Package ‘lidR’

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Type Package

Title Airborne LiDAR Data Manipulation and Visualization for Forestry Applications

Version 4.0.1

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/r-lidar/lidR

BugReports https://github.com/r-lidar/lidR/issues

License GPL-3

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Author Jean-Romain Roussel [aut, cre, cph], David Auty [aut, ctb] (Reviews the documentation), Florian De Boissieu [ctb] (Fixed bugs and improved catalog features), Andrew Sánchez Meador [ctb] (Implemented wing2015() for segment_snags()), Bourdon Jean-François [ctb] (Contributed to Roussel2020() for
track_sensor()
Gatziolis Demetrios [ctb] (Implemented Gatziolis2019() for track_sensor()),
Leon Steinmeier [ctb] (Contributed to parallelization management),
Stanislaw Adaszewski [cph] (Author of the C++ concaveman code)

Maintainer  Jean-Romain Roussel <jean-romain.roussel.1@ulaval.ca>
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Description

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

Details

To learn more about lidR, start with the vignettes: browseVignettes(package = "lidR"). Users can also find unofficial supplementary documentation in the lidR book. To ask "how to" questions please ask on gis.stackexchange.com 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.raster.default** The functions that return a raster are raster agnostic meaning that they work either with rasters from packages 'raster', 'stars' or 'terra'. By default they return rasters from 'stars'. Can be one of "raster", "stars" or "terra". Default: "terra"
- **lidR.check.nested.parallelism** The catalog processing engine (catalog_apply) checks the parallel strategy chosen by the user and verify if C++ parallelization with OpenMP should be disabled to avoid nested parallel loops. Default: TRUE. If FALSE the catalog processing engine will not check for nested parallelism and will respect the settings of set_lidr_threads.

Author(s)

- **Maintainer**: Jean-Romain Roussel <jean-romain.roussel.1@ulaval.ca> [copyright holder]
- **Authors**:
  - 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]
  - Leon Steinmeier (Contributed to parallelization management) [contributor]
  - Stanislaw Adaszewski (Author of the C++ concaveman code) [copyright holder]
See Also

Useful links:

- https://github.com/r-lidar/lidR
- Report bugs at https://github.com/r-lidar/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**

```r
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**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>las</td>
<td>An object of class <strong>LAS</strong></td>
</tr>
<tr>
<td>x</td>
<td>a vector that needs to be added in the LAS object. For <strong>add_lasattribute</strong> it can be missing (see details).</td>
</tr>
<tr>
<td>name</td>
<td>character. The name of the extra bytes attribute to add in the file.</td>
</tr>
<tr>
<td>desc</td>
<td>character. A short description of the extra bytes attribute to add in the file (32 characters).</td>
</tr>
<tr>
<td>type</td>
<td>character. The data type of the extra bytes attribute. Can be &quot;uchar&quot;, &quot;char&quot;, &quot;ushort&quot;, &quot;short&quot;, &quot;uint&quot;, &quot;int&quot;, &quot;uint64&quot;, &quot;int64&quot;, &quot;float&quot;, &quot;double&quot;.</td>
</tr>
</tbody>
</table>
add_attribute

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(header(las))

x <- 1:30

las <- add_attribute(las, x, "mydata")
print(las) # The las object has a new attribute called "mydata"
print(header(las)) # 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"
aggregate

print(header(las)) # 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_attribute(las, x, "newattr")
las <- add_lasattribute(las, name = "newattr", desc = "Amplitude")
print(header(las))

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

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

---

aggregate

Metric derivation at different levels of regularization

Description

`template_metrics()` computes a series of user-defined descriptive statistics for a LiDAR dataset
within each element of a template. Depending on the template it can be for each pixel of a raster
(area-based approach), or each polygon, or each segmented tree, or on the whole point cloud. Other
functions are convenient and simplified wrappers around `template_metrics()` and are expected
to be the actual functions used. See Details and Examples.

Usage

cloud_metrics(las, func, ...)
crown_metrics(
    las,
    func,
    geom = "point",
    concaveman = c(3, 0),
    attribute = "treeID",
    ...
)

hexagon_metrics(las, func, area = 400, ...)

pixel_metrics(las, func, res = 20, start = c(0, 0), ...)

plot_metrics(las, func, geometry, ..., radius)

polygon_metrics(las, func, geometry, ...)
aggregate

```r
template_metrics(las, func, template, filter = NULL, by_echo = "all", ...)

voxel_metrics(las, func, res = 1, ..., all_voxels = FALSE)
```

**Arguments**

- `las` An object of class `LAS` or `LAScatalog`.
- `func` formula or expression. An expression to be applied to each element of the template (see section "Parameter func").
- `...` propagated to `template_metrics` i.e. `filter` and `by_echo`. `pixel_metrics()` also supports `pkg = "terra|raster|stars"` to get an output in `SpatRaster`, `Raster*` or `stars` format. Default is `getOption("lidR.raster.default")`.
- `geom` character. Geometry type of the output. Can be 'point', 'convex', 'concave' or 'bbox'.
- `concaveman` numeric. Only if `type = "concave"`. Vector with the two parameters of the function `concaveman`.
- `attribute` character. The column name of the attribute containing tree IDs. Default is "treeID".
- `area` numeric. Area of the hexagons.
- `res` numeric. The resolution of the output. Can optionally be a `RasterLayer` or a `stars` or a `SpatRaster`. In that case the raster is used as the template.
- `start` vector of x and y coordinates for the reference raster. Default is (0,0) meaning that the grid aligns on (0,0). Not consiered if `res` is a raster
- `geometry` A spatial vector object. `sp` and `sf` objects are supported. `plot_metrics()` supports point and polygons but `polygon_metrics()` supports only polygons.
- `radius` numeric. If the geometry is spatial points a radius must be defined. Support one radius or a vector of radii for variable plot sizes.
- `template` can be of many types and corresponds to the different levels of regularization. `RasterLayer/SpatRaster, sf/sfc` (polygons), `numeric, bbox, NULL`. The metrics are computed for each element of the template. See examples.
- `filter` formula of logical predicates. Enables the function to run only on points of interest in an optimized way. See examples.
- `by_echo` characters. The metrics are computed multiple times for different echo types. Can be one or more of "all", "first", "intermediate", "lastofmany", "single", and "multiple". See examples. Default is "all" meaning that it computes metrics with all points provided.
- `all_voxels` boolean. By default the function returns only voxels that contain 1 or more points. Empty voxels do not exist as the metrics are undefined. If `all_voxels = TRUE` all the voxels are returned and metrics are NA for voxels with 0 points.

**Details**

- `pixel_metrics` Area-based approach. Computes metrics in a square tessellation. The output is a raster.
hexagon_metrics  Computes metrics in an hexagon tessellation. The output is a sf/sfc_POLYGON
plot_metrics  Computes metrics for each plot of a ground inventory by 1. clipping the plot inventories with clip_roi, 2. computing the user’s metrics for each plot with cloud_metrics, and 3. combining spatial data and metrics into one data.frame ready for statistical modelling with cbind. The output is of the class of the input.
cloud_metrics  Computes a series of user-defined descriptive statistics for an entire point cloud. The output is a list
crown_metrics  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. The output can be spatial points or spatial polygons (sf/sfc_POINT or sf/sfc_POLYGON)
voxel_metrics  Is a 3D version of pixel_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. The output is a data.frame
point_metrics  Is a bit more complex and is documented in point_metrics

Value
Depends on the function, the template and the number of metrics. Can be a RasterLayer, a RasterBrick, a stars, a SpatRaster a sf/sfc, a list, a SpatialPolygonDataFrame, or a data.table. Functions are supposed to return an object that is best suited for storing the level of regularization needed.

Parameter func

The function to be applied to each cell is a classical function (see examples) that returns a labelled 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:

pixel_metrics(las, f(Z), res = 20)
voxel_metrics(las, f(Intensity), res = 2)

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. template_metrics will dispatch the point cloud in the user’s function.

Examples

LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile, filter = "-keep_random_fraction 0.5")
col <- sf::sf.colors(15)
fun1 <- ~list(maxz = max(Z))
fun2 <- ~list(q85 = quantile(Z, probs = 0.85))

# ===============
# TEMPLATE METRICS
# ================

# a raster as template
template <- raster::raster(extent(las), nrow = 15, ncol = 15)
raster::crs(template) <- crs(las)
m <- template_metrics(las, fun1, template)
plot(m, col = col)

# a sfc_POLYGON as template
sfc <- sf::st_as_sfc(st_bbox(las))
template <- sf::st_make_grid(sfc, cellsize = 20, square = FALSE)
m <- template_metrics(las, fun1, template)
plot(m)

# a bbox as template
template <- st_bbox(las) + c(50,30,-50,-70)
plot(sf::st_as_sfc(st_bbox(las)), col = "gray")
plot(sf::st_as_sfc(template), col = "darkgreen", add = TRUE)
m <- template_metrics(las, fun2, template)
print(m)

# ================
# CUSTOM METRICS
# ================

# Define a function that computes custom metrics
# in an R&D perspective.
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)
}

# example with a stars template
template <- stars::st_as_stars(st_bbox(las), dx = 10, dy = 10)
m <- template_metrics(las, myMetrics(Z, Intensity), template)
plot(m, col = col)

# ================
# CLOUD METRICS
# ================

cloud_metrics(las, .stdmetrics_z)

# ================
# PIXEL METRICS
# ================

m <- pixel_metrics(las, fun1, 20)
aggregate

```
plot(m, col = col)

m = pixel_metrics(las, myMetrics(Z, Intensity))
plot(m, col = col)

# ================
# PLOT METRICS
# ================

shpfile <- system.file("extdata", "efi_plot.shp", package="lidR")
inventory <- sf::st_read(shpfile, quiet = TRUE)
inventory # contains an ID and a Value Of Interest (VOI) per plot

m <- plot_metrics(las, fun2, inventory, radius = 11.28)
plot(header(las))
plot(m["q85"], pch = 19, cex = 3, add = TRUE)

# Works with polygons as well
inventory <- sf::st_buffer(inventory, 11.28)
plot(header(las))
plot(sf::st_geometry(inventory), add = TRUE)

m <- plot_metrics(las, .stdmetrics_z, inventory)
plot(m["zq85"], pch = 19, cex = 3, add = TRUE)

# ================
# VOXEL METRICS
# ================

m <- voxel_metrics(las, length(Z), 8)
m <- voxel_metrics(las, mean(Intensity), 8)
# plot(m, color = "V1", colorPalette = heat.colors(50), trim = 60)
# plot(m, color = "V1", colorPalette = heat.colors(50), trim = 60, voxel = TRUE)

# ================
# CROWN METRICS
# ================

# Already tree-segmented point cloud
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
trees <- readLAS(LASfile, filter = "-drop_z_below 0")

metrics <- crown_metrics(trees, .stdtreemetrics)
plot(metrics["Z"], pch = 19)

metrics <- crown_metrics(trees, .stdtreemetrics, geom = "convex")
plot(metrics["Z"])

metrics <- crown_metrics(trees, .stdtreemetrics, geom = "bbox")
plot(metrics["Z"])
```
metrics <- crown_metrics(trees, .stdtreemetrics, geom = "concave")
plot(metrics["Z"])

# ================
# ARGUMENT FILTER
# ================

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

# Compute using only some points: optimized
# faster and uses less memory. No intermediate object
metrics = pixel_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 = pixel_metrics(las, mean(Z), 20)

# ================
# ARGUMENT BY_ECHO
# ================

func = ~list(avgI = mean(Intensity))
echo = c("all", "first","multiple")

# func defines one metric but 3 are computed respectively for: (1) all echo types,
# (2) for first returns only and (3) for multiple returns only
metrics <- pixel_metrics(las, func, 20, by_echo = echo)
plot(metrics, col = heat.colors(25))
cloud_metrics(las, func, by_echo = echo)

---

as

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**

<table>
<thead>
<tr>
<th>x</th>
<th>A LASHeader object</th>
</tr>
</thead>
<tbody>
<tr>
<td>...</td>
<td>unused</td>
</tr>
</tbody>
</table>

**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
- LASBRIDGE
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.

Examples

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

print(LASGROUND)

catalog_apply  LAStag processing engine

Description

This function gives users access to the LAStag processing engine. It allows the application of a user-defined routine over a collection of LAS/LAZ files. The LAStag processing engine is explained in the LAStag class

catalog_apply() is the core of the lidR package. It drives every single function that can process a LAStag. It is flexible and powerful but also complex. catalog_map() is a simplified
version of `catalog_apply()` that suits for 90% of use cases.

`catalog_sapply()` is a previous attempt to provide simplified version of `catalog_apply()`. Use `catalog_map()` instead.

**Usage**

\[
\text{catalog\_apply}(ctg, \text{FUN}, \ldots, \text{.options} = \text{NULL}) \\
\text{catalog\_sapply}(ctg, \text{FUN}, \ldots, \text{.options} = \text{NULL}) \\
\text{catalog\_map}(ctg, \text{FUN}, \ldots, \text{.options} = \text{NULL})
\]

**Arguments**

- **ctg**: A LAStool catalog 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 neighbouring 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 LAStool catalog processing engine provides internal tools to load buffered data 'on-the-fly'. `catalog_map()` takes care of removing automatically the results computed in the buffered area to avoid unexpected output with duplicated entries or conflict between values computed twice. It does that in predefined way that may not suit all cases. `catalog_apply()` does not remove the buffer and leave users free to handle this in a custom way. This is why `catalog_apply()` is more complex but gives more freedom to build new applications.

**Buffered data**

The LAS objects loaded in these functions 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** of `catalog_apply` expects a function with a first argument that will be supplied automatically by the LAStool catalog processing engine. This first argument is a `LAStoolCluster`. A `LAStoolCluster` is an internal undocumented class but the user needs to know only three things about this class:

- It represents a chunk of the file collection
• The function `readLAS` can be used with a `LAScluster`
• The function `extent` or `bbox` or `st_bbox` can be used with a `LAScluster` and they return the bounding box of the chunk without the buffer. It must be used to clip the output and remove the buffered region (see examples).

A user-defined function must be templated like this:

```r
myfun <- function(chunk, ...) {
  # Load the chunk + buffer
  las <- readLAS(chunk)
  if (is.empty(las)) return(NULL)

  # do something
  output <- do_something(las, ...)

  # remove the buffer of the output
  bbox <- bbox(chunk)
  output <- remove_buffer(output, bbox)
  return(output)
}
```

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 chunk was empty.

catalog_map is much simpler (but less versatile). It automatically takes care of reading the chunk and checks if the point cloud is empty. It also automatically crop the buffer. The way it crops the buffer suits for most cases but for some special cases it may be advised to handle this in a more specific way i.e. using `catalog_apply()`. For `catalog_map()` the first argument is a LAS and the template is:

```r
myfun <- function(las, ...) {
  # do something
  output <- do_something(las, ...)
  return(output)
}
```

$options$

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 behaviour of the processing engine.

• `drop_null = FALSE`: not intended to be used by regular users. The engine does not remove NULL outputs
• `need_buffer = TRUE`: the function complains if the buffer is 0.
• `need_output_file = TRUE` the function complains if no output file template is provided.
• `raster_alignment = ...` the function checks the alignment of the chunks. This option is important if the output is a raster. See below for more details.

• `automerge = TRUE` by default the engine returns a list with one item per chunk. If `automerge = TRUE`, it tries to merge the outputs into a single object: a `Raster`, a `Spatial`, a `LAS`, an `sf`, a `stars` similarly to other functions of the package. This is a fail-safe option so in the worst case, if the merging fails, the list is returned. This is activated by `catalog_map` making it simpler.

• `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 `bbox` from `sf`. This is activated by `catalog_map` making it simpler.

• `autocrop = TRUE`. Introduced in v4.0.0 this option enables to get rid of the buffer crop steps of the function i.e `something <- remove_buffer(something, bbox)`. In this case the function must take one `LAS` object as input. This is activated by `catalog_map` making it simpler.

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:

```r
# 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))
```

Examples

```r
# More examples might be available in the official lidR vignettes or
```

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

# 1. Build the user-defined function that analyzes each chunk of the catalog.
# The function's first argument is a LAScluster object. The other arguments can be freely
# chosen by the users.
my_tree_detection_method <- function(chunk, ws)
{
  # The chunk argument is a LAScluster object. The users do 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(chunk)
  if (is.empty(las)) return(NULL)

  # Further processing...
}
```
catalog_apply

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

ttops is an sf object that contains the tree tops in our region of interest
# plus the tree tops in the buffered area. We need to remove the buffer otherwise we will get
# some trees more than once.
bbox <- st_bbox(chunk)
ttops <- sf::st_crop(ttops, bbox)
return(ttops)

# 2. Build a collection of file
# (here, a single file LAScatalog for the purposes of this simple example).
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
ctg <- readLAScatalog(LASfile)
plot(ctg)

# 3. Set some processing options.
# For this small single file example, the chunk size is 100 m + 10 m of buffer
opt_chunk_buffer(ctg) <- 10 # Small because this is a dummy example.
opt_chunk_size(ctg) <- 100
opt_chunk_alignment(ctg) <- c(-50, -35) # Align such as it creates 2 chunks only.
opt_select(ctg) <- "xyz" # Read only the coordinates.
opt_filter(ctg) <- "-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(ctg, my_tree_detection_method, ws = 5, .options = opt)
plot(output)

## =========================================================================
## Example 1: simplified. There is nothing that requires special data
##=========================================================================
# 1. Build the user-defined function that analyzes a point cloud.
my_tree_detection_method <- function(las, ws)
{
    # Find the tree tops using a user-developed method
    # (here simply a LMF for the example).
    ttops <- locate_trees(las, lmf(ws))
    return(ttops)
}

# 2. Build a project
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
ctg <- readLAScatalog(LASfile)
plot(ctg)
catalog_boundaries

# 3. Set some processing options.
# For this dummy example, the chunk size is 100 m and the buffer is 10 m
opt_chunk_buffer(ctg) <- 10
opt_chunk_size(ctg) <- 100 # small because this is a dummy example.
opt_chunk_alignment(ctg) <- c(-50, -35) # Align such as it creates 2 chunks only.
opt_select(ctg) <- "xyz" # Read only the coordinates.
opt_filter(ctg) <- "-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
output <- catalog_map(ctg, my_tree_detection_method, ws = 5, .options = opt)

### Example 2: compute a rumple index on surface points
### ==============================================================
rumple_index_surface <- function(las, res)
{
  las <- filter_surfacepoints(las, 1)
  rumple <- pixel_metrics(las, ~rumple_index(X,Y,Z), res)
  return(rumple)
}

LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
ctg <- readLAScatalog(LASfile)
opt_chunk_buffer(ctg) <- 1
opt_chunk_size(ctg) <- 140 # small because this is a dummy example.
opt_select(ctg) <- "xyz" # read only the coordinates.
opt <- list(raster_alignment = 20) # catalog_apply will adjust the chunks if required
output <- catalog_map(ctg, rumple_index_surface, res = 20, .options = opt)
plot(output, col = height.colors(25))

---

catalog_boundaries

*Computes the polygon that encloses the points*

**Description**

Computes the polygon that encloses the points. It reads all the files one by one and computes a concave hull using the `st_concave_hull` function. When all the hulls are computed it updates the LASCatalog to set the true polygons instead of the bounding boxes.

**Usage**

```
catalog_boundaries(ctg, ...)
```
Arguments

c tg  A LAScatalog
... propagated to \texttt{st_concave_hull}

Value

A LAScatalog with true boundaries

Non-supported LAScatalog options

The options `select`, `output files`, `chunk size`, `chunk buffer`, `chunk alignment` are not supported and not respected in `\texttt{catalog_boundaries}` because the function must always process by file, without buffer and knows which attributes to load.

Examples

\begin{verbatim}
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
c tg <- readLAScatalog(LASfile, filter = "-drop_z_below 0.5")
c tg2 <- catalog_boundaries(ctg, concavity = 1, length_threshold = 15)
plot(ctg)
plot(ctg2, add = TRUE)
\end{verbatim}

\begin{verbatim}
catalog_intersect  Subset a LAScatalog
\end{verbatim}

Description

Subset a LAScatalog interactively using the mouse. Subset a LAScatalog with a spatial object to keep only the tiles of interest. It can be used to select tiles of interest that encompass spatial objects.

Usage

\begin{verbatim}
catalog_intersect(
ctg,
y,
...,
subset = c("subset", "flag_unprocessed", "flag_processed")
)
catalog_select(
ctg,
mapview = TRUE,
subset = c("subset", "flag_unprocessed", "flag_processed")
)
\end{verbatim}
Arguments

- `ctg`: A LAScatalog
- `subset`: character. By default it subsets the collection. It is also possible to flag the files to maintain the collection as a whole but process only a subset of its content. `flag_unprocessed` flags the files that will not be processed. `flag_processed` flags the files that will be processed.
- `mapview`: logical. If `FALSE`, use R base plot instead of mapview (no pan, no zoom, see also `plot`)

Value

A LAScatalog object

Examples

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

catalog_retile Retile a LAScatalog

Description

Splits or merges files to reshape the original files collection (.las or .laz) into smaller or larger files. It also enables the addition or removal of a buffer around the tiles. Internally, the function reads and writes the chunks defined by the internal processing options of a LAScatalog. 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). **This function is does not load the point cloud into R memory** It streams from input file(s) to output file(s) and can be applied to large point-cloud with low memory computer.

Note that this function is not actually very useful because 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

Non-supported LASCatalog options

The option select is not supported and not respected because it always preserves the file format and all the attributes. select = "*" is imposed internally.

Examples

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

# Create a new set of 200 x 200 m.las files with first returns only
opt_chunk_buffer(ctg) <- 0
opt_chunk_size(ctg) <- 200
opt_filter(ctg) <- "-keep_first"
opt_chunk_alignment(ctg) <- c(275, 90)
opt_output_files(ctg) <- paste0(tempdir(), "/retile_{XLEFT}_{YBOTTOM}"

# preview the chunk pattern
plot(ctg, chunk = TRUE)

newctg = catalog_retile(ctg)
plot(newctg)

# Create a new set of 200 x 200 m.las files
# but extended with a 50 m buffer in the folder

opt_chunk_buffer(ctg) <- 25
opt_chunk_size(ctg) <- 200
opt_filter(ctg) <- ""
opt_chunk_alignment(ctg) <- c(275, 90)
opt_output_files(ctg) <- paste0(tempdir(), "/{XLEFT}_{YBOTTOM}_buffered"

newctg = catalog_retile(ctg)
plot(newctg)

## Not run:
# 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
classify

```r
classify
Classify points

Description

Classify points that meet some criterion and/or that belong in a region of interest. The functions updates the attribute Classification of the LAS object according to las specifications.

Usage

```r
classify_ground(las, algorithm, last_returns = TRUE)
classify_noise(las, algorithm)
classify_poi(
  las,
  class,
  poi = NULL,
  roi = NULL,
  inverse_roi = FALSE,
  by_reference = FALSE
)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>las</code></td>
<td>An object of class LAS or LASCatalog.</td>
</tr>
<tr>
<td><code>algorithm</code></td>
<td>An algorithm for classification. lidR has has: sor, ivf for noise classification, and pmf, csf, mcc for ground classification (see respective documentation).</td>
</tr>
<tr>
<td><code>last_returns</code></td>
<td>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 attributes 'ReturnNumber' or 'NumberOfReturns' are absent, 'last_returns' is turned to FALSE automatically.</td>
</tr>
<tr>
<td><code>class</code></td>
<td>The ASPRS class to attribute to the points that meet the criterion.</td>
</tr>
<tr>
<td><code>poi</code></td>
<td>a formula of logical predicates. The points that are TRUE will be classified class.</td>
</tr>
<tr>
<td><code>roi</code></td>
<td>A SpatialPolygons*, from sp or a sf/sfc_polygon from sf. The points that are in the region of interest delimited by the polygon(s) are classified class.</td>
</tr>
<tr>
<td><code>inverse_roi</code></td>
<td>bool. Inverses the roi. The points that are outside the polygon(s) are classified class.</td>
</tr>
<tr>
<td><code>by_reference</code></td>
<td>bool. Updates the classification in place (LAS only).</td>
</tr>
</tbody>
</table>
Details

classify_noise  Classify points as 'noise' (outliers) with several possible algorithms. lidR has: sor, ivf. The points classified as 'noise' are assigned a value of 18.

classify_ground  Classify points as 'ground' with several possible algorithms. lidR has pmf, csf and mcc. The points classified as 'ground' are assigned a value of 2

classify_poi  Classify points that meet some logical criterion and/or that belong in a region of interest with class of choice.

Non-supported LAScatalog options

The option select is not supported and not respected because it always preserves the file format and all the attributes. select = "*" is imposed internally.

Examples

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

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

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

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

# Using IVF
las <- classify_noise(las, ivf(5,2))
#plot(las, color = "Classification")

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

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

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

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

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

#plot(las, color = "Classification")

---

**clip**

*Clip points in regions of interest*

**Description**

Clip points within a given region of interest (ROI) from a point cloud (LAS object) or a collection of files (LAScatalog object).

**Usage**

```r
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. spatial points, spatial polygons in sp or sf/sfc format, Extent, bbox, 2x2 matrix
- **...** in clip_roi: optional supplementary options (see supported geometries). Unused in other functions
- **xleft, ybottom, xright, ytop** numeric. coordinates of one or several rectangles.
- **xpoly, ypoly** numeric. x coordinates of a polygon.
- **xcenter, ycenter** numeric. x coordinates of on or several disc centres.
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.

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.

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, or a LASCatalog if the queries are immediately written into files without loading anything in R.

Non-supported LASCatalog options
The option chunk size, buffer, chunk alignment and select are not supported by clip_* because they are meaningless in this context.

Examples

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

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

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

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

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

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

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

decimate_points

plot(subset2)
plot(subset3)

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

## End(Not run)

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, highest, lowest and random_per_voxel.

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

Non-supported LAScatalog options
The option ‘select’ is not supported and not respected because it always preserves the file format and all the attributes. ‘select = "*"’ is imposed internally.
The options ‘chunk buffer’ is not supported and not respected because it is not needed.

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(rasterize_density(las))
#plot(rasterize_density(thinned1))

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

# Select the highest point within each pixel of an overlayed grid
Deprecated functions in lidR

Description

These functions are provided for compatibility with older versions of lidR but are deprecated. They will progressively print a message, throw a warning and eventually be removed. The links below point to the documentation of the new names. In version 4 they now throw an error. In version 4.1 they will be removed definitively.

lasadd lascheck lasclip lasdetectshape lasfilter lasfiltersurfacepoints lasflightline lasground lasmergespatial lasnormalize laspulse lasrangecorrection lasflightline lasreoffset lasrescale lasscanlines lassmooth lassnags lastrees lasvoxelize sensor_tracking tree_detection tree_hull

Usage

lascheck(las)
lasclip(las, geometry, ...)
lasclipRectangle(las, xleft, ybottom, xright, ytop, ...)
lasclipPolygon(las, xpoly, ypoly, ...)
lasclipCircle(las, xcenter, ycenter, radius, ...)
lasdetectshape(las, algorithm, attribute = "Shape", filter = NULL)
lasfilter(las, ...)
lasfilterfirst(las)
lasfilterfirstlast(las)
lasfilterfirstofmany(las)
lasfilterground(las)
lasfilterlast(las)
lasfilternth(las, n)
lasfiltersingle(las)
lasfilterdecimate(las, algorithm)
lasfilterduplicates(las)
lasfiltersurfacepoints(las, res)
lasground(las, algorithm, last_returns = TRUE)
laspulse(las)
lasflightline(las, dt = 30)
lasscanline(las)
lasmergespatial(las, source, attribute = NULL)
lasnormalize(
    las,
    algorithm,
    na.rm = FALSE,
    use_class = c(2L, 9L),
    ..., 
    add_lasattribute = FALSE
)
lasunnormalize(las)
lasrange correction(
    las,
    sensor,
    Rs,
    f = 2.3,
    gpstime = "gpstime",
    elevation = "Z"
)
lasrescale(las, xscale, yscale, zscale)
lasreoffset(las, xoffset, yoffset, zoffset)
lassmooth(
    las,
    size,
    method = c("average", "gaussian"),
    shape = c("circle", "square"),
    sigma = size/6
)
lasunsmooth(las)
lassnags(las, algorithm, attribute = "snagCls")
lastrees(las, algorithm, attribute = "treeID", uniqueness = "incremental")
lasadddata(las, x, name)
lasaddextrabytes(las, x, name, desc)

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

lasremoveextrabytes(las, name)
lasvoxelize(las, res)

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

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

hexbin_metrics(...)

filter_surfacepoints(las, res)
## S3 method for class 'LAS'
filter_surfacepoints(las, res)

## S3 method for class 'LAScatalog'
filter_surfacepoints(las, res)

### 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
- **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
dsm_pitfree  

**Digital Surface Model Algorithm**

**Description**

This function is made to be used in `rasterize_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**


**See Also**

Other digital surface model algorithms: `dsm_point2raster, dsm_tin`

**Examples**

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

# Basic triangulation and rasterization of first returns
chm <- rasterize_canopy(las, res = 0.5, dsmtin())
plot(chm, col = col)
```
# Khosravipour et al. pitfree algorithm

```r
chm <- rasterize_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)

# Because the TIN interpolation is done within the convex hull of the point cloud
# dummy pixels are interpolated that are correct according to the interpolation
# method used, but meaningless in our CHM
chm <- rasterize_canopy(las2, res = 0.5, pitfree(max_edge = c(0, 1.5)))
plot(chm, col = col)

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

## End(Not run)
```

---

**dsm_point2raster**

*Digital Surface Model Algorithm*

**Description**

This function is made to be used in `rasterize_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**

```r
dsm_point2raster(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 `rasterize_terrain` for more details).

**See Also**

Other digital surface model algorithms: `dsm_pitfree`, `dsm_tin`
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 <- rasterize_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 <- rasterize_canopy(las, res = 0.5, p2r(0.2))
plot(chm, col = col)

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

## End(Not run)

---

dsm_tin

Digital Surface Model Algorithm

Description

This function is made to be used in `rasterize_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

dsm_tin(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: `dsm_pitfree`, `dsm_point2raster`
Examples

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

# Basic triangulation and rasterization of first returns
chm <- rasterize_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)

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

# Use 'max_edge' to trim dummy triangles
chm = rasterize_canopy(las2, res = 0.5, dsmtin(max_edge = 3))
plot(chm, col = col)

## End(Not run)

dtm_idw

Spatial Interpolation Algorithm

Description

This function is made to be used in rasterize_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.
rmax numeric. Maximum radius where to search for knn. Default 50.
dtm_kriging

See Also

Other dtm algorithms: dtm_kriging, dtm_tin

Examples

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

#plot(las)
dtm = rasterize_terrain(las, algorithm = knnidw(k = 6L, p = 2))

#plot(dtm)
#plot_dtm3d(dtm)

dtm_kriging

Spatial Interpolation Algorithm

Description

This function is made to be used in rasterize_terrain or normalize_height. It implements an algorithm for spatial interpolation. Spatial interpolation is based on universal kriging using the krig 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.

See Also

Other dtm algorithms: dtm_idw, dtm_tin

Examples

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

plot(las)
dtm_tin = rasterize_terrain(las, algorithm = kriging())

plot(dtm)
plot_dtm3d(dtm)

## End(Not run)

dtm_tin  Spatial Interpolation Algorithm

Description
This function is made to be used in rasterize_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 can be performed with another algorithm.

Usage
tin(..., extrapolate = knnidw(3, 1, 50))

Arguments
... unused
extrapolate There are usually a few points outside the convex hull, determined by the ground points at the very edge of the dataset, that cannot be interpolated with a triangulation. Extrapolation can be performed with another algorithm.

See Also
Other dtm algorithms: dtm_idw, dtm_kriging

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

#plot(las)
dtm = rasterize_terrain(las, algorithm = tin())

#plot(dtm)
#plot_dtm3d(dtm)
Functions for the LAScatalog processing engine not meant to be called directly by users.

Usage

```r
engine_apply(
  .CHUNKS,
  .FUN,
  .PROCESSOPT,
  .OUTPUTOPT,
  .GLOBALS = NULL,
  .AUTOREAD = FALSE,
  .AUTOCROP = FALSE,
  ...
)
```

```r
engine_chunks(ctg, realignment = FALSE, plot = opt_progress(ctg))
```

```r
engine_crop(x, bbox)
```

```r
engine_merge(ctg, any_list, ...)
```

```r
engine_write(x, path, drivers)
```

Arguments

- **.CHUNKS**: list. list of LAScluster
- **.FUN**: function. function that respects a template (see `catalog_apply`)
- **.PROCESSOPT**: list. Processing option
- **.OUTPUTOPT**: list. Output option
- **.GLOBALS**: list. Force export of some object in workers
- **.AUTOREAD**: bool. Enable autoread
- **.AUTOCROP**: bool. Enable autocrop
- **...**: parameters of `.FUN`
- **ctg**: LAScatalog
- **realignment**: FALSE or list(res = x, start = c(y, z)). Sometimes the chunk must be aligned with a raster, for example to ensure the continuity of the output. If the chunk size is 800 and the expected product is a raster with a resolution of 35, 800 and 35 are not compatible and will create 2 different partial pixels on the edges. The realignment option forces the chunk to fit the grid alignment.
### engine_options

#### Description

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

#### Usage

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

---

**plot** logical. Displays the chunk pattern.

**x** LAS, Raster, stars, SpatRaster, sf, sfc, Spatial

**bbox** bbox

**any_list** list of LAS, Raster, stars, SpatRaster, sf, sfc, Spatial, data.frame

**path** strings

**drivers** list. Drivers of a LAScatalog

---

**See Also**

Other LAScatalog processing engine: `engine_options`

Other LAScatalog processing engine: `engine_options`
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.

Details

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

See Also

Other LAScatalog processing engine: engine

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)

---

**Extract or Replace Parts of a LAS* Object**

**Description**

Operators acting on LAS* objects. 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**

```r
## S4 method for signature 'LAS'
x$name

## S4 method for signature 'LAS,ANY,missing'
x[[i, j, ...]]

## S4 replacement method for signature 'LAS'
x$name <- value

## S4 replacement method for signature 'LAS,ANY,missing'
x[[i, j]] <- value

## S4 method for signature 'LAS,numeric,ANY'
x[i]

## S4 method for signature 'LAS,logical,ANY'
x[i]
```
## S4 method for signature 'LAS,sf,ANY'
x[i]

## S4 method for signature 'LAS,sfc,ANY'
x[i]

## S4 method for signature 'LAScatalog'
x$name

## S4 method for signature 'LAScatalog,ANY,missing'
x[[i, j, ...]]

## S4 method for signature 'LAScatalog,ANY,ANY'
x[i, j, ..., drop = FALSE]

## S4 method for signature 'LAScatalog,logical,ANY'
x[i]

## S4 method for signature 'LAScatalog,sf,ANY'
x[i]

## S4 method for signature 'LAScatalog,sfc,ANY'
x[i]

## S4 replacement method for signature 'LAScatalog,ANY,ANY'
x[[i, j]] <- value

## S4 replacement method for signature 'LAScatalog'
x$name <- value

## S4 method for signature 'LASHheader'
x$name

## S4 replacement method for signature 'LASHheader'
x$name <- value

## S4 method for signature 'LASHheader,ANY,missing'
x[[i, j, ...]]

## S4 replacement method for signature 'LASHheader,character,missing'
x[[i]] <- value

### Arguments

- **x**
  - A LAS* object

- **name**
  - A literal character string or a name (possibly backtick quoted).

- **i**
  - string, name of elements to extract or replace.

- **j**
  - Unused.
filters

... Unused
value typically an array-like R object of a similar class as x.
drop Unused

Examples

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

las$Intensity
las[["Z"]]
las[["Number of points by return"]]

## Not run:
las$Z = 2L
las[["Z"]] = 1:10
las$NewCol = 0
las[["NewCol"]]] = 0

## End(Not run)

__________________________

filters  Filter points of interest

Description

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

Usage

filter_poi(las, ...)
filter_first(las)
filter_firstlast(las)
filter_firstofmany(las)
filter_ground(las)
filter_last(las)
filter_nth(las, n)
filter_single(las)
filter_duplicates(las)
## S3 method for class 'LAS'
filter_duplicates(las)

## S3 method for class 'LASCatalog'
filter_duplicates(las)

### Arguments

- **las**
  - An object of class **LAS**

- **...**
  - Logical predicates. Multiple conditions are combined with `&` or `,`

- **n**
  - integer, `ReturnNumber == n`

### Details

- **filter_poi**
  - Select points of interest based on custom logical criteria.

- **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.

- **filter_duplicates**
  - Removes the duplicated points (duplicated by XYZ)

### Value

- An object of class **LAS**

### Non-supported LASCatalog options

- The option **select** is not supported and not respected because it always preserves the file format and all the attributes. **select = "*"** is imposed internally.

### Examples

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

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

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

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

This function is made to be used in `classify_ground`. It implements an algorithm for segmentation of ground points based 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 `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 rigidity 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

See Also

Other ground segmentation algorithms: `gnd_mcc`, `gnd_pmf`

Examples

```r
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")
```

---

**gnd_mcc**

*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 Multiscale Curvature Classification. This method is a strict implementation of the MCC algorithm made by Evans and Hudak. (2007) (see references) that relies on the authors’ original source code written and exposed to R via the `RMCC` package.

**Usage**

```r
mcc(s = 1.5, t = 0.3)
```

**Arguments**

- `s` numeric. Scale parameter. The optimal scale parameter is a function of 1) the scale of the objects (e.g., trees) on the ground, and 2) the sampling interval (post spacing) of the lidar data.
- `t` numeric. Curvature threshold

**Details**

There are two parameters that the user must define, the scale (s) parameter and the curvature threshold (t). The optimal scale parameter is a function of 1) the scale of the objects (e.g., trees) on the ground, and 2) the sampling interval (post spacing) of the lidar data. Current lidar sensors are capable of collecting high density data (e.g., 8 pulses/m2) that translate to a spatial sampling frequency (post spacing) of 0.35 m/pulse (1/sqrt(8 pulses/m2) = 0.35 m/pulse), which is small relative to the size of mature trees and will oversample larger trees (i.e., nominally multiple returns/tree). Sparser lidar data (e.g., 0.25 pulses/m2) translate to a post spacing of 2.0 m/pulse (1/sqrt(0.25 pulses/m2) = 2.0 m/pulse), which would undersample trees and fail to sample some smaller trees (i.e., nominally <1 return/tree).

Therefore, a bit of trial and error is warranted to determine the best scale and curvature parameters to use. Select a las tile containing a good variety of canopy and terrain conditions, as it’s likely...
the parameters that work best there will be applicable to the rest of your project area tiles. As a starting point: if the scale (post spacing) of the lidar survey is 1.5 m, then try 1.5. Try varying it up or down by 0.5 m increments to see if it produces a more desirable digital terrain model (DTM) interpolated from the classified ground returns in the output file. Use units that match the units of the lidar data. For example, if your lidar data were delivered in units of feet with a post spacing of 3 ft, set the scale parameter to 3, then try varying it up or down by 1 ft increments and compare the resulting interpolated DTM s. If the trees are large, then it’s likely that a scale parameter of 1 m (3 ft) will produce a cleaner DTM than a scale parameter of 0.3 m (1 ft), even if the pulse density is 0.3 m (1 ft). As for the curvature threshold, a good starting value to try might be 0.3 (if data are in meters; 1 if data are in feet), and then try varying this up or down by 0.1 m increments (if data are in meters; 0.3 if data are in feet).

References


See Also

Other ground segmentation algorithms: gnd_csf, gnd_pmf

Examples

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

las <- classify_ground(las, mcc(1.5,0.3))
#plot(las, color = "Classification")
```

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)

util_makeZhangParam(
    b = 2,
    dh0 = 0.5,
    dhmax = 3,
    s = 1,
    max_ws = 20,
    exp = FALSE
)

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.

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 \( dh_{\text{max}} \) 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

The progressive morphological filter allows for any sequence of parameters. The 'util_makeZhangParam' function enables computation of the sequences using equations (4), (5) and (7) from Zhang et al. (see reference and 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:

\[
    th_k = s \ast (w_k - w_{k-1}) \ast c + th_0
\]

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.
**Reference**


**See Also**

Other ground segmentation algorithms: *gnd csf, gnd mcc*

**Examples**

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

ws <- seq(3, 12, 3)
th <- seq(0.1, 1.5, length.out = length(ws))
las <- classify_ground(las, pmf(ws, th))
#plot(las, color = "Classification")
```

**interpret_waveform**

*Convert full waveform data into a regular point cloud*

**Description**

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

**Usage**

`interpret_waveform(las)`

**Arguments**

- `las` An object of class LAS with full waveform data

**Value**

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

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

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

Examples

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

is

A set of boolean tests on objects

Description

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

Usage

```r
is.empty(las)
is.overlapping(catalog)
is.indexed(catalog)
is.algorithm(x)
is.parallelised(algorithm)
```
Arguments

- `las`: A LAS object.
- `catalog`: A LAStoc catalog object.
- `x`: Any R object.
- `algorithm`: An algorithm object.

Value

TRUE or FALSE

Examples

```r
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)

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

Description

This function is made to be used in `locate_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

```r
lmf(ws, hmin = 2, shape = c("circular", "square"), ws_args = "Z")
```
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. By default function takes 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. This can be controled with the 'ws_args' parameter.

- **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".

- **ws_args**: list. Named list of argument for the function ‘ws’ if ‘ws’ is a function.

References


See Also

Other individual tree detection algorithms: *itd_manual*

Examples

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

# point-cloud-based

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

#plot(las) |> add_treetops3d(ttops)

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

#plot(las) |> add_treetops3d(ttops)

# Very custom variable windows size
f <- function(x, y, z) { x * 0.07 + y * 0.01 + z}
ws_args <- list(x = "Z", y = "Intensity", z = 3)
ttops <- locate_trees(las, lmf(f, ws_args = ws_args))

# =========
```
Individual Tree Detection Algorithm

Description

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

This algorithm does not preserve tree IDs from detected and renumber all trees. It also loses all attributes.

Usage

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

Arguments

detected: SpatialPoints* or sf/sfc_POINT* with 2 or 3D points of already found tree tops that need manual correction. Can be NULL.

radius: numeric. Radius of the spheres displayed on the point cloud (aesthetic purposes only).

color: character. Colour of the spheres displayed on the point cloud (aesthetic purposes only).

button: Which button to use for selection. One of "left", "middle", "right". lidR using left for rotation and right for dragging using one of left or right will disable either rotation or dragging.

...: supplementary parameters to be passed to plot.
See Also

Other individual tree detection algorithms: \texttt{itd_lmf}

Examples

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

ttops = locate_trees(las, manual())

ttops = locate_trees(las, lmf(5))
ttops = locate_trees(las, manual(ttops))

## End(Not run)
```

its_dalponte2016 \textit{Individual Tree Segmentation Algorithm}

Description

This function is made to be used in \texttt{segment_trees}. It implements an algorithm for tree segmentation based on Dalponte and Coomes (2016) algorithm (see reference). This is a seeds + growing region algorithm. This algorithm exists in the package \texttt{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 \texttt{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

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

Arguments

\texttt{chm} ‘RasterLayer’, ‘SpatRaster’ or ‘stars’. Canopy height model. Can be computed with \texttt{rasterize_canopy} or read from an external file.
treetops  ‘SpatialPoints*‘ or ‘sf/sfc_POINT‘ with 2D or 3D coordinates. Can be computed with `locate_trees` or read from an external file.

`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 treetops contains an attribute with the ID for each tree, the name of this attribute. This way, original IDs will be preserved.

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:

```r
chm <- raster("chm.tif")
ttops <- locate_trees(chm, lmf(3))
crowns <- dalponte2016(chm, ttops())
```

References


See Also

Other individual tree segmentation algorithms: `its_li2012`, `its_silva2016`, `its_watershed`

Other raster based tree segmentation algorithms: `its_silva2016`, `its_watershed`

Examples

```r
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
poi <- "-drop_z_below 0 -inside 481280 3812940 481320 3812980"
las <- readLAS(LASfile, select = "xyz", filter = poi)
col <- pastel.colors(200)

# Using raster because focal does not exist in stars
chm <- rasterize_canopy(las, 0.5, p2r(0.3), pkg = "raster")
ker <- matrix(1,3,3)
chm <- raster::focal(chm, w = ker, fun = mean, na.rm = TRUE)
```
Individual Tree Segmentation Algorithm

Description

This function is made to be used in `segment_trees`. It implements an algorithm for tree segmentation based on Li et al. (2012) (see reference). This method is a growing region method working at the point cloud level. It is an implementation by lidR authors, from the original paper, as close as possible from the original description. However we added a parameter `hmin` to prevent oversegmentation for objects that are too low. This algorithm is known to be slow because it has an algorithmic complexity worst that $O(n^2)$.

Usage

```r
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 by restricting the number of comparisons to perform. The lower the value, the faster the method. Default is 10.

References


See Also

Other individual tree segmentation algorithms: `its_dalponte2016`, `its_silva2016`, `its_watershed`
Examples

```r
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
poi <- "-drop_z_below 0 -inside 481280 3812940 481320 3812980"
las <- readLAS(LASfile, select = "xyz", filter = poi)
col <- pastel.colors(200)

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

Description

This function is made to be used in `segment_trees`. It implements an algorithm for tree segmentation based on Silva et al. (2016) (see reference). This is a simple method based on seed + voronoi tessellation (equivalent to nearest neighbour). This algorithm is implemented in the package rLiDAR. This version is not the version from rLiDAR. It is code written from the original article by the lidR authors and is considerably (between 250 and 1000 times) faster.

Usage

```r
silva2016(chm, treetops, max_cr_factor = 0.6, exclusion = 0.3, ID = "treeID")
```

Arguments

- `chm` ‘RasterLayer’, ‘SpatRaster’ or ‘stars’. Canopy height model. Can be computed with `rasterize_canopy` or read from an external file.
- `treetops` ‘SpatialPoints’ or ‘sf/sfc_POINT’ with 2D or 3D coordinates. Can be computed with `locate_trees` or read from an external file.
- `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 `treetops` contains an attribute with the ID for each tree, the name of this attribute. This way, original IDs will be preserved.

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:

```r
chm <- raster("chm.tif")
ttops <- locate_trees(chm, lmf(3))
crowns <- silva2016(chm, ttops)()
```
its_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. It is based on the bioconductor package EBIimage. You need to install this package to run this method (see its github page). Internally, the function EBIImage::watershed is called.

Usage

watershed(chm, th_tree = 2, tol = 1, ext = 1)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>chm</td>
<td>Canopy height model. Can be computed with rasterize_canopy or read from an external file.</td>
</tr>
<tr>
<td>th_tree</td>
<td>Threshold below which a pixel cannot be a tree. Default is 2.</td>
</tr>
<tr>
<td>tol</td>
<td>Tolerance see ?EBImage::watershed.</td>
</tr>
<tr>
<td>ext</td>
<td>Tolerance see ?EBImage::watershed.</td>
</tr>
</tbody>
</table>
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:

```r
chm <- raster("chm.tif")
crowns <- watershed(chm)(
```

See Also

Other individual tree segmentation algorithms: `its_dalponte2016`, `its_li2012`, `its_silva2016`

Other raster based tree segmentation algorithms: `its_dalponte2016`, `its_silva2016`

Examples

```r
## Not run:
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
poi <- "-drop_z_below 0 -inside 481280 3812940 481320 3812980"
las <- readLAS(LASfile, select = "xyz", filter = poi)
col <- pastel.colors(250)

# Using raster because focal does not exist in stars
chm <- rasterize_canopy(las, res = 0.5, p2r(0.3), pkg = "raster")
ker <- matrix(1,3,3)
chm <- raster::focal(chm, w = ker, fun = mean, na.rm = TRUE)
las <- segment_trees(las, watershed(chm))

plot(las, color = "treeID", colorPalette = col)

## End(Not run)
```

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(), crs = sf::NA_crs_, check = TRUE, index = NULL, ...)`
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.
- **crs**: `crs` object of class `crs` from `sf`.
- **check**: logical. Conformity tests while building the object.
- **index**: list with two elements `list(sensor = 0L, index = 0L)`. See spatial indexing.
- **...**: internal use.

Details

A LAS object contains 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, Y, Z (numeric)
- gpstime (numeric)
- Intensity (integer)
- ReturnNumber, NumberOfReturns (integer)
- ScanDirectionFlag (integer)
- EdgeOfFlightline (integer)
- Classification (integer)
- Synthetic_flag, Keypoint_flag, Withheld_flag (logical)
- ScanAngleRank/ScanAngle (integer/numeric)
- UserData (integer)
- PointSourceID (integer)
- R, G, B, NIR (integer)

Value

An object of class LAS

Functions

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

Slots

- **crs**: Object of class `crs` from `sf`.
- **data**: Object of class `data.table`. Point cloud data according to the LAS file format.
- **header**: Object of class `LASHeader`. LAS file header according to the LAS file format.
- **index**: list. See spatial indexing.
See Also

readLAS

Examples

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

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

# 'data' has many decimal digits
data

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

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

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

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

LAScatalog-class

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

Description

A LAScatalog object is a representation of a collection of las/laz files. A LAScatalog is a way to manage and batch process a lidar coverage. 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.
Details

A LAScatalog contains an sf object to store the geometry and metadata. It is extended with slots that contain processing options. In lidR, each function that supports a LAScatalog as input will respect these processing options. Internally, processing a catalog is almost always the same and relies on a few steps:

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

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

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

Slots

data sf. An sf data.frame with the bounding box of each file as well as all the information read from the header of each LAS/LAZ file.

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

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

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

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

index list. See spatial indexing.

Processing options

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

- **progress**: boolean. Display a progress bar and a chart of progress. Default is TRUE. Progress estimation can be enhanced by installing the package progress. See opt_progress.
• **stop_early**: boolean. Stop the processing if an error occurs in a chunk. If `FALSE` the process can run until the end, removing chunks that failed. Default is `TRUE` and the user should have no reason to change this. See `opt_stop_early`.

• **wall.to.wall** logical. The catalog processing engine always guarantees to return a continuous output without edge effects, assuming that the catalog is a wall-to-wall catalog. To do so, some options are checked internally to guard against bad settings, such as `buffer = 0` for an algorithm that requires a buffer. In rare cases it might be useful to disable these controls. If `wall.to.wall = FALSE` controls are disabled and wall-to-wall outputs cannot be guaranteed. See `opt_wall_to_wall`.

### Chunk options

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

• **chunk_size**: numeric. The size of the chunks that will be sequentially processed. A small size allows small amounts of data to be loaded at once, saving computer memory. With big chunks the computation is usually faster but uses much more memory. If `chunk_size = 0` the chunk pattern is build using the file pattern. The chunks are expecting to be wall-to-wall coverage, which means that `chunk_size = 0` has meaning only if the files are not overlapping. Default is 0 i.e. by default the processing engine respects the existing tiling pattern. See `opt_chunk_size`.

• **buffer**: numeric. Each chunk can be read with an extra buffer around it to ensure there are no edge effects between two independent chunks and that the output is continuous. This is mandatory for some algorithms. Default is 30. See `opt_chunk_buffer`.

• **alignment**: numeric. A vector of size 2 (x and y coordinates, respectively) to align the chunk pattern. By default the alignment is made along (0,0), meaning that the edge of the first chunk will belong on `x = 0` and `y = 0` and all the the other chunks will be multiples of the chunk size. Not relevant if `chunk_size = 0`. See `opt_chunk_alignment`.

• **drop**: integers. A vector of integers that specify the IDs of the chunks that should not be created. This is designed to enable users to restart a computation that failed without reprocessing everything. See `opt_restart<-`. Technically, this option may be used for partial processing of a collection, but it generally should not be. Partial processing is already a feature of the engine. See this vignette.

### Output options

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

• **output_files**: string. If `output_files = ""` outputs are returned in R. Otherwise, if `output_files` is a string the outputs will be written to files. This is useful if the output is too big to be returned in R. A path to a filename template without a file 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 allowed templates are \{XLEFT\}, \{XRIGHT\}, \{YBOTTOM\}, \{YTOP\}, \{ID\}, \{XCENTER\}, \{YCENTER\}, \{ORIGINALFILENAME\}. See opt_output_files.

- **drivers**: list. This contains all the drivers required to seamlessly write Raster\*, SpatRaster, stars, Spatial\*, sf, and LAS objects. It is recommended that only advanced users change this option. A dedicated page describes the drivers in lidR-LAScatalog-drivers.

- **merge**: boolean. Multiple objects are merged into a single object at the end of the processing. See opt_merge.

### Input options

The slot @input_options contains a list of options that are passed to the function readLAS. Indeed, the readLAS function is not called directly by the user but by the internal processing engine. Users can propagate these options through the LAScatalog settings.

- **select**: string. The option select. Usually this option is not respected because each function knows which data must be loaded or not. This is documented in each function. See opt_select.

- **filter**: string. The option filter. See opt_filter.

### Examples

```
## Not run:
# Build a catalog
ctg <- readLAScatalog("folder/to/las/files/", filter = "-keep_first")

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

# We can seamlessly use lidR functions
hmean <- pixel_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 <- rasterize_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 <- rasterize_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 <- rasterize_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 functions catalog_apply
# and catalog_map
output <- catalog_apply(ctg, FUN, ...)

## End(Not run)

---

**LASHeader**

Create a LASHeader object

Description

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

Usage

LASHeader(data = list())

Arguments

data a list containing the data from the header of a LAS file. Can also be a data.frame or data.table

Value

An object of class LASHeader

Examples

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

header = LASheader(data)

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

las <- LAS(data, header)
las

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

---

**LASheader-class**

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

**Description**

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

**Slots**

- **PHB** list. Represents the Public Header Block
- **VLR** list. Represents the Variable Length Records
- **EVLR** list. Represents the Extended Variable Length Records
las_check

Inspect a LAS object

Description

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

For a LAS object it checks:

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

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 and returns a list invisibly. If print = FALSE the function returns a list visibly and do not print the report.

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

See Also

Other las utilities: las_utilities
Examples

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

Description

Package rlas 1.6.0 supports compact representation of non populated attributes. For example UserData is usually populated with zeros (not populated). Yet it takes 32 bits per point to store each 0. With rlas 1.6.0 it can now use 644 bits no matter the number of points loaded if it is not populated or populated with a unique value.

Usage

```r
las_is_compressed(las)
las_size(las)
```

Arguments

las A LAS object.

Details

las_is_compressed test each attributes and returns a named vector with TRUE if the attribute is compressed FALSE otherwise.

las_size returns the true size of a LAS object by considering the compression. object.size from base R does not account for ALTREP and consequently cannot measure properly the size of a LAS object

Examples

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

format(object.size(las), units = "MB")
format(las_size(las), units = "MB")
```
Description

Tools to manipulate LAS objects maintaining compliance with ASPRS specification

Usage

las_rescale(las, xscale, yscale, zscale)
las_reoffset(las, xoffset, yoffset, zoffset)
las_quantize(las, by_reference = TRUE)
las_update(las)
quantize(x, scale, offset, by_reference = TRUE, ...)
is.quantized(x, scale, offset, ...)
count_not_quantized(x, scale, offset)
storable_coordinate_range(scale, offset)
header(las)
payload(las)
phb(las)
vlr(las)
evlr(las)

Arguments

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

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

See Also

Other las utilities: `las_check()`

Examples

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

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

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

# It is important to fix that
las_quantize(las)

# Now the file is almost valid
las_check(las)

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

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

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

This document explains how objects are written on disk when processing a LAScatalog. As mentioned in LAScatalog-class, users can set a templated filename to store the outputs on disk instead of in R memory. By default LAS objects are stored in .las files with writeLAS, raster objects are stored in .tif files using native write function for raster, stars or terra, Spatial* objects are stored in .shp files with after coercion to sf with st_write, sf object are stored to .gpkg files with st_write.data.frame objects are stored in .csv files with fwrite, and other objects are not supported. However, users can modify all these default settings and even add new drivers. This manual page explain how. One may also refer to some unofficial documentation here or here.

Generic form of a driver

A driver is stored in the slot @output_options 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 shapefile instead of a GeoPackage, one must change the sf driver:

```r
ctg@output_options$drivers$sf$extension <- "\.shp"
```

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

```r
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:

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

Add a new driver

The drivers allow LAS, Spatial, sf, Raster, stars, SpatRaster 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 @output_options:

```r
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 sf objects are written into GeoPackage with `st_write`. `st_write` can also write in GeoJSON and even in SQLite database objects. But it cannot add data into an existing SQLite database. Let’s create our own driver for a sf. First we need a function able to write and append a sf into a SQLite database from the object and the path.

```r
dbWrite_sf = function(x, path, name)
{
  x <- sf::st_drop_geometry(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:
```r
ctg$output_options$drivers$sf = list(
  write = dbWrite_sf,
  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.

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

And all the sf will be appended in a single database. To preserve the geometry one can

---

**Description**

This document explains 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:

```r
las <- readLAS("file.las")
tops <- locate_trees(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:

```r
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`.

```r
is.parallelised(lmf(2)) #> TRUE
is.parallelised(li2012()) #> FALSE
```
Chunk-based parallelism

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

```r
ctg <- readLAScatalog("folder/")
out <- pixel_metrics(ctg, ~mean(Z))
```

But this one is evaluated in parallel with two cores:

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

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

Nested parallelism - part 1

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

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

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

Nested parallelism - part 2

We explained rules of precedence. But actually the user can tune the engine more accurately. Let’s define the following function:
myfun = function(las, ws, ...) {
  las <- normalize_height(las, tin())
  tops <- locate_tree(las, lmf(ws))
  return(tops)
}

out <- catalog_map(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_map(ctg, myfun, ws = 5)

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

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

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

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

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

Complex computing architectures

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

options(lidR.check.nested.parallelism = FALSE)

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

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

Usage

sensor(las, h = FALSE)
sensor(las) <- value
index(las, h = FALSE)
index(las) <- value

Arguments

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

Details

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

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

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

By default the spatial index code is 0 ("automatic") meaning that each function is free to choose a different spatial index depending on the recorded sensor. If the code is not 0 then each function will
be forced to used the spatial index that is imposed. This, obviously, applies only to functions that use spatial indexing.

**LASCatalog** objects also record such information that is automatically propagated to the LAS objects when processing.

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

**Examples**

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

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

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

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

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

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

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

# With a LASCatalog, spatial indexing information is propagated to the
# different chunks
```
ctg = readTLSLAScatalog(LASfile)
index(ctg) <- "voxelpartition"
sensor(ctg, h = TRUE)
index(ctg, h = TRUE)

# PERFORMANCE TESTS

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

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

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

# Performance tests on ALS
# ------------------------

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

Individual tree detection

Description

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

Usage

locate_trees(las, algorithm, uniqueness = "incremental")

Arguments

las
An object of class LAS or LAScatalog. Can also be a raster from raster, stars or terra 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

locate_trees returns an sf object with POINT Z geometries. The table of attributes contains a column treeID with an individual ID for each tree. The height of the trees (Z) are also repeated in the table of attribute to be analysed as an attribute and not as a coordinate.
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 LAStile catalog. This is because each chunk/file is processed independently of the others and potentially in parallel on different computers. Thus, the index always restarts at 1 on each chunk/file. Worse, in a tree segmentation process, a tree that is located exactly between 2 chunks/files will have two different IDs for its two halves.

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

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

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

bitmerge This method uses the XY coordinates of the highest point (apex) of a tree to create a single 64-bit number with a bitwise operation. First, XY coordinates are converted to 32-bit integers using the scales and offsets of the point cloud. For example, if the apex is at (10.32, 25.64) with a scale factor of 0.01 and an offset of 0, the 32-bit integer coordinates are X = 1032 and Y = 2564. Their binary representations are, respectively, (here displayed as 16 bits) 0000010000001000 and 0000101000000100. X is shifted by 32 bits and becomes a 64-bit integer. Y is kept as-is and the binary representations are unionized into a 64-bit integer like (here displayed as 32 bit) 0000100000001000010100000001010000000100. The previous steps are done at C++ level and the 64-bit binary representation is reinterpreted into a 64-bit decimal number to be returned in R. The IDs thus generated are somewhat weird. For example, the tree ID 0000100000001000010100000001010000000100 which is 67635716 if interpreted as an integer becomes 3.4164837074751323479078607289E+316 if interpreted as a decimal number. This is far from optimal but at least it is guaranteed to be unique if all files have the same offsets and scale factors.

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

Examples

```r
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile, select = "xyz", filter = "-inside 481250 3812980 481300 3813030")
ttops <- locate_trees(las, lmf(ws = 5))
#plot(las) |> add_treetops3d(ttops)
```
**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*, an sf/sfc, a Raster*, a stars, or a SpatRaster.

- SpatialPolygons*, sf and sfc: 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, single band stars or single layer SpatRaster: it attributes to each point the value found in each pixel of the raster.
- RasterStack, RasterBrick, multibands stars or multilayer SpatRaster must have 3 layers for RGB colors. It colorizes the point cloud with RGB values.

**Usage**

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

**Arguments**

- `las` An object of class LAS
- `source` An object of class SpatialPolygons* or sf or sfc or RasterLayer or RasterStack or RasterBrick or stars.
- `attribute` character. The name of an attribute in the table of attributes or the name of a new column in the LAS object. Not relevant for RGB colorization.

**Value**

A LAS object

**Examples**

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

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

# 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.
```

```r
names(las)
```
forest <- filter_poi(las, inlakes == FALSE)
#plot(forest)

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

---

### noise_ivf

**Noise Segmentation Algorithm**

**Description**

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

**Usage**

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

**Arguments**

- `res` numeric. Resolution of the voxels
- `n` integer. The maximal number of 'other points' in the 27 voxels

**See Also**

Other noise segmentation algorithms: `noise_sor`

**Examples**

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

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

las <- classify_noise(las, ivf(5,2))
```
Description
This function is made to be used in classify\_noise. It implements an algorithm for outliers (noise) segmentation based on Statistical Outliers Removal (SOR) methods first described in the PCL library and also implemented in CloudCompare (see references). For each point, it computes the mean distance to all its k-nearest neighbours. The points that are farther than the average distance plus a number of times (multiplier) the standard deviation are considered noise.

Usage
```r
sor(k = 10, m = 3, quantile = FALSE)
```

Arguments
- **k** numeric. The number of neighbours
- **m** numeric. Multiplier. The maximum distance will be: \( \text{avg distance} + m \times \text{std deviation} \).
  If \( \text{quantile = TRUE} \), \( m \) becomes the quantile threshold.
- **quantile** boolean. Modification of the original SOR to use a quantile threshold instead of a standard deviation multiplier. In this case the maximum distance will be: \( \text{quantile}(\text{distances}, \text{probs} = m) \)

References
- https://pointclouds.org/documentation/tutorials/statistical_outlier.html

See Also
- Other noise segmentation algorithms: noise\_ivf

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

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

las <- classify\_noise(las, sor(15,7))
```
**normalize**

Normalize point cloud

---

**Description**

Normalize elevation or intensity values using multiple methods.

**Usage**

```r
normalize_height(las, algorithm, use_class = c(2L, 9L), dtm = NULL, ...)
```

```r
unnormalize_height(las)
```

## S4 method for signature 'LAS,ANY'

```r
e1 - e2
```

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

**Arguments**

- `las` An object of class LAS or LAScatalog.
- `algorithm` (1) An algorithm for spatial interpolation. lidR has `tin`, `kriging`, `knnidw` or a raster representing a digital terrain model. (2) An algorithm for intensity normalization. lidR currently has `range_correction`.
- `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 normalization without a raster DTM.
- `dtm` raster. If `dtm` is provided, then the DTM is used in place of ground points. This is different than providing a DTM in `algorithm`. If `algorithm = dtm` the dtm is subtracted naively. If `algorithm = tin()` and `dtm = raster` the ground points are not used and the DTM is interpolated as if it were made of regularly-spaced ground points.
- `...` ignored.
- `e1` a LAS object
- `e2` A raster representing a digital terrain model in format from `raster`, `stars` or `terra`.

**Details**

**normalize_height** Subtract digital terrain model (DTM) from a LiDAR point cloud to create a dataset normalized with the ground at 0. The DTM can be a raster, but 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. A new attribute ‘Zref’ records the former elevation values, which enables the use of `unnormalize_height` to restore original point elevations.
**normalize** intensity Normalize intensity values using multiple methods. The attribute 'Intensity' records the normalized intensity. An extra attribute named 'RawIntensity' records the original intensities.

**Non-supported LAScatalog options**

The option `select` is not supported and not respected because it always preserves the file format and all the attributes. `select = "*"` is imposed internally.

**Examples**

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

# ====================
# Normalize elevation
# ====================

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

# restore original elevations
las <- unnormalize_height(nlas)

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

# restore original elevations
las <- unnormalize_height(las)

# Second option: interpolate each point (no discretization)
# ---------------------------------------------------------
nlas <- normalize_height(las, tin())

# operator - can be used. This is equivalent to the previous
las <- unnormalize_height(nlas)
nlas <- 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)
```
```r
# ====================
# Normalize intensity
# ====================

# 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))
```

---

**nstdmetrics**

**Predefined non standard metrics**

### Description

Functions and metrics from the literature. See details and references

### Usage

- `rumple_index(x, y = NULL, z = NULL, ...)`
- `gap_fraction_profile(z, dz = 1, z0 = 2)`
- `LAD(z, dz = 1, k = 0.5, z0 = 2)`
- `entropy(z, by = 1, zmax = NULL)`
- `VCI(z, zmax, by = 1)`

### Arguments

- `x` A RasterLayer, a stars a SpatRaster or a vector of x coordinates.
- `y` numeric. If `x` is a vector of coordinates: the associated y coordinates.
- `z` vector of positive z coordinates
- `...` unused
- `z0` numeric. The bottom limit of the profile
- `k` numeric. is the extinction coefficient
- `by`, `dz` numeric. The thickness of the layers used (height bin)
- `zmax` numeric. Maximum elevation for an entropy normalized to `zmax`.
Details

**rumple_index** Computes the roughness of a surface as the ratio between its area and its projected area on the ground. If the input is a gridded object (raster) the function computes the surfaces using Jenness’s algorithm (see references). If the input is a point cloud the function uses a Delaunay triangulation of the points and computes the area of each triangle.

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

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

**entropy** 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.

**VCI** Vertical Complexity Index. A fixed normalization of the entropy function from van Ewijk et al. (2011) (see references)

Value

numeric. The computed Rumple index.

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

A number between 0 and 1

A number between 0 and 1

References


Examples

```r
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 <- rasterize_canopy(las, 2, p2r())
rumple_index(chm)

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")
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")

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

z <- runif(10000, 0, 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)
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)

---

## Old R Spatial Packages

### Description

lidR 4.0.0 no longer uses the sp and raster packages. New functions are based on sf, terra and stars. However, to maintain backward compatibility the old functions from v<4.0.0 were preserved.

rgdal and rgeos will be retired on Jan 1st 2024. The raster and sp packages are based on rgdal and rgeos. lidR was based on raster and sp because it was created before the sf, terra and stars packages. This means that sooner or later users and packages that are still based on old R spatial packages will run into trouble. According to Edzer Pebesma, Roger Bivand:

*R users who have been around a bit longer, in particular before packages like sf and stars were developed, may be more familiar with older packages like maptools, sp, rgeos, and rgdal. A fair question is whether they should migrate existing code and/or existing R packages depending on these packages. The answer is: yes (see reference).*

The following functions are not formally deprecated but users should definitely move their workflow to modern spatial packages. lidR will maintain the old functions as long as it does not generate issues on CRAN. So, it might be until Jan 1st 2024 or later, who knows...

### Usage

```r
as.spatial(x)

## S3 method for class 'LAS'
as.spatial(x)

## S3 method for class 'LAScatalog'
as.spatial(x)

tree_metrics(las, func = ~list(Z = max(Z)), attribute = "treeID", ...)

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

grid_terrain(
  las,
  res = 1,
  algorithm,
  ...,
  keep_lowest = FALSE,
  full_raster = FALSE,
  use_class = c(2L, 9L),
  Wdegenerated = TRUE,
  is_concave = FALSE
)

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

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

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

Arguments

x, las an object of class LAS*
func see template_metrics
attribute, type see crown_metrics
... ignored
res, start see pixel_metrics
algorithm see rasterize_canopy, rasterize_terrain
full_raster, use_class, Wdegenerated, is_concave, keep_lowest see rasterize_density
filter, by_echo see template_metrics
uniqueness see crown_metrics
concavity, length_threshold
    see concaveman

References
Edzer Pebesma, Roger Bivand Spatial Data Science with applications in R https://keen-swartz-3146c4.netlify.app/older.html

plot

---

### 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, ...)

```r
## S4 method for signature 'LAS,missing'
plot(
  x,
  y,
  ..., 
  color = "Z",
  pal = "auto",
  bg = "black",
  breaks = "pretty",
  nbreaks = "auto",
  backend = "rgl",
  clear_artifacts = TRUE,
  axis = FALSE,
  legend = FALSE,
  add = FALSE,
  voxel = FALSE,
  NAcol = "lightgray"
)
```

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

height.colors(n)
forest.colors(n)
random.colors(n)
pastel.colors(n)

**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.
- **pal**: palette function, similar to `heat.colors`, or palette values. Default is "auto" providing an automatic coloring depending on the attribute `color`.
- **bg**: The color for the background. Default is black.
- **breaks**: either a numeric vector with the actual breaks, or a name of a method accepted by the style argument of `classIntervals`
- **nbreaks**: Number of colors breaks.
- **backend**: character. Can be "rgl" or "lidRviewer". If "rgl" is chosen the display relies on the rgl package. If "lidRviewer" is chosen it relies on the lidRviewer package, which is much more efficient and can handle million of points using less memory. lidRviewer is not available on CRAN yet and should be installed from github (see. [https://github.com/Jean-Romain/lidRviewer](https://github.com/Jean-Romain/lidRviewer)).
- **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.
- **axis**: logical. Display axis on XYZ coordinates.
- **legend**: logical. Display a gradient colour legend.
- **add**: If FALSE normal behaviour otherwise must be the output of a prior plot function to enable the alignment of a second point cloud.
- **voxel**: boolean or numeric. Displays voxels instead of points. Useful to render the output of `voxelize_points`, for example. However it is computationally demanding to render and can easily take 15 seconds for 10000 voxels. It should be reserved for large and/or very large point clouds.
for small scenes. If boolean the voxel resolution is guessed automatically. Otherwise users can provide the size of the voxels. To reduce the rendering time, an internal optimization removes voxels that are not visible when surrounded by other voxels.

**NAcol**  
a color for NA values.

**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.

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

### Examples

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

plot(las)
plot(las, color = "Intensity")
plot(las, color = "ScanAngleRank", pal = rainbow)

# If outliers break the color range, use the breaks parameter
las$Intensity[150] <- 1000L
plot(las, color = "Intensity")
plot(las, color = "Intensity", breaks = "quantile", nbreaks = 50)

plot(las, color = "Classification")

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

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

## End(Not run)
```

---

**plot.lasmetrics3d**  
*Plot voxelized LiDAR data*

### Description

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

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

Arguments

- `x`: An object of the class `lasmetrics3d`
- `y`: Unused (inherited from R base)
- `...`: Supplementary parameters for `plot`. The function internally uses the same plot function than LAS objects.

Examples

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

voxels = voxel_metrics(lidar, list(Imean = mean(Intensity)), res = 5)
plot(voxels, color = "Imean", colorPalette = heat.colors(50), trim=60)
## End(Not run)
```

---

### plot_3d

**Add a spatial object to a point cloud scene**

Description

Add a raster (‘raster’, ‘stars’ ‘terra’) object that represents a digital terrain model or a ‘SpatialPointsDataFrame’ or ‘sf’ 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 offset 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

```r
plot_dtm3d(dtm, bg = "black", clear_artifacts = TRUE, ...)
add_dtm3d(x, dtm, ...)
add_treetops3d(x, ttops, z = "Z", ...)
add_flightlines3d(x, flightlines, z = "Z", ...)
```
**plugins**

**Description**

Tools to build plugin functions for lidR

## Arguments

- **dtm**
  An object of the class ‘RasterLayer’ or ‘stars’ or ‘SpatRaster’

- **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.

- **x**
  The output of the function plot used with a LAS object.

- **ttops**
  A ‘SpatialPointsDataFrame’ or ‘sf/sfc’ that contains tree tops coordinates.

- **z**
  character. The name of the attribute that contains the height of the tree tops or of the flightlines. Only for XY geometries Ignored if the input have XYZ geometries

- **flightlines**
  A ‘SpatialPointsDataFrame’ or ‘sf’ that contains flightlines coordinates.

## Examples

```r
## Not run:
LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las <- readLAS(LASfile)
dtm <- rasterize_terrain(las, algorithm = tin())
ttops <- locate_trees(las, lmf(ws = 5))
plot_dtm3d(dtm)
x <- plot(las)
add_dtm3d(x, dtm)
add_treetops3d(x, ttops)
plot(las) |> add_dtm3d(dtm) |> add_treetops3d(ttops)
## End(Not run)
```
Usage

plugin_dsm(f, omp = FALSE)
plugin_dtm(f, omp = FALSE)
plugin_gnd(f, omp = FALSE)
plugin_decimate(f, omp = FALSE)
plugin_shape(f, omp = FALSE)
plugin_snag(f, omp = FALSE)
plugin_track(f, omp = FALSE)
plugin_nintensity(f, omp = FALSE)
plugin_outliers(f, omp = FALSE)
plugin_itd(f, omp = FALSE, raster_based = FALSE)
plugin_its(f, omp = FALSE, raster_based = FALSE)

Arguments

f        a function
omp      logical is the function natively parallized with OpenMP
raster_based   logical. For ITS and ITD algorithms, is the method raster-based or or point-
                cloud-based?

Examples

```r
## Not run:
mba <- function(n = 1, m = 1, h = 8, extend = TRUE) {
  f <- function(las, where) {
    res <- MBA::mba.points(las@data, where, n, m, h, extend)
    return(res$xyz.est[,3])
  }
  f <- plugin_dtm(f)
  return(f)
}

LASfile <- system.file("extdata", "Topography.laz", package="lidR")
las = readLAS(LASfile)
dtm = rasterize_terrain(las, algorithm = mba())
## End(Not run)
```
**point_metrics**

Point-based metrics

**Description**

Computes a series of user-defined descriptive statistics for a LiDAR dataset for each point based on its k-nearest neighbours or its sphere neighbourhood.

**Usage**

```r
point_metrics(las, func, k, r, xyz = FALSE, filter = NULL, ...)
```

```r
point_eigenvalues(las, k, r, xyz = FALSE, metrics = FALSE, filter = NULL)
```

**Arguments**

- `las`: An object of class LAS
- `func`: formula. An expression to be applied to each point neighbourhood (see also `template_metrics`).
- `k, r`: integer and numeric respectively for k-nearest neighbours and radius of the neighborhood sphere. If k is given and r is missing, computes with the knn, if r is given and k is missing computes with a sphere neighborhood, if k and r are given computes with the knn and a limit on the search distance.
- `xyz`: logical. Coordinates of each point are returned in addition to each metric. Otherwise an ID referring to each point.
- `filter`: formula of logical predicates. Enables the function to run only on points of interest in an optimized way. See examples.
- `...`: unused.
- `metrics`: logical. Compute metrics or not

**Details**

When the neighbourhood is knn the user-defined function is fed with the current processed point and its k-1 neighbours. The current point being considered as the 1-neighbour with a distance 0 to the reference point. The points are ordered by distance to the central point. When the neighbourhood is a sphere the processed point is also included in the query but points are coming in a random order. `point_eigenmetrics` computes the eigenvalues of the covariance matrix and computes associated metrics following Lucas et al, 2019 (see references). It is equivalent to `point_metrics(las, .stdshapemetrics)` but much faster because it is optimized and parallelized internally.

**Performances**

It is important to bear in mind that this function is very fast for the feature it provides i.e. mapping a user-defined function at the point level using optimized memory management. However, it is still computationally demanding.
To help users to get an idea of how computationally demanding this function is, let's compare it to \texttt{pixel_metrics}. Assuming we want to apply \texttt{mean(Z)} on a 1 km² tile with 1 point/m² with a resolution of 20 m (400 m² cells), then the function \texttt{mean} is called roughly 2500 times (once per cell). On the contrary, \texttt{point_metrics} 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.

\textbf{Examples}

```r
# 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_shapes(las, shp_plane(k = 25), "planar")
#> Computed in 0.1 seconds
all.equal(M$planar, las$planar)

# At this stage we can be clever and find that the bottleneck is
# the eigenvalue computation. Let's write a C++ version of it with
# Rcpp and RcppArmadillo
Rcpp::sourceCpp(code = "
#include <RcppArmadillo.h>
// [[Rcpp::depends(RcppArmadillo)]]

// [[Rcpp::export]]
SEXP eigen_values(arma::mat A) {
  arma::mat coeff;
  arma::mat score;
  arma::vec latent;
  arma::princomp(coeff, score, latent, A);
  ")
```
return(Rcpp::wrap(latent));
)

plane_metrics2 = function(x,y,z, th1 = 25, th2 = 6) {
  xyz <- cbind(x,y,z)
  eigen_m <- eigen_values(xyz)
  is_planar <- eigen_m[2] > (th1*eigen_m[3]) && (th2*eigen_m[2]) > eigen_m[1]
  return(list(planar = is_planar))
}

M <- point_metrics(las, ~plane_metrics2(X,Y,Z), k = 25)
#> Computed in 0.5 seconds

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++.

M <- point_eigenvalues(las, k = 25)
is_planar = M$eigen_medium > (25*M$eigen_smallest) & (6*M$eigen_medium) > M$eigen_largest

# 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.

## End(Not run)

print.LAS

Tools inherited from base R for LAS* objects

### Description

Tools inherited from base R for LAS* objects

### Usage

#### S3 method for class 'LAS'
print(x, ...)

#### S3 method for class 'LAScatalog'
print(x, ...)

#### S3 method for class 'lidRAalgorithm'
print(x, ...)

#### S3 method for class 'raster_template'
print(x, ...)

#### S3 method for class 'LAS'
summary(object, ...)
## S3 method for class 'LAScatalog'
summary(object, ...)

## S3 method for class 'LAS'
dim(x)

## S3 method for class 'LAScatalog'
dim(x)

ncol.LAS(x)

nrow.LAScatalog(x)

## S3 method for class 'LAS'
names(x)

## S3 method for class 'LASheader'
names(x)

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

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**: a LAS* object
- **...**: LAS* objects if it is the sole argument (e.g. in rbind())
- **object**: A LAS* object or other lidR related objects.

---

range_correction: *Intensity normalization algorithm*
Description

This function is made to be used in normalize_intensity. It corrects intensity with a range correction according to the formula (see references):

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

To achieve the range correction the position of the sensor must be known at different discrete times. Using the ‘gpstime’ of each point, the position of the sensor is interpolated from the reference and a range correction is applied.

Usage

```r
range_correction(sensor, Rs, f = 2.3, gpstime = "gpstime", elevation = "Z")
get_range(las, sensor, gpstime = "gpstime", elevation = "Z")
```

Arguments

- **sensor**: `SpatialPointsDataFrame` or `sf` 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’). Z can also come from the geometry if the input records XYZ coordinates. It can be computed with `track_sensor`.
- **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 the input contains 3 coordinates points, ‘elevation’ is not considered.
- **las**: an object of class LAS. `get_range()` is a regular function documented here for convenience.

References


Examples

```r
# 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

```r
las <- normalize_intensity(las, range_correction(sensor, Rs = 2000))
```

This might be useful for some applications

```r
R = get_range(las, sensor)
```

---

**rasterize**  
*Rasterize a point cloud*

**Description**

Rasterize a point cloud in different ways to compute a DTM, a CHM or a density map. Most raster products can be computed with `pixel_metrics` but some are more complex and require dedicated and optimized functions. See Details and Examples.

**Usage**

```r
rasterize_canopy(las, res = 1, algorithm = p2r(), ...)
```

```r
rasterize_density(las, res = 4, ...)
```

```r
rasterize_terrain(
  las,
  res = 1,
  algorithm = tin(),
  use_class = c(2L, 9L),
  shape = "convex",
  ...
)
```

**Arguments**

- `las`  
  An object of class LAS or LAScatalog.

- `res`  
  numeric. The size of a grid cell in point cloud coordinates units. Can also be RasterLayer or a stars or a SpatRaster used as layout.

- `algorithm`  
  function. A function that implements an algorithm to compute a digital surface model or a digital terrain model. lidR implements p2r, dsmin, pitfree for digital surface models, and knnmdw, tin, and kriging for digital terrain models (see respective documentation and examples).

- `...`  
  Use pkg = "terra|raster|stars" to get an output in SpatRaster, RasterLayer or stars format. Default is getOption("lidR.raster.default").

- `use_class`  
  integer vector. By default the terrain is computed by using ground points (class 2) and water points (class 9).

- `shape`  
  By default the interpolation is made only within the "convex" hull of the point cloud to get a DTM with the shape of the point cloud. This prevents meaningless interpolations where there is no data. It can also be "concave" or "bbox". It can also be an sfc to define a polygon in which to perform the interpolation.
Details

rasterize_terrain Interpolates the ground points and creates a rasterized digital terrain model. The algorithm uses the points classified as "ground" and "water" (Classification = 2 and 9, respectively, according to LAS file format specifications) to compute the interpolation. How well the edges of the dataset are interpolated depends on the interpolation method used. A buffer around the region of interest is always recommended to avoid edge effects.

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

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

Value

RasterLayer or a stars or a SpatRaster depending on the settings.

Non-supported LAScatalog options

The option select is not supported and not respected in rasterize_* because it is internally known what is best to select.
The option chunk_buffer is not supported and not respected in rasterize_canopy and rasterize_density because it is not necessary.

Examples

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

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

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

# Not run:
plot(dtm1, col = gray(0:25/25))
plot(dtm2, col = gray(0:25/25))
plot(dtm3, col = gray(0:25/25))
plot_dtm3d(dtm1)
plot_dtm3d(dtm2)
plot_dtm3d(dtm3)

## End(Not run)

# Digital Surface Model
```
# ===========
LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
las <- readLAS(LASfile, filter = "-inside 481280 3812940 481330 3812990")
col <- height.colors(15)

# Points-to-raster algorithm with a resolution of 1 meter
chm <- rasterize_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 <- rasterize_canopy(las, res = 0.5, p2r(0.2))
plot(chm, col = col)

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

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

# ===========
# Digital Density Map
# ===========

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

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

las <- retrieve_pulses(las)
d <- rasterize_density(las)
plot(d)

---

**readLAS**

**Read .las or .laz files**

**Description**

Reads .las or .laz files into an object of class **LAS**. If several files are read at once the returned LAS object is considered as one LAS file. The optional parameters enable the user to save a substantial amount of memory by choosing to load only the attributes or points of interest. LAS formats 1.0 to 1.4 are supported. Point Data Record Format 0 to 10 are supported.

**readLAS** is the original function and always works. Using one of the **read*LAS** functions adds information to the returned object to register a point-cloud type. Registering the correct point type
may improve the performance of some functions by enabling users to select an appropriate spatial index. See spatial indexing. Notice that by legacy and for backwards-compatibility reasons, readLAS() and readALSLAS() are equivalent because liR was originally designed for ALS and thus the original function readLAS() was (supposedly) used for ALS. Reading a TLS dataset with readLAS() instead of readTLSLAS() is perfectly valid and performs similarly to versions <= 3.0.0, with neither performance degradation nor improvements.

Usage

readLAS(files, select = "*", filter = "")
readALSLAS(files, select = "*", filter = "")
readTLSLAS(files, select = "*", filter = "")
readUAVLAS(files, select = "*", filter = "")
readDAPLAS(files, select = "*", filter = "")
readMSLAS(files1, files2, files3, select = "+", filter = "+")

Arguments

files characters. Path(s) to one or several a file(s). Can also be a 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).
files1, files2, files3 characters. Path(s) to one or several a file(s). Each argument being one channel (see section 'Multispectral data').

Details

Select: the 'select' argument specifies the data that will actually be loaded. For example, 'xyzia' means that the x, y, and z coordinates, the intensity and the scan angle will be loaded. The supported entries are t - gpstime, a - scan angle, i - intensity, n - number of returns, r - return number, c - classification, s - synthetic flag, k - keypoint flag, w - withheld flag, o - overlap flag (format 6+), u - user data, p - point source ID, e - edge of flight line flag, d - direction of scan flag, R - red channel of RGB color, G - green channel of RGB color, B - blue channel of RGB color, N - near-infrared channel, C - scanner channel (format 6+), W - Full waveform. Also numbers from 1 to 9 for the extra bytes data numbers 1 to 9. 0 enables all extra bytes to be loaded and '+' is the wildcard that enables everything to be loaded from the LAS file. Note that x, y, z are implicit and always loaded. 'xyzia' is equivalent to 'ia'.

Filter: the 'filter' argument allows filtering of the point cloud while reading files. This is much more efficient than filter_poi in many ways. If the desired filters are known before reading the file, the internal filters should always be preferred. The available filters are those from LASlib and can be found by running the following command: readLAS(filter = "-help"). (see also rlas::read.las). From r1as v1.3.6 the transformation commands can also be passed via the argument filter.
Value
A LAS object

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

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

Multispectral data
Multispectral laser data are often stored in 3 different files. If this is the case readMSLAS reads the .las or .laz files of each channel and merges them into an object of class LAS and takes care of attributing an ID to each channel. If the multispectral point cloud is already stored in a single file leave file2 and file3 missing.

Examples

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

readLAScatalog is the original function and always works. Using one of the read*LAScatalog
functions adds information to the returned object to register a point-cloud type. Registering the correct point type may improve the performance of some functions by enabling users to select an appropriate spatial index. See spatial indexing. Notice that by legacy and for backwards-compatibility reasons readLAScatalog() and readALSLAScatalog() are equivalent because lidR was originally designed for ALS and thus the original function readLAScatalog() was (supposedly) used for ALS.

Usage

readLAScatalog(
  folder,
  progress = TRUE,
  select = "*",
  filter = "",
  chunk_size = 0,
  chunk_buffer = 30,
  ...
)

readALSLAScatalog(folder, ...)
readTLSLAScatalog(folder, ...)
readUAVLAScatalog(folder, ...)
readDAPLAScatalog(folder, ...)
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 engine_options.
...
  Extra parameters to list.files. Typically recursive = TRUE. Propagates also to readLAScatalog

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/folder/of/las/>")

# Internal engine will sequentially process chunks of size 500 x 500 m
opt_chunk_size(ctg) <- 500

# Internal engine will align the 500 x 500 m chunks on x = 250 and y = 300
opt_alignment(ctg) <- c(250, 300)

# Internal engine will not display a progress estimation
opt_progress(ctg) <- FALSE

# Internal engine will not return results into R.
# Instead it will write results in files.
# Files will be named e.g.
# filename_256000_1.ext
# filename_257000_2.ext
# filename_258000_3.ext
# ...
# More details in the documentation
opt_output_files(ctg) <- "/path/filename_{XBOTTOM}_{ID}"

# More details in the documentation
help("LAScatalog-class", "lidR")
help("engine_options", "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**

```r
readLASHeader(file)
```

**Arguments**

- **file** characters. Path to one file.

**Value**

A LASHeader object
Examples

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

print(header)
plot(header)

## Not run:
plot(header, mapview = TRUE)
## End(Not run)

---

### retrieve_pulses

#### 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

```r
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile)
las <- retrieve_pulses(las)
las
las <- retrieve_flightlines(las)
#plot(las, color = "flightlineID")
```

---

**sample_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/m² 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

```r
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: `sample_maxima`, `sample_per_voxel`, `sample_random`
### Examples

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

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

### Point Cloud Decimation Algorithm

#### Description

These functions are made to be used in `decimate_points`. They implement algorithms that create a grid with a given resolution and filters the point cloud by selecting the highest/lowest point within each cell.

#### Usage

```
highest(res = 1)

lowest(res = 1)
```

#### Arguments

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

#### See Also

Other point cloud decimation algorithms: `sample_homogenize, sample_per_voxel, sample_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)

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

Description

This function is made to be used in `decimate_points`. It implements an algorithm that creates a 3D grid with a given resolution and filters the point cloud by randomly selecting \( n \) points within each voxel.

Usage

```r
random_per_voxel(res = 1, n = 1)
```

Arguments

- `res`: numeric. The resolution of the voxel grid used to filter the point cloud.
- `n`: integer. The number of points to select.

See Also

Other point cloud decimation algorithms: `sample_homogenize`, `sample_maxima`, `sample_random`

Examples

```r
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile, select = "xyz")
thinned <- decimate_points(las, random_per_voxel(8, 1))
#plot(thinned)
```

sample_random  

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

```r
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: `sample_homogenize`, `sample_maxima`, `sample_per_voxel`

Examples

```r
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))
```

---

**segment**

*Segment a point cloud*

Description

Segment a point cloud using different methods. `segment_*` functions add a new attribute to the point cloud to label each point. They segment either individual trees, snags, or geometrical features.

Usage

```r
segment_shapes(las, algorithm, attribute = "Shape", filter = NULL)
segment_snags(las, algorithm, attribute = "snagCls")
segment_trees(las, algorithm, attribute = "treeID", uniqueness = "incremental")
```

Arguments

- `las`: An object of class `LAS` or `LAScatalog`.
- `algorithm`: function. An algorithm for segmentation. For individual tree segmentation, `lidR` has `dalponte2016`, `watershed`, `li2012`, and `silva2016`. More experimental algorithms may be found in the package `lidRplugins`. For snag segmentation, `lidR` has `wing2015`. For geometry segmentation, `lidR` has `shp_plane`, `shp_hplane`, and `shp_line`.
- `attribute`: character. The returned LAS object as a new attribute (in a new column). This parameter controls the name of the new attribute.
- `filter`: formula of logical predicates. Enables the function to run only on points of interest in an optimized way. See the examples.
- `uniqueness`: character. A method to compute a unique ID. Can be ‘incremental’, ‘gptstime’ or ‘bitmerge’. See section ‘Uniqueness’. This feature must be considered as ‘experimental’.
Details

segment_trees  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.

segment_shapes  Computes, for each point, the eigenvalues of the covariance matrix of the neighbouring points. The eigenvalues are later used either to segment linear/planar points or to compute derived metrics. The points that meet a given criterion based on the eigenvalue are labelled as approximately coplanar/colinear or any other shape supported.

segment_snags  Snag segmentation using several possible algorithms. 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 is implemented, which uses LiDAR intensity thresholds and specified neighbourhoods to differentiate bole and branch from foliage points.

Non-supported LAScatalog options

The option select is not supported and not respected because it always preserves the file format and all the attributes. select = "*" is imposed internally.

Uniqueness

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

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

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

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

bitmerge  This method uses the XY coordinates of the highest point (apex) of a tree to create a single 64-bit number with a bitwise operation. First, XY coordinates are converted to 32-bit integers using the scales and offsets of the point cloud. For example, if the apex is at (10.32, 25.64) with a scale factor of 0.01 and an offset of 0, the 32-bit integer coordinates are X = 1032 and Y = 2564. Their binary representations are, respectively, (here displayed as 16 bits) 0000010000001000 and 0000101000000100. X is shifted by 32 bits and becomes
a 64-bit integer. Y is kept as-is and the binary representations are unionized into a 64-bit integer like (here displayed as 32 bit) 00000100000100000000101000000100 that is guaranteed to be unique. However R does not support 64-bit integers. The previous steps are done at C++ level and the 64-bit binary representation is reinterpreted into a 64-bit decimal number to be returned in R. The IDs thus generated are somewhat weird. For example, the tree ID 00000100000100000000101000000100 which is 67635716 if interpreted as an integer becomes 3.34164837074751323479078607289E-316 if interpreted as a decimal number. This is far from optimal but at least it is guaranteed to be unique if all files have the same offsets and scale factors.

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

Examples

```r
# ==============
# Segment trees
# ==============

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")

# ==============
# Segment shapes
# ==============

LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile, filter = "-keep_random_fraction 0.5")
# Use the eigenvalues to estimate if points are part of a local plan
las <- segment_shapes(las, shp_plane(k = 15), "Coplanar")
#plot(las, color = "Coplanar")

## Not run:
# Drop ground point at runtime
las <- segment_shapes(las, shp_plane(k = 15), "Coplanar", filter = "Classification != 2L")
#plot(las, color = "Coplanar")

# ==============
# Segment snags
# ==============

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)
```

set_lidr_threads <- 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)

---

**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. 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**

```r
set_lidr_threads(threads)
get_lidr_threads()
```

**Arguments**

- `threads` Positive scalar. Default 0 means use all CPU available. Values > 1 mean using `n` cores, values in \( [0, 1] \) mean using a fraction of the cores e.g. 0.5 = half.

**See Also**

lidR-parallelism
Description

These functions are made to be used in `segment_shapes`. They implement algorithms for local neighbourhood 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)
shp_hline(th1 = 10, th2 = 0.02, k = 8)
shp_vline(th1 = 10, th2 = 0.98, k = 8)
```

Arguments

- `th1`, `th2`, `th3` numeric. Threshold values (see details)
- `k` integer. Number of neighbours used to estimate the neighborhood.

Details

In the following, $a_1$, $a_2$, $a_3$ denote the eigenvalues of the covariance matrix of the neighbouring points in ascending order. $|Z_1|$, $|Z_2|$, $|Z_3|$ denote the norm of the Z component of first, second and third axis of the decomposition. $th_1$, $th_2$, $th_3$ denote a set of threshold values. Points are labelled TRUE if they meet the following criteria. FALSE otherwise.

**shp_plane** Detection of plans based on criteria defined by Limberger & Oliveira (2015) (see references). A point is labelled TRUE if the neighborhood is approximately planar, that is:

$$a_2 > (th_1 \times a_1) \& (th_2 \times a_2) > a_3$$

**shp_hplane** The same as 'plane' but with an extra test on the orientation of the Z vector of the principal components to test the horizontality of the surface.

$$a_2 > (th_1 \times a_1) \& (th_2 \times a_2) > a_3 \& |Z_3| > th_3$$

In theory $|Z_3|$ 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 neighbourhood is approximately linear, that is:

$$th_1 \times a_2 < a_3 \& th_1 \times a_1 < a_3$$
**shape_detection**

**shape_detection** Detection of horizontal lines inspired by the Limberger & Oliveira (2015) criterion. A point is labelled TRUE if the neighbourhood is approximately linear and horizontal, that is:

\[
th_1 \times a_2 < a_3 \& th_1 \times a_1 < a_3 \& |Z_1| \leq th_2
\]

In theory \(|Z_1|\) should be exactly equal to 0. In practice 0.02 or 0.01 should be fine.

**shape_detection** Detection of vertical lines inspired by the Limberger & Oliveira (2015) criterion. A point is labelled TRUE if the neighbourhood is approximately linear and vertical, that is:

\[
th_1 \times a_2 < a_3 \& th_1 \times a_1 < a_3 \& |Z_1| > th_2
\]

In theory \(|Z_1|\) should be exactly equal to 1. In practice 0.98 or 0.99 should be fine.

**References**


**Examples**

```r
# Generating some data
n = 400
xplane = runif(n, 0, 6)
yplane = runif(n, 0, 6)
zplane = xplane + 0.8 * yplane + runif(n, 0, 0.1)
plane = data.frame(X = xplane, Y = yplane, Z = zplane)

xhplane = runif(n, 5, 15)
yhplane = runif(n, 0, 10)
zhplane = 5 + runif(n, 0, 0.0)
hplane = data.frame(X = xhplane, Y = yhplane, Z = zhplane)

tline = 1:n
xline = 0.05*tline
yline = 0.01*tline
zline = 0.02*tline + runif(n, 0, 0.1)
line = data.frame(X = xline, Y = yline, Z = zline)

thline = 1:n
xhline = 0.05*thline + runif(n, 0, 0.05)
yhline = 10 - 0.01*thline + runif(n, 0, 0.05)
zhline = 3 + runif(n, 0, 0.05)
hline = data.frame(X = xhline, Y = yhline, Z = zhline)

tvline = 1:n
xvline = 5 + runif(n, 0, 0.05)
yvline = 5 + runif(n, 0, 0.05)
zvline = 0.02*tline
vline = data.frame(X = xvline, Y = yvline, Z = zvline)
```
smooth_height

las <- rbind(plane, line, hplane, hline, vline)
las <- LAS(las)

las <- segment_shapes(las, shp_plane(k = 20), "plane")
las <- segment_shapes(las, shp_hplane(k = 20), "hplane")
las <- segment_shapes(las, shp_line(k = 20), "line")
las <- segment_shapes(las, shp_hline(k = 20), "hline")
las <- segment_shapes(las, shp_vline(k = 20), "vline")

#plot(las)
#plot(las, color = "plane")
#plot(las, color = "hplane")
#plot(las, color = "line")
#plot(las, color = "hline")
#plot(las, color = "vline")

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, for example to develop new algorithms.

Value

An object of the class LAS.

Examples

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

las <- decimate_points(las, highest(1))
#plot(las)

las <- smooth_height(las, 5, "gaussian", "circle", sigma = 2)
#plot(las)

las <- unsmooth_height(las)
#plot(las)
```

snag_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

```r
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.

- **BBPthrsh_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


Examples

LASfile <- system.file("extdata", "MixedConifer.laz", package="lidR")
# Wing also included -keep_single
poi = "-keep_first -inside 481260 3812920 481310 3812960"
las <- readLAS(LASfile, select = "xyzi", filter = poi)

# For the Wing2015 method, supply a matrix of snag BranchBolePtRatio conditional
# assessment thresholds (see Wing et al. 2015, Table 2, pg. 172)
bbpr_thresholds <- matrix(c(0.80, 0.80, 0.70,
                            0.85, 0.85, 0.60,
                            0.80, 0.80, 0.60,
                            0.90, 0.90, 0.55),
                            nrow =3, ncol = 4)

# Run snag classification and assign classes to each point
las <- segment_snags(las, wing2015(neigh_radii = c(1.5, 1, 2), BBPRthrsh_mat = bbpr_thresholds))

# Plot it all, tree and snag points...
#plot(las, color="snagCls", colorPalette = rainbow(5))

# Filter and plot snag points only
snags <- filter_poi(las, snagCls > 0)
#plot(snags, color="snagCls", colorPalette = rainbow(5)[-1])

# Wing et al's (2015) methods ended with performing tree segmentation on the
# classified and filtered point cloud using the watershed method

---

stdmetrics

Predefined standard metrics functions

Description

Predefined metrics functions intended to be used in *metrics function such as pixel_metrics, cloud_metrics, crown_metrics, voxel_metrics and so on. Each function comes with a convenient shortcuts for lazy coding. The lidR package aims to provide an easy way to compute user-defined metrics rather than to provide them. However, for efficiency and to save time, sets of standard metrics have been predefined (see details). Every function can be computed by every *metrics functions however stdmetrics* are more pixel-based metrics, stdtreemetrics are more tree-based metrics and stdshapemetrics are more point-based metrics. For example the metric zmean computed by stdmetrics_z makes sense when computed at the pixel level but brings no information at the voxel level.
stdmetrics

Usage

stdmetrics(x, y, z, i, rn, class, dz = 1, th = 2, zmin = 0)

stdmetrics_z(z, dz = 1, th = 2, zmin = 0)

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

stdmetrics_rn(rn, class = NULL)

stdmetrics_pulse(pulseID, rn)

stdmetrics_ctrl(x, y, z)

stdtreemetrics(x, y, z)

stdshapemetrics(x, y, z)

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.

Details

The function names, their parameters and the output names of the metrics rely on a nomenclature chosen for brevity:

- `z`: refers to the elevation
- `i`: refers to the intensity
- `rn`: refers to the return number
- `q`: refers to quantile
- `a`: refers to the ScanAngleRank or ScanAngle
- `n`: refers to a number (a count)
- `p`: refers to a percentage

For example, the metric named `zq60` refers to the elevation, quantile, 60 i.e. the 60th percentile of elevations. The metric `pground` refers to a percentage. It is the percentage of points classified as ground. The function `stdmetric_i` refers to metrics of intensity. A description of each existing metric can be found on the lidR wiki page.

Some functions have optional parameters. If these parameters are not provided the function computes only a subset of existing metrics. For example, `stdmetrics_i` requires the intensity values, but if the elevation values are also provided it can compute additional metrics such as cumulative intensity at a given percentile of height.

Each function has a convenient associated variable. It is the name of the function, with a dot before the name. This enables the function to be used without writing parameters. The cost of such a feature is inflexibility. It corresponds to a predefined behaviour (see examples)

```
stdmetrics is a combination of stdmetrics_ctrl + stdmetrics_z + stdmetrics_i + stdmetrics_rn
stdtreemetrics is a special function that works with crown_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


 Examples

```r
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile, select = "x", filter = "-keep_random_fraction 0.5")

# All the predefined metrics
m1 <- pixel_metrics(las, ~stdmetrics(X,Y,Z,Intensity,ReturnNumber,Classification,dz=1), res = 40)

# Convenient shortcut
m2 <- pixel_metrics(las, .stdmetrics, res = 40)

# Basic metrics from intensities
m3 <- pixel_metrics(las, ~stdmetrics_i(Intensity), res = 40)

# All the metrics from intensities
m4 <- pixel_metrics(las, ~stdmetrics_i(Intensity, Z, Classification, ReturnNumber), res = 40)

# Convenient shortcut for the previous example
m5 <- pixel_metrics(las, .stdmetrics_i, res = 40)

# Combine some predefined function with your own new metrics
# Here convenient shortcuts are no longer usable.
myMetrics = function(z, i, rn)
{
  first <- rn == 1L
  zfirst <- z[first]
  nfirst <- length(zfirst)
  above2 <- sum(z > 2)
  x <- above2/nfirst*100

  # User's metrics
  metrics <- list(
    above2aboven1st = x,         # Num of returns above 2 divided by num of 1st returns
    zimean = mean(z*i),         # Mean products of z by intensity
    zsqmean = sqrt(mean(z^2))  # Quadratic mean of z
  )

  # Combined with standard metrics
  return( c(metrics, stdmetrics_z(z)) )
}

m10 <- pixel_metrics(las, ~myMetrics(Z, Intensity, ReturnNumber), res = 40)
```

# Users can write their own convenient shortcuts like this:
`.myMetrics = ~myMetrics(Z, Intensity, ReturnNumber)
m1 <- pixel_metrics(las, .myMetrics, res = 40)

---

**st_area**

*Surface covered by a LAS* object

## Description

Surface covered by a LAS* object. The surface covered by a point cloud is mathematically 0. To compute non zero values the function uses different strategies. The area is computed based on the number of occupied cells, or on the area of the convex hull of the points depending on the density and the size of the point cloud. The result is necessarily an approximation that depends on the method used.

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 area covered because some regions are sampled twice. For a LASHeader it is computed with the bounding box. As a consequence, for the same file st_area applied on a LASHeader or on a LAS can return slightly different values. st_area() extends sf:st_area(), area() extends raster:area(). area() is provided for backward compatibility.

## Usage

```r
## S3 method for class 'LAS'
st_area(x, ...)

## S3 method for class 'LASheader'
st_area(x, ...)

## S3 method for class 'LAScatalog'
st_area(x, ...)

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

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

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

## Arguments

- `x`  
  An object of class LAS*.

- `...`  
  Unused.
**Value**

numeric. A number in the same units as the coordinate reference system.

---

**st_bbox**

**Bounding box of a LAS* object**

**Description**

Bounding box of a LAS* object. st_bbox() extends sf, extent() extends raster, bbox() extends sp, and ext() extends terra. The values returned are similar to their parent functions.

**Usage**

```r
## S3 method for class 'LAS'
st_bbox(obj, ...)

## S3 method for class 'LASheader'
st_bbox(obj, ...)

## S3 method for class 'LAScatalog'
st_bbox(obj, ...)

## S3 method for class 'LAScluster'
st_bbox(obj, ...)

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

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

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

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

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

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

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

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

## S4 method for signature 'LASHeader'
bbox(obj)

## S4 method for signature 'LAScatalog'
bbox(obj)

## S4 method for signature 'LAScluster'
bbox(obj)

### Arguments
- obj, x: An object of class LAS*.
- ...: unused

### Value
A bbox from sf, an Extent from raster, a matrix from sp, or a SpatExtent from terra.

### Examples
```r
f <- system.file("extdata", "example.las", package="rlas")
las <- readLAS(f)

st_bbox(las)
bbox(las)
extent(las)
ext(las)
```

---

**st_coordinates**

**Coordinates of a LAS* object in a matrix form**

### Description
Retrieve coordinates of a LAS* object in matrix form. It creates a copy of the coordinates because of the coercion from data.frame to matrix. This function inherits sf::st_coordinates

### Usage
- ## S3 method for class 'LAS'
  st_coordinates(x, z = TRUE, ...)
- ## S3 method for class 'LAScatalog'
  st_coordinates(x, ...)

st_crs

Arguments

x        A LAS* object
z        bool. Return XY or XYZ matrix
...      unused.

Value

matrix

Examples

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

Description

Get or set the projection of a LAS* object. st_crs() extends sf::st_crs(), projection() and crs() extend raster:projection() and raster:crs(). projection() and crs() are provided for backward compatibility. For epsg() and wkt(), see details.

Usage

## S3 method for class 'LAS'
st_crs(x, ...)

## S3 method for class 'LAScatalog'
st_crs(x, ...)

## S3 method for class 'LASheader'
st_crs(x, ...)

## S3 method for class 'LAScluster'
st_crs(x, ...)

## S3 replacement method for class 'LAS'
st_crs(x) <- value

## S3 replacement method for class 'LASheader'
st_crs(x) <- value

## S3 replacement method for class 'LAScatalog'
st_crs(x) <- value
projection(x, asText = TRUE)

projection(x) <- value

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

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

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

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

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

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

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

epsg(object, ...)
epsg(object) <- value

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

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

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

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

wkt(obj)
wkt(obj) <- value

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

\[ \text{wkt(obj)} \leftarrow \text{value} \]

## S4 method for signature 'LAS'

\[ \text{wkt(obj)} \]

## S4 replacement method for signature 'LAS'

\[ \text{wkt(obj)} \leftarrow \text{value} \]

### Arguments

- `x`, `object`, `obj`: An object of class LAS*
- `...`: Unused.
- `value`: A CRS or a crs or a proj4string string or WKT string or an EPSG code.
- `asText`: logical. If TRUE, the projection is returned as text. Otherwise a CRS object is returned.

### Details

There are two ways to store the CRS of a point cloud in a LAS file:

- Store an EPSG code (for LAS 1.0 to 1.3)
- Store a WTK string (for LAS 1.4)

On the other hand, R spatial packages use a crs object 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 crs, and also in a format that can be understood by other R packages.

- `st_crs` return the CRS in sf format.
- `st_crs<-`: assigns a CRS from a CR5 (sp), a crs (sf), a WKT string, a proj4string or an epsg code. It updates the header of the LAS object either with the EPSG code for LAS formats < 1.4 or with a WKT string.
- `epsg`: reads the epsg code from the header.
- `wkt`: reads the WKT string from the header.

### Value

A `st_crs()` returns a `sf::crs`. projection() and crs() return a sp::CRS and should no longer be used.

### Examples

```r
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las <- readLAS(LASfile)
# Get the EPSG code stored in the header (returns 0 if not recorded)
epsg(las)
```
```r
# Get the WKT string stored in the header (LAS >= 1.4)
wkt(las)

# Overwrite the CRS (but does not reproject)
st_crs(las) <- 26918
las
```

---

**st_hull**  
*Concave and convex hulls for LAS objects*

**Description**
Concave and convex hulls for LAS objects. `st_convex_hull` extends `sf::st_convex_hull` for LAS objects. Both functions return a `sfc_POLYGON`. `concaveman` is a very fast 2D concave hull algorithm for a set of points.

**Usage**

```r
st_concave_hull(x, method = "concaveman", ...)
```

```r
## S3 method for class 'LAS'
st_convex_hull(x)
```

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

**Arguments**
- **x, y**  
  An object of class LAS or XY coordinates of points in case of `concaveman`. This can be specified as two vectors x and y, a 2-column matrix x, a list with two components, etc.
- **method**  
  string, currently supports "concaveman".
- **...**  
  Propagate to the method.
- **concavity**  
  numeric a relative measure of concavity. 1 results in a relatively detailed shape, Infinity results in a convex hull. You can use values lower than 1, but they can produce pretty crazy shapes.
- **length_threshold**  
  numeric. When a segment length is below this threshold, it stops being considered for further detailed processing. Higher values result in simpler shapes.

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

Value

A sfc_POLYGON from sf or a data.frame in the case of concaveman

References


Examples

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

```r
LASfile <- system.file("extdata", "Megaplot.laz", package="lidR")
las = readLAS(LASfile, filter = "-drop_z_below 1")
hull = st_concave_hull(las, length_threshold = 10)
plot(hull)
```

---

### st_transform

**Transform or convert coordinates of LAS objects**

#### Description

Transform or convert coordinates of LAS objects `st_transform()` extends `sf::st_transform()`

#### Usage

```r
## S3 method for class 'LAS'
st_transform(x, crs, ...)
```

#### Arguments

- `x`, An object of class LAS
- `crs` crs object from sf or CRS object from sp
- `...` additional arguments `scale` and `xoffset, yoffset, zoffset` for the output LAS objects. It is not mandatory but recommended to consider providing such information. Otherwise it will be guessed automatically which might not be the best choice.
track_sensor

Value

A LAS object

Examples

LASfile <- system.file("extdata", "example.laz", package="rlas")
las = readLAS(LASfile)
st_crs(las)$Name
st_bbox(las)
tlas <- sf::st_transform(las, sf::st_crs(26918))
st_crs(tlas)$Name
st_bbox(tlas)

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
An sf object with POINT Z geometries. Information about the time interval and the score of the positioning (according to the method used) are also in the table of attributes.

Non-supported LAScatalog options
The option ‘select’ is not supported and not respected because it is internally known what is the best to select
The option ‘output_files’ is not supported and not respected because the output must be post-processed as a whole

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.

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(sf::st_geometry(flightlines), add = TRUE)

## Not run:
# With a LAScatalog "-drop_single" and "-thin_pulses_with_time"
# are used by default
c tg = readLAScatalog("folder/")
flightlines <- track_sensor(ctg, Roussel2020(pmin = 15))
plot(flightlines)

## End(Not run)

---

track_sensor_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.
track_sensor_roussel2020

**Author(s)**
Demetrios Gatziolis and Jean-Romain Roussel

**References**

**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)

---

**track_sensor_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 https://doi.org/10.31223/osf.io/k32qw

### Examples

```r
# 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)
```

---

`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**

```r
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`.

**Examples**

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

las2 = voxelize_points(las, 5)
#plot(las2, voxel = TRUE)
```
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"))
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