Package 'lidR'

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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

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'algorithm-trk.R' 'catalog_apply.R' 'catalog_fakerun.R'
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'catalog_makecluster.R' 'catalog_merge_results.R'
'catalog_overlaps.R' 'catalog_retile.R' 'catalog_select.R'
'classify_ground.R' 'clip_roi.R' 'cloud_metrics.R'
'clusters_apply.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'
'generate_las.R' 'grid_canopy.R' 'grid_density.R'
'grid_metrics.R' 'grid_terrain.R' 'hexbin_metrics.R'
'io_readLAS.R' 'io_readLAScatalog.R' 'io_readMSLAS.R'
'io_writeANY.R' 'io_writeLAS.R' 'las_check.R' 'las_tools.R'
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'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'
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`lidR-package` *lidR: airborne LiDAR for forestry applications*

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 github wiki pages. To ask "how to" questions please ask on 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

Author(s)

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- David Auty (Reviews the documentation) [contributor]

Other contributors:

- Florian De Boissieu (Fixed bugs and improved catalog features) [contributor]
- Andrew Sánchez Meador (Implemented wing2015() for segment_snags()) [contributor]
- Bourdon Jean-François (Contributed to Roussel2020() for track_sensor()) [contributor]
- Gatziolis Demetrios (Implemented Gatziolis2019() for track_sensor()) [contributor]

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 LAS
x	a vector that needs to be added in the LAS object. For add_lasattribute* 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 *Transform to a list*

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.
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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.

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 LAScatalog 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 mentionned 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 defaut 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 \link{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 avaible in the official lidR vignettes or
# on the github wiki <http://jean-romain.github.io/lidR/wiki>

## ========================================================================
## 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
# choosen 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 indexation 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 <- tree_detection(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 dummmy example).
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
project <- readLAScatalog(LASfile)
plot(project)

# 3. Set some catalog options.
# For this dummy example, the chunk size is 80 m and the buffer is 10 m
opt_chunk_buffer(project) <- 10
opt_chunk_size(project)   <- 80            # small because this is a dummy example.
opt_select(project)       <- "xyz"         # read only the coordinates.
opt_filter(project)       <- "-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(project, my_tree_detection_method, ws = 5, .options = opt)

spplot(output)

## ================================================
```

```
## 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")
project <- readLAScatalog(LASfile)

opt_chunk_buffer(project) <- 1
opt_chunk_size(project)   <- 120     # small because this is a dummy example.
opt_select(project)       <- "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(project, rumple_index_surface, res = 20, .options = opt)

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

`catalog_intersect` *Subset a LAScatalog with a Spatial* object*

Description

Subset a LAScatalog with a Spatial* object to keep only the tiles of interest. Internally, it uses the function intersect from `raster` with a tweak to make it work with a LAScatalog. It can be used to select tiles of interest that encompass Spatial* objects such as SpatialPoints, SpatialPolygons or SpatialLines.

Usage

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

Arguments

`ctg`	A LAScatalog object
`y`	Extent, Raster*, SpatialPolygons*, SpatialLines* or SpatialPoints* object

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 aligment.
`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.

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_cores(ctg)

opt_cores(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 LAScatalog
value	An appropriate value depending on the expected input.

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 *Retile a LAScatalog*

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 th 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 LAScatalog object
mapview	logical. If FALSE, use R base plot instead of mapview (no pan, no zoom, see also plot)
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. flag_unprocessed enables users to point and click on files that will not be processed. flag_processed 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 *Classify points as 'ground' or 'not ground'*

Description

Classify points as 'ground' or 'not 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 LAS or LAScatalog.
algorithm	a ground-segmentation function. lidR has: pmf and csf.
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")

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

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")

#' # 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")
```

---

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 LAS or LAScatalog.
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 or Polygons
- SpatialPolygons or SpatialPolygonsDataFrame
- SpatialPoints or SpatialPointsDataFrame in that case a parameter 'radius' must be passed in ...
- SimpleFeature that consistently contains POINT or POLYGON/MULTIPOLYGON. In case of POINT a parameter 'radius' must be passed in ...
- Extent
- 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)
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)
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 <- shapefile(f)
subset3 <- clip_roi(ctg, lakes)

# Extract the polygons, 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(mew_ctg)

# Extract a transect
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
ctg <- readLAScatalog(LASfile)
p1 <- c(273357, y = 5274357)
p2 <- c(273642, y = 5274642)
tr1 <- clip_transect(ctg, p1, p2, width = 3)
tr2 <- clip_transect(ctg, p1, p2, width = 3, xz = TRUE)
```

```
plot(tr1, axis = TRUE, clear_artifacts = FALSE)
plot(tr2, axis = TRUE, clear_artifacts = FALSE)

## Not run:
plot(subset1)
plot(subset2)
plot(subset3)

## 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()`, `hexbin_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)
```

---

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

sloop_smooth	logical. When steep slopes exist, set this parameter to TRUE to reduce errors during post-processing.

`class_threshold`
: scalar. The distance to the simulated cloth to classify a point cloud into ground and non-ground. The default is 0.5.

`cloth_resolution`
: 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.

`rigidness`
: 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.

`iterations`
: integer. Maximum iterations for simulating cloth. The default value is 500. Usually, there is no need to change this value.

`time_step`
: 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")
```

---

dalponte2016 *Individual Tree Segmentation Algorithm*

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 grid_canopy or read from an external file.
treetops	SpatialPointsDataFrame. Can be computed with find_trees 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 *Decimate a LAS object*

Description

Reduce the number of points using several possible algorithms.

Usage

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

Arguments

las	An object of class LAS or LAScatalog.
algorithm	function. An algorithm of point decimation. lidR have: random, homogenize and highest.

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 overlayed 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 LAS or LAScatalog.
`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 grid_metrics voxel_metrics or tree_metrics 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 which itself is a wrapper around Vladimir Agafonking's implementation.

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")
las = readLAS(LASfile, select = "xyz0", filter = "-drop_z_below 0")

# 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)
spplot(convex_hulls, "ZTOP")

# The hulls + some user-defined metrics
```

```
convex_hulls = delineate_crowns(las, func = ~list(Zmean = mean(Z)))
spplot(convex_hulls, "Zmean")

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

## Not run:
concave_hulls = delineate_crowns(las, "concave")
sp::plot(concave_hulls)

## End(Not run)
```

---

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 lasrangecorrection lasflightline lasreoffset lasrescale lasscanlines lasssmooth 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)

lasrangecorrection(
  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"
)
```

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 VCI.

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

`las`	An object of class `LAS`
`n`	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()

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Examples

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

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

---

filter_duplicates *Filter duplicated points*

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 LAS
...	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 LAS or LAScatalog.
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`

Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las = readLAS(LASfile)
subset = filter_surfacepoints(las, 2)
plot(subset)
```

---

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")

# 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))
```

---

find_trees *Individual tree detection*

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: lmf and manual. More experimental algorithms may be found in the package lidRplugins.
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 file is processed independently of the others and potentially in parallel on different computers. Thus, the index always restarts at 1 on each file or

chunk. Worse, in a tree segmentation process, a tree that is located exactly between 2 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 exepected 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 to get ID attribution errors.

bitmerge This method uses the XY coordinates of the highest point (apex) of a tree to create a single number with a bitwise operation. First, XY coordinates are converted to integers using the scales and offsets of the point-cloud. Then the ID is computed with X * 2^32 + Y to combine twice the 32-bits of information into a 64-bit number. For example, if the apex is at (10.32, 25.64) with a scale factor of 0.01 and an offset of 0, the integer coordinates are X = 1032 and Y = 2564 and the ID is 4432406252036. Such methods return a 64-bit integer but because 64-bit integers do not exist in R it is converted to a 64-bit decimal number that 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 the very least we expect this to work for simple cases.

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 = "-drop_z_below 0")

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 LAS or LAScatalog.
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 p2r, dsmtin, pitfree (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 .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", "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)

# 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)
```

---

grid_density *Map the pulse or point density*

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 LAS or LAScatalog.
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)

d <- grid_density(las, 5)
plot(d)
d <- grid_density(las, 10)
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)
```

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.

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 .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.

See Also

Other metrics: `cloud_metrics()`, `hexbin_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 ===

# Canopy surface model with 4 m^2 cells
metrics = grid_metrics(las, ~max(Z), 2)
plot(metrics, col = col)

# 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)
```

`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 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
)
```

Arguments

`las`	An object of class LAS or LAScatalog.
`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 knnidw, tin, and kriging (see respective documentation and examples).

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 prevent against 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 check and remove degenerated ground points. If any a warning in thrown.

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 .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 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)
plot(las)

dtm1 = grid_terrain(las, algorithm = knnidw(k = 6L, p = 2))
dtm2 = grid_terrain(las, algorithm = tin())
dtm3 = grid_terrain(las, algorithm = kriging(k = 10L))

## Not run:
plot(dtm1)
plot(dtm2)
plot(dtm3)
plot_dtm3d(dtm1)
plot_dtm3d(dtm2)
plot_dtm3d(dtm3)

## End(Not run)
```

---

hexbin_metrics *Area-Based Approach in hexagonal cells.*

Description

Computes a series of descriptive statistics for a LiDAR dataset within hexagonal cells. This function is identical to grid_metrics but with hexagonal cells instead of square pixels. After all, we conduct circular plot inventories and we map models on pixel-based maps. `hexbin_metrics` provides the opportunity to test something else. Refer to grid_metrics for more information.

Usage

```
hexbin_metrics(las, func, res = 20)
```

Arguments

`las`	An object of class `LAS`.
`func`	formula. An expression to be applied to each hexagonal cell.
`res`	numeric. To be consistent with grid_metrics, the square of `res` give the area of the hexagonal cells, like in `grid_metrics`. The difference being the fact that for square pixels this is obvious. Here `res = 20` gives 400-square-meter hexagonal cells.

Value

A hexbin object from package `hexbin` or a `list` of `hexbin` objects if several metrics are returned.

See Also

Other metrics: cloud_metrics(), grid_metrics(), point_metrics(), tree_metrics(), voxel_metrics()

Examples

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

col = grDevices::colorRampPalette(c("blue", "cyan2", "yellow", "red"))

# Maximum elevation with a resolution of 8 m
hm = hexbin_metrics(lidar, ~max(Z), 8)
hexbin::plot(hm, colramp = col, main = "Max Z")

# Mean height with a resolution of 20 m
hm = hexbin_metrics(lidar, ~mean(Z), 20)
hexbin::plot(hm, colramp = col, main = "Mean Z")

# 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 = hexbin_metrics(lidar, ~myMetrics(Z, Intensity), 10)

hexbin::plot(metrics$zwimean, colramp = col, main = "zwimean")
hexbin::plot(metrics$zimean, colramp = col, main = "zimean")
hexbin::plot(metrics$zsqmean, colramp = col, main = "zsqmean")
```

---

highest *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 selecting the highest point within each cell.

Usage

```
highest(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()

Examples

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

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

---

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^2 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 retrieve_pulses first)

See Also

Other point cloud decimation algorithms: highest(), 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))
```

---

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

`las`	A `LAS` object.
`catalog`	A `LAScatalog` object.
`x`	Any R object.
`algorithm`	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.parallelised(g)

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

---

knnidw *Spatial Interpolation Algorithm*

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` *Spatial Interpolation Algorithm*

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

```
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)
```

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)
```

Arguments

data	a data.table containing the data of a las or laz file.
header	a list or a LASheader containing the header of a las or laz file.
proj4string	projection string of class CRS-class.
check	logical. Conformity tests while building the object.

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)
- Intensity (integer)
- ReturnNumber (integer)
- NumberOfReturns (integer)
- ScanDirectionFlag (integer)
- EdgeOfFlightline (integer)
- Classification (integer)
- Synthetic_flag (logical)
- Keypoint_flag (logical)
- Withheld_flag (logical)
- ScanAngle (integer)
- UserData (integer)
- PointSourceID (integer)

Value

An object of class LAS

Functions

- LAS: creates objects of class LAS. The original data is updated by reference to clamp the coordinates with respect to the scale factor of the header. If header is not provided 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

Extends

Class Spatial, directly.

See Also

readLAS

Examples

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

las <- LAS(data) # /!\ data is updated by reference

data
las
```

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 just 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 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).

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 `@clustering_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, and vice versa. 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 is no edge effect 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 the other chunks will be multiples of the chunk size. Not relevant if `chunk_size = 0`. See opt_chunk_alignment.

Output options

The slot `@output_options` contains a `list` of options that determine how clusters (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 templated filename 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/{ORIGINALFILNAME}_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*, 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 one 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 `select` option. 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 `filter` option. 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

Create a LASheader object

Usage

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

Arguments

data	a list containing the data from the header of a las file.

Value

An object of class LASheader

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

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
- it the coordinate reference sytem 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

las	An object of class LAS or LAScatalog.
print	logical. By default, prints a report into standard ouptut. If print = FALSE the functions returns a list with two elements named 'warnings' and 'errors' containing a vector with the reported warnings and errors.
...	Use deep = TRUE on a LAScatalog only. Instead of a shallow inspection it reads all the files and performs a deep inspection.

Value

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

Examples

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

las_rescale *Rescale and reoffset a LAS object*

Description

Modify the scale factor and the offset of a LAS object. This function modify the header and recompute the coordinates. Coordinates might be moved by few tenth of millimeters or few millimeters depending of the accuracy imposed by the user.

Usage

```
las_rescale(las, xscale, yscale, zscale)

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

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.

Examples

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

las <- las_rescale(las, xscale = 0.01, yscale = 0.01)
las <- las_reoffset(las, xoffset = 300000, yoffset = 5248000)
```

li2012 *Individual Tree Segmentation Algorithm*

Description

This functions 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

dt1	numeric. Threshold number 1. See reference page 79 in Li et al. (2012). Default is 1.5.
dt2	numeric. Threshold number 2. See reference page 79 in Li et al. (2012). Default is 2.
R	numeric. Search radius. See page 79 in Li et al. (2012). Default is 2. If R = 0 all the points are automatically considered as local maxima and the search step is skipped (much faster).
Zu	numeric. If point elevation is greater than Zu, dt2 is used, otherwise dt1 is used. See page 79 in Li et al. (2012). Default is 15.
hmin	numeric. Minimum height of a detected tree. Default is 2.
speed_up	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 defaut 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 writeOGR, 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 writeOGR. writeOGR can write into other file types, such as GeoPackage or GeoJSON and even as SQLlite database objects. But it cannot add data into an existing SQLlite database. Let's create our own driver for a SpatialPointsDataFrame. First we need a function able to write and append a SpatialPointsDataFrame into a SQLlite 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.

lidR-parallelism *Parallel computation in lidR*

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.parallel(lmf(2))   #> TRUE
is.parallel(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 defaut 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.

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 bad! 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. The question of nested parallel loops is irrelevant. The catalog processing engine has precedence rules that are guaranteed to avoid nested parallelism. This precedence rule aims to (1) always work (2) preserve behaviors of lidR version 2.0.y.

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 quadcore machine:

```
# 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)
```

`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 = "-drop_z_below 0")

# 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
# ============

# 5x5 m fixed window size
chm <- grid_canopy(las, res = 1, p2r(0.15))
kernel <- matrix(1,3,3)
chm <- raster::focal(chm, w = kernel, fun = median, na.rm = TRUE)

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 right mouse button. Within the selected region

the highest point will be flagged as 'tree top' in the scene. Once all the trees are labeled 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", ...)
```

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. Color of the spheres displayed on the point cloud (aesthetic purposes only).
...	supplementary parameters to be passed to plot.

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)
```

---

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 SpatialPolygons* or sf or RasterLayer or a RasterStack or RasterBrick 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)
lakes <- shapefile(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(las)
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 LAS or LAScatalog.
algorithm	a spatial interpolation function. lidR have tin, kriging, knnidw or a RasterLayer representing a digital terrain model (can be computed with grid_terrain)

na.rm	logical. When using a RasterLayer 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 RasterLayer, ... is propagated to extract. 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 discared at write time. If TRUE it is maintained as an extrabytes attribute. See also add_lasattribute.
Wdegenerated	logical. The function always check and remove degenerated ground points. If any a warning in thrown.
e1	a LAS object
e2	RasterLayer representing a digital terrain model (can be computed with grid_terrain) or a spatial interpolation function. lidR has tin, kriging, and knnidw.

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)

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 <- unnormalize_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 LAS or LAScatalog.
`algorithm`	an intensity normalizaton algorithm. `lidR` currently has range_correction.

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))
```

---

p2r *Digital Surface Model Algorithm*

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

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).
na.fill	function. A function that implements an algorithm to compute spatial interpolation to fill the empty pixel often left by points-to-raster methods. lidR has knnidw, tin, and kriging (see also grid_terrain 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)
```

---

pitfree *Digital Surface Model Algorithm*

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 dsmtin), 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")
las <- readLAS(LASfile)
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 = c("rgl", "pcv"),
  clear_artifacts = TRUE,
  nbits = 16,
  axis = FALSE,
  legend = FALSE,
  add = 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 points3d (LAS) or plot if mapview = FALSE or to mapview 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 heat.colors, topo.colors, terrain.colors 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 "pcv". If "rgl" is chosen the display relies on the rgl package. If "pcv" is chosen it relies on the PointCloudViewer package, which is much more efficient and can handle million of points using less memory. PointCloudViewer is not available on CRAN yet and should be installed from github (see. https://github.com/Jean-Romain/PointCloudViewer).
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 colors 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 color legend.
add	If FALSE normal behavior otherwise must be the output of a prior plot function to enable the alignment of a second point cloud.
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

```
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 catalog using data provided in lidR
ctg = readLAScatalog(LASfile)
plot(ctg)
```

`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,
  color = "Z",
  colorPalette = height.colors(50),
  bg = "black",
  trim = Inf,
  ...
)
```

Arguments

`x`	An object of the class `'lasmetrics3d'`
`y`	Unused (inherited from R base)
`color`	characters. The field used to color the points. Default is Z coordinates. Or a vector of colors.
`colorPalette`	characters. A color palette name. Default is `height.colors` provided by the package lidR
`bg`	The color for the background. Default is black.
`trim`	numeric. Enables trimming of values when outliers break the color palette range. Default is 1 meaning that the whole range of the values is used for the color palette. 0.9 means that 10 In this case the values higher than the 90th percentile are set to the highest color. They are not removed.
`...`	Supplementary parameters for points3d if the display method is "points".

Examples

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

voxels = voxel_metrics(lidar, list(Imean = mean(Intensity)))
plot(voxels, color = "Imean", colorPalette = heat.colors(50), trim=0.99)
```

`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

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

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)

## Not run:
library(magrittr)
plot(las) %>% add_dtm3d(dtm) %>% add_treetops3d(ttops)

## 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")

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 cell (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, compute the 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 `filter = NULL` coordinates are references to the original coordinates and do not occupy additional memory. If `filter != NULL` it obviously takes memory.
`filter`	formula of logical predicates. Enables the function to run only on points of interest in an optimized way. See also examples.
`...`	unused.

Details

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 km² tile with 1 point/m² with a resolution of 20 m (400 m² 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: is 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 might be meaningless. For example, computing the quantile of elevation does not really makes sense here.

See Also

Other metrics: `cloud_metrics()`, `grid_metrics()`, `hexbin_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 second

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 *Get or set the projection of a LAS* object*

Description

Get or set the projection of a LAS* object with the function projection. Functions epsg and wkt are reserved for advanced users (see details).

Usage

```
epsg(object, ...)

epsg(object) <- value

wkt(object) <- value

## S4 method for signature 'LASheader'
projection(x, asText = TRUE)

## S4 method for signature 'LASheader'
crs(x, asText = FALSE)

## S4 method for signature 'LASheader'
epsg(object, ...)

## S4 replacement method for signature 'LASheader'
epsg(object) <- value

## S4 method for signature 'LASheader'
wkt(obj)

## S4 replacement method for signature 'LASheader'
wkt(object) <- value

## S4 method for signature 'LAS'
projection(x, asText = TRUE)

## S4 replacement method for signature 'LAS'
projection(x) <- value

## S4 method for signature 'LAS'
crs(x, asText = FALSE)

## S4 replacement method for signature 'LAS'
crs(x, ...) <- value

## S4 method for signature 'LAS'
epsg(object)

## S4 replacement method for signature 'LAS'
epsg(object) <- value

## S4 method for signature 'LAS'
wkt(obj)

## S4 replacement method for signature 'LAS'
wkt(object) <- value
```

```
## S4 method for signature 'LAScatalog'
projection(x, asText = TRUE)

## S4 method for signature 'LAScatalog'
crs(x, asText = FALSE)
```

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 for functionprojection. An EPSG code as integer for function epsg. A WKT string for function wkt.
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 1.4)
- Store a WTK string (for LAS 1.4)

On the other hand, all spatial R packages use a proj4string to store the CRS. 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<-: updates the CRS from a proj4string. It updates the header 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. This function should always be preferred.
- epsg<-: updates the CRS from an EPSG code. It adds the EPSG code in the header and updates the proj4string slot.
- wkt<-: updates the CRS from a WKT string. It adds the WKT string in the header and updates the proj4string slot.
- projection: reads the proj4string from the proj4string slot.
- epsg: reads the epsg code from the header.
- wkt: reads the WKT string from the header.
- crs and crs<- are equivalent to projection

Examples

```
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile)
crs <- sp::CRS("+init=epsg:26918")

projection(las)
projection(las) <- crs
```

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

density	numeric. The desired output density.
use_pulse	logical. Decimate by removing random pulses instead of random points (requires running retrieve_pulses first)

See Also

Other point cloud decimation algorithms: highest(), homogenize()

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))
```

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):

$$I_{norm} = I_{obs}(\frac{R}{Rs})^f)$$

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 track_sensor.
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. get_range() is a regular function documented here for convenience.

References

Gatziolis, D. (2013). 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.LAS *Merge LAS objects*

Description

Merge LAS objects

Usage

```
## S3 method for class 'LAS'
rbind(...)
```

Arguments

...	LAS 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. The LAS formats 1.1 to 1.4 are supported. Point Data Record Format 0,1,2,3,5,6,7,8 are supported.

Usage

```
readLAS(files, select = "*", filter = "")
```

Arguments

files	characters. Path(s) to one or several a file(s). Can also be a LAScatalog 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).

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+). 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

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")
```

`readLAScatalog` *Create an object of class LAScatalog*

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 appropriated functions. Careful reading of the LAScatalog class documentation is required to use the `LAScatalog` class correctly.

`catalog()` is softly deprecated for `readLAScatalog()`.

Usage

```
readLAScatalog(
  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 (clusters)
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 *Read a .las or .laz file header*

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)
```

readMSLAS *Read multispectral .las or .laz files*

Description

Multispectral laser data are often stored in 3 differents files. If this is the case this function 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 multisprectral point cloud is already stored in a single file, use readLAS. This function is somewhat experimental and its names could change.

Usage

```
readMSLAS(files1, files2, files3, select = "*", filter = "")
```

Arguments

files1, files2, files3	characters. Path(s) to one or several a file(s). Each argument being one channel.
select, filter	character. See readLAS.

Value

A LAS object

---

retrieve_pulses *Retrieve individual pulses, flightlines or scanlines*

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

interval	numeric. Interval used to bin the gps times and group the pulses to compute a position at a given timepoint t.
pmin	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 pmin.

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

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 (lasmetric or 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 *Estimation of the shape of the points neighborhood*

Description

Computes the eigenvalues of the covariance matrix of the neighbouring points using several possible algorithms. The points that meet a given criterion based on the eigenvalue are labeled as approximately coplanar/colinear or any other shape supported.

Usage

```
segment_shapes(las, algorithm, attribute = "Shape", filter = NULL)
```

Arguments

las	an object of class LAS
algorithm	An algorithm for shape detection. lidR has: shp_plane, shp_hplane and shp_line.
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 also examples.

Value

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).

Examples

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

las <- segment_shapes(las, shp_plane(k = 15), "Coplanar")
plot(las, color = "Coplanar")

# 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 *Snag classification*

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 LAS or LAScatalog.
`algorithm`	function. An algorithm for snag segmentation. `lidR` has wing2015.
`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 LAS or LAScatalog.
`algorithm`	function. An algorithm of individual tree segmentation. `lidR` has: dalponte2016, watershed, li2012 and silva2016. More experimental algorithms may be found in the package lidRplugins.
`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 file is processed independently of the others and

potentially in parallel on different computers. Thus, the index always restarts at 1 on each file or chunk. Worse, in a tree segmentation process, a tree that is located exactly between 2 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 exepected 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 to get ID attribution errors.

bitmerge This method uses the XY coordinates of the highest point (apex) of a tree to create a single number with a bitwise operation. First, XY coordinates are converted to integers using the scales and offsets of the point-cloud. Then the ID is computed with X * 2^32 + Y to combine twice the 32-bits of information into a 64-bit number. For example, if the apex is at (10.32, 25.64) with a scale factor of 0.01 and an offset of 0, the integer coordinates are X = 1032 and Y = 2564 and the ID is 4432406252036. Such methods return a 64-bit integer but because 64-bit integers do not exist in R it is converted to a 64-bit decimal number that 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 the very least we expect this to work for simple cases.

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 *Set or get number of threads that lidR should use*

Description

Set and get number of threads to be used in lidR functions that are parallelized with OpenMP. Default value 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`	An integer >= 0. Default 0 means use all CPU available and leave the operating system to multi task.

See Also

lidR-parallelism

shape_detection *Algorithms for shape detection of the local point neighborhood*

Description

These functions are made to be used in lasdetectshape. 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, $a1, a2, a3$ denote the eigenvalues of the covariance matrix of the neighbouring points in ascending order. $th1, th2, th3$ 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:

$$a2 > (th1 * a1) and (th2 * a2) > a3$$

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.

$$a2 > (th1 * a1) and (th2 * a2) > a3 and |Z| > th3$$

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:

$$th1 * a2 < a3 and th1 * a1 < a3$$

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

`silva2016` *Individual Tree Segmentation Algorithm*

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 tesselation (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 grid_canopy or read from an external file.
`treetops`	`SpatialPointsDataFrame`. Can be computed with find_trees 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")
las <- readLAS(LASfile, select = "xyz", filter = "-drop_z_below 0")
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)
```

---

stdmetrics *Predefined standard metrics functions*

Description

Predefined functions computable at pixel level (grid_metrics), hexagonal cell level (hexbin_metrics), point cloud level (cloud_metrics), tree level (tree_metrics) voxel level (voxel_metrics) and point level (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, a set of standard metrics has been predefined (see details).

Usage

```
stdmetrics(x, y, z, i, rn, class, dz = 1, th = 2)

stdmetrics_z(z, dz = 1, th = 2)

stdmetrics_i(i, z = NULL, class = NULL, rn = NULL)

stdmetrics_rn(rn, class = NULL)

stdmetrics_pulse(pulseID, rn)

stdmetrics_ctrl(x, y, z)
```

`stdtreemetrics(x, y, z)`

`stdshapemetrics(x, y, z)`

`.stdmetrics`

`.stdmetrics_z`

`.stdmetrics_i`

`.stdmetrics_rn`

`.stdmetrics_pulse`

`.stdmetrics_ctrl`

`.stdtreemetrics`

`.stdshapemetrics`

Arguments

`x, y, z, i`	Coordinates of the points, Intensity
`rn, class`	ReturnNumber, Classification
`dz`	numeric. Layer thickness metric entropy
`th`	numeric. Threshold for metrics pzabovex. Can be a vector to compute with several thresholds.
`pulseID`	The number referencing each pulse

Format

An object of class `formula` of length 2.

An object of class `formula` of length 2.

An object of class `formula` of length 2.

An object of class `formula` of length 2.

An object of class `formula` of length 2.

An object of class `formula` of length 2.

An object of class `formula` of length 2.

An object of class `formula` of length 2.

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 behavior (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

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 = "*")

# All the predefined metrics
m1 = grid_metrics(las, ~stdmetrics(X,Y,Z,Intensity,ReturnNumber,Classification,dz=1))

# Convenient shortcut
m2 = grid_metrics(las, .stdmetrics)
```

```
# Basic metrics from intensities
m3 = grid_metrics(las, ~stdmetrics_i(Intensity))

# All the metrics from intensities
m4 = grid_metrics(las, ~stdmetrics_i(Intensity, Z, Classification, ReturnNumber))

# Convenient shortcut for the previous example
m5 = grid_metrics(las, .stdmetrics_i)

# Compute the metrics only on first return
first = filter_first(las)
m6 = grid_metrics(first, .stdmetrics_z)

# Compute the metrics with a threshold at 2 meters
over2 = filter_poi(las, Z > 2)
m7 = grid_metrics(over2, .stdmetrics_z)

# Works also with cloud_metrics and hexbin_metrics
m8 = cloud_metrics(las, .stdmetrics)
m9 = hexbin_metrics(las, .stdmetrics)

# 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))

# Users can write their own convenient shorcuts like this:
.myMetrics = ~myMetrics(Z, Intensity, ReturnNumber)

m11 = grid_metrics(las, .myMetrics)
```

tin *Spatial Interpolation Algorithm*

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(1, 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 knnidw.

See Also

Other spatial interpolation algorithms: knnidw(), kriging()

Examples

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

# 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 LAS or LAScatalog.
`algorithm`	function. An algorithm to compute sensor tracking. `lidR` implements Roussel2020 and Gatziolis2019 (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)
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)

# Load only the data actually useful
las <- readLAS(LASfile,
               select = "xyzrntp",
               filter = "-drop_single -thin_pulses_with_time 0.001")
flightlines <- track_sensor(las,  Roussel2020(pmin = 15))

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 *Compute metrics for each tree*

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 LAS or LAScatalog.
func	formula. An expression to be applied to each tree. It works like in grid_metrics voxel_metrics or delineate_crowns 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 SpatialPoinsDataFrame. 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 SpatialPoinsDataFrame 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(), hexbin_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 *Voxelize a point cloud*

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 LAS or LAScatalog.
`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)
```

Arguments

las	An object of class LAS.
func	formula. An expression to be applied to each voxel (see also grid_metrics).
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

It returns a `data.table` containing the metrics for each voxel. The table has the class `lasmetrics3d` enabling easier plotting.

See Also

Other metrics: `cloud_metrics()`, `grid_metrics()`, `hexbin_metrics()`, `point_metrics()`, `tree_metrics()`

Examples

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

# Cloud of points is voxelized with a 3-meter resolution and in each voxel
# the number of points is computed.
voxel_metrics(las, ~length(Z), 3)

# Cloud of points is voxelized with a 3-meter resolution and in each voxel
# the mean scan angle of points is computed.
voxel_metrics(las, ~mean(Intensity), 3)

## Not run:
# Define your own metric function
myMetrics = function(i)
{
  ret = list(
     npoints = length(i),
     imean   = mean(i)
   )

   return(ret)
}

voxels = voxel_metrics(las, ~myMetrics(Intensity), 3)

plot(voxels, color = "imean", trim = 100)
#etc.

## End(Not run)
```

`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 `EBImage`. You need to install this package to run this method (see its github page). Internally, the function EBImage::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 grid_canopy 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 find_trees 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

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

`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 >= 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")
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
```

---

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 '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

x	A LAS* object
name	A literal character string or a name (possibly backtick quoted).
value	typically an array-like R object of a similar class as x.
i	string, name of elements to extract or replace.
j	Unused.
...	Unused
drop	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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