, yoffset, zoffset	See the new functions that replace the old ones
size, method, shape, sigma	See the new functions that replace the old ones
CRSobj	See the new functions that replace the old ones
uniqueness	See the new functions that replace the old ones
x, name, desc, type, offset, scale, NA_value	See the new functions that replace the old ones
interval, pmin, extra_check, thin_pulse_with_time	See the new functions that replace the old ones
concavity, length_threshold, func	See the new functions that replace the old ones

---

dsmtin

*Digital Surface Model Algorithm*

---

## Description

This function is made to be used in [grid\\_canopy](#). It implements an algorithm for digital surface model computation using a Delaunay triangulation of first returns with a linear interpolation within each triangle.

## Usage

```
dsmtin(max_edge = 0)
```

## Arguments

`max_edge` numeric. Maximum edge length of a triangle in the Delaunay triangulation. If a triangle has an edge length greater than this value it will be removed to trim dummy interpolation on non-convex areas. If `max_edge = 0` no trimming is done (see examples).

## See Also

Other digital surface model algorithms: [p2r\(\)](#), [pitfree\(\)](#)

## Examples

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile)
col <- height.colors(50)

# Basic triangulation and rasterization of first returns
chm <- grid_canopy(las, res = 1, dsmtin())
plot(chm, col = col)

## Not run:
# Potentially complex concave subset of point cloud
x = c(481340, 481340, 481280, 481300, 481280, 481340)
y = c(3812940, 3813000, 3813000, 3812960, 3812940, 3812940)
las2 = clip_polygon(las,x,y)
plot(las2)

# Since the TIN interpolation is done within the convex hull of the point cloud
# dummy pixels are interpolated that are strictly correct according to the interpolation method
# used, but meaningless in our CHM
chm <- grid_canopy(las2, res = 0.5, dsmtin())
plot(chm, col = col)

# Use 'max_edge' to trim dummy triangles
chm = grid_canopy(las2, res = 0.5, dsmtin(max_edge = 3))
```

```
plot(chm, col = col)

## End(Not run)
```

---

entropy

*Normalized Shannon diversity index*

---

## Description

A normalized Shannon vertical complexity index. The Shannon diversity index is a measure for quantifying diversity and is based on the number and frequency of species present. This index, developed by Shannon and Weaver for use in information theory, was successfully transferred to the description of species diversity in biological systems (Shannon 1948). Here it is applied to quantify the diversity and the evenness of an elevational distribution of las points. It makes bins between 0 and the maximum elevation. If there are negative values the function returns NA.

## Usage

```
entropy(z, by = 1, zmax = NULL)
```

## Arguments

z	vector of positive z coordinates
by	numeric. The thickness of the layers used (height bin)
zmax	numeric. Used to turn the function entropy to the function <a href="#">VCI</a> .

## Value

A number between 0 and 1

## References

Pretzsch, H. (2008). Description and Analysis of Stand Structures. Springer Berlin Heidelberg. <http://doi.org/10.1007/978-3-540-88307-4> (pages 279-280) Shannon, Claude E. (1948), "A mathematical theory of communication," Bell System Tech. Journal 27, 379-423, 623-656.

## See Also

[VCI](#)

## Examples

```
z <- runif(10000, 0, 10)

# expected to be close to 1. The highest diversity is given for a uniform distribution
entropy(z, by = 1)

z <- runif(10000, 9, 10)
```

```
# Must be 0. The lowest diversity is given for a unique possibility
entropy(z, by = 1)

z <- abs(rnorm(10000, 10, 1))

# expected to be between 0 and 1.
entropy(z, by = 1)
```

---

extent,LAS-method      *Extent*

---

### Description

Returns an Extent object of a LAS\*.

### Usage

```
## S4 method for signature 'LAS'
extent(x, ...)

## S4 method for signature 'LAScatalog'
extent(x, ...)
```

### Arguments

x	An object of the class LAS or LAScatalog
...	Unused

### Value

Extent object from **raster**

### See Also

[raster::extent](#)

---

filters

*Predefined point of interest filters*

---

### Description

Select only some returns

### Usage

`filter_first(las)`

`filter_firstlast(las)`

`filter_firstofmany(las)`

`filter_ground(las)`

`filter_last(las)`

`filter_nth(las, n)`

`filter_single(las)`

### Arguments

<code>las</code>	An object of class <a href="#">LAS</a>
<code>n</code>	the position in the return sequence

### Details

- `filter_first` Select only the first returns.
- `filter_firstlast` Select only the first and last returns.
- `filter_ground` Select only the returns classified as ground according to LAS specification.
- `filter_last` Select only the last returns i.e. the last returns and the single returns.
- `filter_nth` Select the returns from their position in the return sequence.
- `filter_firstofmany` Select only the first returns from pulses which returned multiple points.
- `filter_single` Select only the returns that return only one point.

### Value

An object of class [LAS](#)



**See Also**

Other filters: [filter\\_duplicates\(\)](#), [filter\\_poi\(\)](#), [filter\\_surfacepoints\(\)](#)  
 Other filters: [filter\\_duplicates\(\)](#), [filter\\_poi\(\)](#), [filter\\_surfacepoints\(\)](#)  
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 Other filters: [filter\\_duplicates\(\)](#), [filter\\_poi\(\)](#), [filter\\_surfacepoints\(\)](#)  
 Other filters: [filter\\_duplicates\(\)](#), [filter\\_poi\(\)](#), [filter\\_surfacepoints\(\)](#)  
 Other filters: [filter\\_duplicates\(\)](#), [filter\\_poi\(\)](#), [filter\\_surfacepoints\(\)](#)  
 Other filters: [filter\\_duplicates\(\)](#), [filter\\_poi\(\)](#), [filter\\_surfacepoints\(\)](#)

**Examples**

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
lidar = readLAS(LASfile)

firstReturns = filter_first(lidar)
groundReturns = filter_ground(lidar)
```

---

filter_duplicates	<i>Filter duplicated points</i>
-------------------	---------------------------------

---

**Description**

Filter points that appear more than once in the point cloud according to their X Y Z coordinates

**Usage**

```
filter_duplicates(las)
```

**Arguments**

las                    An object of class [LAS](#) or [LAScatalog](#).

**Value**

If the input is a LAS object, returns a LAS object. If the input is a LAScatalog, returns a LAScatalog.

**Working with a LAScatalog**

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function

should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- **chunk buffer**: This function guarantee a strict wall-to-wall continuous output. The buffer option is not considered.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files\***: Mandatory because the output is likely to be too big to be returned in R and needs to be written in las/laz files. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The function will write files equivalent to the original ones. Thus select = "\*" and cannot be changed.
- **filter**: Read only points of interest.

### See Also

Other filters: [filter\\_poi\(\)](#), [filter\\_surfacepoints\(\)](#), [filters](#)

---

filter\_poi

*Filter points of interest with matching conditions*

---

### Description

Filter points of interest (POI) from a LAS object where conditions are true.

### Usage

```
filter_poi(las, ...)
```

### Arguments

las	An object of class <a href="#">LAS</a>
...	Logical predicates. Multiple conditions are combined with '&' or ','

**Value**

An object of class [LAS](#)

**See Also**

Other filters: [filter\\_duplicates\(\)](#), [filter\\_surfacepoints\(\)](#), [filters](#)

**Examples**

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
lidar = readLAS(LASfile)

# Select the first returns classified as ground
firstground = filter_poi(lidar, Classification == 2L & ReturnNumber == 1L)

# Multiple arguments are equivalent to &
firstground = filter_poi(lidar, Classification == 2L, ReturnNumber == 1L)

# Multiple criteria
first_or_ground = filter_poi(lidar, Classification == 2L | ReturnNumber == 1L)
```

---

filter\_surfacepoints    *Filter the surface points*

---

**Description**

This function is superseded by the algorithm [highest](#) usable in [decimate\\_points](#)

**Usage**

```
filter_surfacepoints(las, res)
```

**Arguments**

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
res	numeric. The resolution of the grid used to filter the point cloud

**Value**

If the input is a LAS object, returns a LAS object. If the input is a LAScatalog, returns a LAScatalog.

**Supported processing options**

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.

- **chunk buffer**: This function guarantee a strict wall-to-wall continuous output. The buffer option is not considered.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files\***: Mandatory because the output is likely to be too big to be returned in R and needs to be written in las/laz files. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The function will write files equivalent to the original ones. Thus select = "\*" and cannot be changed.
- **filter**: Read only points of interest.

### See Also

Other filters: [filter\\_duplicates\(\)](#), [filter\\_poi\(\)](#), [filters](#)

---

find\_localmaxima

*Local Maximum Filter*

---

### Description

Generic local maximum filter. For individual tree detection use [find\\_trees](#) with the [lmf](#) algorithm that is more adequate for ITD. This function is a more generic method for multiple purposes other than tree segmentation. This function is natively parallelized with OpenMP.

### Usage

```
find_localmaxima(las, w, filter = NULL)
```

### Arguments

las	An object of class LAS
w	numeric. Window shape. 1 number for the diameter of a disc, 2 numbers for a rectangle (width, height), 3 numbers for an oriented rectangle (width, height, angle). The angle must be in radians.
filter	formula. Memory efficient way to work only with a subset of the data without creating a copy of the data.

### Value

SpatialPointsDataFrame with attributes from the corresponding point in the LAS object,

**Examples**

```

LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile, select = "xyzi", filter = "-drop_z_below 0 -keep_random_fraction 0.5")

# Using a 20x5 rectangle with a 45 degrees angle.
# This won't find the tree properly in the general case
# but may find some oriented structure.
lm = find_localmaxima(las, c(20, 5, pi/4))
plot(lm)

```

---

find_trees	<i>Individual tree detection</i>
------------	----------------------------------

---

**Description**

Individual tree detection function that find the position of the trees using several possible algorithms.

**Usage**

```
find_trees(las, algorithm, uniqueness = "incremental")
```

**Arguments**

las	An object of class LAS or LAScatalog. Can also be a RasterLayer representing a canopy height model, in which case it is processed like a regularly-spaced point cloud.
algorithm	An algorithm for individual tree detection. lidR has: <a href="#">lmf</a> and <a href="#">manual</a> . More experimental algorithms may be found in the package <a href="#">lidRplugins</a> .
uniqueness	character. A method to compute a unique ID. Can be 'incremental', 'gpstime' or 'bitmerge'. See section 'Uniqueness'. This feature must be considered as 'experimental'.

**Value**

A SpatialPointsDataFrame with an attribute Z for the tree tops and treeID with an individual ID for each tree.

**Uniqueness**

By default the tree IDs are numbered from 1 to n, n being the number of trees found. The problem with such incremental numbering is that, while it ensures a unique ID is assigned for each tree in a given point-cloud, it also guarantees duplication of tree IDs in different tiles or chunks when processing a LAScatalog. This is because each chunk/file is processed independently of the others and potentially in parallel on different computers. Thus, the index always restarts at 1 on each chunk/file or chunk. Worse, in a tree segmentation process, a tree that is located exactly between 2 chunks/files will have two different IDs for its two halves.

This is why we introduced some uniqueness strategies that are all imperfect and that should be seen as experimental. Please report any troubleshooting. Using a uniqueness-safe strategy ensures that trees from different files will not share the same IDs. Moreover, it also means that two halves of a tree on the edge of a processing chunk will be assigned the same ID.

**incremental** Number from 0 to n. This method **does not** ensure uniqueness of the IDs. This is the legacy method.

**gpstime** This method uses the gpstime of the highest point of a tree (apex) to create a unique ID. This ID is not an integer but a 64-bit decimal number, which is suboptimal but at least it is expected to be unique **if the gpstime attribute is consistent across files**. If inconsistencies with gpstime are reported (for example gpstime records the week time and was reset to 0 in a coverage that takes more than a week to complete), there is a (low) probability of getting ID attribution errors.

**bitmerge** This method uses the XY coordinates of the highest point (apex) of a tree to create a single 64-bit number with a bitwise operation. First, XY coordinates are converted to 32-bit integers using the scales and offsets of the point cloud. For example, if the apex is at (10.32, 25.64) with a scale factor of 0.01 and an offset of 0, the 32-bit integer coordinates are  $X = 1032$  and  $Y = 2564$ . Their binary representations are, respectively, (here displayed as 16 bits) 0000010000001000 and 0000101000000100. X is shifted by 32 bits and becomes a 64-bit integer. Y is kept as-is and the binary representations are unionized into a 64-bit integer like (here displayed as 32 bit) 00000100000010000000101000000100 that is guaranteed to be unique. However R does not support 64-bit integers. The previous steps are done at C++ level and the 64-bit binary representation is reinterpreted into a 64-bit decimal number to be returned in R. The IDs thus generated are somewhat weird. For example, the tree ID 00000100000010000000101000000100 which is 67635716 if interpreted as an integer becomes 3.34164837074751323479078607289E-316 if interpreted as a decimal number. This is far from optimal but at least it is guaranteed to be unique **if all files have the same offsets and scale factors**.

All the proposed options are suboptimal because they either do not guarantee uniqueness in all cases (inconsistencies in the collection of files), or they imply that IDs are based on non-integers or meaningless numbers. But at least it works and deals with some of the limitations of R.

### Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- **chunk buffer\***: Mandatory to get a continuous output without edge effects. The buffer is always removed once processed and will never be returned either in R or in files.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files**: Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: Load only attributes of interest.
- **filter**: Read only points of interest.

**Examples**

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile, select = "xyz", filter = "-inside 481250 3812980 481300 3813030")

ttops <- find_trees(las, lmf(ws = 5))

#x = plot(las)
#add_treetops3d(x, ttops)
```

---

gap\_fraction\_profile *Gap fraction profile*

---

**Description**

Computes the gap fraction profile using the method of Bouvier et al. (see reference)

**Usage**

```
gap_fraction_profile(z, dz = 1, z0 = 2)
```

**Arguments**

z	vector of positive z coordinates
dz	numeric. The thickness of the layers used (height bin)
z0	numeric. The bottom limit of the profile

**Details**

The function assesses the number of laser points that actually reached the layer  $z+dz$  and those that passed through the layer  $[z, z+dz]$ . By definition the layer 0 will always return 0 because no returns pass through the ground. Therefore, the layer 0 is removed from the returned results.

**Value**

A data.frame containing the bin elevations (z) and the gap fraction for each bin (gf)

**References**

Bouvier, M., Durrieu, S., Fournier, R. a, & Renaud, J. (2015). Generalizing predictive models of forest inventory attributes using an area-based approach with airborne las data. Remote Sensing of Environment, 156, 322-334. <http://doi.org/10.1016/j.rse.2014.10.004>

**See Also**

[LAD](#)

**Examples**

```
z <- c(rnorm(1e4, 25, 6), rgamma(1e3, 1, 8)*6, rgamma(5e2, 5,5)*10)
z <- z[z<45 & z>0]

hist(z, n=50)

gapFraction = gap_fraction_profile(z)

plot(gapFraction, type="l", xlab="Elevation", ylab="Gap fraction")
```

---

Gatziolis2019

*Sensor tracking algorithm*

---

**Description**

This function is made to be used in [track\\_sensor](#). It implements an algorithm from Gatziolis and McGaughey 2019 (see reference) for sensor tracking using multiple returns to estimate the positioning of the sensor by computing the intersection in space of the lines passing through the first and last returns.

**Usage**

```
Gatziolis2019(SEGLENFactor = 1.0059, AngleFactor = 0.8824, deltaT = 0.5)
```

**Arguments**

SEGLENFactor	scalar. Weighting factor for the distance b/w 1st and last pulse returns
AngleFactor	scalar. Weighting factor for view angle of mother pulse of a return
deltaT	scalar. TimeBlock duration (in seconds)

**Details**

In the original paper, two steps are described: (1) closest point approach (CPA) and (2) cubic spline fitting. Technically, the cubic spline fitting step is a post-processing step and is not included in this algorithm.

The source code of the algorithm is a slight modification of the original source code provided with the paper to fit with the lidR package.

**Author(s)**

Demetrios Gaziolis and Jean-Romain Roussel

**References**

Gatziolis, D., & McGaughey, R. J. (2019). Reconstructing Aircraft Trajectories from Multi-Return Airborne Laser-Scanning Data. *Remote Sensing*, 11(19), 2258.



**Examples**

```
# A valid file properly populated
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las = readLAS(LASfile)
flightlines <- track_sensor(las, Gatziolis2019())

plot(las@header)
plot(flightlines, add = TRUE)
```

grid\_canopy

*Digital Surface Model***Description**

Creates a digital surface model (DSM) using several possible algorithms. If the user provides a normalised point cloud, the output is indeed a canopy height model (CHM).

**Usage**

```
grid_canopy(las, res, algorithm)
```

**Arguments**

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
res	numeric. The resolution of the output Raster. Can optionally be a RasterLayer. In that case the RasterLayer is used as the layout.
algorithm	function. A function that implements an algorithm to compute a digital surface model. lidR implements <a href="#">p2r</a> , <a href="#">dsmtin</a> , <a href="#">pitfree</a> (see respective documentation and examples).

**Value**

A RasterLayer containing a numeric value in each cell. If the RasterLayers are written on disk when running the function with a LAScatalog, a virtual raster mosaic is returned (see [gdalbuildvrt](#))

**Working with a LAScatalog**

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports `.laz` files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a `.laz` files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog in grid\_\* functions (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once. The chunk size may be slightly modified internally to ensure a strict continuous wall-to-wall output even when chunk size is equal to 0 (processing by file).
- **chunk buffer**: This function guarantees a strict continuous wall-to-wall output. The buffer option is not considered.
- **chunk alignment**: Align the processed chunks. The alignment may be slightly modified internally to ensure a strict continuous wall-to-wall output.
- **progress**: Displays a progress estimate.
- **output files**: Return the output in R or write each cluster's output in a file. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The grid\_\* functions usually 'know' what should be loaded and this option is not considered. In [grid\\_metrics](#) this option is respected.
- **filter**: Read only the points of interest.

### Examples

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile, filter = "-inside 481280 3812940 481330 3812990")
col <- height.colors(50)

# Points-to-raster algorithm with a resolution of 1 meter
chm <- grid_canopy(las, res = 1, p2r())
plot(chm, col = col)

# Points-to-raster algorithm with a resolution of 0.5 meters replacing each
# point by a 20-cm radius circle of 8 points
chm <- grid_canopy(las, res = 0.5, p2r(0.2))
plot(chm, col = col)

# Basic triangulation and rasterization of first returns
chm <- grid_canopy(las, res = 0.5, dsmtin())
plot(chm, col = col)

# Khosravipour et al. pitfree algorithm
chm <- grid_canopy(las, res = 0.5, pitfree(c(0,2,5,10,15), c(0, 1.5)))
plot(chm, col = col)
```

### Description

Creates a map of the point density. If a "pulseID" attribute is found, also returns a map of the pulse density.

### Usage

```
grid_density(las, res = 4)
```

### Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
res	numeric. The size of a grid cell in LiDAR data coordinates units. Default is 4 = 16 square meters.

### Value

A RasterLayer or a RasterBrick containing a numeric value in each cell. If the RasterLayers are written on disk when running the function with a LAScatalog, a virtual raster mosaic is returned (see [gdalbuildvrt](#))

### Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog in grid\_\* functions (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once. The chunk size may be slightly modified internally to ensure a strict continuous wall-to-wall output even when chunk size is equal to 0 (processing by file).
- **chunk buffer**: This function guarantees a strict continuous wall-to-wall output. The buffer option is not considered.
- **chunk alignment**: Align the processed chunks. The alignment may be slightly modified internally to ensure a strict continuous wall-to-wall output.
- **progress**: Displays a progress estimate.

- **output files:** Return the output in R or write each cluster's output in a file. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select:** The grid\_\* functions usually 'know' what should be loaded and this option is not considered. In [grid\\_metrics](#) this option is respected.
- **filter:** Read only the points of interest.

### Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile, filter = "-inside 684800 5017800 684900 5017900")

d <- grid_density(las, 5)
plot(d)

las <- retrieve_pulses(las)
d <- grid_density(las)
plot(d)
```

---

grid\_metrics

*Area-Based Approach*

---

### Description

Computes a series of user-defined descriptive statistics for a LiDAR dataset within each pixel of a raster (area-based approach). The grid cell coordinates are pre-determined for a given resolution, so the algorithm will always provide the same coordinates independently of the dataset. When start = (0,0) and res = 20 grid\_metrics will produce the following cell centers: (10,10), (10,30), (30,10) etc. aligning the corner of a cell on (0,0). When start = (-10, -10) and res = 20 grid\_metrics will produce the following cell centers: (0,0), (0,20), (20,0) etc. aligning the corner of a cell on (-10, -10).

### Usage

```
grid_metrics(
  las,
  func,
  res = 20,
  start = c(0, 0),
  filter = NULL,
  by_echo = "all"
)
```

### Arguments

las                    An object of class [LAS](#) or [LAScatalog](#).

func                    formula. An expression to be applied to each cell (see section "Parameter func").

res	numeric. The resolution of the output Raster. Can optionally be a RasterLayer. In that case the RasterLayer is used as the layout.
start	vector of x and y coordinates for the reference raster. Default is (0,0) meaning that the grid aligns on (0,0).
filter	formula of logical predicates. Enables the function to run only on points of interest in an optimized way. See examples.
by_echo	characters. The metrics are computed multiples times for different echo types. Can be one or more of "all", "first", "intermediate", "lastofmany", "single", "multiple". See examples. Default is "all" meaning that it computes metrics with all points provided.

### Value

A RasterLayer or a RasterBrick containing a numeric value in each cell. If the RasterLayers are written on disk when running the function with a LAScatalog, a virtual raster mosaic is returned (see [gdalbuildvrt](#))

### Parameter func

The function to be applied to each cell is a classical function (see examples) that returns a labeled list of metrics. For example, the following function `f` is correctly formed.

```
f = function(x) {list(mean = mean(x), max = max(x))}
```

And could be applied either on the Z coordinates or on the intensities. These two statements are valid:

```
grid_metrics(las, ~f(Z), res = 20)
grid_metrics(las, ~f(Intensity), res = 20)
```

The following existing functions allow the user to compute some predefined metrics:

- [stdmetrics](#)
- [entropy](#)
- [VCI](#)
- [LAD](#)

But usually users must write their own functions to create metrics. `grid_metrics` will dispatch the point cloud in the user's function.

### Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function

should come with a section that documents the supported engine options.

The LAScatalog engine supports .laz files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .laz files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog in `grid_*` functions (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once. The chunk size may be slightly modified internally to ensure a strict continuous wall-to-wall output even when chunk size is equal to 0 (processing by file).
- **chunk buffer**: This function guarantees a strict continuous wall-to-wall output. The buffer option is not considered.
- **chunk alignment**: Align the processed chunks. The alignment may be slightly modified internally to ensure a strict continuous wall-to-wall output.
- **progress**: Displays a progress estimate.
- **output files**: Return the output in R or write each cluster's output in a file. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The `grid_*` functions usually 'know' what should be loaded and this option is not considered. In [grid\\_metrics](#) this option is respected.
- **filter**: Read only the points of interest.

### See Also

Other metrics: [cloud\\_metrics\(\)](#), [plot\\_metrics\(\)](#), [point\\_metrics\(\)](#), [tree\\_metrics\(\)](#), [voxel\\_metrics\(\)](#)

### Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las = readLAS(LASfile)
col = height.colors(50)

# === Using all points ===

# Mean height with 400 m^2 cells
metrics = grid_metrics(las, ~mean(Z), 20)
plot(metrics, col = col)

# Define your own new metrics
myMetrics = function(z, i) {
  metrics = list(
    zwimean = sum(z*i)/sum(i), # Mean elevation weighted by intensities
    zimean = mean(z*i), # Mean products of z by intensity
    zsqmean = sqrt(mean(z^2)) # Quadratic mean
  )
}
```

```
    return(metrics)
}

metrics = grid_metrics(las, ~myMetrics(Z, Intensity))

plot(metrics, col = col)
#plot(metrics, "zwimean", col = col)
#plot(metrics, "zimean", col = col)

# === With point filters ===

# Compute using only some points: basic
first = filter_poi(las, ReturnNumber == 1)
metrics = grid_metrics(first, ~mean(Z), 20)

# Compute using only some points: optimized
# faster and uses less memory. No intermediate object
metrics = grid_metrics(las, ~mean(Z), 20, filter = ~ReturnNumber == 1)

# Compute using only some points: best
# ~50% faster and uses ~10x less memory
las = readLAS(LASfile, filter = "-keep_first")
metrics = grid_metrics(las, ~mean(Z), 20)

# === Split by echo type ===
func = ~list(avgI = mean(Intensity))
echo = c("all", "first", "multiple")
metrics <- grid_metrics(las, func , 20, by_echo = echo)
plot(metrics, col = heat.colors(25))
```

---

grid\_terrain

*Digital Terrain Model*

---

## Description

Interpolates the ground points and creates a rasterized digital terrain model. The algorithm uses the points classified as "ground" and "water" (Classification = 2 and 9, respectively, according to [LAS file format specifications](#)) to compute the interpolation.

How well the edges of the dataset are interpolated depends on the interpolation method used. A buffer around the region of interest is always recommended to avoid edge effects.

## Usage

```
grid_terrain(
  las,
  res = 1,
  algorithm,
```

```

    ...,
    keep_lowest = FALSE,
    full_raster = FALSE,
    use_class = c(2L, 9L),
    Wdegenerated = TRUE,
    is_concave = FALSE
)

```

### Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
res	numeric. The resolution of the output Raster. Can optionally be a RasterLayer. In that case the RasterLayer is used as the layout.
algorithm	function. A function that implements an algorithm to compute spatial interpolation. lidR implements <a href="#">knnidw</a> , <a href="#">tin</a> , and <a href="#">kriging</a> (see respective documentation and examples).
...	Unused
keep_lowest	logical. This option forces the original lowest ground point of each cell (if it exists) to be chosen instead of the interpolated values.
full_raster	logical. By default the interpolation is made only within the convex hull of the point cloud. This prevents meaningless interpolations where there is no data. If TRUE, each pixel of the raster is interpolated.
use_class	integer vector. By default the terrain is computed by using ground points (class 2) and water points (class 9).
Wdegenerated	logical. The function always checks and removes degenerated ground points for computing the DTM to avoid unexpected behaviours, such as infinite elevation. If TRUE, a warning is thrown to alert users to the presence of degenerated ground points.
is_concave	boolean. By default the function tries to compute a DTM that has the same shape as the point cloud by interpolating only in the convex hull of the points. If the point cloud is concave this may lead to weird values where there are no points. Use <code>is_concave = TRUE</code> to use a concave hull. This is more computationally demanding. It uses <a href="#">concaveman</a> internally.

### Value

A RasterLayer containing a numeric value in each cell. If the RasterLayers are written on disk when running the function with a LAScatalog, a virtual raster mosaic is returned (see [gdalbuildvrt](#))

### Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function



should come with a section that documents the supported engine options.

The LAScatalog engine supports .laz files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .laz files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog in grid\_\* functions (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once. The chunk size may be slightly modified internally to ensure a strict continuous wall-to-wall output even when chunk size is equal to 0 (processing by file).
- **chunk buffer**: This function guarantees a strict continuous wall-to-wall output. The buffer option is not considered.
- **chunk alignment**: Align the processed chunks. The alignment may be slightly modified internally to ensure a strict continuous wall-to-wall output.
- **progress**: Displays a progress estimate.
- **output files**: Return the output in R or write each cluster's output in a file. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The function 'knows' what should be loaded and this option is not considered.
- **filter**: Read only the points of interest.

### Examples

```
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las = readLAS(LASfile, filter = "-inside 273450 5274350 273550 5274450")
#plot(las)

dtm1 = grid_terrain(las, algorithm = knnidw(k = 6L, p = 2))
dtm2 = grid_terrain(las, algorithm = tin())

## Not run:
dtm3 = grid_terrain(las, algorithm = kriging(k = 10L))

plot(dtm1)
plot(dtm2)
plot(dtm3)
plot_dtm3d(dtm1)
plot_dtm3d(dtm2)
plot_dtm3d(dtm3)

## End(Not run)
```

---

homogenize

*Point Cloud Decimation Algorithm*

---

## Description

This function is made to be used in [decimate\\_points](#). It implements an algorithm that creates a grid with a given resolution and filters the point cloud by randomly selecting some points in each cell. It is designed to produce point clouds that have uniform densities throughout the coverage area. For each cell, the proportion of points or pulses that will be retained is computed using the actual local density and the desired density. If the desired density is greater than the actual density it returns an unchanged set of points (it cannot increase the density). The cell size must be large enough to compute a coherent local density. For example, in a 2 points/m<sup>2</sup> point cloud, 25 square meters would be feasible; however 1 square meter cells would not be feasible because density does not have meaning at this scale.

## Usage

```
homogenize(density, res = 5, use_pulse = FALSE)
```

## Arguments

density	numeric. The desired output density.
res	numeric. The resolution of the grid used to filter the point cloud
use_pulse	logical. Decimate by removing random pulses instead of random points (requires running <a href="#">retrieve_pulses</a> first)

## See Also

Other point cloud decimation algorithms: [maxima](#), [random\\_per\\_voxel\(\)](#), [random\(\)](#)

## Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las = readLAS(LASfile, select = "xyz")

# Select points randomly to reach an homogeneous density of 1
thinned <- decimate_points(las, homogenize(1,5))
plot(grid_density(thinned, 10))
```

---

interpret_waveform	<i>Convert full waveform data into a regular point cloud</i>
--------------------	--

---

### Description

Full waveform can be difficult to manipulate and visualize in R. This function converts a LAS object with full waveform data into a regular point cloud. Each waveform record becomes a point with XYZ coordinates and an amplitude (units: volts) and an ID that records each original pulse. Notice that this has the effect of drastically inflating the size of the object in memory, which is likely already very large

### Usage

```
interpret_waveform(las)
```

### Arguments

las                    An object of class LAS with full waveform data

### Value

An object of class LAS 1.2 format 0 with one point per records

### Full waveform

With most recent versions of the 'rlas' package, full waveform (FWF) can be read and 'lidR' provides some compatible functions. However, the support of FWF is still a work-in-progress in the 'rlas' package. How it is read, interpreted and represented in R may change. Consequently, tools provided by 'lidR' may also change until the support of FWF becomes mature and stable in 'rlas'. See also [rlas::read.las](#).

Remember that FWF represents an insanely huge amount of data. In terms of memory it is like having between 10 to 100 times more points. Consequently, loading FWF data in R should be restricted to relatively small point clouds.

### Examples

```
## Not run:
LASfile <- system.file("extdata", "fwf.laz", package="rlas")
fwf <- readLAS(LASfile)
las <- interpret_waveform(fwf)
x <- plot(fwf, size = 3, colorPalette = "red")
plot(las, color = "Amplitude", bg = "white", add = x, size = 2)

## End(Not run)
```

---

is *A set of boolean tests on objects*

---

### Description

`is.empty` tests if a LAS object is a point cloud with 0 points.  
`is.overlapping` tests if a LAScatalog has overlapping tiles.  
`is.indexed` tests if the points of a LAScatalog are indexed with .lax files.  
`is.algorithm` tests if an object is an algorithm of the lidR package.  
`is.parallelised` tests if an algorithm of the lidR package is natively parallelised with OpenMP. Returns TRUE if the algorithm is at least partially parallelised i.e. if some portion of the code is computed in parallel.

### Usage

```
is.empty(las)

is.overlapping(catalog)

is.indexed(catalog)

is.algorithm(x)

is.parallelised(algorithm)
```

### Arguments

<code>las</code>	A LAS object.
<code>catalog</code>	A LAScatalog object.
<code>x</code>	Any R object.
<code>algorithm</code>	An algorithm object.

### Value

TRUE or FALSE

### Examples

```
LASfile <- system.file("extdata", "example.laz", package="rlas")
las = readLAS(LASfile)
is.empty(las)

las = new("LAS")
is.empty(las)

f <- lmf(2)
is.parallelised(f)
```

```
g <- pitfree()
is.parallellised(g)

ctg <- readLAScatalog(LASfile)
is.indexed(ctg)
```

---

*ivf**Noise Segmentation Algorithm*

---

### Description

This function is made to be used in [classify\\_noise](#). It implements an algorithm for outliers (noise) segmentation based on isolated voxels filter (IVF). It is similar to [lasnoise from lastools](#). The algorithm finds points that have only a few other points in their surrounding  $3 \times 3 \times 3 = 27$  voxels.

### Usage

```
ivf(res = 5, n = 6)
```

### Arguments

<code>res</code>	numeric. Resolution of the voxels
<code>n</code>	integer. The maximal number of 'other points' in the 27 voxels

### See Also

Other noise segmentation algorithms: [sor\(\)](#)

### Examples

```
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las <- readLAS(LASfile, filter = "-inside 273450 5274350 273550 5274450")

# Add some artificial outliers
set.seed(314)
id = round(runif(20, 0, npoints(las)))
set.seed(42)
err = runif(20, -50, 50)
las$Z[id] = las$Z[id] + err

las <- classify_noise(las, ivf(5,2))
```

---

knnidw	<i>Spatial Interpolation Algorithm</i>
--------	--

---

### Description

This function is made to be used in [grid\\_terrain](#) or [normalize\\_height](#). It implements an algorithm for spatial interpolation. Interpolation is done using a k-nearest neighbour (KNN) approach with an inverse-distance weighting (IDW).

### Usage

```
knnidw(k = 10, p = 2, rmax = 50)
```

### Arguments

k	integer. Number of k-nearest neighbours. Default 10.
p	numeric. Power for inverse-distance weighting. Default 2.
rmax	numeric. Maximum radius where to search for knn. Default 50.

### See Also

Other spatial interpolation algorithms: [kriging\(\)](#), [tin\(\)](#)

### Examples

```
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las = readLAS(LASfile)

#plot(las)

dtm = grid_terrain(las, algorithm = knnidw(k = 6L, p = 2))

#plot(dtm, col = terrain.colors(50))
#plot_dtm3d(dtm)
```

---

kriging	<i>Spatial Interpolation Algorithm</i>
---------	--

---

### Description

This function is made to be used in [grid\\_terrain](#) or [classify\\_ground](#). It implements an algorithm for spatial interpolation. Spatial interpolation is based on universal kriging using the [krige](#) function from [gstat](#). This method combines the KNN approach with the kriging approach. For each point of interest it kriges the terrain using the k-nearest neighbour ground points. This method is more difficult to manipulate but it is also the most advanced method for interpolating spatial data.

**Usage**

```
kriging(model = gstat::vgm(0.59, "Sph", 874), k = 10L)
```

**Arguments**

**model** A variogram model computed with [vgm](#). If NULL it performs an ordinary or weighted least squares prediction.

**k** numeric. Number of k-nearest neighbours. Default 10.

**See Also**

Other spatial interpolation algorithms: [knnidw\(\)](#), [tin\(\)](#)

**Examples**

```
## Not run:
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las = readLAS(LASfile)

# plot(las)

dtm = grid_terrain(las, algorithm = kriging())

plot(dtm, col = terrain.colors(50))
plot_dtm3d(dtm)

## End(Not run)
```

---

LAD

*Leaf area density*


---

**Description**

Computes a leaf area density profile based on the method of Bouvier et al. (see reference)

**Usage**

```
LAD(z, dz = 1, k = 0.5, z0 = 2)
```

**Arguments**

**z** vector of positive z coordinates

**dz** numeric. The thickness of the layers used (height bin)

**k** numeric. is the extinction coefficient

**z0** numeric. The bottom limit of the profile

**Details**

The function assesses the number of laser points that actually reached the layer  $z+dz$  and those that passed through the layer  $[z, z+dz]$  (see [gap\\_fraction\\_profile](#)). Then it computes the log of this quantity and divides it by the extinction coefficient  $k$  as described in Bouvier et al. By definition the layer 0 will always return infinity because no returns pass through the ground. Therefore, the layer 0 is removed from the returned results.

**Value**

A data.frame containing the bin elevations ( $z$ ) and leaf area density for each bin ( $lad$ )

**References**

Bouvier, M., Durrieu, S., Fournier, R. a, & Renaud, J. (2015). Generalizing predictive models of forest inventory attributes using an area-based approach with airborne las data. Remote Sensing of Environment, 156, 322-334. <http://doi.org/10.1016/j.rse.2014.10.004>

**See Also**

[gap\\_fraction\\_profile](#)

**Examples**

```
z <- c(rnorm(1e4, 25, 6), rgamma(1e3, 1, 8)*6, rgamma(5e2, 5,5)*10)
z <- z[z<45 & z>0]

lad <- LAD(z)

plot(lad, type="l", xlab="Elevation", ylab="Leaf area density")
```

---

LAS-class

*An S4 class to represent a .las or .laz file*

---

**Description**

Class LAS is the representation of a las/laz file according to the [LAS file format specifications](#).

**Usage**

```
LAS(data, header = list(), proj4string = sp::CRS(), check = TRUE, index = NULL)
```

**Arguments**

data	a <a href="#">data.table</a> containing the data of a las or laz file.
header	a list or a <a href="#">LASheader</a> containing the header of a las or laz file.
proj4string	projection string of class <a href="#">CRS-class</a> .
check	logical. Conformity tests while building the object.
index	list with two elements <code>list(sensor = 0L, index = 0L)</code> . See <a href="#">spatial indexing</a>



## Details

A LAS object inherits a [Spatial](#) object from `sp`. Thus it is a `Spatial` object plus a `data.table` with the data read from a las/laz file and a [LASheader](#) (see the ASPRS documentation for the [LAS file format](#) for more information). Because las files are standardized the table of attributes read from the las/laz file is also standardized. Columns are named:

- X (numeric)
- Y (numeric)
- Z (numeric)
- gpstime (numeric)
- Intensity (integer)
- ReturnNumber (integer)
- NumberOfReturns (integer)
- ScanDirectionFlag (integer)
- EdgeOfFlightline (integer)
- Classification (integer)
- Synthetic\_flag (logical)
- Keypoint\_flag (logical)
- Withheld\_flag (logical)
- ScanAngleRank (integer)
- ScanAngle (numeric)
- UserData (integer)
- PointSourceID (integer)
- R,G,B (integer)
- NIR (integer)

## Value

An object of class LAS

## Functions

- LAS: creates objects of class LAS. The original data is updated by reference to quantize the coordinates according to the scale factor of the header if no header is provided. In this case the scale factor is set to 0.001

## Slots

bbox Object of class `matrix`, with bounding box

proj4string Object of class `CRS`, projection string

data Object of class `data.table`. Point cloud data according to the [LAS file format](#)

header Object of class [LASheader](#). las file header according to the [LAS file format](#)

index list. See [spatial indexing](#).

**Extends**

Class [Spatial](#), directly.

**See Also**

[readLAS](#)

**Examples**

```
# Read a las/laz file
LASfile <- system.file("extdata", "example.laz", package="rlas")
las <- readLAS(LASfile)
las

# Creation of a LAS object out of external data
data <- data.frame(X = runif(100, 0, 100),
                  Y = runif(100, 0, 100),
                  Z = runif(100, 0, 20))

# 'data' has many decimal digits
data

# Create a default header and quantize *by reference*
# the coordinates to fit with offset and scale factors
cloud <- LAS(data)

# 'data' has been updated and coordinates were quantized
data
cloud

# Be careful when providing a header the function assumes that
# it corresponds to the data and won't quantize the coordinates
data <- data.frame(X = runif(100, 0, 100),
                  Y = runif(100, 0, 100),
                  Z = runif(100, 0, 20))
header <- las@header

# This works but triggers warnings and creates an invalid LAS object
cloud <- LAS(data, header)

las_check(cloud)
```

---

LAScatalog-class

*An S4 class to represent a catalog of .las or .laz files*

---

**Description**

A LAScatalog object is a representation of a set of las/laz files. A LAScatalog is a way to manage and process an entire dataset. It allows the user to process a large area, or to selectively clip data

from a large area without loading all the data into computer memory. A `LAScatalog` can be built with the function `readLAScatalog` and is formally an extension of a `SpatialPolygonsDataFrame` containing extra data to allow users greater control over how the dataset is processed (see details).

## Details

A `LAScatalog` is formally a `SpatialPolygonsDataFrame` extended with new slots that contain processing options. In `lidR`, each function that supports a `LAScatalog` as input will respect these processing options. Internally, processing a catalog is almost always the same and relies on a few steps:

1. Define chunks. A chunk is an arbitrarily-defined region of interest (ROI) of the catalog. Altogether, the chunks are a wall-to-wall set of ROIs that encompass the whole dataset.
2. Loop over each chunk (in parallel or not).
3. For each chunk, load the points inside the ROI into R, run some R functions, return the expected output.
4. Merge the outputs of the different chunks once they are all processed to build a continuous (wall-to-wall) output.

So basically, a `LAScatalog` is an object that allows for batch processing but with the specificity that `lidR` does not loop through LAS or LAZ files, but loops seamlessly through chunks that do not necessarily match with the file pattern. This way `lidR` can sequentially process tiny ROIs even if each file may be individually too big to fit in memory. This is also why point cloud indexation with `lax` files may significantly speed-up the processing.

It is important to note that catalogs with files that overlap each other are not natively supported by `lidR`. When encountering such datasets the user should always filter any overlaps if possible. This is possible if the overlapping points are flagged, for example in the 'withheld' attribute. Otherwise `lidR` will not be able to process the dataset correctly.

## Slots

`processing_options` list. A list that contains some settings describing how the catalog will be processed (see dedicated section).

`chunk_options` list. A list that contains some settings describing how the catalog will be subdivided into chunks to be processed (see dedicated section).

`output_options` list. A list that contains some settings describing how the catalog will return the outputs (see dedicated section).

`input_options` list. A list of parameters to pass to `readLAS` (see dedicated section).

`index` list. See [spatial indexing](#).

## Processing options

The slot `@processing_options` contains a list of options that determine how chunks (the sub-areas that are sequentially processed) are processed.

- **progress**: boolean. Display a progress bar and a chart of progress. Default is TRUE. Progress estimation can be enhanced by installing the package `progress`. See [opt\\_progress](#).

- **stop\_early**: boolean. Stop the processing if an error occurs in a chunk. If FALSE the process can run until the end, removing chunks that failed. Default is TRUE and the user should have no reason to change this. See [opt\\_stop\\_early](#).
- **wall.to.wall** logical. The catalog processing engine always guarantees to return a continuous output without edge effects, assuming that the catalog is a wall-to-wall catalog. To do so, some options are checked internally to guard against bad settings, such as `buffer = 0` for an algorithm that requires a buffer. In rare cases it might be useful to disable these controls. If `wall.to.wall = FALSE` controls are disabled and wall-to-wall outputs cannot be guaranteed. See [opt\\_wall\\_to\\_wall](#)

### Chunk options

The slot `@chunk_options` contains a list of options that determine how chunks (the sub-areas that are sequentially processed) are made.

- **chunk\_size**: numeric. The size of the chunks that will be sequentially processed. A small size allows small amounts of data to be loaded at once, saving computer memory. With big chunks the computation is usually faster but uses much more memory. If `chunk_size = 0` the catalog is processed sequentially *by file* i.e. a chunk is a file. Default is 0 i.e. by default the processing engine respects the existing tiling pattern. See [opt\\_chunk\\_size](#).
- **buffer**: numeric. Each chunk can be read with an extra buffer around it to ensure there are no edge effects between two independent chunks and that the output is continuous. This is mandatory for some algorithms. Default is 30. See [opt\\_chunk\\_buffer](#).
- **alignment**: numeric. A vector of size 2 (x and y coordinates, respectively) to align the chunk pattern. By default the alignment is made along (0,0), meaning that the edge of the first chunk will belong on `x = 0` and `y = 0` and all the other chunks will be multiples of the chunk size. Not relevant if `chunk_size = 0`. See [opt\\_chunk\\_alignment](#).
- **drop**: integers. A vector of integers that specify the IDs of the chunks that should not be created. This is designed to enable to restart a computation that failed without reprocessing everything. See `opt_restart`. Technically this options may be used for partial processing of a collection but should not. Partial processing is already a feature of the engine. See [this vignette](#)

### Output options

The slot `@output_options` contains a list of options that determine how chunks (the sub-areas that are sequentially processed) are written. By "written" we mean written to files or written in R memory.

- **output\_files**: string. If `output_files = ""` outputs are returned in R. Otherwise, if `output_files` is a string the outputs will be written to files. This is useful if the output is too big to be returned in R. A path to a filename template without extension (the engine guesses it for you) is expected. When several files are going to be written a single string is provided with a template that is automatically filled. For example, the following file names are possible:

```
"/home/user/als/normalized/file_{ID}_segmented"
"C:/user/document/als/zone52_{XLEFT}_{YBOTTOM}_confidential"
"C:/user/document/als/{ORIGINALFILENAME}_normalized"
```

This option will generate as many filenames as needed with custom names for each file. The list of allowed templates is described in the documentation for each function. See [opt\\_output\\_files](#).

- **drivers**: list. This contains all the drivers required to seamlessly write Raster\*, Spatial\*, sf, and LAS objects. It is recommended that only advanced users change this option. A dedicated page describes the drivers in [lidR-LAScatalog-drivers](#).
- **merge**: boolean. Multiple objects are merged into a single object at the end of the processing.

### Input options

The slot @input\_options contains a list of options that are passed to the function [readLAS](#). Indeed, the readLAS function is not called directly by the user but by the internal processing engine. Users can propagate these options through the LAScatalog settings.

- **select**: string. The option select. Usually this option is not respected because each function knows which data must be loaded or not. This is documented in each function. See [opt\\_select](#).
- **filter**: string. The option filter. See [opt\\_filter](#).

### Examples

```
## Not run:
# Build a catalog
ctg <- readLAScatalog("filder/to/las/files/")

# Set some options
opt_filter(ctg) <- "-keep_first"

# Summary gives a summary of how the catalog will be processed
summary(ctg)

# We can seamlessly use lidR functions
hmean <- grid_metrics(ctg, mean(Z), 20)
ttops <- tree_detection(ctg, lmf(5))

# For low memory config it is probably advisable not to load entire files
# and process chunks instead
opt_chunk_size(ctg) <- 500

# Sometimes the output is likely to be very large
# e.g. large coverage and small resolution
dtm <- grid_terrain(ctg, 1, tin())

# In that case it is advisable to write the output(s) to files
opt_output_files(ctg) <- "path/to/folder/DTM_chunk_{XLEFT}_{YBOTTOM}"

# Raster will be written to disk. The list of written files is returned
# or, in this specific case, a virtual raster mosaic.
dtm <- grid_terrain(ctg, 1, tin())

# When chunks are files the original names of the las files can be preserved
opt_chunk_size(ctg) <- 0
opt_output_files(ctg) <- "path/to/folder/DTM_{ORIGINALFILENAME}"
```

```

dtm <- grid_terrain(ctg, 1, tin())

# For some functions, files MUST be written to disk. Indeed, it is certain that R cannot
# handle the entire output.
opt_chunk_size(ctg) <- 0
opt_output_files(ctg) <- "path/to/folder/{ORIGINALFILENAME}_norm"
opt_laz_compression(ctg) <- TRUE
new_ctg <- normalize_height(ctg, tin())

# The user has access to the catalog engine through the function catalog_apply
output <- catalog_apply(ctg, FUN, ...)

## End(Not run)

```

---

LASheader

*Create a LASheader object*


---

## Description

Creates a LASheader object either from a raw list containing all the elements named according to the rlas package or creates a header from a `data.frame` or `data.table` containing a point cloud. In the latter case it will generate a header according to the data using `rlas::header_create()`. It will guess the LAS file format, the point data format, and initialize the scale factors and offsets, but these may not suit a user's needs. Users are advised to manually modify the results to fit their specific needs.

## Usage

```
LASheader(data = list())
```

## Arguments

<code>data</code>	a list containing the data from the header of a LAS file. Can also be a <code>data.frame</code> or <code>data.table</code>
-------------------	--

## Value

An object of class LASheader

## Examples

```

data = data.frame(X = c(339002.889, 339002.983, 339002.918),
                  Y = c(5248000.515, 5248000.478, 5248000.318),
                  Z = c(975.589, 974.778, 974.471),
                  gpstime = c(269347.28141, 269347.28142, 269347.28143),
                  Intensity = c(82L, 54L, 27L),
                  ReturnNumber = c(1L, 1L, 2L),
                  NumberOfReturns = c(1L, 1L, 2L),
                  ScanDirectionFlag = c(1L, 1L, 1L),

```

```

      EdgeOffFlightline = c(1L, 0L, 0L),
      Classification = c(1L, 1L, 1L),
      ScanAngleRank = c(-21L, -21L, -21L),
      UserData = c(32L, 32L, 32L),
      PointSourceID = c(17L, 17L, 17L))

header = LASheader(data)
header

# XYZ values are given with 3 decimals. This was not inferred by the
# function so we changed it manually
# (Note: from package rlas 1.4.1 this is now inferred properly in most cases)
header@PHB[["X scale factor"]] <- 0.001
header@PHB[["Y scale factor"]] <- 0.001
header@PHB[["Z scale factor"]] <- 0.001

# Record an EPSG code
epsg(header) <- 32618
header

las <- LAS(data, header)
las

# The function inferred a LAS 1.2 format 1 which is correct
# Upgrade to LAS 1.4 for the example
header@VLR <- list() # Erase VLR previously written
header@PHB[["Global Encoding"]][["WKT"]] <- TRUE
header@PHB[["Version Minor"]] <- 4L
header@PHB[["Header Size"]] <- 375L
header@PHB[["Offset to point data"]] <- 375L
wkt(header) <- sf::st_crs("EPSG:32618")$wkt
header
las1.4 <- LAS(data, header)
las1.4

```

---

LASheader-class

*An S4 class to represent the header of .las or .laz files*


---

## Description

An S4 class to represent the header of .las or .laz files according to the [LAS file format specifications](#). A LASheader object contains a list in the slot @PHB with the data read from the Public Header Block and list in the slot @VLR with the data read from the Variable Length Records

## Slots

PHB list. Represents the Public Header Block

VLR list. Represents the Variable Length Records

EVLRL list. Represents the Extended Variable Length Records

---

`las_check`*Inspect a LAS object*

---

### Description

Performs a deep inspection of a LAS or LAScatalog object and prints a report.

For a LAS object it checks:

- if the point cloud is valid according to las specification
- if the header is valid according to las specification
- if the point cloud is in accordance with the header
- if the point cloud has duplicated points and degenerated ground points
- if the coordinate reference system is correctly recorded
- if some pre-processing, such as normalization or ground filtering, is already done.

For a LAScatalog object it checks:

- if the headers are consistent across files
- if the files are overlapping
- if some pre-processing, such as normalization, is already done.

For the pre-processing tests the function only makes an estimation and may not be correct.

### Usage

```
las_check(las, print = TRUE, ...)
```

### Arguments

<code>las</code>	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
<code>print</code>	logical. By default, prints a report and returns a list invisibly. If <code>print = FALSE</code> the functions returns a list visibly and do not print the report.
<code>...</code>	Use <code>deep = TRUE</code> on a <a href="#">LAScatalog</a> only. Instead of a shallow inspection it reads all the files and performs a deep inspection.

### Value

A list with three elements named `message`, `warnings` and `errors`. This list is returned invisibly if `print = TRUE`. If `deep = TRUE` a nested list is returned with one element per file.

### See Also

Other las utilities: [las\\_utilities](#)



**Examples**

```

LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile)
las_check(las)

```

---

las\_utilities

*LAS utilities*


---

**Description**

Tools to manipulate LAS objects maintaining compliance with [ASPRS specification](#)

**Usage**

```

las_rescale(las, xscale, yscale, zscale)

las_reoffset(las, xoffset, yoffset, zoffset)

las_quantize(las, by_reference = TRUE)

las_update(las)

quantize(x, scale, offset, by_reference = TRUE, ...)

is.quantized(x, scale, offset, ...)

count_not_quantized(x, scale, offset)

storable_coordinate_range(scale, offset)

```

**Arguments**

las	An object of class LAS
xscale, yscale, zscale	scalar. Can be missing if not relevant.
xoffset, yoffset, zoffset	scalar. Can be missing if not relevant.
by_reference	bool. Update the data in place without allocating new memory.
x	numeric. Coordinates vector
scale, offset	scalar. scale and offset
...	Unused.

## Details

In the specification of the LAS format the coordinates are expected to be given with a certain precision e.g. 0.01 for a millimeter precision (or millifeet), meaning that a file records e.g. 123.46 not 123.45678. Also, coordinates are stored as integers. This is made possible with a scale and offset factor. For example, 123.46 with an offset of 100 and a scale factor of 0.01 is actually stored as  $(123.46 - 100)/0.01 = 2346$ . Storing 123.45678 with a scale factor of 0.01 and an offset of 100 is invalid because it does not convert to an integer:  $(123.45678-100)/0.01 = 2345.678$ . Having an invalid LAS object may be critical in some lidR applications. When writing into a LAS file, users will loose the extra precision without warning and some algorithms in lidR use the integer conversion to make integer-based computation and thus speed-up some algorithms and use less memory. Creation of an invalid LAS object may cause problems and incorrect outputs.

## See Also

Other las utilities: [las\\_check\(\)](#)

## Examples

```
LASfile <- system.file("extdata", "example.laz", package="rlas")
las = readLAS(LASfile)

# Manual modification of the coordinates (e.g. rotation, re-alignment, ...)
las@data$X <- las@data$X + 2/3
las@data$Y <- las@data$Y - 5/3

# The point cloud is no longer valid
las_check(las)

# It is important to fix that
las_quantize(las)

# Now the file is almost valid
las_check(las)

# Update the object to set up-to-date header data
las <- las_update(las)
las_check(las)

# In practice the above code is not useful for regular users because the operators
# $<- already perform such operations on-the-fly. Thus the following
# syntax must be preferred and returns valid objects. Previous tools
# were only intended to be used in very specific cases.
las$X <- las$X + 2/3
las$Y <- las$Y - 5/3

# Rescale and reoffset recompute the coordinates with
# new scales and offsets according to LAS specification
las <- las_rescale(las, xscale = 0.01, yscale = 0.01)
las <- las_reoffset(las, xoffset = 300000, yoffset = 5248000)
```

**Description**

This function is made to be used in [segment\\_trees](#). It implements an algorithm for tree segmentation based on the Li et al. (2012) article (see reference). This method is a growing region method working at the point cloud level. It is an implementation, as strict as possible, made by the lidR author but with the addition of a parameter `hmin` to prevent over-segmentation for objects that are too low.

**Usage**

```
li2012(dt1 = 1.5, dt2 = 2, R = 2, Zu = 15, hmin = 2, speed_up = 10)
```

**Arguments**

<code>dt1</code>	numeric. Threshold number 1. See reference page 79 in Li et al. (2012). Default is 1.5.
<code>dt2</code>	numeric. Threshold number 2. See reference page 79 in Li et al. (2012). Default is 2.
<code>R</code>	numeric. Search radius. See page 79 in Li et al. (2012). Default is 2. If <code>R = 0</code> all the points are automatically considered as local maxima and the search step is skipped (much faster).
<code>Zu</code>	numeric. If point elevation is greater than <code>Zu</code> , <code>dt2</code> is used, otherwise <code>dt1</code> is used. See page 79 in Li et al. (2012). Default is 15.
<code>hmin</code>	numeric. Minimum height of a detected tree. Default is 2.
<code>speed_up</code>	numeric. Maximum radius of a crown. Any value greater than a crown is good because this parameter does not affect the result. However, it greatly affects the computation speed. The lower the value, the faster the method. Default is 10.

**References**

Li, W., Guo, Q., Jakubowski, M. K., & Kelly, M. (2012). A new method for segmenting individual trees from the lidar point cloud. *Photogrammetric Engineering & Remote Sensing*, 78(1), 75-84.

**See Also**

Other individual tree segmentation algorithms: [dalponte2016\(\)](#), [silva2016\(\)](#), [watershed\(\)](#)

**Examples**

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile, select = "xyz", filter = "-drop_z_below 0")
col <- pastel.colors(200)

las <- segment_trees(las, li2012(dt1 = 1.4))
#plot(las, color = "treeID", colorPalette = col)
```

---

 lidR-LAScatalog-drivers

*LAScatalog drivers*


---

## Description

This document explains how objects are written on disk when processing a LAScatalog. As mentioned in [LAScatalog-class](#), users can set a templated filename to store the outputs on disk instead of in R memory. By default LAS objects are stored in .las files with [writeLAS](#), Raster\* objects are stored in .tif files with [writeRaster](#), Spatial\* objects are stored in .shp files with [st\\_write](#), data.frame objects are stored in .csv files with [fwrite](#), and other objects are not supported. However, users can modify all these default settings and even add new drivers. This manual page explain how. One may also refer to some unofficial documentation [here](#) or [here](#).

## Generic form of a driver

A driver is stored in the @output\_options slot of a LAScatalog. It is a list that contains:

**write** A function that receives an object and a path, and writes the object into a file using the path. The function can also have extra options.

**extension** A string that gives the file extension.

**object** A string that gives the name of the argument used to pass the object to write in the function used to write the object.

**path** A string that gives the name of the argument used to pass the path of the file to write in the function used to write the object.

**param** A labelled list of extra parameters for the function used to write the object

For example, the driver to write a Raster\* is

```
list(
  write = raster::writeRaster,
  extension = ".tif",
  object = "x",
  path = "filename",
  param = list(format = "GTiff"))
```

And the driver to write a LAS is

```
list(
  write = lidR::writeLAS,
  extension = ".las",
  object = "las",
  path = "file",
  param = list())
```

**Modify a driver (1/2)**

Users can modify the drivers to write different file types than the default. For example, to write in GeoPackage instead of shapefile, one must change the Spatial driver:

```
ctg@output_options$drivers$Spatial$extension <- ".gpkg"
```

To write in .grd files instead of .tif files one must change the Raster driver:

```
ctg@output_options$drivers$Raster$extension <- ".grd"
ctg@output_options$drivers$Raster$param$format <- "raster"
```

To write in .laz files instead of .las files one must change the LAS driver:

```
ctg@output_options$drivers$LAS$extension <- ".laz"
```

**Add a new driver**

The drivers allow LAS, Spatial\*, Raster\* and data.frame objects to be written. When using the engine ([catalog\\_apply](#)) to build new tools, users may need to be able to write other objects such as a list. To do that users need to add a list element into the output\_options:

```
ctg@output_options$drivers$list = list(
  write = base::saveRDS,
  object = "object",
  path = "file",
  extension = ".rds",
  param = list(compress = TRUE))
```

The LAScatalog now has a new driver capable of writing a list.

**Modify a driver (2/2)**

It is also possible to completely overwrite an existing driver. By default SpatialPointsDataFrame objects are written into ESRI shapefiles with `st_write`. `writeOGR` can write into other file types, such as GeoPackage or GeoJSON and even as SQLite database objects. But it cannot add data into an existing SQLite database. Let's create our own driver for a SpatialPointsDataFrame. First we need a function able to write and append a SpatialPointsDataFrame into a SQLite database from the object and the path.

```
dbWrite_SpatialPointsDataFrame = function(x, path, name)
{
  x <- as.data.frame(x)
  con <- RSQLite::dbConnect(RSQLite::SQLite(), path)
  RSQLite::dbWriteTable(con, name, x, append = TRUE)
  RSQLite::dbDisconnect(con)
}
```

Then we create the driver. User-defined drivers supersede default drivers:

```
ctg@output_options$drivers$SpatialPointsDataFrame = list(
  write = dbWrite_SpatialPointsDataFrame,
  extension = ".sqlite",
  object = "x",
  path = "path",
  param = list(name = "layername"))
```

Then to be sure that we do not write several .sqlite files, we don't use templated filename.

```
opt_output_files(ctg) <- paste0(tempdir(), "/mysqlitefile")
```

And all the SpatialPointsDataFrame will be appended in a single database.

## Description

This document explain how to process point clouds taking advantage of parallel processing in the lidR package. The lidR package has two levels of parallelism, which is why it is difficult to understand how it works. This page aims to provide users with a clear overview of how to take advantage of multicore processing even if they are not comfortable with the parallelism concept.

## Algorithm-based parallelism

When processing a point cloud we are applying an algorithm on data. This algorithm may or may not be natively parallel. In lidR some algorithms are fully computed in parallel, but some are not because they are not parallelizable, while some are only partially parallelized. It means that some portions of the code are computed in parallel and some are not. When an algorithm is natively parallel in lidR it is always a C++ based parallelization with OpenMP. The advantage is that the computation is faster without any consequence for memory usage because the memory is shared between the processors. In short, algorithm-based parallelism provides a significant gain without any cost for your R session and your system (but obviously there is a greater workload for the processors). By default lidR uses half of your cores but you can control this with [set\\_lidr\\_threads](#). For example, the [lmf](#) algorithm is natively parallel. The following code is computed in parallel:

```
las <- readLAS("file.las")
tops <- tree_detection(las, lmf(2))
```

However, as stated above, not all algorithms are parallelized or even parallelizable. For example, [li2012](#) is not parallelized. The following code is computed in serial:

```
las <- readLAS("file.las")
dtm <- segment_trees(las, li2012())
```

To know which algorithms are parallelized users can refer to the documentation or use the function [is\\_parallelised](#).

```
is_parallelised(lmf(2)) #> TRUE
is_parallelised(li2012()) #> FALSE
```

### chunk-based parallelism

When processing a LAScatalog, the internal engine splits the dataset into chunks and each chunk is read and processed sequentially in a loop. But actually this loop can be parallelized with the `future` package. By default the chunks are processed sequentially, but they can be processed in parallel by registering an evaluation strategy. For example, the following code is evaluated sequentially:

```
ctg <- readLAScatalog("folder/")
out <- grid_metrics(ctg, mean(Z))
```

But this one is evaluated in parallel with two cores:

```
library(future)
plan(multisession, workers = 2L)
ctg <- readLAScatalog("folder/")
out <- grid_metrics(ctg, mean(Z))
```

With chunk-based parallelism any algorithm can be parallelized by processing several subsets of a dataset. However, there is a strong cost associated with this type of parallelism. When processing several chunks at a time, the computer needs to load the corresponding point clouds. Assuming the user processes one square kilometer chunks in parallel with 4 cores, then 4 chunks are loaded in the computer memory. This may be too much and the speed-up is not guaranteed since there is some overhead involved in reading several files at a time. Once this point is understood, chunk-based parallelism is very powerful since all the algorithms can be parallelized whether or not they are natively parallel. It also allows to parallelize the computation on several machines on the network or to work on a HPC.

### Nested parallelism - part 1

Previous sections stated that some algorithms are natively parallel, such as `lmf`, and some are not, such as `li2012`. Anyway, users can split the dataset into chunks to process them simultaneously with the LAScatalog processing engine. Let's assume that the user's computer has four cores, what happens in this case:

```
library(future)
plan(multisession, workers = 4L)
set_lidr_threads(4L)
ctg <- readLAScatalog("folder/")
out <- tree_detection(ctg, lmf(2))
```

Here the catalog will be split into chunks that will be processed in parallel. And each computation itself implies a parallelized task. This is a nested parallelism task and it is dangerous! Hopefully the `lidR` package handles such cases and chooses by default to give precedence to chunk-based parallelism. In this case chunks will be processed in parallel and the points will be processed serially by disabling OpenMP.

### Nested parallelism - part 2

We explained rules of precedence. But actually the user can tune the engine more accurately. Let's define the following function:

```
myfun = function(cluster, ...)
{
  las <- readLAS(cluster)
  if (is.empty(las)) return(NULL)
  las <- normalize_height(las, tin())
  tops <- tree_detection(las, lmf(2))
  bbox <- extent(cluster)
  tops <- crop(tops, bbox)
  return(tops)
}
```

```
out <- catalog_apply(ctg, myfun, ws = 5)
```

This function used two algorithms, one is partially parallelized (`tin`) and one is fully parallelized `lmf`. The user can manually use both OpenMP and future. By default the engine will give precedence to chunk-based parallelism because it works in all cases but the user can impose something else. In the following 2 workers are attributed to future and 2 workers are attributed to OpenMP.

```
plan(multisession, workers = 2L)
set_lidr_threads(2L)
catalog_apply(ctg, myfun, ws = 5)
```

The rule is simple. If the number of workers needed is greater than the number of available workers then OpenMP is disabled. Let suppose we have a 4 cores:

```
# 2 chunks 2 threads: OK
plan(multisession, workers = 2L)
set_lidr_threads(2L)

# 4 chunks 1 threads: OK
plan(multisession, workers = 4L)
set_lidr_threads(1L)

# 1 chunks 4 threads: OK
plan(sequential)
set_lidr_threads(4L)

# 3 chunks 2 threads: NOT OK
# Needs 6 workers, OpenMP threads are set to 1 i.e. sequential processing
plan(multisession, workers = 3L)
set_lidr_threads(2L)
```

### Complex computing architectures

For more complex processing architectures such as multiple computers controlled remotely or HPC a finer tuning might be necessary. Using

```
options(lidr.check.nested.parallelism = FALSE)
```

lidR will no longer check for nested parallelism and will never automatically disable OpenMP.



---

 lidR-spatial-index      *Spatial index*


---

## Description

This document explains how to process point-clouds taking advantage of different spatial indices available in the lidR package. lidR can use several types of spatial indexes to apply algorithms (that need a spatial indexing) as fast as possible. The choice of the spatial index depends on the type of point-cloud that is processed and the algorithm that is performed. lidR can use a grid partition, a voxel partition, a quadtree or an octree. See details.

## Usage

```
sensor(las, h = FALSE)
```

```
sensor(las) <- value
```

```
index(las, h = FALSE)
```

```
index(las) <- value
```

## Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
h	boolean. Human readable. Everything is stored as integers that are understood internally. Use h = TRUE for user readable output.
value	integer or character. A code for referring to a sensor type or a spatial index type. Use one of "unknown", "als", "tls", "uav", "dap", "multispectral" for sensor type and one of "auto", "gridpartition", "voxelpartition", "quadtree", "octree" for spatial index type.

## Details

From lidR (>= 3.1.0), a [LAS](#) object records the sensor used to sample the point-cloud (ALS, TLS, UAV, DAP) as well as the spatial index that must be used for processing the point cloud. This can be set manually by the user but the simplest is to use one of the [read\\*LAS\(\)](#) functions. By default a point-cloud is associated to a sensor and the best spatial index is chosen on-the-fly depending on the algorithm applied. It is possible to force the use of a specific spatial index.

Information relative to the spatial indexing is stored in slot @index that contains a list with two elements:

- sensor: an integer that records the sensor type
- index: an integer that records the spatial index to be used

By default the spatial index code is 0 ("automatic") meaning that each function is free to choose a different spatial index depending on the recorded sensor. If the code is not 0 then each function will

be forced to use the spatial index that is imposed. This, obviously, applies only to functions that use spatial indexing.

[LAScatalog](#) objects also record such information that is automatically propagated to the LAS objects when processing.

Note: before version 3.1.0, point-clouds were all considered as ALS because lidR was originally designed for ALS. Consequently, for legacy and backwards-compatibility reasons, `readLAS()` and `readALSLAS()` are actually equivalent. `readLAS()` tags the point cloud with "unknown" sensor while `readALSLAS()` tags it with 'ALS'. Both behave the same and this is especially true compared with versions < 3.1. As a consequence, using `readLAS()` provides the same performance (no degradation) than in previous versions, while using one of the `read*LAS()` functions may improve the performance.

## Examples

```
LASfile <- system.file("extdata", "example.laz", package="rlas")
las <- readLAS(LASfile)

# By default the sensor and spatial index codes are 0
sensor(las)
index(las)

# Codes are used internally and not intended to be known by users
# Use h option for human readable output
sensor(las, h = TRUE)
index(las, h = TRUE)

# Modification of the sensor enables users to select a better spatial index
# when processing the point-cloud.
sensor(las) <- "tls"
sensor(las, h = TRUE)
index(las, h = TRUE)

# Modification of the spatial index forces users to choose one of the available
# spatial indexes.
index(las) <- "quadtree"
sensor(las, h = TRUE)
index(las, h = TRUE)

# The simplest way to take advantage of appropriate spatial indexing is
# to use one of the read*LAS() functions.
las <- readTLAS(LASfile)
sensor(las, h = TRUE)
index(las, h = TRUE)

# But for some specific point-clouds / algorithms it might be advisable to force
# the use of a specific spatial index to perform the computation faster
index(las) <- "voxelpartition"
index(las, h = TRUE)

# With a LAScatalog, spatial indexing information is propagated to the
# different chunks
```

```

ctg = readTLAScatalog(LASfile)
index(ctg) <- "voxelpartition"
sensor(ctg, h = TRUE)
index(ctg, h = TRUE)

# =====
# PERFORMANCE TESTS
# =====

## Not run:
# Performance tests on TLS
# -----

# The package does not include TLS data
# so we can generate something that looks TLS-ish
# >>>>>>>>>>
X = runif(50, -25, 25)
Y = runif(50, -25, 25)
X = as.numeric(sapply(X, function(x) rnorm(2000, x, 2)))
Y = as.numeric(sapply(Y, function(x) rnorm(2000, x, 2)))
Z = abs(rnorm(length(Y), 10, 5))
veg = data.frame(X,Y,Z)
X = runif(5000, -30, 30)
Y = runif(5000, -30, 30)
Z = runif(5000, 0, 1)
ground = data.frame(X,Y,Z)
X = runif(30, -30, 30)
Y = runif(30, -30, 30)
Z = runif(30, 0, 30)
noise = data.frame(X,Y,Z)
las = LAS(rbind(ground, veg, noise))
# <<<<<<<<<<<<<<

plot(las)

# If read with readALSLAS()
sensor(las) <- "als"
system.time(classify_noise(las, sor(20, 8)))
#> 1.5 sec

# If read with readTLASLAS()
sensor(las) <- "tls"
system.time(classify_noise(las, sor(20, 8)))
#> 0.6 sec

# Performance tests on ALS
# -----

# The package does not include large ALS data
# so we can generate something that looks ALS-ish
# >>>>>>>>>>
X = runif(4e5, 0, 1000)
Y = runif(4e5, 0, 1000)

```

```
Z = 40*sin(0.01*X) + 50*cos(0.005*Y) + abs(rnorm(length(Y), 10, 5))
veg = data.frame(X,Y,Z)
X = runif(100, 0, 1000)
Y = runif(100, 0, 1000)
Z = 40*sin(0.01*X) + 50*cos(0.005*Y) + abs(rnorm(length(Y), 10, 5)) + runif(100, 30, 70)
noise = data.frame(X,Y,Z)
las = LAS(rbind(veg, noise))
# <<<<<<<<<<<<<<<<<<<<<

plot(las)

# If read with readALSLAS()
sensor(las) <- "als"
system.time(classify_noise(las, sor(15, 8)))
#> 3 sec

# If read with readTSLAS()
sensor(las) <- "tls"
system.time(classify_noise(las, sor(15, 8)))
#> 4.3 sec

## End(Not run)
```

---

lidrpalettes

Palettes

---

## Description

Create a vector of n contiguous (or not) colors

## Usage

height.colors(n)

forest.colors(n)

random.colors(n)

pastel.colors(n)

## Arguments

n                   The number of colors (> 1) to be in the palette

---

 lmf *Individual Tree Detection Algorithm*


---

**Description**

This function is made to be used in [find\\_trees](#). It implements an algorithm for tree detection based on a local maximum filter. The windows size can be fixed or variable and its shape can be square or circular. The internal algorithm works either with a raster or a point cloud. It is deeply inspired by Popescu & Wynne (2004) (see references).

**Usage**

```
lmf(ws, hmin = 2, shape = c("circular", "square"))
```

**Arguments**

ws	numeric or function. Length or diameter of the moving window used to detect the local maxima in the units of the input data (usually meters). If it is numeric a fixed window size is used. If it is a function, the function determines the size of the window at any given location on the canopy. The function should take the height of a given pixel or point as its only argument and return the desired size of the search window when centered on that pixel/point.
hmin	numeric. Minimum height of a tree. Threshold below which a pixel or a point cannot be a local maxima. Default is 2.
shape	character. Shape of the moving window used to find the local maxima. Can be "square" or "circular".

**References**

Popescu, Sorin & Wynne, Randolph. (2004). Seeing the Trees in the Forest: Using Lidar and Multispectral Data Fusion with Local Filtering and Variable Window Size for Estimating Tree Height. *Photogrammetric Engineering and Remote Sensing*. 70. 589-604. 10.14358/PERS.70.5.589.

**See Also**

Other individual tree detection algorithms: [manual\(\)](#)

**Examples**

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile, select = "xyz", filter = "-inside 481250 3812980 481300 3813050")

# point-cloud-based
# =====

# 5x5 m fixed window size
ttops <- find_trees(las, lmf(5))
```

```

#x <- plot(las)
#add_treetops3d(x, ttops)

# variable windows size
f <- function(x) { x * 0.07 + 3}
ttops <- find_trees(las, lmf(f))

#x <- plot(las)
#add_treetops3d(x, ttops)

# raster-based
# =====

chm <- grid_canopy(las, res = 1, p2r(0.15))
ttops <- find_trees(chm, lmf(5))

plot(chm, col = height.colors(30))
plot(ttops, add = TRUE)

# variable window size
f <- function(x) { x * 0.07 + 3 }
ttops <- find_trees(chm, lmf(f))

plot(chm, col = height.colors(30))
plot(ttops, add = TRUE)

```

---

manual

*Individual Tree Detection Algorithm*


---

## Description

This function is made to be used in [find\\_trees](#). It implements an algorithm for manual tree detection. Users can pinpoint the tree top positions manually and interactively using the mouse. This is only suitable for small-sized plots. First the point cloud is displayed, then the user is invited to select a rectangular region of interest in the scene using the mouse button. Within the selected region the highest point will be flagged as 'tree top' in the scene. Once all the trees are labelled the user can exit the tool by selecting an empty region. Points can also be unflagged. The goal of this tool is mainly for minor correction of automatically-detected tree outputs.

## Usage

```
manual(detected = NULL, radius = 0.5, color = "red", button = "middle", ...)
```

## Arguments

detected	SpatialPointsDataFrame of already found tree tops that need manual correction.
radius	numeric. Radius of the spheres displayed on the point cloud (aesthetic purposes only).

color	character. Colour of the spheres displayed on the point cloud (aesthetic purposes only).
button	Which button to use for selection. One of "left", "middle", "right". lidR using left for rotation and right for dragging using one of left or right will disable either rotation or dragging
...	supplementary parameters to be passed to <a href="#">plot</a> .

### See Also

Other individual tree detection algorithms: [lmf\(\)](#)

### Examples

```
## Not run:
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las = readLAS(LASfile)

# Full manual tree detection
ttops = find_trees(las, manual())

# Automatic detection with manual correction
ttops = find_trees(las, lmf(5))
ttops = find_trees(las, manual(ttops))

## End(Not run)
```

---

maxima

*Point Cloud Decimation Algorithm*


---

### Description

These functions are made to be used in [decimate\\_points](#). They implement algorithms that creates a grid with a given resolution and filters the point cloud by selecting the highest/lowest point within each cell.

### Usage

```
highest(res = 1)
```

```
lowest(res = 1)
```

### Arguments

res                    numeric. The resolution of the grid used to filter the point cloud

### See Also

Other point cloud decimation algorithms: [homogenize\(\)](#), [random\\_per\\_voxel\(\)](#), [random\(\)](#)

Other point cloud decimation algorithms: [homogenize\(\)](#), [random\\_per\\_voxel\(\)](#), [random\(\)](#)

**Examples**

```

LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las = readLAS(LASfile, select = "xyz")

# Select the highest point within each cell of an overlaid grid
thinned = decimate_points(las, highest(4))
#plot(thinned)

# Select the lowest point within each cell of an overlaid grid
thinned = decimate_points(las, lowest(4))
#plot(thinned)

```

---

merge\_spatial

---

*Merge a point cloud with a source of spatial data*


---

**Description**

Merge a point cloud with a source of spatial data. It adds an attribute along each point based on a value found in the spatial data. Sources of spatial data can be a `SpatialPolygons*`, a `sf` data.frame or a `Raster*`.

- `SpatialPolygons*`, `sf`: it checks if the points belongs within each polygon. If the parameter `attribute` is the name of an attribute in the table of attributes it assigns to the points the values of that attribute. Otherwise it classifies the points as boolean. TRUE if the points are in a polygon, FALSE otherwise.
- `RasterLayer`: it attributes to each point the value found in each pixel of the `RasterLayer`.
- `RasterStack` or `RasterBrick` must have 3 channels for RGB colors. It colorizes the point cloud with RGB values.

**Usage**

```
merge_spatial(las, source, attribute = NULL)
```

**Arguments**

las	An object of class LAS
source	An object of class <code>SpatialPolygons*</code> or <code>sf</code> or <code>RasterLayer</code> or a <code>RasterStack</code> or <code>RasterBrick</code> with RGB colors.
attribute	character. The name of an attribute in the table of attributes of the shapefile or the name of a new column in the LAS object. Not relevant for RGB colorization.

**Value**

An object of the class LAS.



**Examples**

```

LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
shp      <- system.file("extdata", "lake_polygons_UTM17.shp", package = "lidR")

las      <- readLAS(LASfile, filter = "-keep_random_fraction 0.1")
lakes    <- sf::st_read(shp)

# The attribute "inlake" does not exist in the shapefile.
# Points are classified as TRUE if in a polygon
las      <- merge_spatial(las, lakes, "inlakes")    # New attribute 'inlakes' is added.
forest   <- filter_poi(las, inlakes == FALSE)
#plot(forest)

# The attribute "LAKENAME_1" exists in the shapefile.
# Points are classified with the values of the polygons
las      <- merge_spatial(las, lakes, "LAKENAME_1") # New column 'LAKENAME_1' is added.

```

---

normalize\_height      *Remove the topography from a point cloud*

---

**Description**

Subtract digital terrain model (DTM) from LiDAR point cloud to create a dataset normalized with the ground at 0. The DTM can originate from an external file or can be computed by the user. It can also be computed on-the-fly. In this case the algorithm does not use rasterized data and each point is interpolated. There is no inaccuracy due to the discretization of the terrain and the resolution of the terrain is virtually infinite.

How well the edges of the dataset are interpolated depends on the interpolation method used. Thus, a buffer around the region of interest is always recommended to avoid edge effects.

The attribute Z of the returned LAS object is the normalized elevation. A new attribute 'Zref' records the former elevation values, which enables the use of [unnormalize\\_height](#) to restore original point elevations.

**Usage**

```

normalize_height(
  las,
  algorithm,
  na.rm = FALSE,
  use_class = c(2L, 9L),
  ...,
  add_lasattribute = FALSE,
  Wdegenerated = TRUE
)

```

```

unnormalize_height(las)

## S4 method for signature 'LAS,RasterLayer'
e1 - e2

## S4 method for signature 'LAS,lidRAlgorithm'
e1 - e2

```

### Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
algorithm	a spatial interpolation function. lidR have <a href="#">tin</a> , <a href="#">kriging</a> , <a href="#">knnidw</a> or a <a href="#">RasterLayer</a> representing a digital terrain model (can be computed with <a href="#">grid_terrain</a> )
na.rm	logical. When using a <a href="#">RasterLayer</a> as DTM, by default the function fails if a point fall in an empty pixel because a Z elevation cannot be NA. If na.rm = TRUE points with an elevation of NA are filtered. Be careful this creates a copy of the point cloud.
use_class	integer vector. By default the terrain is computed by using ground points (class 2) and water points (class 9). Relevant only for a normalisation without a raster DTM.
...	If algorithm is a <a href="#">RasterLayer</a> , ... is propagated to <a href="#">extract</a> . Typically one may use method = "bilinear".
add_lasattribute	logical. By default the above see level elevation is retained in a new attribute. However this new attribute will be discarded at write time. If TRUE it is maintained as an extrabytes attribute. See also <a href="#">add_lasattribute</a> .
Wdegenerated	logical. The function always check and remove degenerated ground points for computing the DTM to avoid unexpected behaviours such as infinite elevation. If TRUE a warning in thrown to alert about the presence of degenerated ground points.
e1	a LAS object
e2	<a href="#">RasterLayer</a> representing a digital terrain model (can be computed with <a href="#">grid_terrain</a> ) or a spatial interpolation function. lidR has <a href="#">tin</a> , <a href="#">kriging</a> , and <a href="#">knnidw</a> .

### Value

If the input is a LAS object, return a LAS object. If the input is a LAScatalog, returns a LAScatalog.

### Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function

should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- **chunk buffer\***: Mandatory to get a continuous output without edge effects. The buffer is always removed once processed and will never be returned either in R or in files.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files\***: Mandatory because the output is likely to be too big to be returned in R and needs to be written in las/laz files. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The function will write files equivalent to the original ones. Thus select = "\*" and cannot be changed.
- **filter**: Read only points of interest.

### See Also

[grid\\_terrain](#)

Other normalize: [normalize\\_intensity\(\)](#)

### Examples

```
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las <- readLAS(LASfile, filter = "-inside 273450 5274350 273550 5274450")

#plot(las)

# First option: use a RasterLayer as DTM
# =====

dtm <- grid_terrain(las, 1, knnidw(k = 6L, p = 2))
las <- normalize_height(las, dtm)

plot(dtm)
#plot(las)

# restore original elevations
las <- unnormailze_height(las)
```

```

#plot(las)

# operator - can be used. This is equivalent to the previous
las <- las - dtm
#plot(las)

# restore original elevations
las <- unnormalize_height(las)

# Second option: interpolate each point (no discretization)
# =====

las <- normalize_height(las, tin())
#plot(las)

# operator - can be used. This is equivalent to the previous
las <- unnormalize_height(las)
las <- las - tin()

## Not run:
# All the following syntaxes are correct
las <- normalize_height(las, knnidw())
las <- normalize_height(las, knnidw(k = 8, p = 2))
las <- las - knnidw()
las <- las - knnidw(k = 8)
las <- normalize_height(las, kriging())
las <- las - kriging(k = 8)

## End(Not run)

```

---

normalize\_intensity    *Normalize intensity*

---

## Description

Normalize intensity values using multiple methods.

## Usage

```
normalize_intensity(las, algorithm)
```

## Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
algorithm	an intensity normalizaton algorithm. lidR currently has <a href="#">range_correction</a> .

## Value

Returns an object of class LAS. The attribute 'Intensity' records the normalized intensity. An extra attribute named 'RawIntensity' records the original intensities.

## Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

## Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- chunk buffer: No buffer needed. A buffer of 0 is used and cannot be changed
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files\***: Mandatory because the output is likely to be too big to be returned in R and needs to be written in las/laz files. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- select: The function will write files equivalent to the original ones. Thus select = "\*" and cannot be changed.
- **filter**: Read only points of interest.

## See Also

Other normalize: [normalize\\_height\(\)](#)

## Examples

```
# A valid file properly populated
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las <- readLAS(LASfile)

# pmin = 15 because it is an extremely small file
# strongly decimated to reduce its size. There are
# actually few multiple returns
sensor <- track_sensor(las, Roussel2020(pmin = 15))

# Here the effect is virtually null because the size of
# the sample is too small to notice any effect of range
las <- normalize_intensity(las, range_correction(sensor, Rs = 2000))
```

**Description**

This function is made to be used in [grid\\_canopy](#). It implements an algorithm for digital surface model computation based on a points-to-raster method: for each pixel of the output raster the function attributes the height of the highest point found. The `subcircle` tweak replaces each point with 8 points around the original one. This allows for virtual 'emulation' of the fact that a lidar point is not a point as such, but more realistically a disc. This tweak densifies the point cloud and the resulting canopy model is smoother and contains fewer 'pits' and empty pixels.

**Usage**

```
p2r(subcircle = 0, na.fill = NULL)
```

**Arguments**

<code>subcircle</code>	numeric. Radius of the circles. To obtain fewer empty pixels the algorithm can replace each return with a circle composed of 8 points (see details).
<code>na.fill</code>	function. A function that implements an algorithm to compute spatial interpolation to fill the empty pixel often left by points-to-raster methods. <code>lidR</code> has <a href="#">knnidw</a> , <a href="#">tin</a> , and <a href="#">kriging</a> (see also <a href="#">grid_terrain</a> for more details).

**See Also**

Other digital surface model algorithms: [dsmtin\(\)](#), [pitfree\(\)](#)

**Examples**

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile)
col <- height.colors(50)

# Points-to-raster algorithm with a resolution of 1 meter
chm <- grid_canopy(las, res = 1, p2r())
plot(chm, col = col)

# Points-to-raster algorithm with a resolution of 0.5 meters replacing each
# point by a 20 cm radius circle of 8 points
chm <- grid_canopy(las, res = 0.5, p2r(0.2))
plot(chm, col = col)

## Not run:
chm <- grid_canopy(las, res = 0.5, p2r(0.2, na.fill = tin()))
plot(chm, col = col)

## End(Not run)
```

## Description

This function is made to be used in [grid\\_canopy](#). It implements the pit-free algorithm developed by Khosravipour et al. (2014), which is based on the computation of a set of classical triangulations at different heights (see references). The subcircle tweak replaces each point with 8 points around the original one. This allows for virtual 'emulation' of the fact that a lidar point is not a point as such, but more realistically a disc. This tweak densifies the point cloud and the resulting canopy model is smoother and contains fewer 'pits' and empty pixels.

## Usage

```
pitfree(thresholds = c(0, 2, 5, 10, 15), max_edge = c(0, 1), subcircle = 0)
```

## Arguments

thresholds	numeric. Set of height thresholds according to the Khosravipour et al. (2014) algorithm description (see references)
max_edge	numeric. Maximum edge length of a triangle in the Delaunay triangulation. If a triangle has an edge length greater than this value it will be removed. The first number is the value for the classical triangulation (threshold = 0, see also <a href="#">dsmtin</a> ), the second number is the value for the pit-free algorithm (for thresholds > 0). If max_edge = 0 no trimming is done (see examples).
subcircle	numeric. radius of the circles. To obtain fewer empty pixels the algorithm can replace each return with a circle composed of 8 points (see details).

## References

Khosravipour, A., Skidmore, A. K., Isenburg, M., Wang, T., & Hussin, Y. A. (2014). Generating pit-free canopy height models from airborne lidar. *Photogrammetric Engineering & Remote Sensing*, 80(9), 863-872.

## See Also

Other digital surface model algorithms: [dsmtin\(\)](#), [p2r\(\)](#)

## Examples

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
poi = "--drop_z_below 0 -inside 481280 3812940 481330 3812990"
las <- readLAS(LASfile, filter = poi)
col <- height.colors(50)

# Basic triangulation and rasterization of first returns
chm <- grid_canopy(las, res = 0.5, dsmtin())
plot(chm, col = col)
```

```

# Khosravipour et al. pitfree algorithm
chm <- grid_canopy(las, res = 0.5, pitfree(c(0,2,5,10,15), c(0, 1.5)))
plot(chm, col = col)

## Not run:
# Potentially complex concave subset of point cloud
x = c(481340, 481340, 481280, 481300, 481280, 481340)
y = c(3812940, 3813000, 3813000, 3812960, 3812940, 3812940)
las2 = clip_polygon(las,x,y)
plot(las2)

# Since the TIN interpolation is done within the convex hull of the point cloud
# dummy pixels are interpolated that are strictly correct according to the interpolation method
# used, but meaningless in our CHM
chm <- grid_canopy(las2, res = 0.5, pitfree())
plot(chm, col = col)

chm = grid_canopy(las2, res = 0.5, pitfree(max_edge = c(3, 1.5)))
plot(chm, col = col)

## End(Not run)

```

---

plot

*Plot a LAS\* object*


---

## Description

Plot displays a 3D interactive windows-based on rgl for [LAS](#) objects

Plot displays an interactive view for [LAScatalog](#) objects with pan and zoom capabilities based on [mapview](#). If the coordinate reference system (CRS) of the LAScatalog is non empty, the plot can be displayed on top of base maps (satellite data, elevation, street, and so on).

Plot displays a [LASheader](#) object exactly like it displays a LAScatalog object.

## Usage

```

plot(x, y, ...)

## S4 method for signature 'LAS,missing'
plot(
  x,
  y,
  color = "Z",
  colorPalette = "auto",
  bg = "black",
  trim = Inf,
  backend = "rgl",

```



```

clear_artifacts = TRUE,
nbits = 16,
axis = FALSE,
legend = FALSE,
add = FALSE,
voxel = FALSE,
...
)

## S4 method for signature 'LAScatalog,missing'
plot(x, y, mapview = FALSE, chunk_pattern = FALSE, overlaps = FALSE, ...)

## S4 method for signature 'LASheader,missing'
plot(x, y, mapview = FALSE, ...)

```

### Arguments

x	A LAS* object
y	Unused (inherited from R base)
...	Will be passed to <a href="#">points3d</a> (LAS) or <a href="#">plot</a> if mapview = FALSE or to <a href="#">mapview</a> if mapview = TRUE (LAScatalog).
color	characters. The attribute used to color the point cloud. Default is Z coordinates. RGB is an allowed string even if it refers to three attributes simultaneously.
colorPalette	characters. A vector of colors such as that generated by <a href="#">heat.colors</a> , <a href="#">topo.colors</a> , <a href="#">terrain.colors</a> or similar functions. Default is "auto" providing an automatic coloring depending on the argument color
bg	The color for the background. Default is black.
trim	numeric. Enables trimming of values when outliers break the color palette range. Every point with a value higher than trim will be plotted with the highest color.
backend	character. Can be "rgl" or "lidRviewer". If "rgl" is chosen the display relies on the rgl package. If "lidRviewer" is chosen it relies on the lidRviewer package, which is much more efficient and can handle million of points using less memory. lidRviewer is not available on CRAN yet and should be installed from github (see. <a href="https://github.com/Jean-Romain/lidRviewer">https://github.com/Jean-Romain/lidRviewer</a> ).
clear_artifacts	logical. It is a known and documented issue that the 3D visualisation with rgl displays artifacts. The points look aligned and/or regularly spaced in some view angles. This is because rgl computes with single precision float. To fix that the point cloud is shifted to (0,0) to reduce the number of digits needed to represent its coordinates. The drawback is that the point cloud is not plotted at its actual coordinates.
nbits	integer. If color = RGB it assumes that RGB colours are coded on 16 bits as described in the LAS format specification. However, this is not always respected. If the colors are stored on 8 bits, set this parameter to 8.
axis	logical. Display axis on XYZ coordinates.
legend	logical. Display a gradient colour legend.

add	If FALSE normal behaviour otherwise must be the output of a prior plot function to enable the alignment of a second point cloud.
voxel	boolean or numeric. Displays voxels instead of points. Useful to render the output of <code>voxelize_points</code> , for example. However it is computationally demanding to render and can easily take 15 seconds for 10000 voxels. It should be reserved for small scenes. If boolean the voxel resolution is guessed automatically. Otherwise users can provide the size of the voxels. To reduce the rendering time, an internal optimization removes voxels that are not visible when surrounded by other voxels.
mapview	logical. If FALSE the catalog is displayed in a regular plot from R base.
chunk_pattern	logical. Display the current chunk pattern used to process the catalog.
overlaps	logical. Highlight the overlaps between files.

### Examples

```
## Not run:
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile)

plot(las)
plot(las, color = "Intensity")

# If outliers break the color range, use the trim parameter
plot(las, color = "Intensity", trim = 150)

plot(las, color = "Classification")

# This dataset is already tree segmented
plot(las, color = "treeID")

# single file LAScatalog using data provided in lidR
ctg = readLAScatalog(LASfile)
plot(ctg)
plot(ctg, map = T, map.types = "Esri.WorldImagery")

## End(Not run)
```

---

plot.lasmetrics3d      *Plot voxelized LiDAR data*

---

### Description

This function implements a 3D plot method for 'lasmetrics3d' objects

### Usage

```
## S3 method for class 'lasmetrics3d'
plot(x, y, ...)
```

**Arguments**

x	An object of the class 'lasmetrics3d'
y	Unused (inherited from R base)
...	Supplementary parameters for <a href="#">plot</a> . The function internally uses the same plot function than LAS objects.

**Examples**

```
## Not run:
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
lidar = readLAS(LASfile)

voxels = voxel_metrics(lidar, list(Imean = mean(Intensity)), res = 5)
plot(voxels, color = "Imean", colorPalette = heat.colors(50), trim=60)

## End(Not run)
```

---

plot\_3d

---

*Add a spatial object to a point cloud scene*


---

**Description**

Add a RasterLayer object that represents a digital terrain model or a SpatialPointsDataFrame that represents tree tops to a point cloud scene. To add elements to a scene with a point cloud plotted with the function plot from lidR, the functions add\_\* take as first argument the output of the plot function (see examples), because the plot function does not plot the actual coordinates of the point cloud, but offsetted values. See function [plot](#) and its argument clear\_artifacts for more details. It works only with rgl i.e. backend = "rgl" which is the default.

**Usage**

```
plot_dtm3d(dtm, bg = "black", clear_artifacts = TRUE, ...)

add_dtm3d(x, dtm, ...)

add_treetops3d(x, ttops, z = "Z", ...)

add_flightlines3d(x, flightlines, z = "Z", ...)
```

**Arguments**

dtm	An object of the class RasterLayer
bg	The color for the background. Default is black.

`clear_artifacts` logical. It is a known and documented issue that 3D visualisation with `rgl` displays artifacts. The points and lines are inaccurately positioned in the space and thus the rendering may look false or weird. This is because `rgl` computes with single precision `float`. To fix this, the objects are shifted to (0,0) to reduce the number of digits needed to represent their coordinates. The drawback is that the objects are not plotted at their actual coordinates.

`...` Supplementary parameters for `surface3d` or `spheres3d`.

`x` The output of the function `plot` used with a LAS object.

`ttops` A `SpatialPointsDataFrame` that contains tree tops coordinates.

`z` character. The name of the attribute that contains the height of the tree tops or of the flightlines.

`flightlines` A `SpatialPointsDataFrame` that contains flightlines coordinates.

### Examples

```
## Not run:
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las = readLAS(LASfile, filter = "-keep_xy 273450 273600 5274450 5274600")

dtm = grid_terrain(las, algorithm = tin())
ttops <- find_trees(las, lmf(ws = 5))

plot_dtm3d(dtm)

x = plot(las)
add_dtm3d(x, dtm)
add_treetops3d(x, ttops)

library(magrittr)
plot(las) %>% add_dtm3d(dtm) %>% add_treetops3d(ttops)

## End(Not run)
```

---

`plot_metrics` *Computes metrics for each plot of a ground inventory*

---

### Description

Computes metrics for each plot of a ground inventory by 1. clipping the plots inventories, 2. computing a user's metrics to each plot, and 3. combining spatial data and metrics into one data.frame ready for statistical modelling. 'plot\_metrics' is basically a seamless wrapper around `clip_roi`, `cloud_metrics`, 'cbind' and adequate processing settings.

### Usage

```
plot_metrics(las, func, geometry, ...)
```

**Arguments**

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
func	formula. An expression to be applied to each cell (see also <a href="#">grid_metrics</a> ).
geometry	a spatial object. Many types are supported (see also <a href="#">clip_roi</a> )
...	optional supplementary options (see also <a href="#">clip_roi</a> )

**Value**

An 'sp' or 'sf' object depending on the input with all the metrics for each plot bound with the original input.

**Working with a LAScatalog**

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

**Supported processing options**

Supported processing options for a LAScatalog in plot\_metrics function (in bold). For more details see the [LAScatalog engine documentation](#):

- chunk size: Not relevant here.
- chunk buffer: Not relevant here.
- chunk alignment: Not relevant here.
- **progress**: Displays a progress estimate.
- output files: plots are extracted in memory.
- **select**: Read only the attributes of interest.
- **filter**: Read only the points of interest.

**See Also**

Other metrics: [cloud\\_metrics\(\)](#), [grid\\_metrics\(\)](#), [point\\_metrics\(\)](#), [tree\\_metrics\(\)](#), [voxel\\_metrics\(\)](#)

## Examples

```

LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
SHPfile <- system.file("extdata", "efi_plot.shp", package="lidR")
las <- readLAS(LASfile)
inventory <- sf::st_read(SHPfile, quiet = TRUE)
inventory # contains an ID and a Value Of Interest (VOI) per plot

M <- plot_metrics(las, ~list(q85 = quantile(Z, probs = 0.85)), inventory, radius = 11.28)
model <- lm(VOI ~ q85, M)

M <- plot_metrics(las, .stdmetrics_z, inventory, radius = 11.28)

## Not run:
# Works with polygons as well
inventory <- sf::st_buffer(inventory, 11.28)
plot(las@header)
plot(sf::st_geometry(inventory), add = TRUE)
M <- plot_metrics(las, .stdmetrics_z, inventory)

## End(Not run)

```

---

pmf

*Ground Segmentation Algorithm*

---

## Description

This function is made to be used in [classify\\_ground](#). It implements an algorithm for segmentation of ground points based on a progressive morphological filter. This method is an implementation of the Zhang et al. (2003) algorithm (see reference). Note that this is not a strict implementation of Zhang et al. This algorithm works at the point cloud level without any rasterization process. The morphological operator is applied on the point cloud, not on a raster. Also, Zhang et al. proposed some formulas (eq. 4, 5 and 7) to compute the sequence of windows sizes and thresholds. Here, these parameters are free and specified by the user. The function [util\\_makeZhangParam](#) enables computation of the parameters according to the original paper.

## Usage

```
pmf(ws, th)
```

## Arguments

ws	numeric. Sequence of windows sizes to be used in filtering ground returns. The values must be positive and in the same units as the point cloud (usually meters, occasionally feet).
th	numeric. Sequence of threshold heights above the parameterized ground surface to be considered a ground return. The values must be positive and in the same units as the point cloud.

## References

Zhang, K., Chen, S. C., Whitman, D., Shyu, M. L., Yan, J., & Zhang, C. (2003). A progressive morphological filter for removing nonground measurements from airborne LIDAR data. *IEEE Transactions on Geoscience and Remote Sensing*, 41(4 PART I), 872–882. <http://doi.org/10.1109/TGRS.2003.810682>.

## See Also

Other ground segmentation algorithms: `csf()`

## Examples

```
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las <- readLAS(LASfile, select = "xyzrn", filter = "-inside 273450 5274350 273550 5274450")

ws <- seq(3,12, 3)
th <- seq(0.1, 1.5, length.out = length(ws))

las <- classify_ground(las, pmf(ws, th))
#plot(las, color = "Classification")
```

---

point\_metrics

*Point-based metrics*

---

## Description

Computes a series of user-defined descriptive statistics for a LiDAR dataset for each point. This function is very similar to [grid\\_metrics](#) but computes metrics **for each point** based on its k-nearest neighbours or its sphere neighbourhood.

## Usage

```
point_metrics(las, func, k, r, xyz = FALSE, filter = NULL, ...)
```

## Arguments

las	An object of class LAS
func	formula. An expression to be applied to each point neighbourhood (see section "Parameter func").
k, r	integer and numeric respectively for k-nearest neighbours and radius of the neighborhood sphere. If k is given and r is missing, computes with the knn, if r is given and k is missing computes with a sphere neighborhood, if k and r are given computes with the knn and a limit on the search distance.
xyz	logical. Coordinates of each point are returned in addition to each metric. If <code>filter = NULL</code> coordinates are references to the original coordinates and do not occupy additional memory. If <code>filter != NULL</code> it obviously takes memory.
filter	formula of logical predicates. Enables the function to run only on points of interest in an optimized way. See examples.
...	unused.

## Details

When the neighbourhood is `knn` the user-defined function is fed with the current processed point and its  $k-1$  neighbours. The current point being considered as the 1-neighbour with a distance 0 to the reference point. The points are ordered by distance to the central point. When the neighbourhood is a sphere the processed point is also included in the query but points are coming in a random order.

## Performances

It is important to bear in mind that this function is very fast for the feature it provides i.e. mapping a user-defined function at the point level using optimized memory management. However, it is still computationally demanding.

To help users to get an idea of how computationally demanding this function is, let's compare it to [grid\\_metrics](#). Assuming we want to apply `mean(Z)` on a 1 km<sup>2</sup> tile with 1 point/m<sup>2</sup> with a resolution of 20 m (400 m<sup>2</sup> cells), then the function `mean` is called roughly 2500 times (once per cell). On the contrary, with `point_metrics`, `mean` is called 1000000 times (once per point). So the function is expected to be more than 400 times slower in this specific case (but it does not provide the same feature).

This is why the user-defined function is expected to be well-optimized, otherwise it might drastically slow down this already heavy computation. See examples.

Last but not least, `grid_metrics()` relies on the `data.table` package to compute a user-defined function in each pixel. `point_metrics()` relies on a similar method but with a major difference: it does not rely on `data.table` and thus has not been tested over many years by thousands of people. Please report bugs, if any.

## Parameter func

The function to be applied to each cell is a classical function (see examples) that returns a labeled list of metrics. For example, the following function `f` is correctly formed.

```
f = function(x) {list(mean = mean(x), max = max(x))}
```

And could be applied either on the Z coordinates or on the intensities. These two statements are valid:

```
point_metrics(las, ~f(Z), k = 8)
point_metrics(las, ~f(Intensity), k = 5)
```

Everything that works in [grid\\_metrics](#) should also work in `point_metrics` but sometimes might be meaningless. For example, computing the quantile of elevation does not really makes sense here.

## See Also

Other metrics: [cloud\\_metrics\(\)](#), [grid\\_metrics\(\)](#), [plot\\_metrics\(\)](#), [tree\\_metrics\(\)](#), [voxel\\_metrics\(\)](#)



**Examples**

```

## Not run:
LASfile <- system.file("extdata", "Topography.laz", package="lidR")

# Read only 0.5 points/m^2 for the purposes of this example
las = readLAS(LASfile, filter = "-thin_with_grid 2")

# Computes the eigenvalues of the covariance matrix of the neighbouring
# points and applies a test on these values. This function simulates the
# 'shp_plane()' algorithm from 'segment_shape()'
plane_metrics1 = function(x,y,z, th1 = 25, th2 = 6) {
  xyz <- cbind(x,y,z)
  cov_m <- cov(xyz)
  eigen_m <- eigen(cov_m)$value
  is_planar <- eigen_m[2] > (th1*eigen_m[3]) && (th2*eigen_m[2]) > eigen_m[1]
  return(list(planar = is_planar))
}

# Apply a user-defined function
M <- point_metrics(las, ~plane_metrics1(X,Y,Z), k = 25)
#> Computed in 6.3 seconds

# We can verify that it returns the same as 'shp_plane'
las <- segment_shape(las, shp_plane(k = 25), "planar")
#> Computed in 0.1 seconds

all.equal(M$planar, las$planar)

# At this stage we can be clever and find that the bottleneck is
# the eigenvalue computation. Let's write a C++ version of it with
# Rcpp and RcppArmadillo
Rcpp::sourceCpp(code = "
#include <RcppArmadillo.h>
// [[Rcpp::depends(RcppArmadillo)]]

// [[Rcpp::export]]
SEXP eigen_values(arma::mat A) {
  arma::mat coeff;
  arma::mat score;
  arma::vec latent;
  arma::princomp(coeff, score, latent, A);
  return(Rcpp::wrap(latent));
}")

plane_metrics2 = function(x,y,z, th1 = 25, th2 = 6) {
  xyz <- cbind(x,y,z)
  eigen_m <- eigen_values(xyz)
  is_planar <- eigen_m[2] > (th1*eigen_m[3]) && (th2*eigen_m[2]) > eigen_m[1]
  return(list(planar = is_planar))
}

M <- point_metrics(las, ~plane_metrics2(X,Y,Z), k = 25)

```

```

#> Computed in 0.5 seconds

all.equal(M$planar, las$planar)
# Here we can see that the optimized version is way better but is still 5-times slower
# because of the overhead of calling R functions and switching back and forth from R to C++.

# Use the filter argument to process only first returns
M1 <- point_metrics(las, ~plane_metrics2(X,Y,Z), k = 25, filter = ~ReturnNumber == 1)
dim(M1) # 13894 instead of 17182 previously.

# is a memory-optimized equivalent to:
first = filter_first(las)
M2 <- point_metrics(first, ~plane_metrics2(X,Y,Z), k = 25)
all.equal(M1, M2)

## End(Not run)

```

---

print

---

*Summary and Print for LAS\* objects*


---

## Description

Summary and Print for LAS\* objects

## Usage

```

print(x, ...)

## S4 method for signature 'LAS'
summary(object, ...)

## S4 method for signature 'LAS'
print(x)

## S4 method for signature 'LAScatalog'
summary(object, ...)

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

```

## Arguments

...	Unused
object, x	A LAS* object or other lidR related objects.

---

projection	<i>Get or set the projection of a LAS* object</i>
------------	---

---

**Description**

Get or set the projection of a LAS\* object.

**Usage**

```
epsg(object, ...)  
  
epsg(object) <- value  
  
## S4 method for signature 'LASheader'  
epsg(object, ...)  
  
## S4 replacement method for signature 'LASheader'  
epsg(object) <- value  
  
## S4 method for signature 'LAS'  
epsg(object)  
  
## S4 replacement method for signature 'LAS'  
epsg(object) <- value  
  
wkt(object) <- value  
  
## S4 method for signature 'LASheader'  
wkt(obj)  
  
## S4 replacement method for signature 'LASheader'  
wkt(object) <- value  
  
## S4 method for signature 'LAS'  
wkt(obj)  
  
## S4 replacement method for signature 'LAS'  
wkt(object) <- value  
  
## S4 method for signature 'LASheader'  
projection(x, asText = TRUE)  
  
## S4 method for signature 'LAS'  
projection(x, asText = TRUE)  
  
## S4 replacement method for signature 'LAS'  
projection(x) <- value
```

```
## S4 method for signature 'LAScatalog'
projection(x, asText = TRUE)

## S4 replacement method for signature 'LAScatalog'
projection(x) <- value

## S4 method for signature 'LASheader'
crs(x, asText = FALSE)

## S4 method for signature 'LAS'
crs(x, asText = FALSE)

## S4 replacement method for signature 'LAS'
crs(x, ...) <- value

## S4 method for signature 'LAScatalog'
crs(x, asText = FALSE)

## S4 replacement method for signature 'LAScatalog'
crs(x, ...) <- value
```

### Arguments

object, x, obj	An object of class LAS or eventually LASheader (regular users don't need to manipulate LASheader objects).
...	Unused.
value	A CRS object or a proj4string string or WKT string or an EPSG code.
asText	logical. If TRUE, the projection is returned as text. Otherwise a CRS object is returned.

### Details

There are two ways to store the CRS of a point cloud in a LAS file:

- Store an EPSG code (for LAS 1.0 to 1.3)
- Store a WTK string (for LAS 1.4)

On the other hand, R spial packages use a proj4string to store the CRS (but the ecosystem is moving to WKT). This is why the CRS is duplicated in a LAS object. The information belongs within the header in a format that can be written in a LAS file and in the slot proj4string in a format that can be understood by R packages.

- `projection<-`: assigns a CRS from a CRS (sp), a crs (sf), a WKT string, a proj4string or an epsg code. It updates the header of the LAS object either with the EPSG code for LAS formats < 1.4 or with a WKT string for LAS format 1.4 and updates the proj4string slot.
- `projection`: returns the CRS in sp format
- `crs` and `crs<-` are equivalent to `projection` and `projection<-`

- `epsg<-`, `wkt<-` : legacy functions superseded by `projection<-`
- `sf::st_crs` return the CRS in sf format.
- `epsg`: reads the epsg code from the header.
- `wkt`: reads the WKT string from the header.

### Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile)

# Get the EPSG code stored in the header (returns 0 if not recorded)
epsg(las)

# Get the WKT string stored in the header (LAS >= 1.4)
wkt(las)

# Uses the EPSG code
projection(las) <- 26919
sf::st_crs(las)$input
```

---

random

*Point Cloud Decimation Algorithm*

---

### Description

This function is made to be used in [decimate\\_points](#). It implements an algorithm that randomly removes points or pulses to reach the desired density over the whole area (see [area](#)).

### Usage

```
random(density, use_pulse = FALSE)
```

### Arguments

<code>density</code>	numeric. The desired output density.
<code>use_pulse</code>	logical. Decimate by removing random pulses instead of random points (requires running <a href="#">retrieve_pulses</a> first)

### See Also

Other point cloud decimation algorithms: [homogenize\(\)](#), [maxima](#), [random\\_per\\_voxel\(\)](#)

## Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las = readLAS(LASfile, select = "xyz")

# Reach a pulse density of 1 on the overall dataset
thinned1 = decimate_points(las, random(1))
plot(grid_density(las))
plot(grid_density(thinned1))
```

---

random\_per\_voxel

*Point Cloud Decimation Algorithm*

---

## Description

This function is made to be used in [decimate\\_points](#). It implements an algorithm that creates a 3D grid with a given resolution and filters the point cloud by randomly selecting  $n$  points within each voxel.

## Usage

```
random_per_voxel(res = 1, n = 1)
```

## Arguments

res	numeric. The resolution of the voxel grid used to filter the point cloud
n	integer. The number of points to select

## See Also

Other point cloud decimation algorithms: [homogenize\(\)](#), [maxima](#), [random\(\)](#)

## Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile, select = "xyz")
thinned <- decimate_points(las, random_per_voxel(8, 1))
#plot(thinned)
```

---

range\_correction      *Intensity normalization algorithm*

---

### Description

This function is made to be used in [normalize\\_intensity](#). It corrects intensity with a range correction according to the formula (see references):

$$I_{norm} = I_{obs} \left( \frac{R}{R_s} \right)^f$$

To achieve the range correction the position of the sensor must be known at different discrete times. Using the 'gpstime' of each point, the position of the sensor is interpolated from the reference and a range correction is applied.

### Usage

```
range_correction(sensor, Rs, f = 2.3, gpstime = "gpstime", elevation = "Z")

get_range(las, sensor, gpstime = "gpstime", elevation = "Z")
```

### Arguments

sensor	SpatialPointsDataDrame object containing the coordinates of the sensor at different timepoints t. The time and elevation are stored as attributes (default names are 'gpstime' and 'Z'). It can be computed with <a href="#">track_sensor</a> .
Rs	numeric. Range of reference.
f	numeric. Exponent. Usually between 2 and 3 in vegetation contexts.
gpstime, elevation	character. The name of the attributes that store the gpstime of the position and the elevation of the sensor respectively. If elevation = NULL the Z coordinates are searched in the third column of the coordinates matrix of the SpatialPoints-DataFrame. This is useful if read from a format that supports 3 coordinates points.
las	an object of class LAS. <code>get_range()</code> is a regular function documented here for convenience.

### References

Gatziolis, D. (2011). Dynamic Range-based Intensity Normalization for Airborne, Discrete Return Lidar Data of Forest Canopies. *Photogrammetric Engineering & Remote Sensing*, 77(3), 251–259. <https://doi.org/10.14358/pers.77.3.251>

## Examples

```
# A valid file properly populated
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las <- readLAS(LASfile)

# pmin = 15 because it is an extremely tiny file
# strongly decimated to reduce its size. There are
# actually few multiple returns
sensor <- track_sensor(las, Roussel2020(pmin = 15))

# Here the effect is virtually null because the size of
# the sample is too small to notice any effect of range
las <- normalize_intensity(las, range_correction(sensor, Rs = 2000))

# This might be useful for some applications
R = get_range(las, sensor)
```

---

rbind

*Merge LAS\* objects*

---

## Description

Merge LAS\* objects

## Usage

```
## S3 method for class 'LAS'
rbind(...)

## S3 method for class 'LAScatalog'
rbind(...)
```

## Arguments

... LAS or LAScatalog objects

---

readLAS

*Read .las or .laz files*

---



## Description

Reads .las or .laz files into an object of class [LAS](#). If several files are read at once the returned LAS object is considered as one LAS file. The optional parameters enable the user to save a substantial amount of memory by choosing to load only the attributes or points of interest. LAS formats 1.1 to 1.4 are supported. Point Data Record Format 0 to 10 are supported.

readLAS is the original function and always works. Using one of the read\*LAS functions adds information to the returned object to register a point-cloud type. Registering the correct point type **may** improve the performance of some functions by enabling users to select an appropriate spatial index. See [spatial indexing](#). Notice that by legacy and for backwards-compatibility reasons, readLAS() and readALSLAS() are equivalent because lidR was originally designed for ALS and thus the original function readLAS() was (supposedly) used for ALS. Reading a TLS dataset with readLAS() instead of readTLSLAS() is perfectly valid and performs similarly to versions <= 3.0.0, with neither performance degradation nor improvements.

## Usage

```
readLAS(files, select = "*", filter = "")
readALSLAS(files, select = "*", filter = "")
readTLSLAS(files, select = "*", filter = "")
readUAVLAS(files, select = "*", filter = "")
readDAPLAS(files, select = "*", filter = "")
readMSLAS(files1, files2, files3, select = "*", filter = "")
```

## Arguments

files	characters. Path(s) to one or several a file(s). Can also be a <a href="#">LAScatalog</a> object.
select	character. Read only attributes of interest to save memory (see details).
filter	character. Read only points of interest to save memory (see details).
files1, files2, files3	characters. Path(s) to one or several a file(s). Each argument being one channel (see section 'Multispectral data').

## Details

**Select:** the 'select' argument specifies the data that will actually be loaded. For example, 'xyzia' means that the x, y, and z coordinates, the intensity and the scan angle will be loaded. The supported entries are t - gpstime, a - scan angle, i - intensity, n - number of returns, r - return number, c - classification, s - synthetic flag, k - keypoint flag, w - withheld flag, o - overlap flag (format 6+), u - user data, p - point source ID, e - edge of flight line flag, d - direction of scan flag, R - red channel of RGB color, G - green channel of RGB color, B - blue channel of RGB color, N - near-infrared channel, C - scanner channel (format 6+), W - Full waveform. Also numbers from 1 to 9 for the extra bytes data numbers 1 to 9. 0 enables all extra bytes to be loaded and '\*' is the wildcard that

enables everything to be loaded from the LAS file.

Note that x, y, z are implicit and always loaded. 'xyzia' is equivalent to 'ia'.

**Filter:** the 'filter' argument allows filtering of the point cloud while reading files. This is much more efficient than [filter\\_poi](#) in many ways. If the desired filters are known before reading the file, the internal filters should always be preferred. The available filters are those from LASlib and can be found by running the following command: `readLAS(filter = "-help")`. (see also [rlas::read.las](#)). From rLas v1.3.6 the transformation commands can also be passed via the argument filter.

## Value

A LAS object

## Full waveform

With most recent versions of the 'rlas' package, full waveform (FWF) can be read and 'lidR' provides some compatible functions. However, the support of FWF is still a work-in-progress in the 'rlas' package. How it is read, interpreted and represented in R may change. Consequently, tools provided by 'lidR' may also change until the support of FWF becomes mature and stable in 'rlas'. See also [rlas::read.las](#).

Remember that FWF represents an insanely huge amount of data. In terms of memory it is like having between 10 to 100 times more points. Consequently, loading FWF data in R should be restricted to relatively small point clouds.

## Multispectral data

Multispectral laser data are often stored in 3 different files. If this is the case `readMSLAS` reads the .las or .laz files of each channel and merges them into an object of class `LAS` and takes care of attributing an ID to each channel. If the multispectral point cloud is already stored in a single file leave `file2` and `file3` missing.

## Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las = readLAS(LASfile)
las = readLAS(LASfile, select = "xyz")
las = readLAS(LASfile, select = "xyzi", filter = "-keep_first")
las = readLAS(LASfile, select = "xyziar", filter = "-keep_first -drop_z_below 0")

# Negation of attributes is also possible (all except intensity and angle)
las = readLAS(LASfile, select = "* -i -a")
```

## Description

Create an object of class [LAScatalog](#) from a folder or a collection of filenames. A `LAScatalog` is a representation of a collection of las/laz files. A computer cannot load all the data at once. A `LAScatalog` is a simple way to manage all the files sequentially. Most functions from `lidR` can be used seamlessly with a `LAScatalog` using the internal `LAScatalog` processing engine. To take advantage of the `LAScatalog` processing engine the user must first adjust some processing options using the [appropriate functions](#). Careful reading of the [LAScatalog class documentation](#) is required to use the `LAScatalog` class correctly.

`readLAScatalog` is the original function and always works. Using one of the `read*LAScatalog` functions adds information to the returned object to register a point-cloud type. Registering the correct point type **may** improve the performance of some functions by enabling users to select an appropriate spatial index. See [spatial indexing](#). Notice that by legacy and for backwards-compatibility reasons `readLAScatalog()` and `readALSLAScatalog()` are equivalent because `lidR` was originally designed for ALS and thus the original function `readLAScatalog()` was (supposedly) used for ALS.

## Usage

```
readLAScatalog(  
  folder,  
  progress = TRUE,  
  select = "*",  
  filter = "",  
  chunk_size = 0,  
  chunk_buffer = 30,  
  ...  
)
```

```
readALSLAScatalog(  
  folder,  
  progress = TRUE,  
  select = "*",  
  filter = "",  
  chunk_size = 0,  
  chunk_buffer = 30,  
  ...  
)
```

```
readTSLAScatalog(  
  folder,  
  progress = TRUE,  
  select = "*",  
  filter = "",  
  chunk_size = 0,  
  chunk_buffer = 30,  
  ...  
)
```

```

readUAVLAScatalog(
  folder,
  progress = TRUE,
  select = "*",
  filter = "",
  chunk_size = 0,
  chunk_buffer = 30,
  ...
)

readDAPLAScatalog(
  folder,
  progress = TRUE,
  select = "*",
  filter = "",
  chunk_size = 0,
  chunk_buffer = 30,
  ...
)

catalog(folder, ...)

```

### Arguments

**folder** string. The path of a folder containing a set of las/laz files. Can also be a vector of file paths.

**progress, select, filter, chunk\_size, chunk\_buffer** Easily accessible processing options tuning. See [LAScatalog-class](#) and [catalog\\_options\\_tools](#).

**...** Extra parameters to [list.files](#). Typically recursive = TRUE.

### Value

A LAScatalog object

### Examples

```

# A single file LAScatalog using data provided with the package
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
ctg = readLAScatalog(LASfile)
plot(ctg)

## Not run:
ctg <- readLAScatalog("/path/to/a/folder/of/las/files")

# Internal engine will sequentially process chunks of size 500 x 500 m
opt_chunk_size(ctg) <- 500

# Internal engine will align the 500 x 500 m chunks on x = 250 and y = 300

```

```
opt_alignment(ctg) <- c(250, 300)

# Internal engine will not display a progress estimation
opt_progress(ctg) <- FALSE

# Internal engine will not return results into R. Instead it will write results in files.
opt_output_files(ctg) <- "/path/to/folder/templated_filename_{XBOTTOM}_{ID}"

# More details in the documentation
help("LAScatalog-class", "lidR")
help("catalog_options_tools", "lidR")

## End(Not run)
```

---

readLASheader	<i>Read a .las or .laz file header</i>
---------------	--

---

## Description

Reads a .las or .laz file header into an object of class [LASheader](#). This function strictly reads the header while the function [readLAS](#) can alter the header to fit the actual data loaded.

## Usage

```
readLASheader(file)
```

## Arguments

file            characters. Path to one file.

## Value

A LASheader object

## Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
header = readLASheader(LASfile)

print(header)
plot(header)

## Not run:
plot(header, mapview = TRUE)
## End(Not run)
```

---

retrieve_pulses	<i>Retrieve individual pulses, flightlines or scanlines</i>
-----------------	---

---

### Description

Retrieve each individual pulse, individual flightline or individual scanline and assigns a number to each point. The LAS object must be properly populated according to LAS specifications otherwise users could find unexpected outputs.

### Usage

```
retrieve_pulses(las)
retrieve_flightlines(las, dt = 30)
retrieve_scanlines(las)
```

### Arguments

las	A LAS object
dt	numeric. The threshold time-lag used to retrieve flightlines

### Details

`retrieve_pulses` Retrieves each individual pulse. It uses GPS time. An attribute `pulseID` is added in the LAS object

`retrieve_scanlines` Retrieves each individual scanline. When data are sampled according to a saw-tooth pattern (oscillating mirror), a scanline is one line, or row of data. The function relies on the GPS field time to order the data. Then, the `ScanDirectionFlag` attribute is used to retrieve each scanline. An attribute `scanlineID` is added in the LAS object

`retrieve_flightlines` Retrieves each individual flightline. It uses GPS time. In a continuous dataset, once points are ordered by GPS time, the time between two consecutive points does not exceed a few milliseconds. If the time between two consecutive points is too long it means that the second point is from a different flightline. The default threshold is 30 seconds. An attribute `flightlineID` is added in the LAS object.

### Value

An object of class LAS

### Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile)

las <- retrieve_pulses(las)
las
```

```
las <- retrieve_flightlines(las)
#plot(las, color = "flightlineID")
```

---

Roussel2020

*Sensor tracking algorithm*

---

## Description

This function is made to be used in [track\\_sensor](#). It implements an algorithm from Roussel et al. 2020 (see reference) for sensor tracking using multiple returns to estimate the positioning of the sensor by computing the intersection in space of the lines passing through the first and last returns.

## Usage

```
Roussel2020(interval = 0.5, pmin = 50)
```

## Arguments

<code>interval</code>	numeric. Interval used to bin the gps times and group the pulses to compute a position at a given timepoint <code>t</code> .
<code>pmin</code>	integer. Minimum number of pulses needed to estimate a sensor position. For a given interval, the sensor position is not computed if the number of pulses is lower than <code>pmin</code> .

## Details

When multiple returns from a single pulse are detected, the sensor computes their positions as being in the center of the footprint and thus all aligned. Because of that behavior, a line drawn between and beyond those returns must cross the sensor. Thus, several consecutive pulses emitted in a tight interval (e.g. 0.5 seconds) can be used to approximate an intersection point in the sky that corresponds to the sensor position given that the sensor carrier hasn't moved much during this interval. A weighted least squares method gives an approximation of the intersection by minimizing the squared sum of the distances between the intersection point and all the lines.

## References

Roussel Jean-Romain, Bourdon Jean-Francois, Achim Alexis, (2020) Range-based intensity normalization of ALS data over forested areas using a sensor tracking method from multiple returns (preprint) Retrieved from [eartharxiv.org/k32qw](https://arxiv.org/abs/2003.03221)

## Examples

```
# A valid file properly populated
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las = readLAS(LASfile)

# pmin = 15 because it is an extremely tiny file
```

```
# strongly decimated to reduce its size. There are
# actually few multiple returns
flightlines <- track_sensor(las, Roussel2020(pmin = 15))

plot(las@header)
plot(flightlines, add = TRUE)
```

---

rumple\_index

*Rumple index of roughness*


---

### Description

Computes the roughness of a surface as the ratio between its area and its projected area on the ground. If the input is a gridded object (raster) the function computes the surfaces using Jenness's algorithm (see references). If the input is a point cloud the function uses a Delaunay triangulation of the points and computes the area of each triangle.

### Usage

```
rumple_index(x, y = NULL, z = NULL, ...)
```

### Arguments

x	A 'RasterLayer' or a vector of x point coordinates.
y	numeric. If x is a vector of coordinates: the associated y coordinates.
z	numeric. If x is a vector of coordinates: the associated z coordinates.
...	unused

### Value

numeric. The computed Rumple index.

### References

Jenness, J. S. (2004). Calculating landscape surface area from digital elevation models. *Wildlife Society Bulletin*, 32(3), 829–839.

### Examples

```
x <- runif(20, 0, 100)
y <- runif(20, 0, 100)

# Perfectly flat surface, rumple_index = 1
z <- rep(10, 20)
rumple_index(x, y, z)

# Rough surface, rumple_index > 1
z <- runif(20, 0, 10)
```



```

rumple_index(x, y, z)

# Rougher surface, rumple_index increases
z <- runif(20, 0, 50)
rumple_index(x, y, z)

# Measure of roughness is scale-dependent
rumple_index(x, y, z)
rumple_index(x/10, y/10, z)

# Use with a canopy height model
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile)
chm <- grid_canopy(las, 2, p2r())
rumple_index(chm)

```

---

segment\_shapes

*Eigenvalues-based features at the point level*


---

### Description

Functions that compute, for each point, the eigenvalues of the covariance matrix of the neighbouring points. The eigenvalues are later used either to segment linear/planar points or to compute derived metrics (see Details).

### Usage

```

segment_shapes(las, algorithm, attribute = "Shape", filter = NULL)

point_eigenvalues(las, k, r, xyz = FALSE, metrics = FALSE, filter = NULL)

```

### Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
algorithm	An algorithm for shape detection. lidR has: <a href="#">shp_plane</a> , <a href="#">shp_hplane</a> and <a href="#">shp_line</a> .
attribute	character. The name of the new column to add into the LAS object.
filter	formula of logical predicates. Enables the function to run only on points of interest in an optimized way. See the examples.
k, r	integer and numeric respectively for k-nearest neighbours and radius of the neighborhood sphere. If k is given and r is missing, computes with the knn, if r is given and k is missing computes with a sphere neighbourhood, if k and r are given computes with the knn and a limit on the search distance.
xyz	logical. Returns the XYZ coordinates of each points instead of IDs.
metrics	logical. Compute additional metrics such as curvature, linearity, planarity based on the eigenvalues.

## Details

All the functions documented here can be reproduced with [point\\_metrics](#). However, [point\\_metrics](#) is a versatile and multipurpose function that is not as fast as is possible because it calls user-defined R code and that implies computational overheads. These functions are parallelized plain C++ versions of tools users can build with [point\\_metrics](#) and are consequently 10-times faster.

**segment\_shape** The points that meet a given criterion based on the eigenvalue are labelled as approximately coplanar/colinear or any other shape supported.

**point\_eigenvalues** Computes the eigenvalues of the covariance matrix and computes associated metrics following Lucas et al, 2019 (see references). It is equivalent to `point_metrics(las, .stdshapemetrics)` but much faster

## Value

**segment\_shape** A LAS object with a new column named after the argument `attribute` that indicates those points that are part of a neighborhood that is approximately of the shape searched (TRUE) or not (FALSE).

**point\_eigenvalues** A data.frame like [point\\_metrics](#)

## References

Lucas, C., Bouten, W., Koma, Z., Kissling, W. D., & Seijmonsbergen, A. C. (2019). Identification of Linear Vegetation Elements in a Rural Landscape Using LiDAR Point Clouds. *Remote Sensing*, 11(3), 292.

## Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile, filter = "-keep_random_fraction 0.5")

# Use the eigenvalues to estimate if points are part of a local plan
las <- segment_shapes(las, shp_plane(k = 15), "Coplanar")
#plot(las, color = "Coplanar")

# Computes the eigenvalue of each point
M <- point_eigenvalues(las, k = 15)
M

## Not run:

# Drop ground point at runtime
las <- segment_shapes(las, shp_plane(k = 15), "Coplanar", filter = ~Classification != 2L)
#plot(las, color = "Coplanar")

## End(Not run)
```

---

segment_snags	<i>Snag classification</i>
---------------	----------------------------

---

### Description

Snag classification/segmentation using several possible algorithms (see details). The function attributes a number identifying a snag class (snagCls attribute) to each point of the point cloud. The classification/segmentation is done at the point cloud level and currently only one algorithm implemented, which uses LiDAR intensity thresholds and specified neighborhoods to differentiate bole and branch from foliage points (see details).

### Usage

```
segment_snags(las, algorithm, attribute = "snagCls")
```

### Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
algorithm	function. An algorithm for snag segmentation. lidR has <a href="#">wing2015</a> .
attribute	character. The returned LAS object automatically has a new attribute (a new column). This parameter is the name of this new attribute.

### Value

If the input is a LAS object, return a LAS object. If the input is a LAScatalog, returns a LAScatalog.

### Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.

- **chunk buffer\***: Mandatory to get a continuous output without edge effects. The buffer is always removed once processed and will never be returned either in R or in files.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files\***: Mandatory because the output is likely to be too big to be returned in R and needs to be written in las/laz files. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The function will write files equivalent to the original ones. Thus select = "\*" and cannot be changed.
- **filter**: Read only points of interest.

## Examples

```
## Not run:
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile, select = "xyzi", filter="-keep_first") # Wing also included -keep_single

# For the Wing2015 method, supply a matrix of snag BranchBolePtRatio conditional
# assessment thresholds (see Wing et al. 2015, Table 2, pg. 172)
bbpr_thresholds <- matrix(c(0.80, 0.80, 0.70,
                           0.85, 0.85, 0.60,
                           0.80, 0.80, 0.60,
                           0.90, 0.90, 0.55),
                          nrow = 3, ncol = 4)

# Run snag classification and assign classes to each point
las <- segment_snags(las, wing2015(neigh_radii = c(1.5, 1, 2), BBPRthrsh_mat = bbpr_thresholds))

# Plot it all, tree and snag points...
plot(las, color="snagCls", colorPalette = rainbow(5))

# Filter and plot snag points only
snags <- filter_poi(las, snagCls > 0)
plot(snags, color="snagCls", colorPalette = rainbow(5)[-1])

# Wing et al's (2015) methods ended with performing tree segmentation on the
# classified and filtered point cloud using the watershed method

## End(Not run)
```

---

segment\_trees

*Individual tree segmentation*

---

## Description

Individual tree segmentation with several possible algorithms. The returned point cloud has a new extra byte attribute named after the parameter attribute independently of the algorithm used.

**Usage**

```
segment_trees(las, algorithm, attribute = "treeID", uniqueness = "incremental")
```

**Arguments**

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
algorithm	function. An algorithm of individual tree segmentation. lidR has: <a href="#">dalponte2016</a> , <a href="#">watershed</a> , <a href="#">li2012</a> and <a href="#">silva2016</a> . More experimental algorithms may be found in the package <a href="#">lidRplugins</a> .
attribute	character. The returned LAS object as a new extra byte attribute (in a new column). This parameter controls the name of the new attribute. Default is "treeID".
uniqueness	character. A method to compute a unique ID. Can be 'incremental', 'gpstime' or 'bitmerge'. See section 'Uniqueness'. This feature must be considered as 'experimental'.

**Value**

If the input is a LAS object, return a LAS object. If the input is a LAScatalog, returns a LAScatalog.

**Uniqueness**

By default the tree IDs are numbered from 1 to n, n being the number of trees found. The problem with such incremental numbering is that, while it ensures a unique ID is assigned for each tree in a given point-cloud, it also guarantees duplication of tree IDs in different tiles or chunks when processing a LAScatalog. This is because each chunk/file is processed independently of the others and potentially in parallel on different computers. Thus, the index always restarts at 1 on each chunk/file or chunk. Worse, in a tree segmentation process, a tree that is located exactly between 2 chunks/files will have two different IDs for its two halves.

This is why we introduced some uniqueness strategies that are all imperfect and that should be seen as experimental. Please report any troubleshooting. Using a uniqueness-safe strategy ensures that trees from different files will not share the same IDs. Moreover, it also means that two halves of a tree on the edge of a processing chunk will be assigned the same ID.

**incremental** Number from 0 to n. This method **does not** ensure uniqueness of the IDs. This is the legacy method.

**gpstime** This method uses the gpstime of the highest point of a tree (apex) to create a unique ID. This ID is not an integer but a 64-bit decimal number, which is suboptimal but at least it is expected to be unique **if the gpstime attribute is consistent across files**. If inconsistencies with gpstime are reported (for example gpstime records the week time and was reset to 0 in a coverage that takes more than a week to complete), there is a (low) probability of getting ID attribution errors.

**bitmerge** This method uses the XY coordinates of the highest point (apex) of a tree to create a single 64-bit number with a bitwise operation. First, XY coordinates are converted to 32-bit integers using the scales and offsets of the point cloud. For example, if the apex is at (10.32, 25.64) with a scale factor of 0.01 and an offset of 0, the 32-bit integer coordinates are X = 1032 and Y = 2564. Their binary representations are, respectively, (here displayed

as 16 bits) 0000010000001000 and 0000101000000100. X is shifted by 32 bits and becomes a 64-bit integer. Y is kept as-is and the binary representations are unionized into a 64-bit integer like (here displayed as 32 bit) 00000100000010000000101000000100 that is guaranteed to be unique. However R does not support 64-bit integers. The previous steps are done at C++ level and the 64-bit binary representation is reinterpreted into a 64-bit decimal number to be returned in R. The IDs thus generated are somewhat weird. For example, the tree ID 00000100000010000000101000000100 which is 67635716 if interpreted as an integer becomes 3.34164837074751323479078607289E-316 if interpreted as a decimal number. This is far from optimal but at least it is guaranteed to be unique **if all files have the same offsets and scale factors**.

All the proposed options are suboptimal because they either do not guarantee uniqueness in all cases (inconsistencies in the collection of files), or they imply that IDs are based on non-integers or meaningless numbers. But at least it works and deals with some of the limitations of R.

### Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- **chunk buffer\***: Mandatory to get a continuous output without edge effects. The buffer is always removed once processed and will never be returned either in R or in files.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files\***: Mandatory because the output is likely to be too big to be returned in R and needs to be written in las/laz files. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The function will write files equivalent to the original ones. Thus `select = "*" and cannot be changed.`
- **filter**: Read only points of interest.

## Examples

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile, select = "xyz", filter = "-drop_z_below 0")

# Using Li et al. (2012)
las <- segment_trees(las, li2012(R = 3, speed_up = 5))
#plot(las, color = "treeID")
```

---

set_lidr_threads	<i>Set or get number of threads that lidR should use</i>
------------------	--

---

## Description

Set and get number of threads to be used in lidR functions that are parallelized with OpenMP. 0 means to utilize all CPU available. `get_lidr_threads()` returns the number of threads that will be used. This affects lidR package but also the `data.table` package by internally calling [setDTthreads](#) because several functions of lidR rely on `data.table` but it does not change R itself or other packages using OpenMP.

## Usage

```
set_lidr_threads(threads)

get_lidr_threads()
```

## Arguments

threads	Positive scalar. Default 0 means use all CPU available. Values > 1 mean using n cores, values in ]0, 1[ mean using a fraction of the cores e.g. 0.5 = half.
---------	---

## See Also

[lidR-parallelism](#)

---

shape_detection	<i>Algorithms for shape detection of the local point neighborhood</i>
-----------------	---

---

## Description

These functions are made to be used in [segment\\_shapes](#). They implement algorithms for local neighborhood shape estimation.

**Usage**

```
shp_plane(th1 = 25, th2 = 6, k = 8)
```

```
shp_hplane(th1 = 25, th2 = 6, th3 = 0.98, k = 8)
```

```
shp_line(th1 = 10, k = 8)
```

**Arguments**

th1, th2, th3    numeric. Threshold values (see details)

k                    integer. Number of neighbours used to estimate the neighborhood.

**Details**

In the following,  $a_1, a_2, a_3$  denote the eigenvalues of the covariance matrix of the neighbouring points in ascending order.  $th_1, th_2, th_3$  denote a set of threshold values. Points are labelled TRUE if they meet the following criteria. FALSE otherwise.

**shp\_plane** Detection of plans based on criteria defined by Limberger & Oliveira (2015) (see references). A point is labelled TRUE if the neighborhood is approximately planar, that is:

$$a_2 > (th_1 * a_1) \text{ and } (th_2 * a_2) > a_3$$

**shp\_hplane** The same as 'plane' but with an extra test on the orientation of the Z vector of the principal components to test the horizontality of the surface.

$$a_2 > (th_1 * a_1) \text{ and } (th_2 * a_2) > a_3 \text{ and } |Z| > th_3$$

In theory  $|Z|$  should be exactly equal to 1. In practice 0.98 or 0.99 should be fine

**shp\_line** Detection of lines inspired by the Limberger & Oliveira (2015) criterion. A point is labelled TRUE if the neighborhood is approximately linear, that is:

$$th_1 * a_2 < a_3 \text{ and } th_1 * a_1 < a_3$$

**References**

Limberger, F. A., & Oliveira, M. M. (2015). Real-time detection of planar regions in unorganized point clouds. *Pattern Recognition*, 48(6), 2043–2053. <https://doi.org/10.1016/j.patcog.2014.12.020>



**Description**

This functions is made to be used in [segment\\_trees](#). It implements an algorithm for tree segmentation based on the Silva et al. (2016) article (see reference). This is a simple method based on seed + voronoi tessellation (equivalent to nearest neighbour). This algorithm is implemented in the package rLiDAR. This version is *not* the version from rLiDAR. It is code written from the original article by the lidR authors and is considerably (between 250 and 1000 times) faster.

**Usage**

```
silva2016(chm, treetops, max_cr_factor = 0.6, exclusion = 0.3, ID = "treeID")
```

**Arguments**

chm	RasterLayer. Image of the canopy. Can be computed with <a href="#">grid_canopy</a> or read from an external file.
treetops	SpatialPointsDataFrame. Can be computed with <a href="#">find_trees</a> or read from an external shapefile.
max_cr_factor	numeric. Maximum value of a crown diameter given as a proportion of the tree height. Default is 0.6, meaning 60% of the tree height.
exclusion	numeric. For each tree, pixels with an elevation lower than exclusion multiplied by the tree height will be removed. Thus, this number belongs between 0 and 1.
ID	character. If the SpatialPointsDataFrame contains an attribute with the ID for each tree, the name of this column. This way, original IDs will be preserved. If there is no such data trees will be numbered sequentially.

**Details**

Because this algorithm works on a CHM only there is no actual need for a point cloud. Sometimes the user does not even have the point cloud that generated the CHM. lidR is a point cloud-oriented library, which is why this algorithm must be used in [segment\\_trees](#) to merge the result into the point cloud. However, the user can use this as a stand-alone function like this:

```
chm = raster("file/to/a/chm/")
ttops = find_trees(chm, lmf(3))
crowns = silva2016(chm, ttops())
```

**References**

Silva, C. A., Hudak, A. T., Vierling, L. A., Loudermilk, E. L., O'Brien, J. J., Hiers, J. K., Khosravipour, A. (2016). Imputation of Individual Longleaf Pine (*Pinus palustris* Mill.) Tree Attributes from Field and LiDAR Data. *Canadian Journal of Remote Sensing*, 42(5), 554–573. <https://doi.org/10.1080/07038992.2016.1196582>.

**See Also**

Other individual tree segmentation algorithms: [dalponte2016\(\)](#), [li2012\(\)](#), [watershed\(\)](#)

Other raster based tree segmentation algorithms: [dalponte2016\(\)](#), [watershed\(\)](#)

**Examples**

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
poi <- "-drop_z_below 0 -inside 481280 3812940 481320 3812980"
las <- readLAS(LASfile, select = "xyz", filter = poi)
col <- pastel.colors(200)

chm <- grid_canopy(las, res = 0.5, p2r(0.3))
ker <- matrix(1,3,3)
chm <- raster::focal(chm, w = ker, fun = mean, na.rm = TRUE)

ttops <- find_trees(chm, lmf(4, 2))
las <- segment_trees(las, silva2016(chm, ttops))
#plot(las, color = "treeID", colorPalette = col)
```

---

smooth\_height

*Smooth a point cloud*

---

**Description**

Point cloud-based smoothing algorithm. Two methods are available: average within a window and Gaussian smooth within a window. The attribute Z of the returned LAS object is the smoothed Z. A new attribute Zraw is added to store the original values and can be used to restore the point cloud with `unsmooth_height`.

**Usage**

```
smooth_height(
  las,
  size,
  method = c("average", "gaussian"),
  shape = c("circle", "square"),
  sigma = size/6
)

unsmooth_height(las)
```

**Arguments**

las	An object of class LAS
size	numeric. The size of the windows used to smooth.
method	character. Smoothing method. Can be 'average' or 'gaussian'.
shape	character. The shape of the windows. Can be circle or square.
sigma	numeric. The standard deviation of the gaussian if the method is gaussian.

## Details

This method does not use raster-based methods to smooth the point cloud. This is a true point cloud smoothing. It is not really useful by itself but may be interesting in combination with filters such as [filter\\_surfacepoints](#), for example to develop new algorithms.

## Value

An object of the class LAS.

## Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile, select = "xyz")

las <- filter_surfacepoints(las, 1)
#plot(las)

las <- smooth_height(las, 5, "gaussian", "circle", sigma = 2)
#plot(las)

las <- unsmooth_height(las)
#plot(las)
```

---

sor

*Noise Segmentation Algorithm*

---

## Description

This function is made to be used in [classify\\_noise](#). It implements an algorithm for outliers (noise) segmentation based on Statistical Outliers Removal (SOR) methods first described in the PCL library and also implemented in CloudCompare (see references). For each point, it computes the mean distance to all its k-nearest neighbours. The points that are farther than the average distance plus a number of times (multiplier) the standard deviation are considered noise.

## Usage

```
sor(k = 10, m = 3, quantile = FALSE)
```

## Arguments

k	numeric. The number of neighbours
m	numeric. Multiplier. The maximum distance will be: avg distance + m * std deviation. If <code>quantile = TRUE</code> , m becomes the quantile threshold.
quantile	boolean. Modification of the original SOR to use a quantile threshold instead of a standard deviation multiplier. In this case the maximum distance will be: <code>quantile(distances, probs = m)</code>

## References

[https://pointclouds.org/documentation/tutorials/statistical\\_outlier.html](https://pointclouds.org/documentation/tutorials/statistical_outlier.html)  
[https://www.cloudcompare.org/doc/wiki/index.php?title=SOR\\_filter](https://www.cloudcompare.org/doc/wiki/index.php?title=SOR_filter)

## See Also

Other noise segmentation algorithms: [ivf\(\)](#)

## Examples

```
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las <- readLAS(LASfile, filter = "-inside 273450 5274350 273550 5274450")

# Add some artificial outliers because the original
# dataset is 'clean'
set.seed(314)
id = round(runif(20, 0, npoints(las)))
set.seed(42)
err = runif(20, -50, 50)
las$Z[id] = las$Z[id] + err

las <- classify_noise(las, sor(15,7))
```

---

stdmetrics

*Predefined standard metrics functions*

---

## Description

Predefined metrics functions intended to be used in `*_metrics` function such as [grid\\_metrics](#), [hexbin\\_metrics](#), [cloud\\_metrics](#), [tree\\_metrics](#), [voxel\\_metrics](#) or [point\\_metrics](#). Each function comes with a convenient shortcuts for lazy coding. The `lidR` package aims to provide an easy way to compute user-defined metrics rather than to provide them. However, for efficiency and to save time, sets of standard metrics have been predefined (see details). Every function can be computed by every `*_metrics` functions however `stdmetrics*` are more pixel-based metrics, `stdtreemetrics` are more tree-based metrics and `stdshapemetrics` are more point-based metrics. For example the metric `zmean` computed by `stdmetrics_z` makes sense when computed at the pixel level but brings no information at the voxel level.

## Usage

```
stdmetrics(x, y, z, i, rn, class, dz = 1, th = 2, zmin = 0)
```

```
stdmetrics_z(z, dz = 1, th = 2, zmin = 0)
```

```
stdmetrics_i(i, z = NULL, class = NULL, rn = NULL)
```

```
stdmetrics_rn(rn, class = NULL)
```



## Details

The function names, their parameters and the output names of the metrics rely on a nomenclature chosen for brevity:

- z: refers to the elevation
- i: refers to the intensity
- rn: refers to the return number
- q: refers to quantile
- a: refers to the ScanAngleRank or ScanAngle
- n: refers to a number (a count)
- p: refers to a percentage

For example the metric named `zq60` refers to the elevation, quantile, 60 i.e. the 60th percentile of elevations. The metric `pground` refers to a percentage. It is the percentage of points classified as ground. The function `stdmetric_i` refers to metrics of intensity. A description of each existing metric can be found on the [lidR wiki page](#).

Some functions have optional parameters. If these parameters are not provided the function computes only a subset of existing metrics. For example, `stdmetrics_i` requires the intensity values, but if the elevation values are also provided it can compute additional metrics such as cumulative intensity at a given percentile of height.

Each function has a convenient associated variable. It is the name of the function, with a dot before the name. This enables the function to be used without writing parameters. The cost of such a feature is inflexibility. It corresponds to a predefined behaviour (see examples)

`stdmetrics` is a combination of `stdmetrics_ctrl` + `stdmetrics_z` + `stdmetrics_i` + `stdmetrics_rn`

`stdtreemetrics` is a special function that works with [tree\\_metrics](#). Actually, it won't fail with other functions but the output makes more sense if computed at the individual tree level.

`stdshapemetrics` is a set of eigenvalue based feature described in Lucas et al, 2019 (see references).

## References

M. Woods, K. Lim, and P. Treitz. Predicting forest stand variables from LiDAR data in the Great Lakes – St. Lawrence forest of Ontario. *The Forestry Chronicle*. 84(6): 827-839. <https://doi.org/10.5558/tfc84827-6>

Lucas, C., Bouten, W., Koma, Z., Kissling, W. D., & Seijmonsbergen, A. C. (2019). Identification of Linear Vegetation Elements in a Rural Landscape Using LiDAR Point Clouds. *Remote Sensing*, 11(3), 292.

## See Also

[cloud\\_metrics](#) [grid\\_metrics](#) [hexbin\\_metrics](#) [voxel\\_metrics](#) [tree\\_metrics](#) [point\\_metrics](#)

**Examples**

```

LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile, select = "*", filter = "-keep_random_fraction 0.5")

# All the predefined metrics
m1 <- grid_metrics(las, ~stdmetrics(X,Y,Z,Intensity,ReturnNumber,Classification,dz=1), res = 40)

# Convenient shortcut
m2 <- grid_metrics(las, .stdmetrics, res = 40)

# Basic metrics from intensities
m3 <- grid_metrics(las, ~stdmetrics_i(Intensity), res = 40)

# All the metrics from intensities
m4 <- grid_metrics(las, ~stdmetrics_i(Intensity, Z, Classification, ReturnNumber), res = 40)

# Convenient shortcut for the previous example
m5 <- grid_metrics(las, .stdmetrics_i, res = 40)

# Combine some predefined function with your own new metrics
# Here convenient shortcuts are no longer usable.
myMetrics = function(z, i, rn)
{
  first <- rn == 1L
  zfirst <- z[first]
  nfirst <- length(zfirst)
  above2 <- sum(z > 2)

  x <- above2/nfirst*100

  # User's metrics
  metrics <- list(
    above2aboven1st = x,      # Num of returns above 2 divided by num of 1st returns
    zimean = mean(z*i),      # Mean products of z by intensity
    zsqmean = sqrt(mean(z^2)) # Quadratic mean of z
  )

  # Combined with standard metrics
  return( c(metrics, stdmetrics_z(z)) )
}

m10 <- grid_metrics(las, ~myMetrics(Z, Intensity, ReturnNumber), res = 40)

# Users can write their own convenient shortcuts like this:
.myMetrics = ~myMetrics(Z, Intensity, ReturnNumber)
m11 <- grid_metrics(las, .myMetrics, res = 40)

```

**Description**

This function is made to be used in [grid\\_terrain](#) or [normalize\\_height](#). It implements an algorithm for spatial interpolation. Spatial interpolation is based on a Delaunay triangulation, which performs a linear interpolation within each triangle. There are usually a few points outside the convex hull, determined by the ground points at the very edge of the dataset, that cannot be interpolated with a triangulation. Extrapolation is done using the nearest neighbour approach.

**Usage**

```
tin(..., extrapolate = knnidw(3, 1, 50))
```

**Arguments**

...	unused
extrapolate	There are usually a few points outside the convex hull, determined by the ground points at the very edge of the dataset, that cannot be interpolated with a triangulation. Extrapolation is done using the nearest neighbour approach by default using <a href="#">knnidw</a> .

**See Also**

Other spatial interpolation algorithms: [knnidw\(\)](#), [kriging\(\)](#)

**Examples**

```
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las = readLAS(LASfile, filter = "-inside 273450 5274350 273550 5274450")

#plot(las)

dtm = grid_terrain(las, algorithm = tin())

plot(dtm, col = terrain.colors(50))
#plot_dtm3d(dtm)
```

---

track\_sensor

---

*Reconstruct the trajectory of the LiDAR sensor using multiple returns*


---

**Description**

Use multiple returns to estimate the positioning of the sensor by computing the intersection in space of the line passing through the first and last returns. To work, this function requires a dataset where the 'gpstime', 'ReturnNumber', 'NumberOfReturns' and 'PointSourceID' attributes are properly populated, otherwise the output may be incorrect or weird. For LAScatalog processing it is recommended to use large chunks and large buffers (e.g. a swath width). The point cloud must not be normalized.



**Usage**

```

track_sensor(
  las,
  algorithm,
  extra_check = TRUE,
  thin_pulse_with_time = 0.001,
  multi_pulse = FALSE
)

```

**Arguments**

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
algorithm	function. An algorithm to compute sensor tracking. lidR implements <a href="#">Rousset2020</a> and <a href="#">Gatziolis2019</a> (see respective documentation and examples).
extra_check	boolean. Datasets are rarely perfectly populated, leading to unexpected errors. Time-consuming checks of data integrity are performed. These checks can be skipped as they account for an significant proportion of the computation time. See also section 'Tests of data integrity'.
thin_pulse_with_time	numeric. In practice, it is not useful to compute the position using all multiple returns. It is more computationally demanding but not necessarily more accurate. This keeps only one pulse every x seconds. Set to 0 to use all multiple returns. Use 0 if the file has already been read with filter = "-thin_pulses_with_time 0.001".
multi_pulse	logical. TRUE only for systems with multiple pulses. Pulse ID must be recorded in the UserData attribute.

**Value**

A `SpatialPointsDataFrame` with the Z elevation stored in the table of attributes. Information about the time interval and the score of the positioning (according to the method used) are also in the table of attributes.

**Test of data integrity**

In theory, sensor tracking is a simple problem to solve as long as each pulse is properly identified from a well-populated dataset. In practice, many problems may arise from datasets that are populated incorrectly. Here is a list of problems that may happen. Those with a \* denote problems already encountered and internally checked to remove weird points:

- 'gpstime' does not record the time at which pulses were emitted and thus pulses are not identifiable
- \*A pulse (two or more points that share the same gpstime) is made of points from different flightlines (different PointSourceID). This is impossible and denotes an improperly populated PointSourceID attribute.
- 'ReturnNumber' and 'NumberOfReturns' are wrongly populated with either some ReturnNumber > NumberOfReturn or several first returns by pulses

For a given time interval, when weird points are not filtered, the position is not computed for this interval.

### Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- **chunk buffer\***: Mandatory to get a continuous output without edge effects. The buffer is always removed once processed and will never be returned either in R or in files.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output\_files**: Saving intermediate results is disabled in 'sensor\_tracking' because the output must be post-processed as a whole.
- **laz\_compression**: write las or laz files
- **select**: is not supported. It is set by default to "xyzrntp"
- **filter**: Read only points of interest. By default it uses "-drop\_single" and "-thin\_pulses\_with\_time" to reduce the number of points loaded.

### Author(s)

Jean-Francois Bourdon & Jean-Romain Roussel

### Examples

```
# A valid file properly populated
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las = readLAS(LASfile,
              select = "xyzrntp",
              filter = "-drop_single -thin_pulses_with_time 0.001")
#plot(las)

# pmin = 15 because it is an extremely small file
```

```

# strongly decimated to reduce its size. There are
# actually few multiple returns
flightlines <- track_sensor(las, Roussel2020(pmin = 15))

plot(las@header)
plot(flightlines, add = TRUE)

#x <- plot(las)
#add_flightlines3d(x, flightlines, radius = 10)

## Not run:
# With a LAScatalog "-drop_single" and "-thin_pulses_with_time"
# are used by default
ctg = readLAScatalog("folder/")
flightlines <- track_sensor(ctg, Roussel2020(pmin = 15))
plot(flightlines)

## End(Not run)

```

---

tree_metrics	<i>Compute metrics for each tree</i>
--------------	--------------------------------------

---

## Description

Once the trees are segmented, i.e. attributes exist in the point cloud that reference each tree, computes a set of user-defined descriptive statistics for each individual tree. This is the "tree version" of [grid\\_metrics](#).

## Usage

```
tree_metrics(las, func = ~max(Z), attribute = "treeID")
```

## Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
func	formula. An expression to be applied to each tree. It works like in <a href="#">grid_metrics</a> , <a href="#">voxel_metrics</a> or <a href="#">delineate_crowns</a> and computes, in addition to tree locations a set of metrics for each tree.
attribute	character. The column name of the attribute containing tree IDs. Default is "treeID"

## Details

By default the function computes the xyz-coordinates of the highest point of each tree and uses xy as tree coordinates in `SpatialPointsDataFrame`. z is stored in the table of attributes along with the id of each tree. All the other attributes are user-defined attributes:

The following existing functions contain a small set of pre-defined metrics:

- [stdmetrics\\_tree](#)

Users must write their own functions to create their own metrics. `tree_metrics` will dispatch the LiDAR data for each segmented tree in the user-defined function. Functions are defined without the need to consider each segmented tree i.e. only the point cloud (see examples).

### Value

A `SpatialPointsDataFrame` that references the xy-position with a table of attributes that associates the z-elevation (highest points) of the trees and the id of the trees, plus the metrics defined by the user.

### Working with a LAScatalog

This section appears in each function that supports a `LAScatalog` as input.

In `lidR` when the input of a function is a `LAScatalog` the function uses the `LAScatalog` processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing `LAScatalogs`. Each `lidR` function should come with a section that documents the supported engine options.

The `LAScatalog` engine supports `.lax` files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a `.lax` files, but this is not mandatory.

### Supported processing options

Supported processing options for a `LAScatalog` (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- **chunk buffer\***: Mandatory to get a continuous output without edge effects. The buffer is always removed once processed and will never be returned either in R or in files.
- **chunk alignment**: Align the processed chunks.
- **progress**: Displays a progression estimation.
- **output files**: Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: Load only attributes of interest.
- **filter**: Read only points of interest.

### See Also

Other metrics: [cloud\\_metrics\(\)](#), [grid\\_metrics\(\)](#), [plot\\_metrics\(\)](#), [point\\_metrics\(\)](#), [voxel\\_metrics\(\)](#)

**Examples**

```

LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las = readLAS(LASfile, filter = "-drop_z_below 0")

# NOTE: This dataset is already segmented
# plot(las, color = "treeID", colorPalette = pastel.colors(200))

# Default computes only Z max
metrics = tree_metrics(las)

# User-defined metrics - mean height and mean intensity for each tree
metrics = tree_metrics(las, ~list(Zmean = mean(Z), Imean = mean(Intensity)))

# Define your own new metrics function
myMetrics = function(z, i)
{
  metrics = list(
    imean = mean(i),
    imax = max(i),
    npoint = length(z)
  )

  return(metrics)
}

metrics = tree_metrics(las, ~myMetrics(Z, Intensity))

# predefined metrics (see ?stdmetrics)
metrics = tree_metrics(las, .stdtreemetrics)

```

---

util\_makeZhangParam     *Parameters for progressive morphological filter*

---

**Description**

The function [classify\\_ground](#) with the progressive morphological filter allows for any sequence of parameters. This function enables computation of the sequences using equations (4), (5) and (7) from Zhang et al. (see reference and details).

**Usage**

```

util_makeZhangParam(
  b = 2,
  dh0 = 0.5,
  dhmax = 3,
  s = 1,
  max_ws = 20,
  exp = FALSE
)

```

**Arguments**

b	numeric. This is the parameter $b$ in Zhang et al. (2003) (eq. 4 and 5).
dh0	numeric. This is $dh_0$ in Zhang et al. (2003) (eq. 7).
dhmax	numeric. This is $dh_{max}$ in Zhang et al. (2003) (eq. 7).
s	numeric. This is $s$ in Zhang et al. (2003) (eq. 7).
max_ws	numeric. Maximum window size to be used in filtering ground returns. This limits the number of windows created.
exp	logical. The window size can be increased linearly or exponentially (eq. 4 or 5).

**Details**

In the original paper the windows size sequence is given by eq. 4 or 5:

$$w_k = 2kb + 1$$

or

$$w_k = 2b^k + 1$$

In the original paper the threshold sequence is given by eq. 7:

$$th_k = s * (w_k - w_{k-1}) * c + th_0$$

Because the function `classify_ground` applies the morphological operation at the point cloud level the parameter  $c$  is set to 1 and cannot be modified.

**Value**

A list with two components: the windows size sequence and the threshold sequence.

**References**

Zhang, K., Chen, S. C., Whitman, D., Shyu, M. L., Yan, J., & Zhang, C. (2003). A progressive morphological filter for removing nonground measurements from airborne LIDAR data. *IEEE Transactions on Geoscience and Remote Sensing*, 41(4 PART I), 872–882. <http://doi.org/10.1109/TGRS.2003.810682>.

**Examples**

```
p = util_makeZhangParam()
```

---

VCI

*Vertical Complexity Index*

---

### Description

A fixed normalization of the entropy function (see references)

### Usage

```
VCI(z, zmax, by = 1)
```

### Arguments

z	vector of z coordinates
zmax	numeric. Used to turn the function entropy to the function vci.
by	numeric. The thickness of the layers used (height bin)

### Value

A number between 0 and 1

### References

van Ewijk, K. Y., Treitz, P. M., & Scott, N. A. (2011). Characterizing Forest Succession in Central Ontario using LAS-derived Indices. *Photogrammetric Engineering and Remote Sensing*, *77*(3), 261-269. Retrieved from <Go to ISI>://WOS:000288052100009

### See Also

[entropy](#)

### Examples

```
z <- runif(10000, 0, 10)
VCI(z, by = 1, zmax = 20)

z <- abs(rnorm(10000, 10, 1))

# expected to be closer to 0.
VCI(z, by = 1, zmax = 20)
```

---

voxelize_points	<i>Voxelize a point cloud</i>
-----------------	-------------------------------

---

### Description

Reduce the number of points by voxelizing the point cloud. If the Intensity is part of the attributes it is preserved and aggregated as mean(Intensity). Other attributes cannot be aggregated and are lost.

### Usage

```
voxelize_points(las, res)
```

### Arguments

las	An object of class <a href="#">LAS</a> or <a href="#">LAScatalog</a> .
res	numeric. The resolution of the voxels. res = 1 for a 1x1x1 cubic voxels. Optionally res = c(1, 2) for non-cubic voxels (1x1x2 cuboid voxel).

### Value

If the input is a LAS object, returns a LAS object. If the input is a LAScatalog, returns a LAScatalog.

### Working with a LAScatalog

This section appears in each function that supports a LAScatalog as input.

In lidR when the input of a function is a [LAScatalog](#) the function uses the LAScatalog processing engine. The user can modify the engine options using the [available options](#). A careful reading of the [engine documentation](#) is recommended before processing LAScatalogs. Each lidR function should come with a section that documents the supported engine options.

The LAScatalog engine supports .lax files that *significantly* improve the computation speed of spatial queries using a spatial index. Users should really take advantage a .lax files, but this is not mandatory.

### Supported processing options

Supported processing options for a LAScatalog (in bold). For more details see the [LAScatalog engine documentation](#):

- **chunk size**: How much data is loaded at once.
- **chunk buffer\***: Mandatory to get a continuous output without edge effects. The buffer is always removed once processed and will never be returned either in R or in files.
- **chunk alignment**: Align the processed chunks.



- **progress**: Displays a progression estimation.
- **output files\***: Mandatory because the output is likely to be too big to be returned in R and needs to be written in las/laz files. Supported templates are {XLEFT}, {XRIGHT}, {YBOTTOM}, {YTOP}, {XCENTER}, {YCENTER} {ID} and, if chunk size is equal to 0 (processing by file), {ORIGINALFILENAME}.
- **select**: The function will write files equivalent to the original ones. Thus `select = "*"`  and cannot be changed.
- **filter**: Read only points of interest.

### Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las = readLAS(LASfile, select = "xyz")

las2 = voxelize_points(las, 2)
#plot(las2)
```

---

voxel\_metrics

*Voxelize the space and compute metrics for each voxel*

---

### Description

This is a 3D version of [grid\\_metrics](#). It creates a 3D matrix of voxels with a given resolution. It creates a voxel from the cloud of points if there is at least one point in the voxel. For each voxel the function allows computation of one or several derived metrics in the same way as the [grid\\_metrics](#) functions. The function will dispatch the LiDAR data for each voxel in the user's function (see [grid\\_metrics](#)).

### Usage

```
voxel_metrics(las, func, res = 1, ..., all_voxels = FALSE)
```

### Arguments

<code>las</code>	An object of class LAS.
<code>func</code>	formula. An expression to be applied to each voxel (see also <a href="#">grid_metrics</a> ).
<code>res</code>	numeric. The resolution of the voxels. <code>res = 1</code> for a 1x1x1 cubic voxels. Optionally <code>res = c(1, 2)</code> for non-cubic voxels (1x1x2 cuboid voxel).
<code>...</code>	Unused
<code>all_voxels</code>	boolean. By default the function returns only voxels that contain 1 or more points. Empty voxels do not exist as the metrics are undefined. If <code>all_voxels = TRUE</code> all the voxels are returned and metrics are NA for voxels with 0 points.

### Value

It returns a `data.table` containing the metrics for each voxel. The table has the class `lasmetrics3d` enabling easier plotting. It also has an attribute `res` that stores the resolution.

**See Also**

Other metrics: `cloud_metrics()`, `grid_metrics()`, `plot_metrics()`, `point_metrics()`, `tree_metrics()`

**Examples**

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile)

# Cloud of points is voxelized with a 8-meter resolution and in each voxel
# the number of points is computed.
vm <- voxel_metrics(las, ~length(Z), 8)

# Cloud of points is voxelized with a 8-meter resolution and in each voxel
# the mean intensity of points is computed.
vm <- voxel_metrics(las, ~mean(Intensity), 8)
#plot(vm, color = "V1", colorPalette = heat.colors(50), trim = 60)

# Define your own metric function
myMetrics = function(i)
{
  ret = list(
    npoints = length(i),
    imean   = mean(i)
  )
  return(ret)
}

voxels <- voxel_metrics(las, ~myMetrics(Intensity), 8)

#plot(voxels, color = "imean", colorPalette = heat.colors(50), trim = 60)
#etc.

attr(voxels, "res")
```

---

watershed

*Individual Tree Segmentation Algorithm*

---

**Description**

This function is made to be used in `segment_trees`. It implements an algorithm for tree segmentation based on a watershed or a marker-controlled watershed.

- **Simple watershed** is based on the bioconductor package `EBIimage`. You need to install this package to run this method (see its [github page](#)). Internally, the function `EBIimage::watershed` is called.
- **Marker-controlled watershed** is based on the `imager` package and has been removed because `imager` is an orphaned package.

**Usage**

```
watershed(chm, th_tree = 2, tol = 1, ext = 1)

mcwatershed(chm, treetops, th_tree = 2, ID = "treeID")
```

**Arguments**

chm	RasterLayer. Image of the canopy. Can be computed with <a href="#">grid_canopy</a> or read from an external file.
th_tree	numeric. Threshold below which a pixel cannot be a tree. Default is 2.
tol	numeric. Tolerance see ?EBImage::watershed.
ext	numeric. see ?EBImage::watershed.
treetops	SpatialPointsDataFrame. Can be computed with <a href="#">find_trees</a> or read from an external shapefile.
ID	character. If the SpatialPointsDataFrame contains an attribute with the ID for each tree, the name of this column. This way, original IDs will be preserved. If there is no such data trees will be numbered sequentially.

**Details**

Because this algorithm works on a CHM only there is no actual need for a point cloud. Sometimes the user does not even have the point cloud that generated the CHM. `lidR` is a point cloud-oriented library, which is why this algorithm must be used in [segment\\_trees](#) to merge the result into the point cloud. However, the user can use this as a stand-alone function like this:

```
chm = raster("file/to/a/chm/")
ttops = find_trees(chm, lmf(3))
crowns = watershed(chm())
```

**See Also**

Other individual tree segmentation algorithms: [dalponte2016\(\)](#), [li2012\(\)](#), [silva2016\(\)](#)  
 Other raster based tree segmentation algorithms: [dalponte2016\(\)](#), [silva2016\(\)](#)

**Examples**

```
## Not run:
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
poi <- "-drop_z_below 0 -inside 481280 3812940 481320 3812980"
las <- readLAS(LASfile, select = "xyz", filter = poi)
col <- pastel.colors(250)

chm <- grid_canopy(las, res = 0.5, p2r(0.3))
ker <- matrix(1,3,3)
chm <- raster::focal(chm, w = ker, fun = mean, na.rm = TRUE)
las <- segment_trees(las, watershed(chm))

plot(las, color = "treeID", colorPalette = col)
```

```
## End(Not run)
```

---

 wing2015

*Snags Segmentation Algorithm*


---

### Description

This function is made to be used in [segment\\_snags](#). It implements an algorithms for snags segmentation based on Wing et al (2015) (see references). This is an automated filtering algorithm that utilizes three dimensional neighborhood lidar point-based intensity and density statistics to remove lidar points associated with live trees and retain lidar points associated with snags.

### Usage

```
wing2015(
  neigh_radii = c(1.5, 1, 2),
  low_int_thrsh = 50,
  uppr_int_thrsh = 170,
  pt_den_req = 3,
  BBPRthrsh_mat = NULL
)
```

### Arguments

neigh_radii	numeric. A vector of three radii used in quantifying local-area centered neighborhoods. See Wing et al. (2015) reference page 171 and Figure 4. Defaults are 1.5, 1, and 2 for the sphere, small cylinder and large cylinder neighborhoods, respectively.
low_int_thrsh	numeric. The lower intensity threshold filtering value. See Wing et al. (2015) page 171. Default is 50.
uppr_int_thrsh	numeric. The upper intensity threshold filtering value. See Wing et al. (2015) page 171. Default is 170.
pt_den_req	numeric. Point density requirement based on plot-level point density defined classes. See Wing et al. (2015) page 172. Default is 3.
BBPRthrsh_mat	matrix. A 3x4 matrix providing the four average BBPR (branch and bole point ratio) values for each of the three neighborhoods (sphere, small cylinder and large cylinder) to be used for conditional assessments and classification into the following four snag classes: 1) general snag 2) small snag 3) live crown edge snag 4) high canopy cover snag. See Wing et al. (2015) page 172 and Table 2. This matrix must be provided by the user.

## Details

Note that this algorithm strictly performs a classification based on user input while the original publication's methods also included a segmentation step and some pre- (filtering for first and single returns only) and post-process (filtering for only the snag classified points prior to segmentation) tasks which are now expected to be performed by the user. Also, this implementation may have some differences compared with the original method due to potential mis-interpretation of the Wing et al. manuscript, specifically Table 2 where they present four groups of conditional assessments with their required neighborhood point density and average BBPR values (BBPR = branch and bole point ratio; PDR = point density requirement).

This algorithm attributes each point in the point cloud (snagCls column) into the following five snag classes:

- 0: live tree - not a snag
- 1: general snag - the broadest range of snag point situations
- 2: small snag - isolated snags with lower point densities
- 3: live crown edge snag - snags located directly adjacent or intermixing with live trees crowns
- 4: high canopy cover snag - snags protruding above the live canopy in dense conditions (e.g., canopy cover  $\geq 55\%$ ).

## Author(s)

Implementation by Andrew Sánchez Meador & Jean-Romain Roussel

## References

Wing, Brian M.; Ritchie, Martin W.; Boston, Kevin; Cohen, Warren B.; Olsen, Michael J. 2015. Individual snag detection using neighborhood attribute filtered airborne lidar data. *Remote Sensing of Environment*. 163: 165-179 <https://doi.org/10.1016/j.rse.2015.03.013>

## Examples

```
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
# Wing also included -keep_single
poi = "-keep_first -inside 481260 3812920 481310 3812960"
las <- readLAS(LASfile, select = "xyzi", filter = poi)

# For the Wing2015 method, supply a matrix of snag BranchBolePtRatio conditional
# assessment thresholds (see Wing et al. 2015, Table 2, pg. 172)
bbpr_thresholds <- matrix(c(0.80, 0.80, 0.70,
                           0.85, 0.85, 0.60,
                           0.80, 0.80, 0.60,
                           0.90, 0.90, 0.55),
                          nrow = 3, ncol = 4)
```

```
# Run snag classification and assign classes to each point
las <- segment_snags(las, wing2015(neigh_radii = c(1.5, 1, 2), BBPRthrsh_mat = bbpr_thresholds))

# Plot it all, tree and snag points...
#plot(las, color="snagCls", colorPalette = rainbow(5))

# Filter and plot snag points only
snags <- filter_poi(las, snagCls > 0)
#plot(snags, color="snagCls", colorPalette = rainbow(5)[-1])

# Wing et al's (2015) methods ended with performing tree segmentation on the
# classified and filtered point cloud using the watershed method
```

---

writeLAS

*Write a .las or .laz file*

---

## Description

Write a [LAS](#) object into a binary .las or .laz file (compression specified in filename)

## Usage

```
writeLAS(las, file, index = FALSE)
```

## Arguments

las	an object of class LAS.
file	character. A character string naming an output file.
index	boolean. Also write a lax file to index the points in the files

## Value

Nothing. This function is used for its side-effect of writing a file.

## Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las = readLAS(LASfile)
subset = clip_rectangle(las, 684850, 5017850, 684900, 5017900)
writeLAS(subset, tempfile(fileext = ".laz"))
```

---

\$<-,LAS-method                    *Inherited but modified methods from sp*

---

### Description

LAS\* objects are [Spatial](#) objects so they inherit several methods from `sp`. However, some have modified behaviors to prevent some irrelevant modifications. Indeed, a LAS\* object cannot contain anything, as the content is restricted by the LAS specifications. If a user attempts to use one of these functions inappropriately an informative error will be thrown.

### Usage

```
## S4 replacement method for signature 'LAS'
x$name <- value

## S4 replacement method for signature 'LAS,ANY,missing'
x[[i, j]] <- value

## S4 method for signature 'LAS,numeric,ANY'
x[i]

## S4 method for signature 'LAScatalog,ANY,ANY'
x[i, j, ..., drop = TRUE]

## S4 replacement method for signature 'LAScatalog,ANY,ANY'
x[[i, j]] <- value

## S4 replacement method for signature 'LAScatalog'
x$name <- value
```

### Arguments

<code>x</code>	A LAS* object
<code>name</code>	A literal character string or a name (possibly backtick quoted).
<code>value</code>	typically an array-like R object of a similar class as <code>x</code> .
<code>i</code>	string, name of elements to extract or replace.
<code>j</code>	Unused.
<code>...</code>	Unused
<code>drop</code>	Unused

### Examples

```
## Not run:
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las = readLAS(LASfile)
```

```
las$Z = 2L
las[["Z"]] = 1:10
las$NewCol = 0
las[["NewCol"]] = 0

## End(Not run)
```



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