

Package ‘pliman’

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Title Tools for Plant Image Analysis

Version 2.0.1

Description Tools for single or batch image manipulation and analysis as described by Olivoto (2022) <[doi:10.1111/2041-210X.13803](https://doi.org/10.1111/2041-210X.13803)> that can be used to quantify plant leaf area, assess disease severity, count objects, obtain shape measures, object landmarks, and compute Elliptical Fourier Analysis of the object outline, as described by Claude (2008) <[doi:10.1007/978-0-387-77789-4](https://doi.org/10.1007/978-0-387-77789-4)>. Additionally, the package includes tools for analyzing grids, which enables high throughput field phenotyping using RGB imagery captured by unmanned aerial vehicles.

License GPL (>= 3)

URL <https://github.com/TiagoOlivoto/pliman>

BugReports <https://github.com/TiagoOlivoto/pliman/issues>

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R topics documented:

analyze_objects	4
analyze_objects_shp	15
apply_fun_to_imgs	18
as_image	20
calibrate	21
contours	22
custom_palette	22
dist_transform	23
efourier	24
efourier_coefs	25
efourier_error	26
efourier_inv	27
efourier_norm	28
efourier_power	29
efourier_shape	30
ellipse	32
get_pliman_viewer	33
ggplot_color	33
image_align	34
image_binary	35
image_combine	37
image_create	38
image_expand	39
image_index	40
image_prepare_mv	43
image_segment	44
image_segment_kmeans	47
image_segment_manual	48
image_segment_mask	49
image_shp	50
image_square	52
image_thinning_guo_hall	52
image_to_mat	53
image_view	54
landmarks	55
landmarks_add	56
landmarks_angle	57
landmarks_dist	58
landmarks_regradi	59
leading_zeros	60
make_brush	61
make_mask	62
measure_disease	63
measure_disease_byl	68
measure_disease_shp	71
object_edge	73

object_export	74
object_export_shp	77
object_label	79
object_map	81
object_mark	82
object_rgb	83
object_split	84
object_split_shp	86
object_to_color	87
otsu	88
palettes	89
pipe	90
pixel_index	91
pliman_images	92
pliman_viewer	93
plot.image_shp	93
plot_index	94
plot_index_shp	95
plot_lw	97
poly_apex_base_angle	98
poly_pcv	99
poly_width_at	100
prepare_to_shp	101
random_color	102
sad	103
separate_col	104
set_pliman_viewer	105
summary_index	105
utils_colorspace	107
utils_dpi	108
utils_file	110
utils_image	112
utils_measures	113
utils_objects	116
utils_pca	119
utils_pick	121
utils_polygon	123
utils_polygon_plot	129
utils_rows_cols	130
utils_shapes	131
utils_stats	134
utils_transform	134
utils_wd	141
watershed2	142

analyze_objects	<i>Analyzes objects in an image</i>
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Description

- `analyze_objects()` provides tools for counting and extracting object features (e.g., area, perimeter, radius, pixel intensity) in an image. See more at the **Details** section.
- `analyze_objects_iter()` provides an iterative section to measure object features using an object with a known area.
- `plot.anal_obj()` produces a histogram for the R, G, and B values when argument `object_index` is used in the function `analyze_objects()`.

Usage

```
analyze_objects(  
  img,  
  foreground = NULL,  
  background = NULL,  
  pick_palettes = FALSE,  
  viewer = get_pliman_viewer(),  
  reference = FALSE,  
  reference_area = NULL,  
  back_fore_index = "R/(G/B)",  
  fore_ref_index = "B-R",  
  reference_larger = FALSE,  
  reference_smaller = FALSE,  
  pattern = NULL,  
  parallel = FALSE,  
  workers = NULL,  
  watershed = TRUE,  
  veins = FALSE,  
  sigma_veins = 1,  
  ab_angles = FALSE,  
  ab_angles_percentiles = c(0.25, 0.75),  
  haralick = FALSE,  
  har_nbins = 32,  
  har_scales = 1,  
  har_band = 1,  
  pcv = FALSE,  
  pcv_niter = 100,  
  resize = FALSE,  
  trim = FALSE,  
  fill_hull = FALSE,  
  filter = FALSE,  
  invert = FALSE,  
  object_size = "medium",
```

```
    index = "NB",
    object_index = NULL,
    pixel_level_index = FALSE,
    return_mask = FALSE,
    efourier = FALSE,
    nharm = 10,
    threshold = "Otsu",
    k = 0.1,
    window_size = NULL,
    tolerance = NULL,
    extension = NULL,
    lower_noise = 0.1,
    lower_size = NULL,
    upper_size = NULL,
    topn_lower = NULL,
    topn_upper = NULL,
    lower_eccent = NULL,
    upper_eccent = NULL,
    lower_circ = NULL,
    upper_circ = NULL,
    randomize = TRUE,
    nrows = 1000,
    plot = TRUE,
    show_original = TRUE,
    show_chull = FALSE,
    show_contour = TRUE,
    contour_col = "red",
    contour_size = 1,
    show_lw = FALSE,
    show_background = TRUE,
    show_segmentation = FALSE,
    col_foreground = NULL,
    col_background = NULL,
    marker = FALSE,
    marker_col = NULL,
    marker_size = NULL,
    save_image = FALSE,
    prefix = "proc_",
    dir_original = NULL,
    dir_processed = NULL,
    verbose = TRUE
)

## S3 method for class 'anal_obj'
plot(
  x,
  which = "measure",
  measure = "area",
```

```

    type = c("density", "histogram"),
    ...
)

analyze_objects_iter(pattern, known_area, verbose = TRUE, ...)

```

Arguments

img	The image to be analyzed.
foreground, background	A color palette for the foreground and background, respectively (optional). If a character is used (eg., foreground = "fore"), the function will search in the current working directory a valid image named "fore".
pick_palettes	Logical argument indicating whether the user needs to pick up the color palettes for foreground and background for the image. If TRUE <code>pick_palette()</code> will be called internally so that the user can sample color points representing foreground and background.
viewer	The viewer option. This option controls the type of viewer to use for interactive plotting (eg., when pick_palettes = TRUE). If not provided, the value is retrieved using <code>get_pliman_viewer()</code> .
reference	Logical to indicate if a reference object is present in the image. This is useful to adjust measures when images are not obtained with standard resolution (e.g., field images). See more in the details section.
reference_area	The known area of the reference objects. The measures of all the objects in the image will be corrected using the same unit of the area informed here.
back_fore_index	A character value to indicate the index to segment the foreground (objects and reference) from the background. Defaults to "R/(G/B)". This index is optimized to segment white backgrounds from green leaves and a blue reference object.
fore_ref_index	A character value to indicate the index to segment objects and the reference object. It can be either an available index in pliman (see <code>pliman_indexes()</code>) or an own index computed with the R, G, and B bands. Defaults to "B-R". This index is optimized to segment green leaves from a blue reference object after a white background has been removed.
reference_larger, reference_smaller	Logical argument indicating when the larger/smaller object in the image must be used as the reference object. This only is valid when reference is set to TRUE and reference_area indicates the area of the reference object. IMPORTANT. When reference_smaller is used, objects with an area smaller than 1% of the mean of all the objects are ignored. This is used to remove possible noise in the image such as dust. So, be sure the reference object has an area that will be not removed by that cutpoint.
pattern	A pattern of file name used to identify images to be imported. For example, if pattern = "im" all images in the current working directory that the name matches the pattern (e.g., img1., image1., im2.-) will be imported as a list.

	Providing any number as pattern (e.g., pattern = "1") will select images that are named as 1.-, 2.-, and so on. An error will be returned if the pattern matches any file that is not supported (e.g., img1.pdf).
parallel	If TRUE processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time, especially when pattern is used is informed. When object_index is informed, multiple sections will be used to extract the RGB values for each object in the image. This may significantly speed up processing time when an image has lots of objects (say >1000).
workers	A positive numeric scalar or a function specifying the number of parallel processes that can be active at the same time. By default, the number of sections is set up to 50% of available cores.
watershed	If TRUE (default) performs watershed-based object detection. This will detect objects even when they are touching one other. If FALSE, all pixels for each connected set of foreground pixels are set to a unique object. This is faster but is not able to segment touching objects.
veins	Logical argument indicating whether vein features are computed. This will call <code>object_edge()</code> and applies the Sobel-Feldman Operator to detect edges. The result is the proportion of edges in relation to the entire area of the object(s) in the image. Note that THIS WILL BE AN OPERATION ON AN IMAGE LEVEL, NOT OBJECT! .
sigma_veins	Gaussian kernel standard deviation used in the gaussian blur in the edge detection algorithm
ab_angles	Logical argument indicating whether apex and base angles should be computed. Defaults to FALSE. If TRUE, <code>poly_apex_base_angle()</code> are called and the base and apex angles are computed considering the 25th and 75th percentiles of the object height. These percentiles can be changed with the argument <code>ab_angles_percentiles</code> .
ab_angles_percentiles	The percentiles indicating the heights of the object for which the angle should be computed (from the apex and the bottom). Defaults to <code>c(0.25, 0.75)</code> , which means considering the 25th and 75th percentiles of the object height.
haralick	Logical value indicating whether Haralick features are computed. Defaults to FALSE.
har_nbins	An integer indicating the number of bins using to compute the Haralick matrix. Defaults to 32. See Details
har_scales	A integer vector indicating the number of scales to use to compute the Haralick features. See Details.
har_band	The band to compute the Haralick features (1 = R, 2 = G, 3 = B). Defaults to 1.
pcv	Computes the Perimeter Complexity Value? Defaults to FALSE.
pcv_niter	An integer specifying the number of smoothing iterations for computing the Perimeter Complexity Value. Defaults to 100.
resize	Resize the image before processing? Defaults to FALSE. Use a numeric value of range 0-100 (proportion of the size of the original image).

trim	Number of pixels removed from edges in the analysis. The edges of images are often shaded, which can affect image analysis. The edges of images can be removed by specifying the number of pixels. Defaults to FALSE (no trimmed edges).
fill_hull	Fill holes in the binary image? Defaults to FALSE. This is useful to fill holes in objects that have portions with a color similar to the background. IMPORTANT: Objects touching each other can be combined into one single object, which may underestimate the number of objects in an image.
filter	Performs median filtering in the binary image? See more at image_filter() . Defaults to FALSE. Use a positive integer to define the size of the median filtering. Larger values are effective at removing noise, but adversely affect edges.
invert	Inverts the binary image if desired. This is useful to process images with a black background. Defaults to FALSE. If <code>reference = TRUE</code> is use, <code>invert</code> can be declared as a logical vector of length 2 (eg., <code>invert = c(FALSE, TRUE)</code>). In this case, the segmentation of objects and reference from the foreground using <code>back_fore_index</code> is performed using the default (not inverted), and the segmentation of objects from the reference is performed by inverting the selection (selecting pixels higher than the threshold).
object_size	The size of the object. Used to automatically set up tolerance and extension parameters. One of the following. "small" (e.g, wheat grains), "medium" (e.g, soybean grains), "large"(e.g, peanut grains), and "elarge" (e.g, soybean pods)‘.
index	A character value specifying the target mode for conversion to binary image when foreground and background are not declared. Defaults to "NB" (normalized blue). See image_index() for more details. User can also calculate your own index using the bands names, e.g. <code>index = "R+B/G"</code>
object_index	Defaults to FALSE. If an index is informed, the average value for each object is returned. It can be the R, G, and B values or any operation involving them, e.g., <code>object_index = "R/B"</code> . In this case, it will return for each object in the image, the average value of the R/B ratio. Use pliman_indexes_eq() to see the equations of available indexes.
pixel_level_index	Return the indexes computed in <code>object_index</code> in the pixel level? Defaults to FALSE to avoid returning large data.frames.
return_mask	Returns the mask for the analyzed image? Defaults to FALSE.
efourier	Logical argument indicating if Elliptical Fourier should be computed for each object. This will call efourier() internally. If <code>efourier = TRUE</code> is used, both standard and normalized Fourier coefficients are returned.
nharm	An integer indicating the number of harmonics to use. Defaults to 10. For more details see efourier() .
threshold	The threshold method to be used. <ul style="list-style-type: none"> • By default (<code>threshold = "Otsu"</code>), a threshold value based on Otsu’s method is used to reduce the grayscale image to a binary image. If a numeric value is informed, this value will be used as a threshold.

- If threshold = "adaptive", adaptive thresholding (Shafait et al. 2008) is used, and will depend on the k and windowsize arguments.
- If any non-numeric value different than "Otsu" and "adaptive" is used, an iterative section will allow you to choose the threshold based on a raster plot showing pixel intensity of the index.

k	a numeric in the range 0-1. when k is high, local threshold values tend to be lower. when k is low, local threshold value tend to be higher.
windowsize	windowsize controls the number of local neighborhood in adaptive thresholding. By default it is set to $1/3 * \text{minxy}$, where minxy is the minimum dimension of the image (in pixels).
tolerance	The minimum height of the object in the units of image intensity between its highest point (seed) and the point where it contacts another object (checked for every contact pixel). If the height is smaller than the tolerance, the object will be combined with one of its neighbors, which is the highest.
extension	Radius of the neighborhood in pixels for the detection of neighboring objects. Higher value smooths out small objects.
lower_noise	To prevent noise from affecting the image analysis, objects with lesser than 10% of the mean area of all objects are removed (lower_noise = 0.1). Increasing this value will remove larger noises (such as dust points), but can remove desired objects too. To define an explicit lower or upper size, use the lower_size and upper_size arguments.
lower_size, upper_size	Lower and upper limits for size for the image analysis. Plant images often contain dirt and dust. Upper limit is set to NULL, i.e., no upper limit used. One can set a known area or use lower_limit = 0 to select all objects (not advised). Objects that matches the size of a given range of sizes can be selected by setting up the two arguments. For example, if lower_size = 120 and upper_size = 140, objects with size greater than or equal 120 and less than or equal 140 will be considered.
topn_lower, topn_upper	Select the top n objects based on its area. topn_lower selects the n elements with the smallest area whereas topn_upper selects the n objects with the largest area.
lower_eccent, upper_eccent, lower_circ, upper_circ	Lower and upper limit for object eccentricity/circularity for the image analysis. Users may use these arguments to remove objects such as square papers for scale (low eccentricity) or cut petioles (high eccentricity) from the images. Defaults to NULL (i.e., no lower and upper limits).
randomize	Randomize the lines before training the model?
nrows	The number of lines to be used in training step. Defaults to 2000.
plot	Show image after processing?
show_original	Show the count objects in the original image?
show_chull	Show the convex hull around the objects? Defaults to FALSE.
show_contour	Show a contour line around the objects? Defaults to TRUE.

contour_col, contour_size	The color and size for the contour line around objects. Defaults to contour_col = "red" and contour_size = 1.
show_lw	If TRUE, plots the length and width lines on each object calling <code>plot_lw()</code> .
show_background	Show the background? Defaults to TRUE. A white background is shown by default when show_original = FALSE.
show_segmentation	Shows the object segmentation colored with random permutations. Defaults to FALSE.
col_foreground, col_background	Foreground and background color after image processing. Defaults to NULL, in which "black", and "white" are used, respectively.
marker, marker_col, marker_size	The type, color and size of the object marker. Defaults to NULL, which plots the object id. Use marker = "point" to show a point in each object or marker = FALSE to omit object marker.
save_image	Save the image after processing? The image is saved in the current working directory named as proc_* where * is the image name given in img.
prefix	The prefix to be included in the processed images. Defaults to "proc_".
dir_original, dir_processed	The directory containing the original and processed images. Defaults to NULL. In this case, the function will search for the image img in the current working directory. After processing, when save_image = TRUE, the processed image will be also saved in such a directory. It can be either a full path, e.g., "C:/Desktop/imgs", or a subfolder within the current working directory, e.g., "/imgs".
verbose	If TRUE (default) a summary is shown in the console.
x	An object of class anal_obj.
which	Which to plot. Either 'measure' (object measures) or 'index' (object index). Defaults to "measure".
measure	The measure to plot. Defaults to "area".
type	The type of plot. Either "hist" or "density". Partial matches are recognized.
...	Depends on the function: <ul style="list-style-type: none"> • For <code>analyze_objects_iter()</code>, further arguments passed on to <code>analyze_objects()</code>.
known_area	The known area of the template object.

Details

A binary image is first generated to segment the foreground and background. The argument `index` is useful to choose a proper index to segment the image (see `image_binary()` for more details). It is also possible to provide color palettes for background and foreground (arguments `background` and `foreground`, respectively). When this is used, a general linear model (binomial family) fitted to the RGB values to segment fore- and background.

Then, the number of objects in the foreground is counted. By setting up arguments such as `lower_size` and `upper_size`, it is possible to set a threshold for lower and upper sizes of the objects, respectively. The argument `object_size` can be used to set up pre-defined values of `tolerance` and `extension` depending on the image resolution. This will influence the watershed-based object segmentation. Users can also tune up `tolerance` and `extension` explicitly for a better precision of watershed segmentation.

If `watershed = FALSE` is used, all pixels for each connected set of foreground pixels in `img` are set to a unique object. This is faster, especially for a large number of objects, but it is not able to segment touching objects.

There are some ways to correct the measures based on a reference object. If a reference object with a known area (`reference_area`) is used in the image and `reference = TRUE` is used, the measures of the objects will be corrected, considering the unit of measure informed in `reference_area`. There are two main ways to work with reference objects.

- The first, is to provide a reference object that has a contrasting color with both the background and object of interest. In this case, the arguments `back_fore_index` and `fore_ref_index` can be used to define an index to first segment the reference object and objects to be measured from the background, then the reference object from objects to be measured.
- The second one is to use a reference object that has a similar color to the objects to be measured, but has a contrasting size. For example, if we are counting small brown grains, we can use a brown reference template that has an area larger (says 3 times the area of the grains) and then uses `reference_larger = TRUE`. With this, the larger object in the image will be used as the reference object. This is particularly useful when images are captured with background light, such as the example 2. Some types: (i) It is suggested that the reference object is not too much larger than the objects of interest (mainly when the `watershed = TRUE`). In some cases, the reference object can be broken into several pieces due to the watershed algorithm. (ii) Since the reference object will increase the mean area of the object, the argument `lower_noise` can be increased. By default (`lower_noise = 0.1`) objects with lesser than 10% of the mean area of all objects are removed. Since the mean area will be increased, increasing `lower_noise` will remove dust and noises more reliably. The argument `reference_smaller` can be used in the same way

By using `pattern`, it is possible to process several images with common pattern names that are stored in the current working directory or in the subdirectory informed in `dir_original`. To speed up the computation time, one can set `parallel = TRUE`.

`analyze_objects_iter()` can be used to process several images using an object with a known area as a template. In this case, all the images in the current working directory that match the `pattern` will be processed. For each image, the function will compute the features for the objects and show the identification (`id`) of each object. The user only needs to inform which is the `id` of the known object. Then, given the `known_area`, all the measures will be adjusted. In the end, a `data.frame` with the adjusted measures will be returned. This is useful when the images are taken at different heights. In such cases, the image resolution cannot be conserved. Consequently, the measures cannot be adjusted using the argument `dpi` from `get_measures()`, since each image will have a different resolution. NOTE: This will only work in an interactive section.

- Additional measures: By default, some measures are not computed, mainly due to computational efficiency when the user only needs simple measures such as area, length, and width.

- If `haralick = TRUE`, The function computes 13 Haralick texture features for each object based on a gray-level co-occurrence matrix (Haralick et al. 1979). Haralick features depend on the configuration of the parameters `har_nbins` and `har_scales`. `har_nbins` controls the number of bins used to compute the Haralick matrix. A smaller `har_nbins` can give more accurate estimates of the correlation because the number of events per bin is higher. While a higher value will give more sensitivity, `har_scales` controls the number of scales used to compute the Haralick features. Since Haralick features compute the correlation of intensities of neighboring pixels it is possible to identify textures with different scales, e.g., a texture that is repeated every two pixels or 10 pixels. By default, the Haralick features are computed with the R band. To change this default, use the argument `har_band`. For example, `har_band = 2` will compute the features with the green band.
- If `efourier = TRUE` is used, an Elliptical Fourier Analysis (Kuhl and Giardina, 1982) is computed for each object contour using `efourier()`.
- If `veins = TRUE` (experimental), vein features are computed. This will call `object_edge()` and applies the Sobel-Feldman Operator to detect edges. The result is the proportion of edges in relation to the entire area of the object(s) in the image. Note that THIS WILL BE AN OPERATION ON AN IMAGE LEVEL, NOT an OBJECT LEVEL! So, If vein features need to be computed for leaves, it is strongly suggested to use one leaf per image.
- If `ab_angles = TRUE` the apex and base angles of each object are computed with `poly_apex_base_angle()`. By default, the function computes the angle from the first pixel of the apex of the object to the two pixels that slice the object at the 25th percentile of the object height (apex angle). The base angle is computed in the same way but from the first base pixel.

Value

`analyze_objects()` returns a list with the following objects:

- `results` A data frame with the following variables for each object in the image:
 - `id`: object identification.
 - `x,y`: x and y coordinates for the center of mass of the object.
 - `area`: area of the object (in pixels).
 - `area_ch`: the area of the convex hull around object (in pixels).
 - `perimeter`: perimeter (in pixels).
 - `radius_min`, `radius_mean`, and `radius_max`: The minimum, mean, and maximum radius (in pixels), respectively.
 - `radius_sd`: standard deviation of the mean radius (in pixels).
 - `diam_min`, `diam_mean`, and `diam_max`: The minimum, mean, and maximum diameter (in pixels), respectively.
 - `major_axis`, `minor_axis`: elliptical fit for major and minor axes (in pixels).
 - `caliper`: The longest distance between any two points on the margin of the object. See `poly_caliper()` for more details
 - `length`, `width` The length and width of objects (in pixels). These measures are obtained as the range of x and y coordinates after aligning each object with `poly_align()`.
 - `radius_ratio`: radius ratio given by `radius_max / radius_min`.
 - `theta`: object angle (in radians).

- eccentricity: elliptical eccentricity computed using the ratio of the eigen values (inertia axes of coordinates).
- form_factor (Wu et al., 2007): the difference between a leaf and a circle. It is defined as $4\pi A/P$, where A is the area and P is the perimeter of the object.
- narrow_factor (Wu et al., 2007): Narrow factor (caliper / length).
- asp_ratio (Wu et al., 2007): Aspect ratio (length / width).
- rectangularity (Wu et al., 2007): The similarity between a leaf and a rectangle (length * width/ area).
- pd_ratio (Wu et al., 2007): Ratio of perimeter to diameter (perimeter / caliper)
- plw_ratio (Wu et al., 2007): Perimeter ratio of length and width (perimeter / (length + width))
- solidity: object solidity given by area / area_ch.
- convexity: The convexity of the object computed using the ratio between the perimeter of the convex hull and the perimeter of the polygon.
- elongation: The elongation of the object computed as $1 - \text{width} / \text{length}$.
- circularity: The object circularity given by $\text{perimeter}^2 / \text{area}$.
- circularity_haralick: The Haralick's circularity (CH), computed as $CH = m/sd$, where m and sd are the mean and standard deviations from each pixels of the perimeter to the centroid of the object.
- circularity_norm: The normalized circularity (Cn), to be unity for a circle. This measure is computed as $Cn = \text{perimeter}^2 / 4\pi * \text{area}$ and is invariant under translation, rotation, scaling transformations, and dimensionless.
- asm: The angular second-moment feature.
- con: The contrast feature
- cor: Correlation measures the linear dependency of gray levels of neighboring pixels.
- var: The variance of gray levels pixels.
- idm: The Inverse Difference Moment (IDM), i.e., the local homogeneity.
- sav: The Sum Average.
- sva: The Sum Variance.
- sen: Sum Entropy.
- dva: Difference Variance.
- den: Difference Entropy
- f12: Difference Variance.
- f13: The angular second-moment feature.
- statistics: A data frame with the summary statistics for the area of the objects.
- count: If pattern is used, shows the number of objects in each image.
- obj_rgb: If object_index is used, returns the R, G, and B values for each pixel of each object.
- object_index: If object_index is used, returns the index computed for each object.
- Elliptical Fourier Analysis: If efourier = TRUE is used, the following objects are returned.
 - efourier: The Fourier coefficients. For more details see [efourier\(\)](#).
 - efourier_norm: The normalized Fourier coefficients. For more details see [efourier_norm\(\)](#).

- `efourier_error`: The error between original data and reconstructed outline. For more details see `efourier_error()`.
- `efourier_power`: The spectrum of harmonic Fourier power. For more details see `efourier_power()`.
- `veins`: If `veins = TRUE` is used, returns, for each image, the proportion of veins (in fact the object edges) related to the total object(s)' area.
- `analyze_objects_iter()` returns a data.frame containing the features described in the results object of `analyze_objects()`.
- `plot.anal_obj()` returns a trellis object containing the distribution of the pixels, optionally for each object when `facet = TRUE` is used.

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References

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Examples

```
library(pliman)
img <- image_pliman("soybean_touch.jpg")
obj <- analyze_objects(img)
obj$statistics

##### Example 1 #####
# Enumerate the objects in the original image
# Return the top-5 grains with the largest area
```

```

top <-
  analyze_objects(img,
                 marker = "id",
                 topn_upper = 5)
top$results

#' ##### Example 1 #####
# Correct the measures based on the area of the largest object
# note that since the reference object

img <- image_pliman("flax_grains.jpg")
res <-
  analyze_objects(img,
                 index = "GRAY",
                 marker = "point",
                 show_contour = FALSE,
                 reference = TRUE,
                 reference_area = 6,
                 reference_larger = TRUE,
                 lower_noise = 0.3)

library(pliman)

img <- image_pliman("soy_green.jpg")
# Segment the foreground (grains) using the normalized blue index (NB, default)
# Shows the average value of the blue index in each object

rgb <-
  analyze_objects(img,
                 marker = "id",
                 object_index = "B",
                 pixel_level_index = TRUE)
# density of area
plot(rgb)

# histogram of perimeter
plot(rgb, measure = "perimeter", type = "histogram") # or 'hist'

# density of the blue (B) index
plot(rgb, which = "index")

```

analyze_objects_shp *Analyzes objects using shapefiles*

Description

Analyzes objects using shapefiles

Usage

```
analyze_objects_shp(
  img,
  nrow = 1,
  ncol = 1,
  buffer_x = 0,
  buffer_y = 0,
  prepare = FALSE,
  viewer = get_pliman_viewer(),
  index = "R",
  shapefile = NULL,
  interactive = FALSE,
  plot = FALSE,
  parallel = FALSE,
  workers = NULL,
  watershed = TRUE,
  filter = FALSE,
  object_size = "medium",
  efourier = FALSE,
  object_index = NULL,
  veins = FALSE,
  verbose = TRUE,
  invert = FALSE,
  ...
)
```

Arguments

<code>img</code>	An Image object
<code>nrow, ncol</code>	The number of rows and columns to generate the shapefile when shapefile is not declared. Defaults to 1.
<code>buffer_x, buffer_y</code>	Buffering factor for the width and height, respectively, of each individual shape's side. A value between 0 and 0.5 where 0 means no buffering and 0.5 means complete buffering (default: 0). A value of 0.25 will buffer the shape by 25% on each side.
<code>prepare</code>	Logical value indicating whether to prepare the image for analysis using image_prepare_mv() function. Defaults to FALSE. Set to TRUE to interactively align and crop the image before processing.
<code>viewer</code>	The viewer option. If not provided, the value is retrieved using get_pliman_viewer() . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the set_pliman_viewer() function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.

index	A character value specifying the target mode for conversion to binary image when foreground and background are not declared. Defaults to "NB" (normalized blue). See image_index() for more details. User can also calculate your own index using the bands names, e.g. <code>index = "R+B/G"</code>
shapefile	(Optional) An object created with image_shp() . If NULL (default), both <code>nrow</code> and <code>ncol</code> must be declared.
interactive	If FALSE (default) the grid is created automatically based on the image dimension and number of <code>nrow/columns</code> . If <code>interactive = TRUE</code> , users must draw points at the diagonal of the desired bounding box that will contain the grid.
plot	Plots the processed images? Defaults to FALSE.
parallel	If TRUE processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time, especially when <code>pattern</code> is used is informed. When <code>object_index</code> is informed, multiple sections will be used to extract the RGB values for each object in the image. This may significantly speed up processing time when an image has lots of objects (say >1000).
workers	A positive numeric scalar or a function specifying the number of parallel processes that can be active at the same time. By default, the number of sections is set up to 50% of available cores.
watershed	If TRUE (default) performs watershed-based object detection. This will detect objects even when they are touching one other. If FALSE, all pixels for each connected set of foreground pixels are set to a unique object. This is faster but is not able to segment touching objects.
filter	Performs median filtering in the binary image? See more at image_filter() . Defaults to FALSE. Use a positive integer to define the size of the median filtering. Larger values are effective at removing noise, but adversely affect edges.
object_size	Argument to control control the watershed segmentation. See analyze_objects() for more details.
efourier	Logical argument indicating if Elliptical Fourier should be computed for each object. This will call efourier() internally. If <code>efourier = TRUE</code> is used, both standard and normalized Fourier coefficients are returned.
object_index	Defaults to FALSE. If an index is informed, the average value for each object is returned. It can be the R, G, and B values or any operation involving them, e.g., <code>object_index = "R/B"</code> . In this case, it will return for each object in the image, the average value of the R/B ratio. Use pliman_indexes_eq() to see the equations of available indexes.
veins	Logical argument indicating whether vein features are computed. This will call object_edge() and applies the Sobel-Feldman Operator to detect edges. The result is the proportion of edges in relation to the entire area of the object(s) in the image. Note that THIS WILL BE AN OPERATION ON AN IMAGE LEVEL, NOT OBJECT! .
verbose	If TRUE (default) a summary is shown in the console.
invert	Inverts the binary image if desired. This is useful to process images with a black background. Defaults to FALSE. If <code>reference = TRUE</code> is use, <code>invert</code> can be declared as a logical vector of length 2 (eg., <code>invert = c(FALSE, TRUE)</code>). In

this case, the segmentation of objects and reference from the foreground using `back_fore_index` is performed using the default (not inverted), and the segmentation of objects from the reference is performed by inverting the selection (selecting pixels higher than the threshold).

... Additional arguments passed on to [analyze_objects](#).

Details

The `analyze_objects_shp` function performs object analysis on an image and generates shapefiles representing the analyzed objects. The function first prepares the image for analysis using the [image_prepare_mv\(\)](#) function if the `prepare` argument is set to `TRUE`. If a shapefile object is provided, the number of rows and columns for splitting the image is obtained from the shapefile. Otherwise, the image is split into multiple sub-images based on the specified number of rows and columns using the [object_split_shp\(\)](#) function. The objects in each sub-image are analyzed using the [analyze_objects\(\)](#) function, and the results are stored in a list. If parallel processing is enabled, the analysis is performed in parallel using multiple workers. The analysis results is

The output object provides access to various components of the analysis results, such as the analyzed object coordinates and properties. Additionally, the shapefiles representing the analyzed objects are included in the output object for further analysis or visualization.

Value

An object of class `anal_obj`. See more details in the Value section of [analyze_objects\(\)](#).

Examples

```
if(interactive()){
  library(pliman)

  # Computes the DGCI index for each flax leaf
  flax <- image_pliman("flax_leaves.jpg", plot =TRUE)
  res <-
    analyze_objects_shp(flax,
                        nrow = 3,
                        ncol = 5,
                        plot = FALSE,
                        object_index = "DGCI")

  plot(flax)
  plot(res$shapefiles)
  plot_measures(res, measure = "DGCI")
}
```

Description

Most of the functions in `pliman` can be applied to a list of images, but this can be not ideal to deal with lots of images, mainly if they have a high resolution. For curiosity, a 6000 x 4000 image use nearly 570 Megabytes of RAM. So, it would be impossible to deal with lots of images within R. `apply_fun_to_img()` applies a function to images stored in a given directory as follows:

- Create a vector of image names that contain a given pattern of name.
- Import each image of such a list.
- Apply a function to the imported image.
- Export the mutated image to the computer.

If `parallel` is set to `FALSE` (default), the images are processed sequentially, which means that one image needs to be imported, processed, and exported so that the other image can be processed. If `parallel` is set to `TRUE`, the images are processed asynchronously (in parallel) in separate R sessions (3) running in the background on the same machine. It may speed up the processing time when lots of images need to be processed.

Usage

```
apply_fun_to_imgs(
  pattern,
  fun,
  ...,
  dir_original = NULL,
  dir_processed = NULL,
  prefix = "",
  suffix = "",
  parallel = FALSE,
  workers = 3,
  verbose = TRUE
)
```

Arguments

<code>pattern</code>	A pattern to match the images' names.
<code>fun</code>	A function to apply to the images.
<code>...</code>	Arguments passed on to <code>fun</code> .
<code>dir_original, dir_processed</code>	The directory containing the original and processed images. Defaults to <code>NULL</code> , which means that the current working directory will be considered. The processed image will overwrite the original image unless a prefix/suffix be used or a subfolder is informed in <code>dir_processed</code> argument.
<code>prefix, suffix</code>	A prefix and/or suffix to be included in the name of processed images. Defaults to <code>""</code> .
<code>parallel</code>	If <code>TRUE</code> processes the images asynchronously (in parallel) in separate R sessions (3 by default) running in the background on the same machine. It may speed up the processing time, especially when <code>pattern</code> is used is informed.

workers	A positive numeric scalar or a function specifying the number of parallel processes that can be active at the same time. Defaults to 3.
verbose	Shows the progress in console? Defaults to TRUE.

Value

Nothing. The processed images are saved to the current working directory.

Examples

```
# apply_fun_to_imgs("pattern", image_resize, rel_size = 50)
```

as_image	<i>Create an Image object</i>
----------	-------------------------------

Description

This function is a simple wrapper around [EBImage::Image\(\)](#).

Usage

```
as_image(data, ...)
```

Arguments

data	A vector or array containing the pixel intensities of an image. If missing, the default 1x1 zero-filled array is used.
...	Additional arguments passed to EBImage::Image() .

Value

An Image object.

Examples

```
img <-
as_image(rnorm(150 * 150 * 3),
         dim = c(150, 150, 3),
         colormode = 'Color')
plot(img)
```

calibrate	<i>Calibrates distances of landmarks</i>
-----------	--

Description

Calibrating the actual size is possible if any interlandmark distance on the image is known. `calibrate()` can be used to determine the size of a known distance (cm) on the graph. I invite users to photograph the object together with a scale (e.g., ruler, micrometer...).

Usage

```
calibrate(img, viewer = get_pliman_viewer())
```

Arguments

<code>img</code>	An Image object
<code>viewer</code>	The viewer option. If not provided, the value is retrieved using <code>get_pliman_viewer()</code> . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the <code>set_pliman_viewer()</code> function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.

Value

A numeric (double) scalar value indicating the scale (in pixels per unit of known distance).

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Examples

```
if(isTRUE(interactive())){
  library(pliman)
  ##### compute scale (dots per unit of known distance) #####
  # only works in an interactive section
  # objects_300dpi.jpg has a known resolution of 300 dpi
  img <- image_pliman("objects_300dpi.jpg")
  # Larger square: 10 x 10 cm
  # 1) Run the function calibrate()
  # 2) Use the left mouse button to create a line in the larger square
  # 3) Declare a known distance (10 cm)
  # 4) See the computed scale (pixels per cm)
  calibrate(img)
```

```
# scale ~118
# 118 * 2.54 ~300 DPI
}
```

contours *Contour outlines from five leaves*

Description

A list of contour outlines from five leaves. It may be used as example in some functions such as [efourier\(\)](#)

Format

A list with five objects

- leaf_1
- leaf_2
- leaf_3
- leaf_4
- leaf_5

Each object is a `data.frame` with the coordinates for the outline perimeter

Author(s)

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Source

Personal data. The images were obtained in the Flavia data set downloadable at <https://flavia.sourceforge.net/>

custom_palette *Generate Custom Color Palette*

Description

This function generates a custom color palette using the specified colors and number of colors.

Usage

```
custom_palette(
  colors = c("#4B0055", "#00588B", "#009B95", "#53CC67", "yellow"),
  n = 100
)
```

Arguments

`colors` A vector of colors to create the color palette. Default is `c("steelblue", "salmon", "forestgreen")`.

`n` The number of gradient colors in the color palette. Default is 100.

Value

A vector of colors representing the custom color palette.

Examples

```
# Generate a custom color palette with default colors and 10 colors
custom_palette()

# Generate a custom color palette with specified colors and 20 colors
custom_palette(colors = c("blue", "red"), n = 20)

# example code
library(pliman)
custom_palette(n = 5)
```

`dist_transform` *Distance map transform*

Description

Computes the distance map transform of a binary image. The distance map is a matrix which contains for each pixel the distance to its nearest background pixel.

Usage

```
dist_transform(binary)
```

Arguments

`binary` A binary image

Value

An Image object or an array, with pixels containing the distances to the nearest background points

Examples

```
library(pliman)
img <- image_pliman("soybean_touch.jpg")
binary <- image_binary(img, "B")[[1]]
wts <- dist_transform(binary)
range(wts)
```

 efourier

Elliptical Fourier Analysis

Description

Computes Elliptical Fourier Analysis of closed outlines based on x and y-coordinates coordinates.

Usage

```
efourier(x, nharm = 10, align = FALSE, center = FALSE, smooth_iter = 0)
```

Arguments

x	A matrix, a data.frame a list of perimeter coordinates, often produced with <code>object_contour()</code> or a vector of landmarks produced with <code>landmarks()</code> or <code>landmarks_regradi()</code> .
nharm	An integer indicating the number of harmonics to use. Defaults to 10.
align	Align the objects before computing Fourier analysis? Defaults to FALSE. If TRUE, the object is first aligned along the major caliper with <code>poly_align()</code> .
center	Center the objects on the origin before computing Fourier analysis? Defaults to FALSE. If TRUE, the object is first centered on the origin with <code>poly_center()</code> .
smooth_iter	The number of smoothing iterations to perform. This will smooth the perimeter of the objects using <code>poly_smooth()</code> .

Details

Adapted from Claude (2008). pp. 222-223.

Value

A list of class `efourier` with:

- the harmonic coefficients (a_n , b_n , c_n and d_n)
- the estimates of the coordinates of the centroid of the configuration (a_0 and c_0).
- The number of rows (points) of the perimeter outline (nr).
- The number of harmonics used ($nharm$).
- The original coordinates (`coords`).

If `x` is a list of perimeter coordinates, a list of `efourier` objects will be returned as an object of class `iefourier_lst`.

References

- Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.
- Kuhl, F. P., and Giardina, C. R. (1982). Elliptic Fourier features of a closed contour. *Computer Graphics and Image Processing* 18, 236–258. doi: [doi:10.1016/0146664X\(82\)90034X](https://doi.org/10.1016/0146664X(82)90034X)

Examples

```
library(pliman)
leaf1 <- contours[[4]]
plot_polygon(leaf1)

#### default options
# 10 harmonics (default)
# without alignment

ef <- efourier(leaf1)
efourier_coefs(ef)

# object is aligned along the major caliper with `poly_align()`
# object is centered on the origin with `poly_center()`
# using a list of object coordinates
ef2 <- efourier(contours, align = TRUE, center = TRUE)
efourier_coefs(ef2)

# reconstruct the perimeter of the object
# Use only the first one for simplicity
plot_polygon(contours[[1]] |> poly_align() |> poly_center())
efourier_inv(ef2[[1]]) |> plot_contour(col = "red", lwd = 4)
```

efourier_coefs

Get Fourier coefficients

Description

Extracts the Fourier coefficients from objects computed with `efourier()` and `efourier_norm()` returning a 'ready-to-analyze' data frame.

Usage

```
efourier_coefs(x)
```

Arguments

x An object computed with `efourier()` or `efourier_norm()`.

Value

A data.frame object

Examples

```
library(pliman)

# a list of objects
efourier(contours) |> efourier_coefs()
```

```
# one object, normalized coefficients
efourier(contours[[4]]) |>
  efourier_norm() |>
  efourier_coefs()
```

efourier_error

Erros between the original and reconstructed outline

Description

Computes the sum of squared distances between the original data and reconstructed outline. It allows examining reconstructed outlines with the addition of successive contributing harmonics indicated in the argument `nharm`.

Usage

```
efourier_error(
  x,
  nharm = NULL,
  type = c("error", "outline", "deviations"),
  plot = TRUE,
  ncol = NULL,
  nrow = NULL
)
```

Arguments

<code>x</code>	An object computed with <code>efourier()</code> .
<code>nharm</code>	An integer or vector of integers indicating the number of harmonics to use. If not specified the number of harmonics used in <code>x</code> is used.
<code>type</code>	The type of plot to produce. By default, a line plot with the sum of squared distances (y-axis) and the number of harmonics (x-axis) is produced. If <code>type = "outline"</code> is used, a plot with the original polygon and the constructed outline is produced. If <code>type = "deviations"</code> is used, a plot with the deviations from the original outline and reconstructed outline (y-axis) and points along the outline (x-axis) is produced.
<code>plot</code>	A logical to inform if a plot should be produced. Defaults to <code>TRUE</code> .
<code>ncol, nrow</code>	The number of rows or columns in the plot grid. Defaults to <code>NULL</code> , i.e., a square grid is produced.

Value

A list with the objects:

- `dev_points` A list with the deviations (distances) from original and predicted outline for each pixel of the outline.

- data.frame object with the minimum, maximum and average deviations (based on the outline points).

If x is an object of class efourier_lst, a list will be returned.

Examples

```
library(pliman)
ef <-
  contours[[1]] |>
  efourier(nharm = 30)

efourier_error(ef)

efourier_error(ef,
              nharm = 30,
              type = "outline")

efourier_error(ef,
              nharm = c(1, 4, 20),
              type = "deviations")
```

 efourier_inv

Inverse Elliptical Fourier Analysis

Description

Performs an inverse elliptical Fourier transformation to construct a shape, given a list with Fourier coefficients computed with [efourier\(\)](#).

Usage

```
efourier_inv(x, nharm = NULL, a0 = NULL, c0 = NULL, npoints = 500)
```

Arguments

x	An object of class efourier or efourier_lst computed with efourier() .
nharm	An integer indicating the number of harmonics to use. If not specified the number of harmonics used in x is used.
a0, c0	the estimates of the coordinates of the centroid of the configuration. If NULL (default), the generated coordinates will be centered on the position of the original shape given by efourier() .
npoints	The number of interpolated points on the constructed outline. Defaults to 500.

Details

Adapted from Claude (2008). pp. 223.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Examples

```
library(pliman)
plot_polygon(contours, aspect_ratio = 1)
# without alignment
ef <- efourier(contours, nharm = 10, align = FALSE)
ief <- efourier_inv(ef)
plot_contour(ief, col = "red", lwd = 2)
```

efourier_norm	<i>Normalized Fourier coefficients</i>
---------------	--

Description

The first harmonic defines an ellipse that best fits the outlines. One can use the parameters of the first harmonic to “normalize” the data so that they can be invariant to size, rotation, and starting position of the outline trace. This approach is referred to in the literature as the normalized elliptic Fourier. `efourier_norm()` calculates a new set of Fourier coefficients A_n , B_n , C_n , D_n that one can use for further multivariate analyses (Claude, 2008).

Usage

```
efourier_norm(x, start = FALSE)
```

Arguments

x	An object computed with <code>efourier()</code> .
start	Logical value telling whether the position of the starting point has to be preserved or not.

Details

Adapted from Claude (2008). pp. 226.

Value

A list with the following components:

- A, B, C, D for harmonic coefficients.
- size the magnitude of the semi-major axis of the first fitting ellipse.
- theta angle, in radians, between the starting and the semi-major axis of the first fitting ellipse.
- psi orientation of the first fitting ellipse
- a0 and c0, harmonic coefficients.
- lnef the concatenation of coefficients.
- nharm the number of harmonics used.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Examples

```
library(pliman)
leaf1 <- contours[[4]]
plot_polygon(leaf1)

# compute the Fourier coefficients
ef <- efourier(leaf1)
efourier_coefs(ef)

# Normalized Fourier coefficients

efn <- efourier_norm(ef)
efourier_coefs(efn)
```

efourier_power

Power in Fourier Analysis

Description

Computes an spectrum of harmonic Fourier power. The power is proportional to the harmonic amplitude and can be considered as a measure of shape information. As the rank of harmonic increases, the power decreases and adds less and less information. We can evaluate the number of harmonics that we must select, so their cumulative power gathers 99% of the total cumulative power (Claude, 2008).

Usage

```
efourier_power(
  x,
  first = TRUE,
  thresh = c(0.8, 0.85, 0.9, 0.95, 0.99, 0.999),
  plot = TRUE,
  ncol = NULL,
  nrow = NULL
)
```

Arguments

x	An object of class <code>efouriercomputed</code> with <code>efourier()</code> .
first	Logical argument indicating whether to include the first harmonic for computing the power. See Details.
thresh	A numeric vector indicating the threshold power. The number of harmonics needed for such thresholds will then be computed.

plot	Logical argument indicating whether to produce a plot.
ncol, nrow	The number of rows or columns in the plot grid. Defaults to NULL, i.e., a square grid is produced.

Details

Most of the shape "information" is contained in the first harmonic. This is not surprising because this is the harmonic that best fits the outline, and the size of ellipses decreases as for explaining successive residual variation. However, one may think that the first ellipse does not contain relevant shape information, especially when differences one wants to investigate concern complex outlines. By using `first = FALSE` it is possible to remove the first harmonic for this computation. When working on a set of outlines, high-rank-harmonics can contain information that may allow groups to be distinguished (Claude, 2008).

Adapted from Claude (2008). pp. 229.

Value

A list with the objects:

- `cum_power`, a `data.frame` object with the accumulated power depending on the number of harmonics
-

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Examples

```
library(pliman)
pw <- efourier(contours) |> efourier_power()
```

efourier_shape *Draw shapes based on Fourier coefficients*

Description

Calculates a 'Fourier elliptical shape' given Fourier coefficients

Usage

```
efourier_shape(
  an = NULL,
  bn = NULL,
  cn = NULL,
  dn = NULL,
```

```

n = 1,
nharm = NULL,
npoints = 150,
alpha = 4,
plot = TRUE
)

```

Arguments

an	The a_n Fourier coefficients on which to calculate a shape.
bn	The b_n Fourier coefficients on which to calculate a shape.
cn	The c_n Fourier coefficients on which to calculate a shape.
dn	The d_n Fourier coefficients on which to calculate a shape.
n	The number of shapes to generate. Defaults to 1. If more than one shape is used, a list of coordinates is returned.
nharm	The number of harmonics to use. It must be less than or equal to the length of *_n coefficients.
npoints	The number of points to calculate.
alpha	The power coefficient associated with the (usually decreasing) amplitude of the Fourier coefficients.
plot	Logical indicating Whether to plot the shape. Defaults to 'TRUE'

Details

efourier_shape can be used by specifying nharm and alpha. The coefficients are then sampled in an uniform distribution $(-\pi; \pi)$ and this amplitude is then divided by $harmonicrank^\alpha$. If alpha is lower than 1, consecutive coefficients will thus increase. See Claude (2008) pp.223 for the maths behind inverse elliptical Fourier

Adapted from Claude (2008). pp. 223.

Value

A list with components:

- x vector of x-coordinates
- y vector of y-coordinates.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Examples

```

library(pliman)
# approximation of the third leaf's perimeter
# 4 harmonics
image_pliman("potato_leaves.jpg", plot = TRUE)

```

```
efourier_shape(an = c(-7.34, 1.81, -1.32, 0.50),  
               bn = c(-113.88, 21.90, -0.31, -6.14),  
               cn = c(-147.51, -20.89, 0.66, -14.06),  
               dn = c(-0.48, 2.36, -4.36, 3.03))
```

ellipse

Confidence ellipse

Description

Produces a confidence ellipse that is an iso-contour of the Gaussian distribution, allowing to visualize a 2D confidence interval.

Usage

```
ellipse(  
  x,  
  conf = 0.95,  
  np = 100,  
  plot = TRUE,  
  fill = "green",  
  alpha = 0.3,  
  random_fill = TRUE  
)
```

Arguments

x	A matrix, a data.frame or a list of perimeter coordinates, often produced with <code>object_contour()</code> .
conf	The confidence level. Defaults to 0.95
np	Number of sampled points on the ellipse.
plot	Create a plot? Defaults to TRUE.
fill	The color to fill the ellipse. Defaults to "green".
alpha	The alpha value to define the opacity of ellipse. Defaults to 0.3
random_fill	Fill multiple ellipses with random colors? Defaults to TRUE.

Value

A matrix with coordinates of points sampled on the ellipse.

Note

Borrowed from Claude (2008), pp. 85

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Examples

```
library(pliman)
ellipse(contours)
```

get_pliman_viewer	<i>Get the value of the pliman_viewer option</i>
-------------------	--

Description

Retrieves the current value of the pliman_viewer option used in the package.

Usage

```
get_pliman_viewer()
```

Value

The current value of the pliman_viewer option.

ggplot_color	<i>ggplot2-like colors generation</i>
--------------	---------------------------------------

Description

Generate ggplot2

Usage

```
ggplot_color(n = 1)
```

Arguments

n	The number of colors. This works well for up to about eight colours, but after that it becomes hard to tell the different colours apart.
---	--

Examples

```
library(pliman)
ggplot_color(n = 3)
```

image_align	<i>Aligns an Image object by hand</i>
-------------	---------------------------------------

Description

`image_rotate()` rotate an image given a line of desired alignment along the y axis that corresponds to the alignment of the objects (e.g., field plots). By default, the alignment will be to the vertical, which means that if the drawn line have an angle $< 90^\circ$ parallel to the x axis, the rotation angle will be negative (anticlockwise rotation).

Usage

```
image_align(
  img,
  align = c("vertical", "horizontal"),
  viewer = get_pliman_viewer(),
  plot = TRUE
)
```

Arguments

<code>img</code>	An Image object
<code>align</code>	The desired alignment. Either "vertical" (default) or "horizontal".
<code>viewer</code>	The viewer option. If not provided, the value is retrieved using <code>get_pliman_viewer()</code> . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the <code>set_pliman_viewer()</code> function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.
<code>plot</code>	Plots the aligned image? Defaults to TRUE.

Details

The `image_align` function aligns an image along the vertical or horizontal axis based on user-selected points. The alignment can be performed in either the base plotting system or using the mapview package for interactive visualization. If the viewer option is set to "base", the function prompts the user to select two points on the image to define the alignment line. If the viewer option is set to "mapview", the function opens an interactive map where the user can draw a polyline to define the alignment line. The alignment angle is calculated based on the selected points, and the image is rotated accordingly using the `image_rotate` function. The function returns the aligned image object.

Value

The `img` aligned

Examples

```
if(interactive()){
  library(pliman)
  flax <- image_pliman("flax_leaves.jpg", plot = TRUE)
  aligned <- image_align(flax)
}
```

image_binary	<i>Creates a binary image</i>
--------------	-------------------------------

Description

Reduce a color, color near-infrared, or grayscale images to a binary image using a given color channel (red, green blue) or even color indexes. The Otsu's thresholding method (Otsu, 1979) is used to automatically perform clustering-based image thresholding.

Usage

```
image_binary(
  img,
  index = NULL,
  threshold = c("Otsu", "adaptive"),
  k = 0.1,
  windowsize = NULL,
  has_white_bg = FALSE,
  resize = FALSE,
  fill_hull = FALSE,
  filter = FALSE,
  re = NULL,
  nir = NULL,
  invert = FALSE,
  plot = TRUE,
  nrow = NULL,
  ncol = NULL,
  parallel = FALSE,
  workers = NULL,
  verbose = TRUE
)
```

Arguments

img	An image object.
index	A character value (or a vector of characters) specifying the target mode for conversion to binary image. See the available indexes with pliman_indexes() and image_index() for more details.
threshold	The threshold method to be used.

- By default (threshold = "Otsu"), a threshold value based on Otsu's method is used to reduce the grayscale image to a binary image. If a numeric value is informed, this value will be used as a threshold.
- If threshold = "adaptive", adaptive thresholding (Shafait et al. 2008) is used, and will depend on the k and windowsize arguments.
- If any non-numeric value different than "Otsu" and "adaptive" is used, an interactive section will allow you to choose the threshold based on a raster plot showing pixel intensity of the index.

k	a numeric in the range 0-1. when k is high, local threshold values tend to be lower. when k is low, local threshold value tend to be higher.
windowsize	windowsize controls the number of local neighborhood in adaptive thresholding. By default it is set to $1/3 * \text{minxy}$, where minxy is the minimum dimension of the image (in pixels).
has_white_bg	Logical indicating whether a white background is present. If TRUE, pixels that have R, G, and B values equals to 1 will be considered as NA. This may be useful to compute an image index for objects that have, for example, a white background. In such cases, the background will not be considered for the threshold computation.
resize	Resize the image before processing? Defaults to FALSE. Use a numeric value as the percentage of desired resizing. For example, if resize = 30, the resized image will have 30% of the size of original image.
fill_hull	Fill holes in the objects? Defaults to FALSE.
filter	Performs median filtering in the binary image? (Defaults to FALSE). Provide a positive integer > 1 to indicate the size of the median filtering. Higher values are more efficient to remove noise in the background but can dramatically impact the perimeter of objects, mainly for irregular perimeters such as leaves with serrated edges.
re	Respective position of the red-edge band at the original image file.
nir	Respective position of the near-infrared band at the original image file.
invert	Inverts the binary image, if desired.
plot	Show image after processing?
nrow, ncol	The number of rows or columns in the plot grid. Defaults to NULL, i.e., a square grid is produced.
parallel	Processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time when image is a list. The number of sections is set up to 70% of available cores.
workers	A positive numeric scalar or a function specifying the maximum number of parallel processes that can be active at the same time.
verbose	If TRUE (default) a summary is shown in the console.

Value

A list containing binary images. The length will depend on the number of indexes used.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

References

- Otsu, N. 1979. Threshold selection method from gray-level histograms. *IEEE Trans Syst Man Cybern SMC-9*(1): 62–66. doi:[10.1109/tsmc.1979.4310076](https://doi.org/10.1109/tsmc.1979.4310076)
- Shafait, F., D. Keysers, and T.M. Breuel. 2008. Efficient implementation of local adaptive thresholding techniques using integral images. *Document Recognition and Retrieval XV*. SPIE. p. 317–322 doi:[10.1117/12.767755](https://doi.org/10.1117/12.767755)

Examples

```
library(pliman)
img <- image_pliman("soybean_touch.jpg")
image_binary(img, index = c("R", "G"))
```

image_combine	<i>Combines images to a grid</i>
---------------	----------------------------------

Description

Combines several images to a grid

Usage

```
image_combine(
  ...,
  labels = NULL,
  nrow = NULL,
  ncol = NULL,
  col = "black",
  verbose = TRUE
)
```

Arguments

- | | |
|------------|---|
| ... | a comma-separated name of image objects or a list containing image objects. |
| labels | A character vector with the same length of the number of objects in ... to indicate the plot labels. |
| nrow, ncol | The number of rows or columns in the plot grid. Defaults to NULL, i.e., a square grid is produced. |
| col | The color for the plot labels. Defaults to col = "black". |
| verbose | Shows the name of objects declared in ... or a numeric sequence if a list with no names is provided. Set to FALSE to suppress the text. |

Value

A grid with the images in . . .

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(pliman)
img1 <- image_pliman("sev_leaf.jpg")
img2 <- image_pliman("sev_leaf_nb.jpg")
image_combine(img1, img2)
```

image_create

Create an Image object of a given color

Description

image_create() can be used to create an Image object with a desired color and size.

Usage

```
image_create(color, width = 200, height = 200, plot = FALSE)
```

Arguments

color	either a color name (as listed by <code>grDevices::colors()</code>), or a hexadecimal string of the form "#rrggbb".
width, height	The width and height of the image in pixel units.
plot	Plots the image after creating it? Defaults to FALSE.

Value

An object of class Image.

Examples

```
image_create("red")
image_create("#009E73", width = 300, height = 100)
```

image_expand	<i>Expands an image</i>
--------------	-------------------------

Description

Expands an image towards the left, top, right, or bottom by sampling pixels from the image edge. Users can choose how many pixels (rows or columns) are sampled and how many pixels the expansion will have.

Usage

```
image_expand(
  img,
  left = NULL,
  top = NULL,
  right = NULL,
  bottom = NULL,
  edge = NULL,
  sample_left = 10,
  sample_top = 10,
  sample_right = 10,
  sample_bottom = 10,
  random = FALSE,
  filter = NULL,
  plot = TRUE
)
```

Arguments

img	An Image object.
left, top, right, bottom	The number of pixels to expand in the left, top, right, and bottom directions, respectively.
edge	The number of pixels to expand in all directions. This can be used to avoid calling all the above arguments
sample_left, sample_top, sample_right, sample_bottom	The number of pixels to sample from each side. Defaults to 20.
random	Randomly sampling of the edge's pixels? Defaults to FALSE.
filter	Apply a median filter in the sampled pixels? Defaults to FALSE.
plot	Plots the extended image? defaults to FALSE.

Value

An Image object

Examples

```
library(pliman)
img <- image_pliman("soybean_touch.jpg")
image_expand(img, left = 200)
image_expand(img, right = 150, bottom = 250, filter = 5)
```

image_index

Image indexes

Description

image_index() Builds image indexes using Red, Green, Blue, Red-Edge, and NIR bands.
 Generates a raster or density plot of the index values computed with image_index().

Usage

```
image_index(
  img,
  index = NULL,
  resize = FALSE,
  re = NULL,
  nir = NULL,
  has_white_bg = FALSE,
  plot = TRUE,
  nrow = NULL,
  ncol = NULL,
  parallel = FALSE,
  workers = NULL,
  verbose = TRUE,
  ...
)
```

```
## S3 method for class 'image_index'
plot(x, type = c("raster", "density"), nrow = NULL, ncol = NULL, ...)
```

Arguments

img An image object.

index A character value (or a vector of characters) specifying the target mode for conversion to binary image. Use [pliman_indexes\(\)](#) or the details section to see the available indexes. Defaults to NULL ((normalized) Red, Green and Blue). One can also use "RGB" for RGB only, "NRGB" for normalized RGB, or "all" for all indexes. User can also calculate your own index using the bands names, e.g. index = "R+B/G".

resize	Resize the image before processing? Defaults to <code>resize = FALSE</code> . Use <code>resize = 50</code> , which resizes the image to 50% of the original size to speed up image processing.
re	Respective position of the red-edge band at the original image file.
nir	Respective position of the near-infrared band at the original image file.
has_white_bg	Logical indicating whether a white background is present. If TRUE, pixels that have R, G, and B values equals to 1 will be considered as NA. This may be useful to compute an image index for objects that have, for example, a white background. In such cases, the background will not be considered for the threshold computation.
plot	Show image after processing?
nrow, ncol	The number of rows or columns in the plot grid. Defaults to NULL, i.e., a square grid is produced.
parallel	Processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time when image is a list. The number of sections is set up to 70% of available cores.
workers	A positive numeric scalar or a function specifying the maximum number of parallel processes that can be active at the same time.
verbose	If TRUE (default) a summary is shown in the console.
...	Additional arguments passed to <code>plot_index()</code> for customization.
x	An object of class <code>image_index</code> .
type	The type of plot. Use <code>type = "raster"</code> (default) to produce a raster plot showing the intensity of the pixels for each image index or <code>type = "density"</code> to produce a density plot with the pixels' intensity.

Details

The following indexes are available in `pliman`.

- RGB color space
- R red
- G green
- B blue
- NR normalized red $R/(R+G+B)$.
- NG normalized green $G/(R+G+B)$
- NB normalized blue $B/(R+G+B)$
- GB green blue ratio G/B
- RB red blue ratio R/B
- GR green red ratio G/R
- BI brightness Index $\sqrt{(R^2+G^2+B^2)}/3$
- BIM brightness Index 2 $\sqrt{(R*2+G*2+B*2)}/3$

- SCI Soil Colour Index $(R-G)/(R+G)$
- GLI Green leaf index Vis Louhaichi et al. (2001) $(2*G-R-B)/(2*G+R+B)$
- HI Primary colours Hue Index $(2*R-G-B)/(G-B)$
- NDGRI Normalized green red difference index (Tucker, 1979) $(G-R)/(G+R)$
- NDGBI Normalized green blue difference index $(G-B)/(G+B)$
- NDRBI Normalized red blue difference index $(R-B)/(R+B)$
- I $R+G+B$
- S $((R+G+B)-3*B)/(R+G+B)$
- L $R+G+B/3$
- VARI A Visible Atmospherically Resistant Index $(G-R)/(G+R-B)$
- HUE Overall Hue Index $\text{atan}(2*(B-G-R)/30.5*(G-R))$
- HUE2 $\text{atan}(2*(R-G-R)/30.5*(G-B))$
- BGI B/G
- GRAY $0.299*R + 0.587*G + 0.114*B$
- GRAY2 $((R^2.2+(1.5*G)^2.2+(0.6*B)^2.2)/(1+1.5^2.2+0.6^2.2))^{1/2.2}$
- GLAI $(25*(G-R)/(G+R-B)+1.25)$
- CI Coloration Index $(R-B)/R$
- SAT Overall Saturation Index $(\max(R, G, B) - \min(R, G, B)) / \max(R, G, B)$
- SHP Shape Index $2*(R-G-B)/(G-B)$
- RI Redness Index $R^{**2}/(B*G^{**3})$
- HSB color space
- DGC I Dark Green Color Index, based on HSB color space $60*((G - B) / (\max(R, G, B) - \min(R, G, B)))$
- CIE-Lab color space
- L*: relative luminance $(0.2126 * R + 0.7152 * G + 0.0722 * B)$
- a*: $0.55*(R - (0.2126 * R + 0.7152 * G + 0.0722 * B)) / (1.0 - 0.2126)$

When type = "raster" (default), the function calls `plot_index()` to create a raster plot for each index present in x. If type = "density", a for loop is used to create a density plot for each index. Both types of plots can be arranged in a grid controlled by the ncol and nrow arguments.

Value

A list containing Grayscale images. The length will depend on the number of indexes used.

A NULL object

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

References

Nobuyuki Otsu, "A threshold selection method from gray-level histograms". IEEE Trans. Sys., Man., Cyber. 9 (1): 62-66. 1979. doi:10.1109/TSMC.1979.4310076

Examples

```
library(pliman)
img <- image_pliman("soybean_touch.jpg")
image_index(img, index = c("R, NR"))

# Example for S3 method plot()
library(pliman)
img <- image_pliman("sev_leaf.jpg")
# compute the index
ind <- image_index(img, index = c("R, G, B, NGRDI"), plot = FALSE)
plot(ind)

# density plot
plot(ind, type = "density")
```

image_prepare_mv	<i>Prepare an image (align and crop)</i>
------------------	--

Description

This function aligns and crops the image using either base or mapview visualization. This is useful to prepare the images to be analyzed with [analyze_objects_shp\(\)](#)

Usage

```
image_prepare_mv(img, viewer = get_pliman_viewer())
```

Arguments

img	An optional Image object
viewer	The viewer option. If not provided, the value is retrieved using get_pliman_viewer() . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the set_pliman_viewer() function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.

Value

The aligned/cropped image for further visualization or analysis.

Examples

```
# Example usage:
if(interactive()){
img <- image_pliman("mult_leaves.jpg")
image_prepare_mv(img, viewer = "mapview")
}
```

image_segment

Image segmentation

Description

- `image_segment()` reduces a color, color near-infrared, or grayscale images to a segmented image using a given color channel (red, green blue) or even color indexes (See [image_index\(\)](#) for more details). The Otsu's thresholding method (Otsu, 1979) is used to automatically perform clustering-based image thresholding.
- `image_segment_iter()` Provides an iterative image segmentation, returning the proportions of segmented pixels.

Usage

```
image_segment(
  img,
  index = NULL,
  threshold = c("Otsu", "adaptive"),
  k = 0.1,
  windowsize = NULL,
  col_background = NULL,
  has_white_bg = FALSE,
  fill_hull = FALSE,
  filter = FALSE,
  re = NULL,
  nir = NULL,
  invert = FALSE,
  plot = TRUE,
  nrow = NULL,
  ncol = NULL,
  parallel = FALSE,
  workers = NULL,
  verbose = TRUE
)
```

```
image_segment_iter(
  img,
  nseg = 2,
  index = NULL,
  invert = NULL,
```

```

    threshold = NULL,
    k = 0.1,
    windowsize = NULL,
    has_white_bg = FALSE,
    plot = TRUE,
    verbose = TRUE,
    nrow = NULL,
    ncol = NULL,
    parallel = FALSE,
    workers = NULL,
    ...
)

```

Arguments

img	An image object or a list of image objects.
index	<ul style="list-style-type: none"> • For <code>image_segment()</code>, a character value (or a vector of characters) specifying the target mode for conversion to binary image. See the available indexes with <code>pliman_indexes()</code>. See <code>image_index()</code> for more details. • For <code>image_segment_iter()</code> a character or a vector of characters with the same length of <code>nseg</code>. It can be either an available index (described above) or any operation involving the RGB values (e.g., "B/R+G").
threshold	<p>The threshold method to be used.</p> <ul style="list-style-type: none"> • By default (<code>threshold = "Otsu"</code>), a threshold value based on Otsu's method is used to reduce the grayscale image to a binary image. If a numeric value is informed, this value will be used as a threshold. • If <code>threshold = "adaptive"</code>, adaptive thresholding (Shafait et al. 2008) is used, and will depend on the <code>k</code> and <code>windowsize</code> arguments. • If any non-numeric value different than "Otsu" and "adaptive" is used, an interactive section will allow you to choose the threshold based on a raster plot showing pixel intensity of the index.
k	a numeric in the range 0-1. when <code>k</code> is high, local threshold values tend to be lower. when <code>k</code> is low, local threshold value tend to be higher.
windowsize	<code>windowsize</code> controls the number of local neighborhood in adaptive thresholding. By default it is set to $1/3 * \text{minxy}$, where <code>minxy</code> is the minimum dimension of the image (in pixels).
col_background	The color of the segmented background. Defaults to NULL (white background).
has_white_bg	Logical indicating whether a white background is present. If TRUE, pixels that have R, G, and B values equals to 1 will be considered as NA. This may be useful to compute an image index for objects that have, for example, a white background. In such cases, the background will not be considered for the threshold computation.
fill_hull	Fill holes in the objects? Defaults to FALSE.
filter	Performs median filtering in the binary image? See more at <code>image_filter()</code> . Defaults to FALSE. Use a positive integer to define the size of the median filtering. Larger values are effective at removing noise, but adversely affect edges.

re	Respective position of the red-edge band at the original image file.
nir	Respective position of the near-infrared band at the original image file.
invert	Inverts the binary image, if desired. For <code>image_segmentation_iter()</code> use a vector with the same length of <code>nseg</code> .
plot	Show image after processing?
nrow, ncol	The number of rows or columns in the plot grid. Defaults to NULL, i.e., a square grid is produced.
parallel	Processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time when <code>image</code> is a list. The number of sections is set up to 70% of available cores.
workers	A positive numeric scalar or a function specifying the maximum number of parallel processes that can be active at the same time.
verbose	If TRUE (default) a summary is shown in the console.
nseg	The number of iterative segmentation steps to be performed.
...	Additional arguments passed on to <code>image_segment()</code> .

Value

- `image_segment()` returns list containing `n` objects where `n` is the number of indexes used. Each objects contains:
 - `image` an image with the RGB bands (layers) for the segmented object.
 - `mask` A mask with logical values of 0 and 1 for the segmented image.
- `image_segment_iter()` returns a list with (1) a data frame with the proportion of pixels in the segmented images and (2) the segmented images.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

References

Nobuyuki Otsu, "A threshold selection method from gray-level histograms". IEEE Trans. Sys., Man., Cyber. 9 (1): 62-66. 1979. doi:[10.1109/TSMC.1979.4310076](https://doi.org/10.1109/TSMC.1979.4310076)

Examples

```
library(pliman)
img <- image_pliman("soybean_touch.jpg", plot = TRUE)
image_segment(img, index = c("R", "G", "B"))

# adaptive thresholding
```

image_segment_kmeans *Image segmentation using k-means clustering*

Description

Segments image objects using clustering by the k-means clustering algorithm

Usage

```
image_segment_kmeans(  
  img,  
  bands = 1:3,  
  nclasses = 2,  
  invert = FALSE,  
  filter = FALSE,  
  fill_hull = FALSE,  
  plot = TRUE  
)
```

Arguments

img	An Image object.
bands	A numeric integer/vector indicating the RGB band used in the segmentation. Defaults to 1:3, i.e., all the RGB bands are used.
nclasses	The number of desired classes after image segmentation.
invert	Invert the segmentation? Defaults to FALSE. If TRUE the binary matrix is inverted.
filter	Applies a median filtering in the binary matrix? Defaults to FALSE. Use a numeric integer to indicate the size of the median filter.
fill_hull	Fill holes in the objects? Defaults to FALSE.
plot	Plot the segmented image?

Value

A list with the following values:

- `image` The segmented image considering only two classes (foreground and background)
- `clusters` The class of each pixel. For example, if `ncluster = 3`, `clusters` will be a two-way matrix with values ranging from 1 to 3.
- `masks` A list with the binary matrices showing the segmentation.

References

Hartigan, J. A. and Wong, M. A. (1979). Algorithm AS 136: A K-means clustering algorithm. *Applied Statistics*, 28, 100–108. [doi:10.2307/2346830](https://doi.org/10.2307/2346830)

Examples

```
img <- image_pliman("la_leaves.jpg", plot = TRUE)
seg <- image_segment_kmeans(img)
seg <- image_segment_kmeans(img, fill_hull = TRUE, invert = TRUE, filter = 10)
```

image_segment_manual *Image segmentation by hand*

Description

This R code is a function that allows the user to manually segment an image based on the parameters provided. This only works in an interactive section.

Usage

```
image_segment_manual(
  img,
  shape = c("free", "circle", "rectangle"),
  type = c("select", "remove"),
  viewer = get_pliman_viewer(),
  resize = TRUE,
  edge = 5,
  plot = TRUE
)
```

Arguments

img	An Image object.
shape	The type of shape to use. Defaults to "free". Other possible values are "circle" and "rectangle". Partial matching is allowed.
type	The type of segmentation. By default (type = "select") objects are selected. Use type = "remove" to remove the selected area from the image.
viewer	The viewer option. If not provided, the value is retrieved using get_pliman_viewer() . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the set_pliman_viewer() function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.
resize	By default, the segmented object is resized to fill the original image size. Use <code>resize = FALSE</code> to keep the segmented object in the original scale.
edge	Number of pixels to add in the edge of the segmented object when <code>resize = TRUE</code> . Defaults to 5.
plot	Plot the segmented object? Defaults to TRUE.

Details

If the shape is "free", it allows the user to draw a perimeter to select/remove objects. If the shape is "circle", it allows the user to click on the center and edge of the circle to define the desired area. If the shape is "rectangle", it allows the user to select two points to define the area.

Value

A list with the segmented image and the mask used for segmentation.

Examples

```
if (interactive()) {  
  img <- image_pliman("la_leaves.jpg")  
  seg <- image_segment_manual(img)  
  plot(seg$mask)  
}
```

image_segment_mask *Segment an Image object using a brush mask*

Description

It combines `make_mask()` and `make_brush()` to segment an Image object using a brush of desired size, shape, and position.

Usage

```
image_segment_mask(  
  img,  
  size,  
  shape = "disc",  
  rel_pos_x = 0.5,  
  rel_pos_y = 0.5,  
  type = c("binary", "shadow"),  
  plot = TRUE,  
  ...  
)
```

Arguments

img	A Image object
size	A numeric containing the size of the brush in pixels. This should be an odd number; even numbers are rounded to the next odd one.
shape	A character vector indicating the shape of the brush. Can be "box", "disc", "diamond", "Gaussian" or "line" Defaults to "disc".

rel_pos_x, rel_pos_y	A relative position to include the brush in the image. Defaults to 0.5. This means that the brush will be centered in the original image. Smaller values move the brush toward the left and top, respectively.
type	Defines the type of the mask. By default, a binary mask is applied. This results in white pixels in the original image that matches the 0s pixels in the brush. If type = "shadow" is used, a shadow mask is produced
plot	Plots the generated mask? Defaults to TRUE.
...	Further arguments passed on to <code>EImage::makeBrush()</code> .

Value

A color Image object

Examples

```
img <- image_pliman("soybean_touch.jpg")
plot(img)
image_segment_mask(img, size = 601)
image_segment_mask(img,
  size = 401,
  shape = "diamond",
  rel_pos_x = 0,
  rel_pos_y = 0,
  type = "shadow")
```

image_shp

Construct a shape file from an image

Description

Creates a list of object coordinates given the desired number of nrow and columns. It starts by selecting 4 points at the corners of objects of interest in the plot space. Then, given nrow and ncol, a grid is drawn and the objects' coordinates are returned.

Usage

```
image_shp(
  img,
  nrow = 1,
  ncol = 1,
  buffer_x = 0,
  buffer_y = 0,
  interactive = FALSE,
  viewer = get_pliman_viewer(),
  col_line = "red",
  size_line = 2,
```

```

    col_text = "red",
    size_text = 1,
    plot = TRUE
  )

```

Arguments

img	An object of class Image
nrow	The number of desired rows in the grid. Defaults to 1.
ncol	The number of desired columns in the grid. Defaults to 1.
buffer_x, buffer_y	Buffering factor for the width and height, respectively, of each individual shape's side. A value between 0 and 0.5 where 0 means no buffering and 0.5 means complete buffering (default: 0). A value of 0.25 will buffer the shape by 25% on each side.
interactive	If FALSE (default) the grid is created automatically based on the image dimension and number of rows/columns. If interactive = TRUE, users must draw points at the diagonal of the desired bounding box that will contain the grid.
viewer	The viewer option. If not provided, the value is retrieved using get_pliman_viewer() . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the set_pliman_viewer() function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.
col_line, col_text	The color of the line/text in the grid. Defaults to "red".
size_line, size_text	The size of the line/text in the grid. Defaults to 2.5.
plot	Plots the grid on the image? Defaults to TRUE.

Value

A list with row * col objects containing the plot coordinates.

Examples

```

library(pliman)
flax <- image_pliman("flax_leaves.jpg")
shape <- image_shp(flax, nrow = 3, ncol = 5)

```

image_square	<i>Squares an image</i>
--------------	-------------------------

Description

Converts a rectangular image into a square image by expanding the rows/columns using `image_expand()`.

Usage

```
image_square(img, plot = TRUE, ...)
```

Arguments

<code>img</code>	An Image object.
<code>plot</code>	Plots the extended image? defaults to FALSE.
<code>...</code>	Further arguments passed on to <code>image_expand()</code> .

Value

The modified Image object.

Examples

```
library(pliman)
img <- image_pliman("soybean_touch.jpg")
dim(img)
square <- image_square(img)
dim(square)
```

image_thinning_guo_hall

Perform Guo-Hall thinning on a binary image or list of binary images

Description

This function performs the Guo-Hall thinning algorithm (Guo and Hall, 1989) on a binary image or a list of binary images.

Usage

```
image_thinning_guo_hall(  
  img,  
  parallel = FALSE,  
  workers = NULL,  
  verbose = TRUE,  
  plot = FALSE,  
  ...  
)
```

Arguments

img	The binary image or a list of binary images to be thinned. It can be either a single binary image of class 'Image' or a list of binary images.
parallel	Logical, whether to perform thinning using multiple cores (parallel processing). If TRUE, the function will use multiple cores for processing if available. Default is FALSE.
workers	Integer, the number of workers (cores) to use for parallel processing. If NULL (default), it will use 40% of available cores.
verbose	Logical, whether to display progress messages during parallel processing. Default is TRUE.
plot	Logical, whether to plot the thinned images. Default is FALSE.
...	Additional arguments to be passed to <code>image_binary()</code> if img is not a binary image.

Value

If img is a single binary image, the function returns the thinned binary image. If img is a list of binary images, the function returns a list containing the thinned binary images.

References

Guo, Z., and R.W. Hall. 1989. Parallel thinning with two-subiteration algorithms. *Commun. ACM* 32(3): 359–373. doi:10.1145/62065.62074

Examples

```
library(pliman)
img <- image_pliman("potato_leaves.jpg", plot = TRUE)
image_thinning_guo_hall(img, index = "R", plot = TRUE)
```

image_to_mat

Convert an image to a data.frame

Description

Given an object image, converts it into a data frame where each row corresponds to the intensity values of each pixel in the image.

Usage

```
image_to_mat(img, parallel = FALSE, workers = NULL, verbose = TRUE)
```

Arguments

img	An image object.
parallel	Processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time when image is a list. The number of sections is set up to 70% of available cores.
workers	A positive numeric scalar or a function specifying the maximum number of parallel processes that can be active at the same time.
verbose	If TRUE (default) a summary is shown in the console.

Value

A list containing three matrices (R, G, and B), and a data frame containing four columns: the name of the image in image and the R, G, B values.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(pliman)
img <- image_pliman("sev_leaf.jpg")
dim(img)
mat <- image_to_mat(img)
dim(mat[[1]])
```

image_view

Create an interactive map view of an image

Description

This function allows users to interactively edit and analyze an image using mapview and mapedit packages.

Usage

```
image_view(
  img,
  title = "Edit the image",
  show = c("rgb", "index"),
  index = "B",
  max_pixels = 2500000,
  color_regions = custom_palette(),
  ...
)
```

Arguments

<code>img</code>	An Image object.
<code>title</code>	The title of the map view. Use to provide short orientations to the user.
<code>show</code>	The display option for the map view. Options are "rgb" for RGB view and "index" for index view.
<code>index</code>	The index to use for the index view. Defaults to "B".
<code>max_pixels</code>	integer > 0. Maximum number of cells to use for the plot. If <code>max_pixels < npixels(img)</code> , regular sampling is used before plotting.
<code>color_regions</code>	The color palette for displaying index values. Default is <code>custom_palette()</code> .
<code>...</code>	Additional arguments to be passed to <code>mapview::mapview()</code> .

Value

An sf object, the same object returned by `mapedit::editMap()`.

Examples

```
if(interactive()){
# Example usage:
img <- image_pliman("sev_leaf.jpg")
image_view(img)
}
```

landmarks

Create image landmarks

Description

An interactive section where the user will be able to click on the image to select landmarks manually is open. With each mouse click, a point is drawn and an upward counter is shown in the console. After `n` counts or after the user press Esc, the interactive process is interrupted and a `data.frame` with the `x` and `y` coordinates for the landmarks is returned.

Usage

```
landmarks(
  img,
  n = Inf,
  viewer = get_pliman_viewer(),
  scale = NULL,
  calibrate = FALSE
)
```

Arguments

img	An Image object.
n	The number of landmarks to produce. Defaults to Inf. In this case, landmarks are chosen up to the user press Esc.
viewer	The viewer option. If not provided, the value is retrieved using <code>get_pliman_viewer()</code> . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the <code>set_pliman_viewer()</code> function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.
scale	A known scale of the coordinate values. If NULL (default) scale = 1 is used.
calibrate	A logical argument indicating whether a calibration step must be performed before picking up the landmarks. If so, <code>calibrate()</code> is called internally. Users must then select two points and indicate a known distance. A scale value will internally be computed and used in the correction of the coordinates (from pixels to the unit of the known distance).

Value

A data.frame with the x and y-coordinates from the landmarks.

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Examples

```
if(isTRUE(interactive())){
  library(pliman)
  img <- image_pliman("potato_leaves.jpg")
  x <- landmarks(img)
}
```

landmarks_add

Artificially inflates the number of landmarks

Description

Interpolates supplementary landmarks that correspond to the mean coordinates of two adjacent landmarks.

Usage

```
landmarks_add(x, n = 3, smooth_iter = 0, plot = TRUE, nrow = NULL, ncol = NULL)
```


Arguments

x	A matrix, a data.frame a list of perimeter coordinates, often produced with <code>object_contour()</code> , <code>landmarks()</code> , or <code>landmarks_regradi()</code> .
n	The number of iterations. Defaults to 3.
smooth_iter	The number of smoothing iterations to perform. This will smooth the perimeter of the interpolated landmarks using <code>poly_smooth()</code> .
plot	Creates a plot? Defaults to TRUE.
ncol, nrow	The number of rows or columns in the plot grid when a list is used in x. Defaults to NULL, i.e., a square grid is produced.

Value

A Matrix of interpolated coordinates.

Examples

```
library(pliman)

# equally spaced landmarks
plot_polygon(contours[[4]])
ldm <- landmarks_regradi(contours[[4]], plot = FALSE)
points(ldm$coords, pch = 16)
segments(mean(ldm$coords[,1]),
         mean(ldm$coords[,2]),
         ldm$coords[,1],
         ldm$coords[,2])

ldm_add <- landmarks_add(ldm, plot = FALSE)
points(ldm_add, col = "red")
points(ldm$coords, pch = 16)

# smoothed version
ldm_add_smo <- landmarks_add(ldm, plot = FALSE, smooth_iter = 10)
lines(ldm_add_smo, col = "blue", lwd = 3)
```

landmarks_angle	<i>Angles between landmarks</i>
-----------------	---------------------------------

Description

Computes the angle from two interlandmark vectors using the difference of their arguments using complex vectors (Claude, 2008).

Usage

```
landmarks_angle(x, unit = c("rad", "deg"))
```

Arguments

- `x` An object computed with `landmarks()`.
- `unit` The unit of the angle. Defaults to radian (rad). Use `unit = "deg"` to return the angles in degrees.

Value

A matrix with the angles for each landmark combination.

Note

Borrowed from Claude (2008), pp. 50

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Examples

```
if(isTRUE(interactive())){
  library(pliman)
  img <- image_pliman("potato_leaves.jpg")
  x <- landmarks(img)
  landmarks_angle(x)
}
```

landmarks_dist	<i>Distances between landmarks</i>
----------------	------------------------------------

Description

Computes the distance between two landmarks as the square root of the sum of the squared differences between each coordinate (Claude, 2008).

Usage

```
landmarks_dist(x)
```

Arguments

- `x` An object computed with `landmarks()`.

Value

A matrix with the distances for each landmark combination.

Note

Borrowed from Claude (2008), pp. 49

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Examples

```
if(isTRUE(interactive())){
  library(pliman)
  img <- image_pliman("potato_leaves.jpg")
  x <- landmarks(img)
  landmarks_dist(x)
}
```

landmarks_regradi *Pseudolandmarks with equally spaced angles*

Description

Select n landmarks that are spaced with a regular sequence of angles taken between the outline coordinates and the centroid.

Usage

```
landmarks_regradi(
  x,
  n = 50,
  close = TRUE,
  plot = TRUE,
  ncol = NULL,
  nrow = NULL
)
```

Arguments

<code>x</code>	A matrix, a data.frame a list of perimeter coordinates, often produced with object_contour() .
<code>n</code>	Number of points to be sampled. Defaults to 50.
<code>close</code>	Return a closed polygon? Defaults to TRUE.
<code>plot</code>	Create a plot? Defaults to TRUE.
<code>ncol, nrow</code>	The number of rows or columns in the plot grid when a list is used in <code>x</code> . Defaults to NULL, i.e., a square grid is produced.

Value

A list with the following objects:

- `pixindices`: Vector of radius indices.
- `radii`: Vector of sampled radii lengths.
- `Xc`: The centroid coordinate of x axis.
- `Yc`: The centroid coordinate of y axis.
- `coords`: Coordinates of sampled points arranged in a two-column matrix.

If `x` is a list, a list of objects described above is returned.

Note

Borrowed from Claude (2008), pp. 53

References

Claude, J. (2008) *Morphometrics with R*, Use R! series, Springer 316 pp.

Examples

```
library(pliman)
plot_polygon(contours[[1]])
ldm <- landmarks_regradi(contours)
```

leading_zeros

Add leading zeros to a numeric sequence

Description

Add `n` leading zeros to a numeric sequence. This is useful to create a character vector to rename files in a folder.

Usage

```
leading_zeros(x, n = 3)
```

Arguments

`x` A numeric vector or a list of numeric vectors.

`n` The number of leading zeros to add. Defaults to 3.

Value

A character vector or a list of character vectors.

Examples

```
library(pliman)
leading_zeros(1:5)
leading_zeros(list(a = 1:3,
                  b = 1:5),
              n = 2)
```

make_brush	<i>Makes a brush</i>
------------	----------------------

Description

Generates brushes of various sizes and shapes that can be used as structuring elements. See [EBImage::makeBrush\(\)](#).

Usage

```
make_brush(size, shape = "disc", ...)
```

Arguments

size	A numeric containing the size of the brush in pixels. This should be an odd number; even numbers are rounded to the next odd one.
shape	A character vector indicating the shape of the brush. Can be "box", "disc", "diamond", "Gaussian" or "line" Defaults to "disc".
...	Further arguments passed on to EBImage::makeBrush() .

Value

A 2D matrix of 0s and 1s containing the desired brush.

Examples

```
make_brush(size = 51) |> image()
make_brush(size = 51, shape = "diamond") |> image()
```

make_mask	<i>Makes a mask in an image</i>
-----------	---------------------------------

Description

Make a mask using an Image object and a brush.

Usage

```
make_mask(img, brush, rel_pos_x = 0.5, rel_pos_y = 0.5, plot = TRUE)
```

Arguments

img	A Image object
brush	An object created with <code>make_brush()</code>
rel_pos_x, rel_pos_y	A relative position to include the brush in the image. Defaults to 0.5. This means that the brush will be centered in the original image. Smaller values move the brush toward the left and top, respectively.
plot	Plots the generated mask? Defaults to TRUE.

Details

It applies a brush to an Image, selecting the Image pixels that match the brush values equal to 1. The position of the brush in the original image is controlled by the relative positions x (`rel_pos_x`) and y (`rel_pos_y`) arguments. The size of the brush must be smaller or equal to the smaller dimension of image.

Value

A binary image with 0s and 1s.

Examples

```
img <- image_pliman("soybean_touch.jpg")
make_mask(img, brush = make_brush(size = 201))
make_mask(img,
  brush = make_brush(size = 401, shape = "diamond"),
  rel_pos_x = 0.1,
  rel_pos_y = 0.8)
```

measure_disease	<i>Performs plant disease measurements</i>
-----------------	--

Description

- `measure_disease()` computes the percentage of symptomatic leaf area and (optionally) counts and compute shapes (area, perimeter, radius, etc.) of lesions in a sample or entire leaf using color palettes. See more at **Details**.
- `measure_disease_iter()` provides an iterative section for `measure_disease()`, where the user picks up samples in the image to create the needed color palettes.

Usage

```
measure_disease(  
  img,  
  img_healthy = NULL,  
  img_symptoms = NULL,  
  img_background = NULL,  
  pattern = NULL,  
  filter = 10,  
  parallel = FALSE,  
  workers = NULL,  
  resize = FALSE,  
  fill_hull = TRUE,  
  index_lb = NULL,  
  index_dh = "GLI",  
  has_white_bg = FALSE,  
  threshold = NULL,  
  invert = FALSE,  
  lower_size = NULL,  
  upper_size = NULL,  
  topn_lower = NULL,  
  topn_upper = NULL,  
  randomize = TRUE,  
  nsample = 3000,  
  watershed = FALSE,  
  lesion_size = "medium",  
  tolerance = NULL,  
  extension = NULL,  
  show_features = FALSE,  
  show_segmentation = FALSE,  
  plot = TRUE,  
  show_original = TRUE,  
  show_background = TRUE,  
  show_contour = TRUE,  
  contour_col = "white",
```

```

contour_size = 1,
col_leaf = NULL,
col_lesions = NULL,
col_background = NULL,
marker = FALSE,
marker_col = NULL,
marker_size = NULL,
save_image = FALSE,
prefix = "proc_",
name = NULL,
dir_original = NULL,
dir_processed = NULL,
verbose = TRUE
)

measure_disease_iter(
  img,
  has_background = TRUE,
  r = 2,
  viewer = get_pliman_viewer(),
  show = "rgb",
  index = "NGRDI",
  ...
)

```

Arguments

<code>img</code>	The image to be analyzed.
<code>img_healthy</code>	A color palette of healthy tissues.
<code>img_symptoms</code>	A color palette of lesioned tissues.
<code>img_background</code>	A color palette of the background (if exists). These arguments can be either an Image object stored in the global environment or a character value. If a character is used (e.g., <code>img_healthy = "leaf"</code>), the function will search in the current working directory a valid image that contains "leaf" in the name. Note that if two images matches this pattern, an error will occur.
<code>pattern</code>	A pattern of file name used to identify images to be processed. For example, if <code>pattern = "im"</code> all images that the name matches the pattern (e.g., <code>img1.-</code> , <code>imge1.-</code> , <code>im2.-</code>) will be analyzed. Providing any number as pattern (e.g., <code>pattern = "1"</code>) will select images that are named as <code>1.-</code> , <code>2.-</code> , and so on.
<code>filter</code>	Performs median filtering in the binary image that segments the leaf from background? By default, a median filter of <code>size = 10</code> is applied. This is useful to reduce the noise and segment the leaf and background more accurately. See more at image_filter() . Set to <code>FALSE</code> to cancel median filtering.
<code>parallel</code>	Processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time, especially when <code>pattern</code> is used is informed. The number of sections is set up to 70% of available cores.

workers	A positive numeric scalar or a function specifying the maximum number of parallel processes that can be active at the same time.
resize	Resize the image before processing? Defaults to FALSE. Use a numeric value of range 0-100 (proportion of the size of the original image).
fill_hull	Fill holes in the image? Defaults to TRUE. This is useful to fill holes in leaves, e.g., those caused by insect attack, ensuring the hole area will be accounted for the leaf, not background.
index_lb	The index used to segment the foreground (e.g., leaf) from the background. If not declared, the entire image area (pixels) will be considered in the computation of the severity.
index_dh	The index used to segment diseased from healthy tissues when <code>img_healthy</code> and <code>img_symptoms</code> are not declared. Defaults to "GLI". See image_index() for more details.
has_white_bg	Logical indicating whether a white background is present. If TRUE, pixels that have R, G, and B values equals to 1 will be considered as NA. This may be useful to compute an image index for objects that have, for example, a white background. In such cases, the background will not be considered for the threshold computation.
threshold	By default (<code>threshold = NULL</code>), a threshold value based on Otsu's method is used to reduce the grayscale image to a binary image. If a numeric value is informed, this value will be used as a threshold. Inform any non-numeric value different than "Otsu" to iteratively choose the threshold based on a raster plot showing pixel intensity of the index. Must be a vector of length 2 to indicate the threshold for <code>index_lb</code> and <code>index_dh</code> , respectively.
invert	Inverts the binary image if desired. This is useful to process images with black background. Defaults to FALSE.
lower_size	Lower limit for size for the image analysis. Leaf images often contain dirt and dust. To prevent dust from affecting the image analysis, the lower limit of analyzed size is set to 0.1, i.e., objects with lesser than 10% of the mean of all objects are removed. One can set a known area or use <code>lower_limit = 0</code> to select all objects (not advised).
upper_size	Upper limit for size for the image analysis. Defaults to NULL, i.e., no upper limit used.
topn_lower, topn_upper	Select the top n lesions based on its area. <code>topn_lower</code> selects the n lesions with the smallest area whereas <code>topn_upper</code> selects the n lesions with the largest area.
randomize	Randomize the lines before training the model? Defaults to TRUE.
nsample	The number of sample pixels to be used in training step. Defaults to 3000.
watershed	If TRUE (Default) implements the Watershed Algorithm to segment lesions connected by a fairly few pixels that could be considered as two distinct lesions. If FALSE, lesions that are connected by any pixel are considered unique lesions. For more details see EBImage::watershed() .
lesion_size	The size of the lesion. Used to automatically tune tolerance and extension parameters. One of the following. "small" (2-5 mm in diameter, e.g. rust pustules), "medium" (0.5-1.0 cm in diameter, e.g. wheat leaf spot), "large" (1-2 cm in diameter, and "elarge" (2-3 cm in diameter, e.g. target spot of soybean).

tolerance	The minimum height of the object in the units of image intensity between its highest point (seed) and the point where it contacts another object (checked for every contact pixel). If the height is smaller than the tolerance, the object will be combined with one of its neighbors, which is the highest. Defaults to NULL, i.e., starting values are set up according to the argument lesion_size.
extension	Radius of the neighborhood in pixels for the detection of neighboring objects. Defaults to 20. Higher value smooths out small objects.
show_features	If TRUE returnS the lesion features such as number, area, perimeter, and radius. Defaults to FALSE.
show_segmentation	Shows the object segmentation colored with random permutations. Defaults to TRUE.
plot	Show image after processing? Defaults to TRUE.
show_original	Show the symptoms in the original image?
show_background	Show the background? Defaults to TRUE. A white background is shown by default when show_original = FALSE.
show_contour	Show a contour line around the lesions? Defaults to TRUE.
contour_col, contour_size	The color and size for the contour line around objects. Defaults to contour_col = "white" and contour_size = 1.
col_leaf	Leaf color after image processing. Defaults to "green"
col_lesions	Symptoms color after image processing. Defaults to "red".
col_background	Background color after image processing. Defaults to "NULL".
marker, marker_col, marker_size	The type, color and size of the object marker. Defaults to NULL, which shows nothing. Use marker = "point" to show a point in each lesion or marker = "*" where "*" is any variable name of the shape data frame returned by the function.
save_image	Save the image after processing? The image is saved in the current working directory named as proc_* where * is the image name given in img.
prefix	The prefix to be included in the processed images. Defaults to "proc_".
name	The name of the image to save. Use this to overwrite the name of the image in img.
dir_original, dir_processed	The directory containing the original and processed images. Defaults to NULL. In this case, the function will search for the image img in the current working directory. After processing, when save_image = TRUE, the processed image will be also saved in such a directory. It can be either a full path, e.g., "C:/Desktop/imgs", or a subfolder within the current working directory, e.g., "/imgs".
verbose	If TRUE (default) a summary is shown in the console.
has_background	A logical indicating if the image has a background to be segmented before processing.

r	The radius of neighborhood pixels. Defaults to 2. A square is drawn indicating the selected pixels.
viewer	The viewer option. If not provided, the value is retrieved using <code>get_pliman_viewer()</code> . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the <code>set_pliman_viewer()</code> function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.
show	The show option for the mapview viewer, either "rgb" or "index".
index	The index to be shown when show = "rgb".
...	Further parameters passed on to <code>measure_disease()</code> .

Details

In `measure_disease()`, a general linear model (binomial family) fitted to the RGB values is used to segment the lesions from the healthy leaf. If a pallet of background is provided, the function takes care of the details to isolate it before computing the number and area of lesions. By using `pattern` it is possible to process several images with common pattern names that are stored in the current working directory or in the subdirectory informed in `dir_original`.

If `img_healthy` and `img_symptoms` are not declared, RGB-based phenotyping of foliar disease severity is performed using the index informed in `index_lb` to first segment leaf from background and `index_dh` to segment diseased from healthy tissues.

`measure_disease_iter()` only run in an interactive section. In this function, users will be able to pick up samples of images to iteratively create the needed color palettes. This process calls `pick_palette()` internally. If `has_background` is TRUE (default) the color palette for the background is first created. The sample of colors is performed in each left-button mouse click and continues until the user press Esc. Then, a new sampling process is performed to sample the color of healthy tissues and then diseased tissues. The generated palettes are then passed on to `measure_disease()`. All the arguments of such function can be passed using the ... (three dots).

When `show_features = TRUE`, the function computes a total of 36 lesion features (23 shape features and 13 texture features). The Haralick texture features for each object based on a gray-level co-occurrence matrix (Haralick et al. 1979). See more details in `analyze_objects()`.

Value

- `measure_disease()` returns a list with the following objects:
 - `severity` A data frame with the percentage of healthy and symptomatic areas.
 - `shape,statistics` If `show_features = TRUE` is used, returns the shape (area, perimeter, etc.) for each lesion and a summary statistic of the results.
- `measure_disease_iter()` returns a list with the following objects:
 - `results` A list with the objects returned by `measure_disease()`.
 - `leaf` The color palettes for the healthy leaf.
 - `disease` The color palettes for the diseased leaf.
 - `background` The color palettes for the background.

Author(s)

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Examples

```
library(pliman)
img <- image_pliman("sev_leaf_nb.jpg")
healthy <- image_pliman("sev_healthy.jpg")
lesions <- image_pliman("sev_sympt.jpg")
image_combine(img, healthy, lesions, ncol = 3)

sev <-
  measure_disease(img = img,
                 img_healthy = healthy,
                 img_symptoms = lesions,
                 lesion_size = "large",
                 plot = TRUE)

# an interactive section
measure_disease_iter(img)
```

measure_disease_byl *Performs plant disease measurements by leaf*

Description

Computes the percentage of symptomatic leaf area using color palettes or RGB indexes by each leaf of an image. This allows, for example, processing replicates of the same treatment and obtaining the results for each replication with a single image. To do that, leaf samples are first splitted with `object_split()` and then, `measure_disease()` is applied to the list of leaves.

Usage

```
measure_disease_byl(
  img,
  index = "B",
  index_lb = "B",
  index_dh = "NGRDI",
  lower_size = NULL,
  watershed = TRUE,
  invert = FALSE,
  fill_hull = FALSE,
  filter = 3,
  threshold = "Otsu",
  extension = NULL,
```

```

    tolerance = NULL,
    object_size = "large",
    dir_original = NULL,
    img_healthy = NULL,
    img_symptoms = NULL,
    pattern = NULL,
    parallel = FALSE,
    workers = NULL,
    plot = TRUE,
    show_features = FALSE,
    save_image = FALSE,
    verbose = TRUE,
    ...
)

```

Arguments

<code>img</code>	The image to be analyzed.
<code>index</code>	A character value specifying the target mode for conversion to binary to segment the leaves from background. Defaults to "B" (blue). See image_index() for more details. Personalized indexes can be informed as, e.g., <code>index = "R*G/B"</code> .
<code>index_lb</code>	The index used to segment the foreground (e.g., leaf) from the background. If not declared, the entire image area (pixels) will be considered in the computation of the severity.
<code>index_dh</code>	The index used to segment diseased from healthy tissues when <code>img_healthy</code> and <code>img_symptoms</code> are not declared. Defaults to "GLI". See image_index() for more details.
<code>lower_size</code>	To prevent dust from affecting object segmentation, objects with lesser than 10% of the mean of all objects are removed. . One can set a known area or use <code>lower_limit = 0</code> to select all objects (not advised).
<code>watershed</code>	If TRUE (default) performs watershed-based object detection. This will detect objects even when they are touching one other. If FALSE, all pixels for each connected set of foreground pixels are set to a unique object. This is faster but is not able to segment touching objects.
<code>invert</code>	Inverts the binary image if desired. This is useful to process images with a black background. Defaults to FALSE. If <code>reference = TRUE</code> is use, <code>invert</code> can be declared as a logical vector of length 2 (eg., <code>invert = c(FALSE, TRUE)</code>). In this case, the segmentation of objects and reference from the foreground using <code>back_fore_index</code> is performed using the default (not inverted), and the segmentation of objects from the reference is performed by inverting the selection (selecting pixels higher than the threshold).
<code>fill_hull</code>	Fill holes in the binary image? Defaults to FALSE. This is useful to fill holes in objects that have portions with a color similar to the background. IMPORTANT: Objects touching each other can be combined into one single object, which may underestimate the number of objects in an image.

filter	Performs median filtering in the binary image? See more at image_filter() . Defaults to FALSE. Use a positive integer to define the size of the median filtering. Larger values are effective at removing noise, but adversely affect edges.
threshold	The threshold method to be used. <ul style="list-style-type: none"> • By default (threshold = "Otsu"), a threshold value based on Otsu's method is used to reduce the grayscale image to a binary image. If a numeric value is informed, this value will be used as a threshold. • If threshold = "adaptive", adaptive thresholding (Shafait et al. 2008) is used, and will depend on the k and windowsize arguments. • If any non-numeric value different than "Otsu" and "adaptive" is used, an iterative section will allow you to choose the threshold based on a raster plot showing pixel intensity of the index.
extension	Radius of the neighborhood in pixels for the detection of neighboring objects. Higher value smooths out small objects.
tolerance	The minimum height of the object in the units of image intensity between its highest point (seed) and the point where it contacts another object (checked for every contact pixel). If the height is smaller than the tolerance, the object will be combined with one of its neighbors, which is the highest.
object_size	The size of the object. Used to automatically set up tolerance and extension parameters. One of the following. "small" (e.g, wheat grains), "medium" (e.g, soybean grains), "large"(e.g, peanut grains), and "elarge" (e.g, soybean pods)'.
dir_original	The directory containing the original and processed images. Defaults to NULL. In this case, the function will search for the image img in the current working directory.
img_healthy	A color palette of healthy tissues.
img_symptoms	A color palette of lesioned tissues.
pattern	A pattern of file name used to identify images to be processed. For example, if pattern = "im" all images that the name matches the pattern (e.g., img1.-, image1.-, im2.-) will be analyzed. Providing any number as pattern (e.g., pattern = "1") will select images that are named as 1.-, 2.-, and so on.
parallel	Processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time, especially when pattern is used is informed. The number of sections is set up to 70% of available cores.
workers	A positive numeric scalar or a function specifying the maximum number of parallel processes that can be active at the same time.
plot	Show image after processing?
show_features	If TRUE returnS the lesion features such as number, area, perimeter, and radius. Defaults to FALSE.
save_image	Save the image after processing? The image is saved in the current working directory named as proc_* where * is the image name given in img.
verbose	If TRUE (default) a summary is shown in the console.
...	Additional arguments passed on to measure_disease() .

Value

- A list with the following objects:
 - severity A data frame with the percentage of healthy and symptomatic areas for each leaf in the image(s).
 - shape,statistics If show_features = TRUE is used, returns the shape (area, perimeter, etc.) for each lesion and a summary statistic of the results.

Examples

```
library(pliman)
img <- image_pliman("mult_leaves.jpg", plot = TRUE)
sev <-
  measure_disease_byl(img = img,
                     index_lb = "B",
                     index_dh = "NGRDI",
                     workers = 2)
sev$severity
```

measure_disease_shp *Measure disease using shapefiles*

Description

This function calls [measure_disease\(\)](#) in each image polygon of a shapefile object generated with [image_shp\(\)](#) and bind the results into read-ready data frames.

Usage

```
measure_disease_shp(
  img,
  nrow = 1,
  ncol = 1,
  buffer_x = 0,
  buffer_y = 0,
  prepare = FALSE,
  viewer = "mapview",
  index_lb = "HUE2",
  index_dh = "NGRDI",
  pattern = NULL,
  threshold = NULL,
  invert = FALSE,
  dir_original = NULL,
  show_features = FALSE,
  interactive = FALSE,
  plot = TRUE,
```

```

parallel = FALSE,
workers = NULL,
verbose = TRUE,
...
)

```

Arguments

<code>img</code>	The image to be analyzed. Either an image of class <code>Image</code> or a character string containing the image name. In the last, the image will be searched in the root directory. Declare <code>dir_original</code> to inform a subfolder that contains the images to be processed.
<code>nrow, ncol</code>	The number of rows and columns to generate the shapefile. Defaults to 1.
<code>buffer_x, buffer_y</code>	Buffering factor for the width and height, respectively, of each individual shape's side. A value between 0 and 0.5 where 0 means no buffering and 0.5 means complete buffering (default: 0). A value of 0.25 will buffer the shape by 25% on each side.
<code>prepare</code>	Logical value indicating whether to prepare the image for analysis using <code>image_prepare_mv()</code> function. This allows to align and crop the image before processing. Defaults to FALSE.
<code>viewer</code>	The viewer option. If not provided, the value is retrieved using <code>get_pliman_viewer()</code> . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the <code>set_pliman_viewer()</code> function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.
<code>index_lb</code>	The index used to segment the foreground (e.g., leaf) from the background. If not declared, the entire image area (pixels) will be considered in the computation of the severity.
<code>index_dh</code>	The index used to segment diseased from healthy tissues when <code>img_healthy</code> and <code>img_symptoms</code> are not declared. Defaults to "GLI". See <code>image_index()</code> for more details.
<code>pattern</code>	A pattern of file name used to identify images to be processed. For example, if <code>pattern = "im"</code> all images that the name matches the pattern (e.g., <code>img1.-</code> , <code>image1.-</code> , <code>im2.-</code>) will be analyzed. Providing any number as pattern (e.g., <code>pattern = "1"</code>) will select images that are named as 1.-, 2.-, and so on.
<code>threshold</code>	By default (<code>threshold = NULL</code>), a threshold value based on Otsu's method is used to reduce the grayscale image to a binary image. If a numeric value is informed, this value will be used as a threshold. Inform any non-numeric value different than "Otsu" to iteratively choose the threshold based on a raster plot showing pixel intensity of the index. Must be a vector of length 2 to indicate the threshold for <code>index_lb</code> and <code>index_dh</code> , respectively.
<code>invert</code>	Inverts the binary image if desired. This is useful to process images with black background. Defaults to FALSE.

dir_original	The directory containing the original and processed images. Defaults to NULL. In this case, the function will search for the image <code>img</code> in the current working directory.
show_features	If TRUE returnS the lesion features such as number, area, perimeter, and radius. Defaults to FALSE.
interactive	If FALSE (default) the grid is created automatically based on the image dimension and number of rows/columns. If <code>interactive = TRUE</code> , users must draw points at the diagonal of the desired bounding box that will contain the grid.
plot	Show image after processing? Defaults to TRUE.
parallel	Processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time, especially when <code>pattern</code> is used is informed. The number of sections is set up to 70% of available cores.
workers	A positive numeric scalar or a function specifying the maximum number of parallel processes that can be active at the same time.
verbose	If TRUE (default) a summary is shown in the console.
...	Additional arguments passed on to measure_disease .

Value

An object of class `plm_disease_by1`. See more details in the Value section of [measure_disease\(\)](#).

Examples

```
if(interactive()){
# severity for the three leaflets (from left to right)
img <- image_pliman("mult_leaves.jpg", plot = TRUE)
sev <-
  measure_disease_shp(img = img,
                     nrow = 1,
                     ncol = 3,
                     index_lb = "B",
                     index_dh = "NGRDI")
sev$severity
}
```

object_edge

Object edges

Description

Applies the Sobel-Feldman Operator to detect edges. The operator is based on convolving the image with a small, separable, and integer-valued filter in the horizontal and vertical directions.

Usage

```
object_edge(img, sigma = 1, threshold = "Otsu", thinning = FALSE, plot = TRUE)
```

Arguments

img	An image or a list of images of class Image.
sigma	Gaussian kernel standard deviation used in the gaussian blur.
threshold	The threshold method to be used. If threshold = "Otsu" (default), a threshold value based on Otsu's method is used to reduce the grayscale image to a binary image. If any non-numeric value different than "Otsu" is used, an interactive section will allow you to choose the threshold based on a raster plot showing pixel intensity of the index. Alternatively, provide a numeric value to be used as the threshold value.
thinning	Logical value indicating whether a thinning procedure should be applied to the detected edges. See image_skeleton()
plot	Logical value indicating whether a plot should be created

Value

A binary version of image.

References

Sobel, I., and G. Feldman. 1973. A 3x3 isotropic gradient operator for image processing. *Pattern Classification and Scene Analysis*: 271–272.

Examples

```
library(pliman)
img <- image_pliman("sev_leaf_nb.jpg", plot = TRUE)
object_edge(img)
```

object_export

Export multiple objects from an image to multiple images

Description

Given an image with multiple objects, `object_export()` will split the objects into a list of objects using `object_split()` and then export them to multiple images into the current working directory (or a subfolder). Batch processing is performed by declaring a file name pattern that matches the images within the working directory.

Usage

```
object_export(
  img,
  pattern = NULL,
  dir_original = NULL,
  dir_processed = NULL,
```

```

format = ".jpg",
squaresize = FALSE,
index = "NB",
lower_size = NULL,
watershed = TRUE,
invert = FALSE,
fill_hull = FALSE,
filter = 2,
threshold = "Otsu",
extension = NULL,
tolerance = NULL,
object_size = "medium",
edge = 20,
remove_bg = FALSE,
parallel = FALSE,
verbose = TRUE
)

```

Arguments

img	The image to be analyzed.
pattern	A pattern of file name used to identify images to be processed. For example, if pattern = "im" all images in the current working directory that the name matches the pattern (e.g., img1.-, image1.-, im2.-) will be imported and processed. Providing any number as pattern (e.g., pattern = "1") will select images that are named as 1.-, 2.-, and so on. An error will be returned if the pattern matches any file that is not supported (e.g., img1.pdf).
dir_original	The directory containing the original images. Defaults to NULL. It can be either a full path, e.g., "C:/Desktop/imgs", or a subfolder within the current working directory, e.g., "/imgs".
dir_processed	Optional character string indicating a subfolder within the current working directory to save the image(s). If the folder doesn't exist, it will be created.
format	The format of image to be exported.
squaresize	Squaresizes the image before the exportation? If TRUE, image_square() will be called internally.
index	A character value specifying the target mode for conversion to binary image when foreground and background are not declared. Defaults to "NB" (normalized blue). See image_index() for more details. User can also calculate your own index using the bands names, e.g. index = "R+B/G"
lower_size	Plant images often contain dirt and dust. To prevent dust from affecting the image analysis, objects with lesser than 10% of the mean of all objects are removed. Set lower_limit = 0 to keep all the objects.
watershed	If TRUE (default) performs watershed-based object detection. This will detect objects even when they are touching one other. If FALSE, all pixels for each connected set of foreground pixels are set to a unique object. This is faster but is not able to segment touching objects.

invert	Inverts the binary image if desired. This is useful to process images with a black background. Defaults to FALSE. If reference = TRUE is use, invert can be declared as a logical vector of length 2 (eg., invert = c(FALSE, TRUE). In this case, the segmentation of objects and reference from the foreground using back_fore_index is performed using the default (not inverted), and the segmentation of objects from the reference is performed by inverting the selection (selecting pixels higher than the threshold).
fill_hull	Fill holes in the binary image? Defaults to FALSE. This is useful to fill holes in objects that have portions with a color similar to the background. IMPORTANT: Objects touching each other can be combined into one single object, which may underestimate the number of objects in an image.
filter	Performs median filtering in the binary image? See more at image_filter() . Defaults to FALSE. Use a positive integer to define the size of the median filtering. Larger values are effective at removing noise, but adversely affect edges.
threshold	The threshold method to be used. <ul style="list-style-type: none"> • By default (threshold = "Otsu"), a threshold value based on Otsu's method is used to reduce the grayscale image to a binary image. If a numeric value is informed, this value will be used as a threshold. • If threshold = "adaptive", adaptive thresholding (Shafait et al. 2008) is used, and will depend on the k and windowsize arguments. • If any non-numeric value different than "Otsu" and "adaptive" is used, an iterative section will allow you to choose the threshold based on a raster plot showing pixel intensity of the index.
extension	Radius of the neighborhood in pixels for the detection of neighboring objects. Higher value smooths out small objects.
tolerance	The minimum height of the object in the units of image intensity between its highest point (seed) and the point where it contacts another object (checked for every contact pixel). If the height is smaller than the tolerance, the object will be combined with one of its neighbors, which is the highest.
object_size	The size of the object. Used to automatically set up tolerance and extension parameters. One of the following. "small" (e.g, wheat grains), "medium" (e.g, soybean grains), "large"(e.g, peanut grains), and "elarge" (e.g, soybean pods)'.
edge	The number of pixels to be added in the edge of the segmented object. Defaults to 5.
remove_bg	If TRUE, the pixels that are not part of objects are converted to white.
parallel	If TRUE processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time, especially when pattern is used is informed. When object_index is informed, multiple sections will be used to extract the RGB values for each object in the image. This may significantly speed up processing time when an image has lots of objects (say >1000).
verbose	If TRUE (default) a summary is shown in the console.

Value

A NULL object.

Examples

```
if(interactive()){  
  library(pliman)  
  img <- image_pliman("la_leaves.jpg")  
  object_export(img)  
  
}
```

object_export_shp	<i>Export multiple objects from an image to multiple images</i>
-------------------	---

Description

Given an image with multiple objects, `object_export_shp()` will split the objects into a list of objects using `object_split_shp()` and then export them to multiple images into the current working directory (or a subfolder). Batch processing is performed by declaring a file name pattern that matches the images within the working directory.

Usage

```
object_export_shp(  
  img,  
  pattern = NULL,  
  dir_original = NULL,  
  dir_processed = NULL,  
  format = ".jpg",  
  subfolder = NULL,  
  squarize = FALSE,  
  nrow = 1,  
  ncol = 1,  
  buffer_x = 0,  
  buffer_y = 0,  
  interactive = FALSE,  
  parallel = FALSE,  
  verbose = TRUE,  
  viewer = get_pliman_viewer()  
)
```

Arguments

`img` An object of class Image

pattern	A pattern of file name used to identify images to be processed. For example, if pattern = "im" all images in the current working directory that the name matches the pattern (e.g., img1., image1., im2.-) will be imported and processed. Providing any number as pattern (e.g., pattern = "1") will select images that are named as 1., 2., and so on. An error will be returned if the pattern matches any file that is not supported (e.g., img1.pdf).
dir_original	The directory containing the original images. Defaults to NULL. It can be either a full path, e.g., "C:/Desktop/imgs", or a subfolder within the current working directory, e.g., "/imgs".
dir_processed	Optional character string indicating a subfolder within the current working directory to save the image(s). If the folder doesn't exist, it will be created.
format	The format of image to be exported.
subfolder	Optional character string indicating a subfolder within the current working directory to save the image(s). If the folder doesn't exist, it will be created.
squarize	Squarizes the image before the exportation? If TRUE, <code>image_square()</code> will be called internally.
nrow	The number of desired rows in the grid. Defaults to 1.
ncol	The number of desired columns in the grid. Defaults to 1.
buffer_x, buffer_y	Buffering factor for the width and height, respectively, of each individual shape's side. A value between 0 and 0.5 where 0 means no buffering and 0.5 means complete buffering (default: 0). A value of 0.25 will buffer the shape by 25% on each side.
interactive	If FALSE (default) the grid is created automatically based on the image dimension and number of rows/columns. If interactive = TRUE, users must draw points at the diagonal of the desired bounding box that will contain the grid.
parallel	If TRUE processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time, especially when pattern is used is informed. When object_index is informed, multiple sections will be used to extract the RGB values for each object in the image. This may significantly speed up processing time when an image has lots of objects (say >1000).
verbose	If TRUE (default) a summary is shown in the console.
viewer	The viewer option. If not provided, the value is retrieved using <code>get_pliman_viewer()</code> . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the <code>set_pliman_viewer()</code> function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.

Value

A NULL object.

Examples

```

if(interactive()){
  library(pliman)
  flax <- image_pliman("flax_leaves.jpg", plot = TRUE)
  object_export_shp(flax)
}

```

object_label

Labels objects

Description

All pixels for each connected set of foreground (non-zero) pixels in *x* are set to a unique increasing integer, starting from 1. Hence, `max(x)` gives the number of connected objects in *x*. This is a wrapper to `EImage::bwlabel` or `EImage::watershed` (if `watershed = TRUE`).

Usage

```

object_label(
  img,
  index = "B",
  invert = FALSE,
  fill_hull = FALSE,
  threshold = "Otsu",
  k = 0.1,
  window_size = NULL,
  filter = FALSE,
  watershed = FALSE,
  tolerance = NULL,
  extension = NULL,
  object_size = "medium",
  plot = TRUE,
  ncol = NULL,
  nrow = NULL,
  verbose = TRUE
)

```

Arguments

<code>img</code>	An image object.
<code>index</code>	A character value (or a vector of characters) specifying the target mode for conversion to binary image. See the available indexes with <code>pliman_indexes()</code> and <code>image_index()</code> for more details.
<code>invert</code>	Inverts the binary image, if desired.
<code>fill_hull</code>	Fill holes in the objects? Defaults to FALSE.

threshold	<p>The threshold method to be used.</p> <ul style="list-style-type: none"> • By default (threshold = "Otsu"), a threshold value based on Otsu's method is used to reduce the grayscale image to a binary image. If a numeric value is informed, this value will be used as a threshold. • If threshold = "adaptive", adaptive thresholding (Shafait et al. 2008) is used, and will depend on the k and windowsize arguments. • If any non-numeric value different than "Otsu" and "adaptive" is used, an interactive section will allow you to choose the threshold based on a raster plot showing pixel intensity of the index.
k	a numeric in the range 0-1. when k is high, local threshold values tend to be lower. when k is low, local threshold value tend to be higher.
windowsize	windowsize controls the number of local neighborhood in adaptive thresholding. By default it is set to $1/3 * \text{minxy}$, where minxy is the minimum dimension of the image (in pixels).
filter	Performs median filtering in the binary image? (Defaults to FALSE). Provide a positive integer > 1 to indicate the size of the median filtering. Higher values are more efficient to remove noise in the background but can dramatically impact the perimeter of objects, mainly for irregular perimeters such as leaves with serrated edges.
watershed	If TRUE (default) performs watershed-based object detection. This will detect objects even when they are touching one other. If FALSE, all pixels for each connected set of foreground pixels are set to a unique object. This is faster but is not able to segment touching objects.
tolerance	The minimum height of the object in the units of image intensity between its highest point (seed) and the point where it contacts another object (checked for every contact pixel). If the height is smaller than the tolerance, the object will be combined with one of its neighbors, which is the highest.
extension	Radius of the neighborhood in pixels for the detection of neighboring objects. Higher value smooths out small objects.
object_size	The size of the object. Used to automatically set up tolerance and extension parameters. One of the following. "small" (e.g, wheat grains), "medium" (e.g, soybean grains), "large"(e.g, peanut grains), and "elarge" (e.g, soybean pods)'. '.
plot	Show image after processing?
nrow, ncol	The number of rows or columns in the plot grid. Defaults to NULL, i.e., a square grid is produced.
verbose	If TRUE (default) a summary is shown in the console.

Value

A list with the same length of img containing the labeled objects.

Examples

```
img <- image_pliman("soybean_touch.jpg")
```



```
# segment the objects using the "B" (blue) band.
object_label(img, index = "B")
object_label(img, index = "B", watershed = TRUE)
```

object_map	<i>Map Object Distances</i>
------------	-----------------------------

Description

Computes distances between objects in an `anal_obj` object and returns a list of distances, coefficient of variation (CV), and means.

Usage

```
object_map(object, by_column = "img", direction = c("horizontal", "vertical"))
```

Arguments

<code>object</code>	An <code>anal_obj</code> object computed with <code>analyze_objects_shp()</code> .
<code>by_column</code>	The column name in the object's results data frame to group objects by. Default is "img".
<code>direction</code>	The direction of mapping. Should be one of "horizontal" or "vertical". Default is "horizontal".

Value

A list with the following components:

<code>distances</code>	A list of distances between objects grouped by unique values in the specified column/row.
<code>cvs</code>	A vector of coefficient of variation (CV) values for each column/row.
<code>means</code>	A vector of mean distances for each column/row.

See Also

[analyze_objects_shp](#)

Examples

```
if(interactive()){
  library(pliman)
  flax <- image_pliman("flax_leaves.jpg", plot =TRUE)
  res <-
    analyze_objects_shp(flax,
      nrow = 3,
      ncol = 1,
      watershed = FALSE,
      index = "R/(G/B)",
```

```

                                plot = FALSE)
plot(res$final_image_mask)
plot(res$shapefiles)

# distance from each leave within each row
result <- object_map(res)
result$distances
result$cvs
result$means
}

```

object_mark

Mark Object Points

Description

Marks the coordinates of objects in an `anal_obj` object on a plot.

Usage

```
object_mark(object, col = "white")
```

Arguments

`object` An `anal_obj` object computed with `analyze_objects_shp()` or `analyze_objects_shp()`.
`col` The color of the marked points. Default is "white".

See Also

[analyze_objects_shp](#)

Examples

```

library(pliman)
flax <- image_pliman("flax_leaves.jpg", plot =TRUE)
res <-
  analyze_objects(flax,
                  watershed = FALSE,
                  index = "R/(G/B)",
                  plot = FALSE)
object_mark(res)

```

object_rgb	<i>Extract red, green and blue values from objects</i>
------------	--

Description

Given an image and a matrix of labels that identify each object, the function extracts the red, green, and blue values from each object.

Usage

```
object_rgb(img, labels)
```

Arguments

img	An Image object
labels	A mask containing the labels for each object. This can be obtained with <code>EImage::bwlabel()</code> or <code>EImage::watershed()</code>

Value

A data.frame with n rows (number of pixels for all the objects) and the following columns:

- id: the object id;
- R: the value for the red band;
- G: the value for the blue band;
- B: the value for the green band;

Examples

```
library(pliman)
img <- image_pliman("soybean_touch.jpg")
# segment the objects using the "B" (blue) band (default)

labs <- object_label(img, watershed = TRUE)
rgb <- object_rgb(img, labs[[1]])
head(rgb)
```

 object_split

Splits objects from an image into multiple images

Description

Using threshold-based segmentation, objects are first isolated from background. Then, a new image is created for each single object. A list of images is returned.

Usage

```
object_split(
  img,
  index = "NB",
  lower_size = NULL,
  watershed = TRUE,
  invert = FALSE,
  fill_hull = FALSE,
  filter = 2,
  threshold = "Otsu",
  extension = NULL,
  tolerance = NULL,
  object_size = "medium",
  edge = 3,
  remove_bg = FALSE,
  plot = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

img	The image to be analyzed.
index	A character value specifying the target mode for conversion to binary image when foreground and background are not declared. Defaults to "NB" (normalized blue). See <code>image_index()</code> for more details. User can also calculate your own index using the bands names, e.g. <code>index = "R+B/G"</code>
lower_size	Plant images often contain dirt and dust. To prevent dust from affecting the image analysis, objects with lesser than 10% of the mean of all objects are removed. Set <code>lower_limit = 0</code> to keep all the objects.
watershed	If TRUE (default) performs watershed-based object detection. This will detect objects even when they are touching one other. If FALSE, all pixels for each connected set of foreground pixels are set to a unique object. This is faster but is not able to segment touching objects.
invert	Inverts the binary image if desired. This is useful to process images with a black background. Defaults to FALSE. If <code>reference = TRUE</code> is use, <code>invert</code> can be declared as a logical vector of length 2 (eg., <code>invert = c(FALSE, TRUE)</code>). In

this case, the segmentation of objects and reference from the foreground using `back_fore_index` is performed using the default (not inverted), and the segmentation of objects from the reference is performed by inverting the selection (selecting pixels higher than the threshold).

<code>fill_hull</code>	Fill holes in the binary image? Defaults to FALSE. This is useful to fill holes in objects that have portions with a color similar to the background. IMPORTANT: Objects touching each other can be combined into one single object, which may underestimate the number of objects in an image.
<code>filter</code>	Performs median filtering in the binary image? See more at image_filter() . Defaults to FALSE. Use a positive integer to define the size of the median filtering. Larger values are effective at removing noise, but adversely affect edges.
<code>threshold</code>	The threshold method to be used. <ul style="list-style-type: none"> • By default (<code>threshold = "otsu"</code>), a threshold value based on Otsu's method is used to reduce the grayscale image to a binary image. If a numeric value is informed, this value will be used as a threshold. • If <code>threshold = "adaptive"</code>, adaptive thresholding (Shafait et al. 2008) is used, and will depend on the <code>k</code> and <code>window_size</code> arguments. • If any non-numeric value different than <code>"otsu"</code> and <code>"adaptive"</code> is used, an interactive section will allow you to choose the threshold based on a raster plot showing pixel intensity of the index.
<code>extension</code>	Radius of the neighborhood in pixels for the detection of neighboring objects. Higher value smooths out small objects.
<code>tolerance</code>	The minimum height of the object in the units of image intensity between its highest point (seed) and the point where it contacts another object (checked for every contact pixel). If the height is smaller than the tolerance, the object will be combined with one of its neighbors, which is the highest.
<code>object_size</code>	The size of the object. Used to automatically set up <code>tolerance</code> and <code>extension</code> parameters. One of the following. <code>"small"</code> (e.g, wheat grains), <code>"medium"</code> (e.g, soybean grains), <code>"large"</code> (e.g, peanut grains), and <code>"elarge"</code> (e.g, soybean pods)'.
<code>edge</code>	The number of pixels to be added in the edge of the segmented object. Defaults to 5.
<code>remove_bg</code>	If TRUE, the pixels that are not part of objects are converted to white.
<code>plot</code>	Show image after processing?
<code>verbose</code>	If TRUE (default) a summary is shown in the console.
<code>...</code>	Additional arguments passed on to image_combine()

Value

A list of objects of class `Image`.

See Also

[analyze_objects\(\)](#), [image_binary\(\)](#)

Examples

```
library(pliman)
img <- image_pliman("la_leaves.jpg", plot = TRUE)
imgs <- object_split(img) # set to NULL to use 50% of the cores
```

object_split_shp *Splits image objects based on a shape file*

Description

Here, `image_shp()` is used to create a shape file based on the desired number of rows and columns. Then, using the object coordinates, a list of Image objects is created.

Usage

```
object_split_shp(
  img,
  nrow = 1,
  ncol = 1,
  buffer_x = 0,
  buffer_y = 0,
  interactive = FALSE,
  viewer = get_pliman_viewer(),
  only_shp = FALSE,
  ...
)
```

Arguments

<code>img</code>	An object of class Image
<code>nrow</code>	The number of desired rows in the grid. Defaults to 1.
<code>ncol</code>	The number of desired columns in the grid. Defaults to 1.
<code>buffer_x, buffer_y</code>	Buffering factor for the width and height, respectively, of each individual shape's side. A value between 0 and 0.5 where 0 means no buffering and 0.5 means complete buffering (default: 0). A value of 0.25 will buffer the shape by 25% on each side.
<code>interactive</code>	If FALSE (default) the grid is created automatically based on the image dimension and number of rows/columns. If <code>interactive = TRUE</code> , users must draw points at the diagonal of the desired bounding box that will contain the grid.
<code>viewer</code>	The viewer option. If not provided, the value is retrieved using <code>get_pliman_viewer()</code> . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview

package is used. To set this argument globally for all functions in the package, you can use the `set_pliman_viewer()` function. For example, you can run `set_pliman_viewer("mapview")` to set the viewer option to "mapview" for all functions.

`only_shp` If TRUE returns only the shapefiles with the coordinates for each image. If FALSE (default) returns the splitted image according to `nrow` and `ncol` arguments.

`...` Other arguments passed on to `image_shp()`

Value

A list of Image objects

Examples

```
if(interactive()){
  library(pliman)
  flax <- image_pliman("flax_leaves.jpg", plot = TRUE)
  objects <- object_split_shp(flax, nrow = 3, ncol = 5)
  image_combine(objects$imgs)
}
```

`object_to_color` *Apply color to image objects*

Description

The function applies the color informed in the argument `color` to segmented objects in the image. The segmentation is performed using image indexes. Use `image_index()` to identify the better candidate index to segment objects.

Usage

```
object_to_color(img, index = "NB", color = "blue", plot = TRUE, ...)
```

Arguments

`img` An image object.

`index` A character value (or a vector of characters) specifying the target mode for conversion to binary image. See the available indexes with `pliman_indexes()` and `image_index()` for more details.

`color` The color to apply in the image objects. Defaults to "blue".

`plot` Plots the modified image? Defaults to TRUE.

`...` Additional arguments passed on to `image_binary()`.

Value

An object of class Image

Examples

```
library(pliman)
img <- image_pliman("la_leaves.jpg")
img2 <- object_to_color(img, index = "G-R")
image_combine(img, img2)
```

otsu

Calculate Otsu's threshold

Description

Given a numeric vector with the pixel's intensities, returns the threshold value based on Otsu's method, which minimizes the combined intra-class variance

Usage

```
otsu(values)
```

Arguments

values A numeric vector with the pixel values.

Value

A double (threshold value).

References

Otsu, N. 1979. Threshold selection method from gray-level histograms. IEEE Trans Syst Man Cybern SMC-9(1): 62–66. doi: [doi:10.1109/tsmc.1979.4310076](https://doi.org/10.1109/tsmc.1979.4310076)

Examples

```
img <- image_pliman("soybean_touch.jpg")
thresh <- otsu(img@.Data[, , 3])
plot(img[, , 3] < thresh)
```

palettes *Create image palettes*

Description

`image_palette()` creates image palettes by applying the k-means algorithm to the RGB values.

Usage

```
image_palette(img, npal = 5, proportional = TRUE, plot = TRUE)
```

Arguments

<code>img</code>	An image object.
<code>npal</code>	The number of color palettes.
<code>proportional</code>	Creates a joint palette with proportional size equal to the number of pixels in the image? Defaults to TRUE.
<code>plot</code>	Plot the generated palette? Defaults to TRUE.

Value

`image_palette()` returns a list with two elements:

- `palette_list` A list with `npal` color palettes of class `Image`.
- `joint` An object of class `Image` with the color palettes
- `proportions` The proportion of the entire image corresponding to each color in the palette
- `rgbs` The average RGB value for each palette

Examples

```
library(pliman)
img <- image_pliman("sev_leaf.jpg")
pal <- image_palette(img, npal = 4)

image_combine(pal$palette_list)
```

pipe

Forward-pipe operator

Description

Pipe an object forward into a function or call expression.

Usage

```
lhs %>% rhs
```

Arguments

lhs	The result you are piping.
rhs	Where you are piping the result to.

Author(s)

Nathan Eastwood <nathan.eastwood@icloud.com> and Antoine Fabri <antoine.fabri@gmail.com>. The code was obtained from poorman package at <https://github.com/nathaneastwood/poorman/blob/master/R/pipe.R>

Examples

```
library(pliman)

# Basic use:
iris %>% head()

# use to apply several functions to an image
img <- image_pliman("la_leaves.jpg")

img %>%
  image_resize(50) %>%      # resize to 50% of the original size
  object_isolate(id = 1) %>% # isolate object 1
  image_filter() %>%      # apply a median filter
  plot()                  # plot
```

pixel_index	<i>Get the pixel indices for a given row of a binary image</i>
-------------	--

Description

This function finds the first row in the bin matrix that has a value greater than 0 (TRUE). It then calculates the minimum, median, and maximum values for the pixels in that row and creates an array containing the row index, the minimum pixel index, the median pixel index, and the maximum pixel index.

Usage

```
pixel_index(bin, row = NULL, direction = "updown")
```

Arguments

bin	A logical matrix representing a binary image
row	An optional row index. If not provided, the function selects the first non-zero row.
direction	The direction for row selection when row is not provided. If set to "updown", the function starts scanning from the top of the image towards the bottom. If set to "downup", the function starts scanning from the bottom towards the top.

Value

A numeric vector containing the row index, the minimum pixel index, the median pixel index, and the maximum pixel index.

Examples

```
library(pliman)
leaf <- image_pliman("sev_leaf.jpg")
bin <- image_binary(leaf, "NB")[[1]]

# first row with leaf (17)
pixel_index(bin)

# index at the row 100
pixel_index(bin, row = 100)

plot(leaf)
points(x = 248, y = 17, pch = 16, col = "red", cex = 2)
points(x = 163, y = 100, pch = 16, col = "red", cex = 2)
points(x = 333, y = 100, pch = 16, col = "red", cex = 2)
```

pliman_images

Sample images

Description

Sample images installed with the **pliman** package

Format

*.jpg format

- flax_leaves.jpg Flax leaves in a white background
- flax_grains.jpg Flax grains with background light.
- la_back.jpg A cyan palette representing the background of images la_pattern, la_leaves, and soybean_touch.
- la_leaf.jpg A sample of the leaves in la_leaves
- la_leaves.jpg Tree leaves with a sample of known area.
- mult_leaves.jpg Three soybean leaflets with soybean rust symptoms.
- objects_300dpi.jpg An image with 300 dpi resolution.
- potato_leaves.jpg Three potato leaves, which were gathered from Gupta et al. (2020).
- sev_leaf.jpg A soybean leaf with a blue background.
- sev_leaf_nb.jpg A soybean leaf without background.
- sev_back.jpg A blue palette representing the background of sev_leaf.
- sev_healthy.jpg Healthy area of sev_leaf.
- sev_symp.jpg The symptomatic area sev_leaf.
- shadow.jpg A shaded leaf, useful to test adaptive thresholding
- soy_green.jpg Soybean grains with a white background.
- soybean_grain.jpg A sample palette of the grains in soy_green.
- soybean_touch.jpg Soybean grains with a cyan background touching one each other.
- field_mosaic.jpg An UVA image from a soybean field.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Source

Personal data, Gupta et al. (2020).

References

Gupta, S., Rosenthal, D. M., Stinchcombe, J. R., & Baucom, R. S. (2020). The remarkable morphological diversity of leaf shape in sweet potato (*Ipomoea batatas*): the influence of genetics, environment, and G×E. *New Phytologist*, 225(5), 2183–2195. doi:10.1111/NPH.16286

pliman_viewer	<i>Global option for controlling the viewer in pliman package</i>
---------------	---

Description

Users can set the value of this option using `options("pliman_viewer", value)`. The default value is "base". Use "mapview" to allow image to be plotted/edited using the R packages `mapview` and `mapedit`

plot.image_shp	<i>S3 method plot for image_shp objects</i>
----------------	---

Description

Draws the bounding boxes for each object computed with `image_shp()`.

Usage

```
## S3 method for class 'image_shp'
plot(
  x,
  img = NULL,
  col_line = "black",
  size_line = 2,
  col_text = "black",
  size_text = 0.75,
  ...
)
```

Arguments

<code>x</code>	An object computed with <code>image_shp()</code> .
<code>img</code>	The image that was used to compute the shapefile (optional)
<code>col_line, col_text</code>	The color of the line/text in the grid. Defaults to "red".
<code>size_line, size_text</code>	The size of the line/text in the grid. Defaults to 2.5.
<code>...</code>	Currently not used.

Value

A NULL object

Examples

```

library(pliman)
flax <- image_pliman("flax_leaves.jpg")
shape <- image_shp(flax, nrow = 3, ncol = 5)

# grid on the existing image
plot(flax)
plot(shape)

```

plot_index

Plot an image index

Description

Plot an image index

Usage

```

plot_index(
  img = NULL,
  object = NULL,
  index = NULL,
  remove_bg = TRUE,
  viewer = get_pliman_viewer(),
  layer = 1,
  max_pixels = 1e+06,
  color_regions = custom_palette(),
  ncol = NULL,
  nrow = NULL,
  aspect_ratio = NA
)

```

Arguments

img	An optional Image object or an object computed with image_index() . If object is provided, then the input image is obtained internally.
object	An object computed with analyze_objects_shp() . By using this object you can ignore img.
index	The index to plot. Defaults to the index computed from the object if provided. Otherwise, the B index is computed. See image_index() for more details.
remove_bg	Logical value indicating whether to remove the background when object is provided. Defaults to TRUE.
viewer	The viewer option. If not provided, the value is retrieved using get_pliman_viewer() . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview

package is used. To set this argument globally for all functions in the package, you can use the `set_pliman_viewer()` function. For example, you can run `set_pliman_viewer("mapview")` to set the viewer option to "mapview" for all functions.

layer	The layer to plot when <code>img</code> is an object computed with <code>image_index()</code> and <code>viewer = "mapview"</code> . Defaults to the first layer (first index computed).
max_pixels	integer > 0. Maximum number of cells to plot the index. If <code>max_pixels < npixels(img)</code> , regular sampling is used before plotting. Using a large number of pixels may slow down the plotting time.
color_regions	The color palette for displaying index values. Default is <code>custom_palette()</code> .
nrow, ncol	The number of rows or columns in the plot grid. Defaults to NULL, i.e., a square grid is produced.
aspect_ratio	Numeric, giving the aspect ratio y/x. Defaults to NA. See <code>graphics::plot.window()</code> for more details.

Value

None

Examples

```
if(interactive()){
# Example usage:
library(pliman)
img <- image_pliman("sev_leaf.jpg")
plot_index(img, index = "B")
}
```

plot_index_shp	<i>Plot rectangles colored by a quantitative attribute and overlay on an RGB image</i>
----------------	--

Description

This function plots rectangles on top of an RGB image, where each rectangle is colored based on a quantitative variable. The quantitative variable is specified in the `attribute` argument and should be present in the `object_index` of the object computed using `analyze_objects_shp()`. The rectangles are colored using a color scale.

Usage

```
plot_index_shp(
  object,
  attribute = "coverage",
  color = c("red", "green"),
```

```

alpha = 0.5,
legend.position = "bottom",
na.color = "gray",
classes = 6,
round = 3,
horiz = TRUE
)

```

Arguments

object	An object computed with <code>analyze_objects_shp()</code> .
attribute	The name of the quantitative variable in the <code>object_index</code> to be used for coloring the rectangles.
color	A vector of two colors to be used for the color scale.
alpha	The transparency level of the rectangles' color (between 0 and 1).
legend.position	The position of the color legend, either "bottom" or "right".
na.color	The color to be used for rectangles with missing values in the quantitative variable.
classes	The number of classes in the color scale.
round	The number of decimal places to round the legend values.
horiz	Logical, whether the legend should be horizontal (TRUE) or vertical (FALSE).

Value

The function plots rectangles colored by the specified quantitative variable on top of the RGB image and shows the continuous color legend outside the plot.

Examples

```

if(interactive()){
library(pliman)

# Computes the DGCI index for each flax leaf
flax <- image_pliman("flax_leaves.jpg", plot =TRUE)
res <-
  analyze_objects_shp(flax,
    buffer_x = 0.2,
    buffer_y = 0.2,
    nrow = 3,
    ncol = 5,
    plot = FALSE,
    object_index = "DGCI")
plot(res$final_image)
plot_index_shp(res)
}

```

`plot_lw`*Plot length and width lines on objects*

Description

This function plots the length and width lines given an object computed with `analyze_objects()`. The function does not call `plot.new`, so it must be called after an image is plotted. This can be done either using, e.g., `plot(img)`, or `analyze_objects(..., plot = TRUE)`.

Usage

```
plot_lw(  
  object,  
  col_length = "red",  
  col_width = "green",  
  lwd_length = 2,  
  lwd_width = 2  
)
```

Arguments

<code>object</code>	An object computed with <code>analyze_objects()</code> .
<code>col_length</code>	The color of the length line. Default is "red".
<code>col_width</code>	The color of the width line. Default is "green".
<code>lwd_length</code>	The line width of the length line. Default is 2.
<code>lwd_width</code>	The line width of the width line. Default is 2.

Details

This function takes an object computed with `analyze_objects()` and plots the length and width lines of each object onto an image. The length and width lines are calculated based on the position and orientation of the object, and are plotted using the specified colors and line widths.

Examples

```
img <- image_pliman("flax_leaves.jpg")  
res <- analyze_objects(img, watershed = FALSE, show_contour = FALSE)  
plot_lw(res)
```

poly_apex_base_angle *Calculate the apex and base angles of an object*

Description

This function calculates the apex and base angles of an object. It takes as input a matrix of coordinates and returns the apex angle, base angle, and the coordinates of the apex and base as a list. The angles are computed after the object is aligned in the vertical axis with `poly_align()`.

Usage

```
poly_apex_base_angle(  
  x,  
  percentiles = c(0.25, 0.75),  
  invert = FALSE,  
  plot = TRUE  
)
```

Arguments

x	A matrix of coordinates representing the contour of the object, often obtained with <code>object_contour()</code> .
percentiles	A numeric vector of two percentiles between 0 and 1 indicating the height of the points from the top to the bottom. The function calculates the apex angle between the two percentiles and the base angle between the lowest point and the highest point.
invert	If TRUE, aligns the object along the horizontal axis.
plot	Plots the polygon with the points? Defaults to TRUE.

Value

A list containing the apex angle, base angle, apex coordinates, and base coordinates.

Examples

```
library(pliman)  
# a matrix of coordinates  
angls <- poly_apex_base_angle(contours[[2]])  
angls  
  
# or a list of coordinates  
poly_apex_base_angle(contours)
```

`poly_pcv`*Compute Perimeter Complexity Value (PCV)*

Description

This function calculates the Perimeter Complexity Value (PCV) for a given set of coordinates representing a contour. The PCV measures the variation of distances between the original coordinates and the smoothed coordinates relative to the perimeter length of the original contour. See more in details section.

Usage

```
poly_pcv(x, niter = 100)
```

Arguments

<code>x</code>	A matrix or a list of matrices representing the coordinates of the polygon(s).
<code>niter</code>	An integer specifying the number of smoothing iterations. See poly_smooth() for more details.

Details

The PCV is computed using the following formula:

$$PCV = \frac{\text{sum}(dists) \times \text{sd}(dists)}{\text{perim}}$$

where *dists* represents the distances between corresponding points in the original and smoothed coordinates, and *perim* is the perimeter length of the smoothed contour.

The PCV is computed by first smoothing the input contour using a specified number of iterations. The smoothed contour is then used to compute the distances between corresponding points in the original and smoothed coordinates. These distances reflect the variations in the contour shape after smoothing. The sum of these distances represents the overall magnitude of the variations. Next, the sum of distances is multiplied by the standard deviation of the distances to capture the dispersion or spread of the variations. Finally, this value is divided by the perimeter length of the original contour to provide a relative measure of complexity. Therefore, the PCV provides a relative measure of complexity by considering both the magnitude and spread of the variations in the contour shape after smoothing.

Value

The PCV value(s) computed for the contour(s).

If `x` is a matrix, returns the complexity value of the polygon's perimeter. If `x` is a list of matrices, returns a numeric vector of complexity values for each polygon.

Examples

```

library(pliman)
set.seed(20)
shp <- efourier_shape(npoints = 1000)
poly_pcv(shp)

# increase the complexity of the outline
shp2 <- poly_jitter(shp, noise_x = 20, noise_y = 250, plot = TRUE)

smo <- poly_smooth(shp2, niter = 100, plot = FALSE)
plot_contour(smo, col = "red")
poly_pcv(shp2)

```

poly_width_at	<i>Width at a given height</i>
---------------	--------------------------------

Description

The function computes the polygonal convex hull of the points in `x` and then returns the number of points that lie below a specified set of heights along the vertical axis of the convex hull.

Usage

```

poly_width_at(
  x,
  at = c(0.05, 0.25, 0.5, 0.75, 0.95),
  unify = FALSE,
  plot = FALSE
)

```

Arguments

<code>x</code>	A vector containing two-dimensional data points (often produced with object_contour).
<code>at</code>	A vector of heights along the vertical axis of the convex hull at which to count the number of points below. The default value is <code>c(0.05, 0.25, 0.5, 0.75, 0.95)</code> , which means the function will return the number of points below the 5th, 25th, 50th, 75th, and 95th percentiles of the convex hull. If <code>at = "heights"</code> is used, the function returns the width for each point of the object length.
<code>unify</code>	A logical value indicating whether to use the unified convex hull calculation method. If <code>unify = TRUE</code> , coordinates in <code>x</code> will be first bound before computing the convex hull.
<code>plot</code>	A logical value that specifies whether the widths should be plotted.

Details

The convex hull computed from `x` is aligned along the major axis and then converted to a binary image. For each height in the `at` vector, the function computes the corresponding row number in the binary image (i.e., the row number that corresponds to the specified height along the vertical axis of the convex hull) and sums the values in that row to obtain the number of points that lie below the specified height. If the convex hull contains multiple polygons and `unify = FALSE`, the function loops over each polygon and returns a list of the number of points below the specified heights for each polygon. If the convex hull contains only one polygon or multiple polygons and `unify = TRUE`, the function returns a vector of the number of points below the specified heights for that single polygon.

Value

A vector with the widths of the convex hull at the specified heights or a list of vectors with the widths of each component.

Examples

```
cont <- contours[[2]]
plot_polygon(cont |> conv_hull() |> poly_align())
# width below 5th, 25th, 50th, 75th, and 95th percentiles of the length
wd <- poly_width_at(cont)
wd

# width along the height
poly_width_at(cont, at = "height", plot = TRUE)
```

```
prepare_to_shp
```

```
Prepare images to analyze_objects_shp()
```

Description

It is a simple wrapper around `image_align()` and `image_crop()`. In this case, only the option `viewer = "base"` is used. To use `viewer = "mapview"`, please, use such functions separately.

Usage

```
prepare_to_shp(img, align = "vertical")
```

Arguments

<code>img</code>	A Image object
<code>align</code>	The desired alignment. Either "vertical" (default) or "horizontal".

Value

An aligned and cropped Image object.

Examples

```
if(interactive()){  
img <- image_pliman("flax_leaves.jpg")  
prepare_to_shp(img)  
}
```

random_color

Random built-in color names

Description

Randomly chooses single or multiple built-in color names which R knows about. See more at [grDevices::colors\(\)](#)

Usage

```
random_color(n = 1, distinct = FALSE)
```

Arguments

n The number of color names. Defaults to 1.

distinct Logical indicating if the colors returned should all be distinct. Defaults to FALSE.

Value

A character vector of color names

Examples

```
library(pliman)  
random_color(n = 3)
```

sad

*Produces Santandard Area Diagrams***Description**

Given an object computed with `measure_disease()` a Standard Area Diagram (SAD) with n images are returned with the respective severity values.

Usage

```
sad(
  object,
  n,
  show_original = FALSE,
  show_contour = FALSE,
  nrow = NULL,
  ncol = NULL,
  ...
)
```

Arguments

<code>object</code>	An object computed with <code>measure_disease()</code> .
<code>n</code>	The number of leaves in the Standard Area Diagram.
<code>show_original</code>	Show original images? Defaults to FALSE, i.e., a mask is returned.
<code>show_contour</code>	Show original images? Defaults to FALSE, i.e., a mask is returned.
<code>nrow, ncol</code>	The number of rows and columns in the plot. See <code>[image_combine()]</code> <code>[image_combine()]</code> : <code>R:image_combine()</code>
<code>...</code>	Other arguments passed on to <code>measure_disease()</code> .

Details

The leaves with the smallest and highest severity will always be in the SAD. If $n = 1$, the leaf with the smallest severity will be returned. The others are sampled sequentially to achieve the n images after severity has been ordered in an ascending order. For example, if there are 30 leaves and n is set to 3, the leaves sampled will be the 1st, 15th, and 30th with the smallest severity values.

The SAD can be only computed if an image pattern name is used in argument `pat tern` of `measure_disease()`. If the images are saved, the n images will be retrieved from `dir_processed` directory. Otherwise, the severity will be computed again to generate the images.

Value

A data frame with the severity values for the n sampled leaves. A plot with the standard area diagram can be saved by wrapping `sad()` with `png()`.

References

Del Ponte EM, Pethybridge SJ, Bock CH, et al (2017) Standard area diagrams for aiding severity estimation: Scientometrics, pathosystems, and methodological trends in the last 25 years. *Phytopathology* 107:1161–1174. doi:10.1094/PHYTO02170069FI

Examples

```
## Not run:
library(pliman)
sev <-
measure_disease(pattern = "sev_leaf",
                img_healthy = "sev_healthy",
                img_symptoms = "sev_symp",
                img_background = "sev_back",
                plot = FALSE,
                save_image = TRUE,
                show_original = FALSE,
                dir_original = image_pliman(),
                dir_processed = tempdir())
sad(sev, n = 2)

## End(Not run)
```

separate_col	<i>Turns a single character column into multiple columns.</i>
--------------	---

Description

Given either a regular expression or a vector of character positions, `separate_col()` turns a single character column into multiple columns.

Usage

```
separate_col(.data, col, into, sep = "[^[:alnum:]]+")
```

Arguments

.data	A data frame
col	Column name
into	Names of new variables to create as character vector
sep	The separator between columns. By default, a regular expression that matches any sequence of non-alphanumeric values.

Value

A mutated `.data`

Examples

```
library(pliman)
df <- data.frame(x = paste0("TRAT_", 1:5),
                 y = 1:5)
df
separate_col(df, x, into = c("TRAT", "REP"))
```

set_pliman_viewer	<i>Set the value of the pliman_viewer option</i>
-------------------	--

Description

Sets the value of the pliman_viewer option used in the package.

Usage

```
set_pliman_viewer(value)
```

Arguments

value	The value to be set for the pliman_viewer option.
-------	---

summary_index	<i>Summary an object index</i>
---------------	--------------------------------

Description

If more than one index is available, the function performs a Principal Component Analysis and produces a plot showing the contribution of the indexes to the PC1 (see [pca\(\)](#)). If an index is declared in index and a cut point in cut_point, the number and proportion of objects with mean value of index bellow and above cut_point are returned. Additionally, the number and proportion of pixels bellow and above the cutpoint is shown for each object (id).

Usage

```
summary_index(
  object,
  index = NULL,
  cut_point = NULL,
  select_higher = FALSE,
  plot = TRUE,
  type = "var",
  ...
)
```

Arguments

object	An object computed with analyze_objects() .
index	The index desired, e.g., "B". Note that these value must match the index(es) used in the argument object_index of analyze_objects() .
cut_point	The cut point.
select_higher	If FALSE (default) selects the objects with index smaller than the cut_point. Use select_higher = TRUE to select the objects with index higher than cut_point.
plot	Shows the contribution plot when more than one index is available? Defaults to TRUE.
type	The type of plot to produce. Defaults to "var". See more at get_biplot() .
...	Further arguments passed on to get_biplot() .

Value

A list with the following elements:

- ids The identification of selected objects.
- between_id A data frame with the following columns
 - n The number of objects.
 - nsel The number of selected objects.
 - prop The proportion of objects selected.
 - mean_index_sel, and mean_index_nsel The mean value of index for the selected and non-selected objects, respectively.
- within_id A data frame with the following columns
 - id The object identification
 - n_less The number of pixels with values lesser than or equal to cut_point.
 - n_greater The number of pixels with values greater than cut_point.
 - less_ratio The proportion of pixels with values lesser than or equal to cut_point.
 - greater_ratio The proportion of pixels with values greater than cut_point.
- pca_res An object computed with [pca\(\)](#)

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(pliman)
soy <- image_pliman("soy_green.jpg")
anal <- analyze_objects(soy, object_index = "G", pixel_level_index = TRUE)
plot_measures(anal, measure = "G")

summary_index(anal, index = "G", cut_point = 0.5)
```

utils_colorspace *Convert between colour spaces*

Description

`rgb_to_srgb()` Transforms colors from RGB space (red/green/blue) to Standard Red Green Blue (sRGB), using a gamma correction of 2.2.

- `rgb_to_hsb()` Transforms colors from RGB space (red/green/blue) to HSB space (hue/saturation/brightness).
- `rgb_to_lab()` Transforms colors from RGB space (red/green/blue) to CIE-LAB space

It is assumed that

Usage

```
rgb_to_hsb(object)
```

```
rgb_to_srgb(object)
```

```
rgb_to_lab(object)
```

Arguments

`object` An Image object, an object computed with `analyze_objects()` with a valid `object_index` argument, or a `data.frame/matrix`. For the last, a three-column data (R, G, and B, respectively) is required.

Value

A data frame with the columns of the converted color space

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
if(interactive()){
  library(pliman)
  img <- image_pliman("sev_leaf.jpg")
  rgb_to_lab(img)

  # analyze the object and convert the pixels
  anal <- analyze_objects(img, object_index = "B", pixel_level_index = TRUE)
  rgb_to_lab(anal)
}
```

Description

Provides useful conversions between size (cm), number of pixels (px) and dots per inch (dpi).

- `dpi_to_cm()` converts a known dpi value to centimeters.
- `cm_to_dpi()` converts a known centimeter values to dpi.
- `pixels_to_cm()` converts the number of pixels to centimeters, given a known resolution (dpi).
- `cm_to_pixels()` converts a distance (cm) to number of pixels, given a known resolution (dpi).
- `distance()` Computes the distance between two points in an image based on the Pythagorean theorem.
- `dpi()` An interactive function to compute the image resolution given a known distance informed by the user. See more information in the **Details** section.
- `npixels()` returns the number of pixels of an image.

Usage

```
dpi_to_cm(dpi)
```

```
cm_to_dpi(cm)
```

```
pixels_to_cm(px, dpi)
```

```
cm_to_pixels(cm, dpi)
```

```
npixels(img)
```

```
dpi(img, viewer = get_pliman_viewer())
```

```
distance(img, viewer = get_pliman_viewer())
```

Arguments

<code>dpi</code>	The image resolution in dots per inch.
<code>cm</code>	The size in centimeters.
<code>px</code>	The number of pixels.
<code>img</code>	An image object.
<code>viewer</code>	The viewer option. If not provided, the value is retrieved using <code>get_pliman_viewer()</code> . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package,

you can use the `set_pliman_viewer()` function. For example, you can run `set_pliman_viewer("mapview")` to set the viewer option to "mapview" for all functions.

Details

`dpi()` only run in an interactive section. To compute the image resolution (dpi) the user must use the left button mouse to create a line of known distance. This can be done, for example, using a template with known distance in the image (e.g., `la_leaves.jpg`).

Value

- `dpi_to_cm()`, `cm_to_dpi()`, `pixels_to_cm()`, and `cm_to_pixels()` return a numeric value or a vector of numeric values if the input data is a vector.
- `dpi()` returns the computed dpi (dots per inch) given the known distance informed in the plot.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(pliman)
# Convert dots per inch to centimeter
dpi_to_cm(c(1, 2, 3))

# Convert centimeters to dots per inch
cm_to_dpi(c(1, 2, 3))

# Convert centimeters to number of pixels with resolution of 96 dpi.
cm_to_pixels(c(1, 2, 3), 96)

# Convert number of pixels to cm with resolution of 96 dpi.
pixels_to_cm(c(1, 2, 3), 96)

if(isTRUE(interactive())){
#### compute the dpi (dots per inch) resolution ####
# only works in an interactive section
# objects_300dpi.jpg has a known resolution of 300 dpi
img <- image_pliman("objects_300dpi.jpg")
# Higher square: 10 x 10 cm
# 1) Run the function dpi()
# 2) Use the left mouse button to create a line in the higher square
# 3) Declare a known distance (10 cm)
# 4) See the computed dpi
dpi(img)

img2 <- image_pliman("la_leaves.jpg")
# square leaf sample (2 x 2 cm)
dpi(img2)
}
```

`utils_file`*Utilities for file manipulation*

Description

- `file_extension()` Get the extension of a file.
- `file_name()` Get the name of a file.
- `file_dir()` Get or directory of a file
- `manipulate_files()` Manipulate files in a directory with options to rename (insert prefix or suffix) and save the new files to the same or other provided directory.
- `pliman_indexes()` Get the indexes available in pliman.
- `pliman_indexes_eq()` Get the equation of the indexes available in pliman.

Usage

```
file_extension(file)
```

```
file_name(file)
```

```
file_dir(file)
```

```
manipulate_files(  
    pattern,  
    dir = NULL,  
    prefix = NULL,  
    name = NULL,  
    suffix = NULL,  
    extension = NULL,  
    sep = "",  
    save_to = NULL,  
    overwrite = FALSE,  
    remove_original = FALSE,  
    verbose = TRUE  
)
```

```
pliman_indexes()
```

```
pliman_indexes_eq()
```

Arguments

<code>file</code>	The file name.
<code>pattern</code>	A file name pattern.
<code>dir</code>	The working directory containing the files to be manipulated. Defaults to the current working directory.

prefix, suffix	A prefix or suffix to be added in the new file names. Defaults to NULL (no prefix or suffix).
name	The name of the new files. Defaults to NULL (original names). name can be either a single value or a character vector of the same length as the number of files manipulated. If one value is informed, a sequential vector of names will be created as "name_1", "name_2", and so on.
extension	The new extension of the file. If not declared (default), the original extensions will be used.
sep	An optional separator. Defaults to "".
save_to	The directory to save the new files. Defaults to the current working directory. If the file name of a file is not changed, nothing will occur. If save_to refers to a subfolder in the current working directory, the files will be saved to the given folder. In case of the folder doesn't exist, it will be created. By default, the files will not be overwritten. Set overwrite = TRUE to overwrite the files.
overwrite	Overwrite the files? Defaults to FALSE.
remove_original	Remove original files after manipulation? defaults to FALSE. If TRUE the files in pattern will be removed.
verbose	If FALSE, the code is run silently.

Value

- file_extension(), file_name(), and file_dir() return a character string.
- manipulate_files() No return value. If verbose == TRUE, a message is printed indicating which operation succeeded (or not) for each of the files attempted.

Examples

```
library(pliman)
# get file name, directory and extension
file <- "E:/my_folder/my_subfolder/image1.png"
file_dir(file)
file_name(file)
file_extension(file)

# manipulate files
dir <- tempdir()
list.files(dir)
file.create(paste0(dir, "/test.txt"))
list.files(dir)
manipulate_files("test",
  dir = paste0(dir, "\\"),
  prefix = "chang_",
  save_to = paste0(dir, "\\"),
  overwrite = TRUE)
list.files(dir)
```

utils_image

*Import and export images***Description**

Import images from files and URLs and write images to files, possibly with batch processing.

Usage

```
image_import(
  img,
  ...,
  which = 1,
  pattern = NULL,
  path = NULL,
  resize = FALSE,
  plot = FALSE,
  nrow = NULL,
  ncol = NULL
)
```

```
image_export(img, name, prefix = "", extension = NULL, subfolder = NULL, ...)
```

```
image_pliman(img, plot = FALSE)
```

Arguments

img	<ul style="list-style-type: none"> • For <code>image_import()</code>, a character vector of file names or URLs. • For <code>image_export()</code>, an Image object, an array or a list of images. • For <code>image_pliman()</code>, a character value specifying the image example. See <code>?pliman_images</code> for more details.
...	Alternative arguments passed to the corresponding functions from the <code>jpeg</code> , <code>png</code> , and <code>tiff</code> packages.
which	logical scalar or integer vector to indicate which image are imported if a TIFF files is informed. Defaults to 1 (the first image is returned).
pattern	A pattern of file name used to identify images to be imported. For example, if <code>pattern = "im"</code> all images in the current working directory that the name matches the pattern (e.g., <code>img1.-</code> , <code>image1.-</code> , <code>im2.-</code>) will be imported as a list. Providing any number as pattern (e.g., <code>pattern = "1"</code>) will select images that are named as <code>1.-</code> , <code>2.-</code> , and so on. An error will be returned if the pattern matches any file that is not supported (e.g., <code>img1.pdf</code>).
path	A character vector of full path names; the default corresponds to the working directory, <code>getwd()</code> . It will overwrite (if given) the path informed in <code>image</code> argument.
resize	Resize the image after importation? Defaults to <code>FALSE</code> . Use a numeric value of range 0-100 (proportion of the size of the original image).

plot	Plots the image after importing? Defaults to FALSE.
nrow, ncol	Passed on to <code>image_combine()</code> . The number of rows and columns to use in the composite image when <code>plot = TRUE</code> .
name	An string specifying the name of the image. It can be either a character with the image name (e.g., "img1") or name and extension (e.g., "img1.jpg"). If none file extension is provided, the image will be saved as a *.jpg file.
prefix	A prefix to include in the image name when exporting a list of images. Defaults to "", i.e., no prefix.
extension	When <code>image</code> is a list, <code>extension</code> can be used to define the extension of exported files. This will overwrite the file extensions given in <code>image</code> .
subfolder	Optional character string indicating a subfolder within the current working directory to save the image(s). If the folder doesn't exist, it will be created.

Value

- `image_import()` returns a new Image object.
- `image_export()` returns an invisible vector of file names.
- `image_pliman()` returns a new Image object with the example image required. If an empty call is used, the path to the `tmp_images` directory installed with the package is returned.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(pliman)
folder <- image_pliman()
full_path <- paste0(folder, "/sev_leaf.jpg")
(path <- file_dir(full_path))
(file <- basename(full_path))
image_import(img = full_path)
image_import(img = file, path = path)
```

Description

- `get_measures()` computes object measures (area, perimeter, radius) by using either a known resolution (dpi) or an object with known measurements.
- `plot_measures()` draws the object measures given in an object to the current plot. The object identification ("id") is drawn by default.

Usage

```

get_measures(
  object,
  measure = NULL,
  id = NULL,
  dpi = NULL,
  sep = "\\_|-",
  verbose = TRUE,
  digits = 5
)

plot_measures(
  object,
  measure = "id",
  id = NULL,
  hjust = NULL,
  vjust = NULL,
  digits = 2,
  size = 0.9,
  col = "white",
  ...
)

```

Arguments

object	An object computed with <code>analyze_objects()</code> .
measure	For <code>plot_measures()</code> , a character string; for <code>get_measures()</code> , a two-sided formula, e.g., <code>measure = area ~ 100</code> indicating the known value of object id. The right-hand side is the known value and the left-hand side can be one of the following. <ul style="list-style-type: none"> • <code>area</code> The known area of the object. • <code>perimeter</code> The known perimeter of the object. • <code>radius_mean</code> The known radius of the object. • <code>radius_min</code> The known minimum radius of the object. If the object is a square, then the <code>radius_min</code> of such object will be $L/2$ where L is the length of the square side. • <code>radius_max</code> The known maximum radius of the object. If the object is a square, then the <code>radius_max</code> of such object according to the Pythagorean theorem will be $L \times \sqrt{2} / 2$ where L is the length of the square side.
id	An object in the image to indicate a known value.
dpi	A known resolution of the image in DPI (dots per inch).
sep	Regular expression to manage file names. The function combines in the merge object the object measures (sum of area and mean of all the other measures) of all images that share the same filename prefix, defined as the part of the filename preceding the first hyphen (-) or underscore (_) (no hyphen or underscore is required). For example, the measures of images named <code>L1-1.jpeg</code> , <code>L1-2.jpeg</code> ,

	and L1-3. jpeg would be combined into a single image information (L1). This feature allows the user to treat multiple images as belonging to a single sample, if desired. Defaults to <code>sep = "_ -"</code> .
<code>verbose</code>	If FALSE, runs the code silently.
<code>digits</code>	The number of significant figures. Defaults to 2.
<code>hjust, vjust</code>	A numeric value to adjust the labels horizontally and vertically. Positive values will move labels to right (<code>hjust</code>) and top (<code>vjust</code>). Negative values will move the labels to left and bottom, respectively.
<code>size</code>	The size of the text. Defaults to 0.9.
<code>col</code>	The color of the text. Defaults to "white".
<code>...</code>	Further arguments passed on to <code>graphics::text()</code> .

Value

- For `get_measures()`, if `measure` is informed, the pixel values will be corrected by the value of the known object, given in the unit of the right-hand side of `meae`. If `dpi` is informed, then all the measures will be adjusted to the `knosurwn` dpi.
- If applied to an object of class `anal_obj`, returns a data frame with the object id and the (corrected) measures.
 - If applied to an object of class `anal_obj_ls`, returns a list of class `measures_ls`, with two objects: (i) `results`, a data frame containing the identification of each image (`img`) and object within each image (`id`); and (ii) `summary` a data frame containing the values for each image. If more than one object is detected in a given image, the number of objects (`n`), total area (`area_sum`), mean area (`area_mean`) and the standard deviation of the area (`area_sd`) will be computed. For the other measures (perimeter and radius), the mean values are presented.
- `plot_measures()` returns a NULL object, drawing the text according to the x and y coordinates of the objects in `object`.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(pliman)
img <- image_pliman("objects_300dpi.jpg")
plot(img)
# Image with four objects with a known resolution of 300 dpi
# Higher square: 10 x 10 cm
# Lower square: 5 x 5 cm
# Rectangle: 4 x 2 cm
# Circle: 3 cm in diameter

# Count the objects using the blue band to segment the image
```

```
results <-
  analyze_objects(img,
                 index = "B",
                 lower_noise = 0.1)
plot_measures(results, measure = "id")

# Get object measures by declaring the known resolution in dots per inch
(measures <- get_measures(results, dpi = 300))

# Calculated diagonal of the object 1
# 10 * sqrt(2) = 14.14

# Observed diagonal of the object 1
measures[1, "radius_max"] * 2

# Get object measures by declaring the known area of object 1
get_measures(results,
             id = 1,
             area ~ 100)
```

utils_objects

Utilities for working with image objects

Description

- `object_id()` get the object identification in an image.
- `object_coord()` get the object coordinates and (optionally) draw a bounding rectangle around multiple objects in an image.
- `object_contour()` returns the coordinates (x and y) for the contours of each object in the image.
- `object_isolate()` isolates an object from an image.

Usage

```
object_coord(
  img,
  id = NULL,
  index = "NB",
  watershed = TRUE,
  invert = FALSE,
  filter = FALSE,
  fill_hull = FALSE,
  threshold = "Otsu",
  edge = 2,
```

```

    extension = NULL,
    tolerance = NULL,
    object_size = "medium",
    parallel = FALSE,
    workers = NULL,
    plot = TRUE
)

object_contour(
  img,
  pattern = NULL,
  dir_original = NULL,
  center = FALSE,
  index = "NB",
  invert = FALSE,
  filter = FALSE,
  fill_hull = FALSE,
  threshold = "Otsu",
  watershed = TRUE,
  extension = NULL,
  tolerance = NULL,
  object_size = "medium",
  parallel = FALSE,
  workers = NULL,
  plot = TRUE,
  verbose = TRUE
)

object_isolate(img, id = NULL, parallel = FALSE, workers = NULL, ...)

object_id(img, parallel = FALSE, workers = NULL, ...)

```

Arguments

<code>img</code>	An image of class <code>Image</code> or a list of <code>Image</code> objects.
<code>id</code>	<ul style="list-style-type: none"> For <code>object_coord()</code>, a vector (or scalar) of object <code>id</code> to compute the bounding rectangle. Object <code>ids</code> can be obtained with <code>object_id()</code>. Set <code>id = "all"</code> to compute the coordinates for all objects in the image. If <code>id = NULL</code> (default) a bounding rectangle is drawn including all the objects. For <code>object_isolate()</code>, a scalar that identifies the object to be extracted.
<code>index</code>	The index to produce a binary image used to compute bounding rectangle coordinates. See <code>image_binary()</code> for more details.
<code>watershed</code>	If <code>TRUE</code> (default) performs watershed-based object detection. This will detect objects even when they are touching one other. If <code>FALSE</code> , all pixels for each connected set of foreground pixels are set to a unique object. This is faster but is not able to segment touching objects.
<code>invert</code>	Inverts the binary image, if desired. Defaults to <code>FALSE</code> .

filter	Performs median filtering in the binary image? See more at image_filter() . Defaults to FALSE. Use a positive integer to define the size of the median filtering. Larger values are effective at removing noise, but adversely affect edges.
fill_hull	Fill holes in the objects? Defaults to FALSE.
threshold	By default (threshold = "Otsu"), a threshold value based on Otsu's method is used to reduce the grayscale image to a binary image. If a numeric value is informed, this value will be used as a threshold. Inform any non-numeric value different than "Otsu" to iteratively chosen the threshold based on a raster plot showing pixel intensity of the index.
edge	The number of pixels in the edge of the bounding rectangle. Defaults to 2.
extension, tolerance, object_size	Controls the watershed segmentation of objects in the image. See analyze_objects() for more details.
parallel	Processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time when image is a list. The number of sections is set up to 50% of available cores.
workers	A positive numeric scalar or a function specifying the maximum number of parallel processes that can be active at the same time.
plot	Shows the image with bounding rectangles? Defaults to TRUE.
pattern	A pattern of file name used to identify images to be imported. For example, if pattern = "im" all images in the current working directory that the name matches the pattern (e.g., img1., image1., im2.-) will be imported as a list. Providing any number as pattern (e.g., pattern = "1") will select images that are named as 1., 2., and so on. An error will be returned if the pattern matches any file that is not supported (e.g., img1.pdf).
dir_original	The directory containing the original images. Defaults to NULL, which means that the current working directory will be considered.
center	If TRUE returns the object contours centered on the origin.
verbose	If TRUE (default) a summary is shown in the console.
...	<ul style="list-style-type: none"> • For object_isolate(), further arguments passed on to object_coord(). • For object_id(), further arguments passed on to analyze_objects().

Value

- [object_id\(\)](#) An image of class "Image" containing the object's identification.
- [object_coord\(\)](#) A list with the coordinates for the bounding rectangles. If id = "all" or a numeric vector, a list with a vector of coordinates is returned.
- [object_isolate\(\)](#) An image of class "Image" containing the isolated object.

Examples

```
library(pliman)
img <- image_pliman("la_leaves.jpg")
# Get the object's (leaves) identification
```

```

object_id(img)

# Get the coordinates and draw a bounding rectangle around leaves 1 and 3
object_coord(img, id = c(1, 3))

# Isolate leaf 3
isolated <- object_isolate(img, id = 3)
plot(isolated)

```

utils_pca

Utilities for Principal Component Axis analysis

Description

- `pca()` Computes a Principal Component Analysis. It wrappers `stats::prcomp()`, but returns more results such as data, scores, contributions and quality of measurements for individuals and variables.
- `get_biplot()`: Produces a biplot for an object computed with `pca()`.
- `plot.pca()`: Produces several types of plots, depending on the type and which arguments.
 - `type = "var"` Produces a barplot with the contribution (which = "contrib"), quality of adjustment which = "cos2", and a scatter plot with coordinates (which = "coord") for the variables.
 - `type = "ind"` Produces a barplot with the contribution (which = "contrib"), quality of adjustment which = "cos2", and a scatter plot with coordinates (which = "coord") for the individuals.
 - `type = "biplot"` Produces a biplot.

Usage

```

pca(x, scale = TRUE)

get_biplot(
  x,
  axes = c(1, 2),
  show = c("both"),
  show_ind_id = TRUE,
  show_unit_circle = TRUE,
  expand = NULL
)

## S3 method for class 'pca'
plot(x, type = "var", which = "contrib", axis = 1, ...)

```

Arguments

x	<ul style="list-style-type: none"> • For <code>pca()</code>, a numeric or complex matrix (or data frame) which provides the data for the principal components analysis. • For <code>plot.pca()</code> and <code>get_biplot()</code>, an object computed with <code>pca()</code>.
scale	A logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. Defaults to TRUE.
axes	The principal component axes to plot. Defaults to <code>axes = c(1, 2)</code> , i.e., the first and second interaction principal component axis.
show	Which to show in the biplot. Defaults to "both" (both variables and individuals). One can also use "var", or "ind".
show_ind_id	Shows the labels for individuals? Defaults to TRUE.
show_unit_circle	Shows the unit variance circle? Defaults to TRUE.
expand	An expansion factor to apply when plotting the second set of points relative to the first. This can be used to tweak the scaling of the two sets to a physically comparable scale. Setting to TRUE will automatically compute the expansion factor. Alternatively, a numeric value can be informed.
type	One of "var" (to plot variables), "ind" (to plot individuals), or "biplot" to create a biplot.
which	Which measure to plot. Either <code>which = "contribution"</code> (default), <code>which = "cos2"</code> (quality of representation), or <code>which = "coord"</code> (coordinates)
axis	The axis to plot the contribution/cos2. Defaults to 1.
...	Further arguments passed on to <code>get_biplot()</code> when <code>type = "biplot"</code> . Otherwise, When <code>which = "coord"</code> , further arguments passed on to <code>get_biplot()</code> . When <code>which = "contrib"</code> , or <code>which = "cos2"</code> further arguments passed on to <code>graphics::barplot()</code> .

Value

- `pca()` returns a list including:
 - `data`: The raw data used to compute the PCA.
 - `variances`: Variances (eigenvalues), and proportion of explained variance for each component.
 - `center, scale`: the centering and scaling used.
 - `ind, var`: A list with the following objects for individuals/variables, respectively.
 - `coord`: coordinates for the individuals/variables (`loadings * the component standard deviations`)
 - `cos2`: `cos2` for the individuals/variables (`coord^2`)
 - `contrib`: The contribution (in percentage) of a variable to a given principal component: $(\text{cos2} * 100) / (\text{total cos2 of the component})$
- `plot.pca()` returns a list with the coordinates used.
- `get_biplot()` returns a NULL object

Examples

```
library(pliman)
pc <- pca(mtcars[1:10 ,1:6])
plot(pc)
plot(pc, type = "ind")
plot(pc, type = "var", which = "coord")
plot(pc, type = "ind", which = "coord")
plot(pc, type = "biplot")
```

utils_pick

Utilities for picking up points in an image

Description

- `pick_count()` opens an interactive section where the user will be able to click in the image to count objects (points) manually. In each mouse click, a point is drawn and an upward counter is shown in the console. After n counts or after the user press Esc, the interactive process is terminated and the number of counts is returned.
- `pick_coord()` Picks coordinates from the image
- `pick_palette()` creates an image palette by picking up color point(s) from the image.
- `pick_rgb()` Picks up the RGB values from selected point(s) in the image.

Usage

```
pick_count(  
  img,  
  n = Inf,  
  col = "red",  
  viewer = get_pliman_viewer(),  
  size = 0.8,  
  plot = TRUE,  
  verbose = TRUE  
)
```

```
pick_coords(  
  img,  
  n = Inf,  
  col = "red",  
  viewer = get_pliman_viewer(),  
  size = 0.8,  
  verbose = TRUE  
)
```

```
pick_rgb(  
  img,  
  n = Inf,
```

```

    col = "red",
    viewer = get_pliman_viewer(),
    size = 0.8,
    plot = TRUE,
    verbose = TRUE
)

pick_palette(
  img,
  n = Inf,
  r = 1,
  shape = "box",
  viewer = get_pliman_viewer(),
  show = "rgb",
  title = "Pick colors in the image",
  index = "B",
  random = TRUE,
  width = 100,
  height = 100,
  col = "red",
  size = 0.8,
  plot = TRUE,
  palette = TRUE,
  verbose = TRUE
)

```

Arguments

<code>img</code>	An Image object.
<code>n</code>	The number of points of the <code>pick_*</code> function. Defaults to <code>Inf</code> . This means that picking will run until the user press Esc.
<code>col, size</code>	The color and size for the marker point.
<code>viewer</code>	The viewer option. If not provided, the value is retrieved using <code>get_pliman_viewer()</code> . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the <code>set_pliman_viewer()</code> function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.
<code>plot</code>	Call a new <code>plot(img)</code> before processing? Defaults to <code>TRUE</code> .
<code>verbose</code>	If <code>TRUE</code> (default) shows a counter in the console.
<code>r</code>	The radius of neighborhood pixels. Defaults to 1.
<code>shape</code>	A character vector indicating the shape of the brush around the selected pixel. It can be "box", "disc", "diamond", "Gaussian" or "line". Defaults to "box". In this case, if <code>'r = 1'</code> , all the 8 surrounding pixels are sampled. Setting to

	"disc" and increasing the radius (r) will select surrounding pixels towards the format of a sphere around the selected pixel.
show	How to plot in mapview viewer, either 'rgb' or 'index'.
title	The title of the map view when viewer is used.
index	The index to use for the index view. Defaults to 'B'.
random	Randomize the selected pixels? Defaults to TRUE.
width, height	The width and height of the generated palette. Defaults to 100 for both, i.e., a square image of 100 x 100.
palette	Plot the generated palette? Defaults to TRUE.

Value

- pick_count() returns data.frame with the x and y coordinates of the selected point(x).
- pick_rgb() returns a data.frame with the R, G, and B values of the selected point(s).
- pick_palette() returns an object of class Image.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
if(interactive()){
  library(pliman)
  img <- image_pliman("soybean_touch.jpg")

  # start a counting process
  pick_count(img)

  # get rgb from point(s)
  pick_rgb(img)

  # create a palette from point(s)
  pick_palette(img)
}
```

Description

Several useful functions for analyzing polygons. All of them are based on a set of coordinate points that describe the edge of the object(s). If a list of polygons is provided, it loops through the list and computes what is needed for each element of the list.

- Polygon measures

- `conv_hull()` Computes the convex hull of a set of points.
- `conv_hull_unified()` Computes the convex hull of a set of points. Compared to `conv_hull()`, `conv_hull_unified()` binds (unifies) the coordinates when `x` is a list of coordinates.
- `poly_area()` Computes the area of a polygon given by the vertices in the vectors `x` and `y` using the Shoelace formula, as follows (Lee and Lim, 2017):

$$A = \frac{1}{2} \left| \sum_{i=1}^n (x_i y_{i+1} - x_{i+1} y_i) \right|$$

where `x` and `y` are the coordinates that form the corners of a polygon, and `n` is the number of coordinates.

- `poly_angles()` Calculates the internal angles of the polygon using the law of cosines.
 - `poly_lw()` Returns the length and width of a polygon based on its alignment to the `y`-axis (with `poly_align()`). The length is defined as the range along the `x`-axis, and the width is defined as the range on the `y`-axis.
 - `poly_mass()` Computes the center of mass of a polygon given by the vertices in the vectors in `x`.
 - `poly_solidity()` Computes the solidity of a shape as the ratio of the shape area and the convex hull area.
- Perimeter measures
 - `poly_slide()` Slides the coordinates of a polygon given by the vertices in the vectors `x` and `y` so that the `id`-th point becomes the first one.
 - `poly_distpts()` Computes the Euclidean distance between every point of a polygon given by the vertices in the vectors `x` and `y`.
 - `poly_centdist()` Computes the Euclidean distance between every point on the perimeter and the centroid of the object.
 - `poly_perimeter()` Computes the perimeter of a polygon given by the vertices in the vectors `x` and `y`.
 - `poly_caliper()` Computes the caliper (also called the Feret's diameter) of a polygon given by the vertices in the vectors `x` and `y`.
 - Circularity measures (Montero et al. 2009).
 - `poly_circularity()` computes the circularity (`C`), also called shape compactness or roundness measure, of an object. It is given by $C = P^2 / A$, where `P` is the perimeter and `A` is the area of the object.
 - `poly_circularity_norm()` computes the normalized circularity (`Cn`), which is unity for a circle. This measure is invariant under translation, rotation, scaling transformations, and is dimensionless. It is given by: $Cn = P^2 / 4 * \pi * A$.
 - `poly_circularity_haralick()` computes Haralick's circularity (`CH`). The method is based on computing all Euclidean distances from the object centroid to each boundary pixel. With this set of distances, the mean (`m`) and the standard deviation (`sd`) are computed. These statistical parameters are used to calculate the circularity, `CH`, of a shape as $CH = m / sd$.
 - `poly_convexity()` computes the convexity of a shape using the ratio between the perimeter of the convex hull and the perimeter of the polygon.
 - `poly_eccentricity()` computes the eccentricity of a shape using the ratio of the eigenvalues (inertia axes of coordinates).

- `poly_elongation()` computes the elongation of a shape as $1 - \text{width} / \text{length}$.
- Utilities for polygons
 - `poly_check()` Checks a set of coordinate points and returns a matrix with x and y columns.
 - `poly_is_closed()` Returns a logical value indicating if a polygon is closed.
 - `poly_close()` and `poly_unclose()` close and unclose a polygon, respectively.
 - `poly_rotate()` Rotates the polygon coordinates by an angle (0-360 degrees) in the counterclockwise direction.
 - `poly_flip_x()`, `poly_flip_y()` flip shapes along the x-axis and y-axis, respectively.
 - `poly_align()` Aligns the coordinates along their longer axis using the var-cov matrix and eigen values.
 - `poly_center()` Centers the coordinates on the origin.
 - `poly_sample()` Samples n coordinates from existing points. Defaults to 50.
 - `poly_sample_prop()` Samples a proportion of coordinates from existing points. Defaults to 0.1.
 - `poly_spline()` Interpolates the polygon contour.
 - `poly_smooth()` Smooths the polygon contour using a simple moving average.
 - `poly_jitter()` Adds a small amount of noise to a set of point coordinates. See [base::jitter\(\)](#) for more details.
- `poly_measures()` Is a wrapper around the `poly_*`() functions.

Usage

```
poly_check(x)
poly_is_closed(x)
poly_close(x)
poly_unclose(x)
poly_angles(x)
poly_limits(x)
conv_hull(x)
conv_hull_unified(x)
poly_area(x)
poly_slide(x, fp = 1)
poly_distpts(x)
poly_censtdist(x)
```

```
poly_perimeter(x)
poly_rotate(x, angle, plot = TRUE)
poly_align(x, plot = TRUE)
poly_center(x, plot = TRUE)
poly_lw(x)
poly_eccentricity(x)
poly_convexity(x)
poly_caliper(x)
poly_elongation(x)
poly_solidity(x)
poly_flip_y(x)
poly_flip_x(x)
poly_sample(x, n = 50)
poly_sample_prop(x, prop = 0.1)
poly_jitter(x, noise_x = 1, noise_y = 1, plot = TRUE)
poly_circularity(x)
poly_circularity_norm(x)
poly_circularity_haralick(x)
poly_mass(x)
poly_spline(x, vertices = 100, k = 2)
poly_smooth(x, niter = 10, n = NULL, prop = NULL, plot = TRUE)
poly_measures(x)
```

Arguments

x A 2-column matrix with the x and y coordinates. If x is a list of vector coordinates, the function will be applied to each element using `base::lapply()` or

	<code>base::sapply()</code> .
<code>fp</code>	The ID of the point that will become the new first point. Defaults to 1.
<code>angle</code>	The angle (0-360) to rotate the object.
<code>plot</code>	Should the object be plotted? Defaults to TRUE.
<code>n, prop</code>	The number and proportion of coordinates to sample from the perimeter coordinates. In <code>poly_smooth()</code> , these arguments can be used to sample points from the object's perimeter before smoothing.
<code>noise_x, noise_y</code>	A numeric factor to define the noise added to the x and y axes, respectively. See <code>base::jitter()</code> for more details.
<code>vertices</code>	The number of spline vertices to create.
<code>k</code>	The number of points to wrap around the ends to obtain a smooth periodic spline.
<code>niter</code>	An integer indicating the number of smoothing iterations.

Value

- `conv_hull()` and `poly_spline()` returns a matrix with x and y coordinates for the convex hull/smooth line in clockwise order. If x is a list, a list of points is returned.
- `poly_area()` returns a double, or a numeric vector if x is a list of vector points.
- `poly_mass()` returns a `data.frame` containing the coordinates for the center of mass, as well as for the maximum and minimum distance from contour to the center of mass.
- `poly_slides()`, `poly_distpts()`, `poly_spline()`, `poly_close()`, `poly_unclose()`, `poly_rotate()`, `poly_jitter()`, `poly_sample()`, `poly_sample_prop()`, and `poly_measures` returns a `data.frame`.
- `poly_perimeter()`, `poly_lw()`, `poly_eccentricity()`, `poly_convexity()`, `poly_caliper()`, `poly_elongation()`, `poly_circularity_norm()`, `poly_circularity_haralick()` returns a double.

References

- Lee, Y., & Lim, W. (2017). Shoelace Formula: Connecting the Area of a Polygon and the Vector Cross Product. *The Mathematics Teacher*, 110(8), 631–636. doi:10.5951/mathteacher.110.8.0631
- Montero, R. S., Bribiesca, E., Santiago, R., & Bribiesca, E. (2009). State of the Art of Compactness and Circularity Measures. *International Mathematical Forum*, 4(27), 1305–1335.
- Chen, C.H., and P.S.P. Wang. 2005. *Handbook of Pattern Recognition and Computer Vision*. 3rd ed. World Scientific.

Examples

```
library(pliman)
# A 2 x 2 square
df <- draw_square(side = 2)

# square area
poly_area(df)
```

```

# polygon perimeter
poly_perimeter(df)

# center of mass of the square
cm <- poly_mass(df)
plot_mass(cm)

# The convex hull will be the vertices of the square
(conv_square <- conv_hull(df) |> poly_close())
plot_contour(conv_square,
             col = "blue",
             lwd = 6)
poly_area(conv_square)

##### Example with a polygon #####
x <- c(0, 1, 2, 3, 5, 2, -1, 0, 0)
y <- c(5, 6.5, 7, 3, 1, 1, 0, 2, 5)
df_poly <- cbind(x, y)

# area of the polygon
plot_polygon(df_poly, fill = "red")
poly_area(df_poly)

# perimeter of the polygon
poly_perimeter(df_poly)

# center of mass of polygon
cm <- poly_mass(df_poly)
plot_mass(cm, col = "blue")

# vertices of the convex hull
(conv_poly <- conv_hull(df_poly))

# area of the convex hull
poly_area(conv_poly)

plot_polygon(conv_poly,
            fill = "red",
            alpha = 0.2,
            add = TRUE)

##### example of circularity measures #####
tri <- draw_circle(n = 200, plot = FALSE)
plot_polygon(tri, aspect_ratio = 1)
poly_circularity_norm(tri)

set.seed(1)
tri2 <-
  draw_circle(n = 200, plot = FALSE) |>
  poly_jitter(noise_x = 100, noise_y = 100, plot = FALSE)

```



```
plot_polygon(tri2, aspect_ratio = 1)
poly_circularity_norm(tri2)
```

utils_polygon_plot *Utilities for plotting polygons*

Description

- plot_contour() Plot contour lines.
- plot_polygon() Plots a polygon describing the objects.
- plot_mass() Plots the center of mass along with maximum and minimum radius.
- plot_ellipse() Plots an ellipse that fits the major and minor axis for each object.

Usage

```
plot_contour(x, id = NULL, col = "black", lwd = 1, ...)
```

```
plot_polygon(
  x,
  fill = "gray",
  random_fill = TRUE,
  points = FALSE,
  merge = TRUE,
  border = "black",
  alpha = 1,
  add = FALSE,
  nrow = NULL,
  ncol = NULL,
  aspect_ratio = 1,
  show_id = TRUE,
  xlim = NULL,
  ylim = NULL,
  ...
)
```

```
plot_mass(x, id = NULL, col = "black", cex = 1, lwd = 1)
```

```
plot_ellipse(object, id = NULL, col = "black", lwd = 1)
```

Arguments

- | | |
|---------------|---|
| x | A 2-column matrix with the x and y coordinates. |
| id | The object identification (numeric) to plot the contour/ellipse. By default (id = NULL), the contour is plotted to all objects. |
| col, lwd, cex | The color, width of the lines, and size of point, respectively. |

...	<ul style="list-style-type: none"> • For <code>plot_contour()</code> and <code>plot_ellipse()</code> further arguments passed on to <code>graphics::lines()</code>. • For <code>plot_mass()</code>, further arguments passed on to <code>graphics::points()</code>. • For <code>plot_polygon()</code>, further arguments passed on to <code>graphics::polygon()</code>.
fill, border, alpha	The color to fill the polygon, the color of the polygon's border, and the alpha transparency (1 opaque, 0 transparent).
random_fill	Fill multiple objects with random colors? Defaults to TRUE.
points	Plot the points? Defaults to FALSE.
merge	Merge multiple objects into a single plot? Defaults to TRUE. If FALSE, a single call <code>plot()</code> will be used for each objects. Use <code>nrow</code> and <code>ncol</code> to control the number of rows and columns of the window.
add	Add the current plot to a previous one? Defaults to FALSE.
nrow, ncol	The number of rows and columns to use in the composite image. Defaults to NULL, i.e., a square grid is produced.
aspect_ratio	The x/y aspect ratio. Defaults to 1. This will set up the window so that one data unit in the y direction is equal to one data unit in the x direction. Set <code>aspect_ratio = NULL</code> to fit the object to the window size.
show_id	Shows the object id? Defaults to TRUE.
xlim, ylim	A numeric vector of length 2 (min; max) indicating the range of x and y-axes.
object	An object computed with <code>analyze_objects()</code> .

Value

a NULL object.

Examples

```
plot_polygon(contours)
plot_contour(contours[[1]], id = 6, col = "red", lwd = 3)
```

 utils_rows_cols

Utilities for handling with rows and columns

Description

- `columns_to_rownames()`: Move a column of `.data` to its row names.
- `rownames_to_column()`: Move the row names of `.data` to a new column.
- `remove_rownames()`: Remove the row names of `.data`.
- `round_cols()` Rounds the values of all numeric variables to the specified number of decimal places (default 2).

Usage

```
column_to_rownames(.data, var = "rowname")  
rownames_to_column(.data, var = "rowname")  
remove_rownames(.data)  
round_cols(.data, digits = 2)
```

Arguments

.data	A data frame
var	Name of column to use for rownames.
digits	The number of significant figures. Defaults to 2.

Author(s)

Tiago Olivoto <tiagoolivoto@gmail.com>

Examples

```
library(pliman)  
iris2 <- iris |> rownames_to_column()  
head(iris2)  
iris2$rowname <- paste0("r", iris2$rowname)  
iris2 |> column_to_rownames("rowname") |> head()
```

utils_shapes

Utilities for drawing coordinates of known shapes

Description

The functions computes the coordinates of common shapes such as squares triangles, rectangles and circles.

- `draw_circle()` Draws a perfect circle with a desired radius.
- `draw_square()` Draws a square with a desired side.
- `draw_rectangle()` Draws a rectangle given two desired sides.
- `draw_trian_equi()` Draws an equilateral triangle with a desired side.
- `draw_trian_rect()` Draws a triangle rectangle given two cathetus.
- `draw_n_tagon()` Draws polygons with n sides

Usage

```
draw_circle(radius = 1, n = 1000, plot = TRUE)

draw_square(side = 2, plot = TRUE)

draw_rectangle(side1 = 2, side2 = 3, plot = TRUE)

draw_trian_equi(side = 2, plot = TRUE)

draw_trian_rect(cat1 = 1, cat2 = 2, plot = TRUE)

draw_n_tagon(n, plot = TRUE)
```

Arguments

radius	The radius of the circle. Defaults to 1.
n	The number of sides in the n-tagon.
plot	Plots the result? Defaults to TRUE.
side	The side of the square/equilateral triangle. Defaults to 2.
side1, side2	The first and second sides of the rectangle. Defaults to 2 and 3, respectively.
cat1, cat2	The first and second cathetus of the right triangle. Defaults to 1, and 2, respectively.

Value

A data frame with the x and y coordinates

Examples

```
##### An example of a circle #####
library(pliman)
radius <- 3
circ <- draw_circle(radius = radius)

# area
pi * radius ^ 2
poly_area(circ)

# perimeter
2 * pi * radius
poly_perimeter(circ)

##### An example of a square #####
side <- 2
(square <- draw_square(side = side))

# area
side ^ 2
poly_area(square)
```

```
# perimeter
side * 4
poly_perimeter(square)

##### An example of a rectangle #####
side1 <- 2
side2 <- 3
(rect <- draw_rectangle())

# area
poly_area(rect)

# perimeter
poly_perimeter(rect)
##### An example of an equilateral triangle #####
side <- 1 # defaults
(trig <- draw_trian_equi(side = side))

### area (b*h / 2)
# height of the triangle
(h <- (side * sqrt(3)) / 2)
side * h / 2

poly_area(trig)

### perimeter (side * 3)
poly_perimeter(trig)

##### An example of a rectangle triangle #####
cat1 <- 2
cat2 <- 3
(df <- draw_trian_rect(cat1, cat2))
# area
(cat1 * cat2) / 2
poly_area(df)

# perimeter
cat1 + cat2 + sqrt(cat1^2 + cat2^2)
poly_perimeter(df)
##### An creating shapes with n sides #####
side <- 2
(square <- draw_square(side = side))

# area
side ^ 2
poly_area(square)

# perimeter
side * 4
poly_perimeter(square)
```

utils_stats	<i>These functions applies common statistics to a list of objects, returning a numeric vector.</i>
-------------	--

Description

These functions applies common statistics to a list of objects, returning a numeric vector.

Usage

```
mean_list(x, ...)
```

```
sd_list(x, ...)
```

```
max_list(x, ...)
```

```
min_list(x, ...)
```

Arguments

x A data.frame or matrix with numeric values.

... Further arguments passed on to the R base function (e.g, mean(), sd(), etc.)

Value

A numeric vector.

Examples

```
mean_list(list(a = 1:10, b = 2:20))
```

utils_transform	<i>Spatial transformations</i>
-----------------	--------------------------------

Description

Performs image rotation and reflection

- image_autocrop() Crops automatically an image to the area of objects.
- image_crop() Crops an image to the desired area.
- image_trim() Remove pixels from the edges of an image (20 by default).
- image_dimension() Gives the dimension (width and height) of an image.
- image_rotate() Rotates the image clockwise by the given angle.
- image_horizontal() Converts (if needed) an image to a horizontal image.

- `image_vertical()` Converts (if needed) an image to a vertical image.
- `image_hreflect()` Performs horizontal reflection of the image.
- `image_vreflect()` Performs vertical reflection of the image.
- `image_resize()` Resize the image. See more at [EBImage::resize\(\)](#).
- `image_contrast()` Improve contrast locally by performing adaptive histogram equalization. See more at [EBImage::clahe\(\)](#).
- `image_dilate()` Performs image dilatation. See more at [EBImage::dilate\(\)](#).
- `image_erode()` Performs image erosion. See more at [EBImage::erode\(\)](#).
- `image_opening()` Performs an erosion followed by a dilation. See more at [EBImage::opening\(\)](#).
- `image_closing()` Performs a dilation followed by an erosion. See more at [EBImage::closing\(\)](#).
- `image_filter()` Performs median filtering in constant time. See more at [EBImage::medianFilter\(\)](#).
- `image_blur()` Performs blurring filter of images. See more at [EBImage::gblur\(\)](#).
- `image_skeleton()` Performs image skeletonization.

Usage

```
image_autocrop(  
  img,  
  index = "NB",  
  edge = 5,  
  filter = 3,  
  parallel = FALSE,  
  workers = NULL,  
  verbose = TRUE,  
  plot = FALSE  
)
```

```
image_crop(  
  img,  
  width = NULL,  
  height = NULL,  
  viewer = get_pliman_viewer(),  
  show = "rgb",  
  parallel = FALSE,  
  workers = NULL,  
  verbose = TRUE,  
  plot = FALSE  
)
```

```
image_dimension(img, parallel = FALSE, workers = NULL, verbose = TRUE)
```

```
image_rotate(  
  img,  
  angle,  
  bg_col = "white",
```

```
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = TRUE  
  )  
  
  image_horizontal(  
    img,  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
  )  
  
  image_vertical(  
    img,  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
  )  
  
  image_hreflect(  
    img,  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
  )  
  
  image_vreflect(  
    img,  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
  )  
  
  image_resize(  
    img,  
    rel_size = 100,  
    width,  
    height,  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
  )
```



```
image_trim(  
    img,  
    edge = NULL,  
    top = NULL,  
    bottom = NULL,  
    left = NULL,  
    right = NULL,  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
)
```

```
image_dilate(  
    img,  
    kern = NULL,  
    size = NULL,  
    shape = "disc",  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
)
```

```
image_erode(  
    img,  
    kern = NULL,  
    size = NULL,  
    shape = "disc",  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
)
```

```
image_opening(  
    img,  
    kern = NULL,  
    size = NULL,  
    shape = "disc",  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
)
```

```
image_closing(  
    img,  
    kern = NULL,  
    size = NULL,  
    shape = "disc",  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
)
```

```
    img,  
    kern = NULL,  
    size = NULL,  
    shape = "disc",  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
  )  
  
  image_skeleton(  
    img,  
    kern = NULL,  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE,  
    ...  
  )  
  
  image_thinning(  
    img,  
    niter = 3,  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE,  
    ...  
  )  
  
  image_filter(  
    img,  
    size = 2,  
    cache = 512,  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
  )  
  
  image_blur(  
    img,  
    sigma = 3,  
    parallel = FALSE,  
    workers = NULL,  
    verbose = TRUE,  
    plot = FALSE  
  )
```

```

image_contrast(
  img,
  parallel = FALSE,
  workers = NULL,
  verbose = TRUE,
  plot = FALSE
)

```

Arguments

img	An image or a list of images of class Image.
index	The index to segment the image. See image_index() for more details. Defaults to "NB" (normalized blue).
edge	<ul style="list-style-type: none"> for image_autocrop() the number of pixels in the edge of the cropped image. If edge = 0 the image will be cropped to create a bounding rectangle (x and y coordinates) around the image objects. for image_trim(), the number of pixels removed from the edges. By default, 20 pixels are removed from all the edges.
filter	Performs median filtering in the binary image. This is useful to remove noise (like dust) and improve the image autocropping method. See more at image_filter() . Set to FALSE to remove the median filtering.
parallel	Processes the images asynchronously (in parallel) in separate R sessions running in the background on the same machine. It may speed up the processing time when image is a list. The number of sections is set up to 70% of available cores.
workers	A positive numeric scalar or a function specifying the maximum number of parallel processes that can be active at the same time.
verbose	If TRUE (default) a summary is shown in the console.
plot	If TRUE plots the modified image. Defaults to FALSE.
width, height	<ul style="list-style-type: none"> For image_resize() the Width and height of the resized image. These arguments can be missing. In this case, the image is resized according to the relative size informed in <code>rel_size</code>. For image_crop() a numeric vector indicating the pixel range (x and y, respectively) that will be maintained in the cropped image, e.g., width = 100:200
viewer	The viewer option. If not provided, the value is retrieved using get_pliman_viewer() . This option controls the type of viewer to use for interactive plotting. The available options are "base" and "mapview". If set to "base", the base R graphics system is used for interactive plotting. If set to "mapview", the mapview package is used. To set this argument globally for all functions in the package, you can use the set_pliman_viewer() function. For example, you can run <code>set_pliman_viewer("mapview")</code> to set the viewer option to "mapview" for all functions.
show	How to plot in mapview viewer, either "rgb" or "index".
angle	The rotation angle in degrees.

bg_col	Color used to fill the background pixels, defaults to "white".
rel_size	The relative size of the resized image. Defaults to 100. For example, setting rel_size = 50 to an image of width 1280 x 720, the new image will have a size of 640 x 360.
top, bottom, left, right	The number of pixels removed from top, bottom, left, and right when using <code>image_trim()</code> .
kern	An Image object or an array, containing the structuring element. Defaults to a brushe generated with <code>EImage::makeBrush()</code> .
size	<ul style="list-style-type: none"> • For <code>image_filter()</code> is the median filter radius (integer). Defaults to 3. • For <code>image_dilate()</code> and <code>image_erode()</code> is an odd number containing the size of the brush in pixels. Even numbers are rounded to the next odd one. The default depends on the image resolution and is computed as the image resolution (megapixels) times 20.
shape	A character vector indicating the shape of the brush. Can be box, disc, diamond, Gaussian or line. Default is disc.
...	Additional arguments passed on to <code>image_binary()</code> .
niter	The number of iterations to perform in the thinning procedure. Defaults to 3. Set to NULL to iterate until the binary image is no longer changing.
cache	The the L2 cache size of the system CPU in kB (integer). Defaults to 512.
sigma	A numeric denoting the standard deviation of the Gaussian filter used for blurring. Defaults to 3.

Value

- `image_skeleton()` returns a binary Image object.
- All other functions returns a modified version of image depending on the `image_*`() function used.
- If image is a list, a list of the same length will be returned.

Author(s)

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Examples

```
library(pliman)
img <- image_pliman("sev_leaf.jpg")
plot(img)
img <- image_resize(img, 50)
img1 <- image_rotate(img, 45)
img2 <- image_hreflect(img)
img3 <- image_vreflect(img)
img4 <- image_vertical(img)
image_combine(img1, img2, img3, img4)
```

Description

- `get_wd_here()` gets the working directory to the path of the current script.
- `set_wd_here()` sets the working directory to the path of the current script.
- `open_wd_here()` Open the File Explorer at the directory path of the current script.
- `open_wd()` Open the File Explorer at the current working directory.

Usage

```
set_wd_here(path = NULL)
```

```
get_wd_here(path = NULL)
```

```
open_wd_here(path = get_wd_here())
```

```
open_wd(path = getwd())
```

Arguments

path	Path components below the project root. Defaults to NULL. This means that the directory will be set to the path of the file. If the path doesn't exist, the user will be asked if he wants to create such a folder.
------	---

Value

- `get_wd_here()` returns a full-path directory name.
- `get_wd_here()` returns a message showing the current working directory.
- `open_wd_here()` Opens the File Explorer of the path returned by `get_wd_here()`.

Examples

```
## Not run:  
get_wd_here()  
set_wd_here()  
open_wd_here()  
  
## End(Not run)
```

`watershed2`*Alternative watershed algorithm*

Description

This is a basic watershed algorithm that can be used as a faster alternative to `EImage::watershed()`. I strongly suggest using this only with round objects, since it doesn't consider both 'extension' and 'tolerance' arguments of `EImage::watershed()`.

Usage

```
watershed2(binary, dist_thresh = 0.75, plot = TRUE)
```

Arguments

<code>binary</code>	A binary image
<code>dist_thresh</code>	The distance threshold to create the
<code>plot</code>	If TRUE (default) plots the labeled objects

Value

The labelled version of binary.

Examples

```
library(pliman)
img <- image_pliman("soybean_touch.jpg")
binary <- image_binary(img, "B")[[1]]
wts <- watershed2(binary)
range(wts)
```

Index

- * **data**
 - contours, [22](#)
- * **images**
 - pliman_images, [92](#)
- %>% (pipe), [90](#)

- analyze_objects, [4](#), [18](#)
- analyze_objects(), [4](#), [10](#), [14](#), [17](#), [18](#), [67](#), [85](#),
[97](#), [106](#), [114](#), [118](#), [130](#)
- analyze_objects_iter (analyze_objects),
[4](#)
- analyze_objects_iter(), [4](#), [10](#), [11](#)
- analyze_objects_shp, [15](#), [81](#), [82](#)
- analyze_objects_shp(), [43](#), [94–96](#)
- apply_fun_to_imgs, [18](#)
- as_image, [20](#)

- base::jitter(), [125](#), [127](#)
- base::lapply(), [126](#)
- base::sapply(), [127](#)

- calibrate, [21](#)
- calibrate(), [56](#)
- cm_to_dpi (utils_dpi), [108](#)
- cm_to_dpi(), [108](#), [109](#)
- cm_to_pixels (utils_dpi), [108](#)
- cm_to_pixels(), [108](#), [109](#)
- column_to_rownames (utils_rows_cols),
[130](#)
- contours, [22](#)
- conv_hull (utils_polygon), [123](#)
- conv_hull_unified (utils_polygon), [123](#)
- custom_palette, [22](#)
- custom_palette(), [55](#), [95](#)

- dist_transform, [23](#)
- distance (utils_dpi), [108](#)
- distance(), [108](#)
- dpi (utils_dpi), [108](#)
- dpi(), [108](#), [109](#)

- dpi_to_cm (utils_dpi), [108](#)
- dpi_to_cm(), [108](#), [109](#)
- draw_circle (utils_shapes), [131](#)
- draw_n_tagon (utils_shapes), [131](#)
- draw_rectangle (utils_shapes), [131](#)
- draw_square (utils_shapes), [131](#)
- draw_trian_equi (utils_shapes), [131](#)
- draw_trian_rect (utils_shapes), [131](#)

- EImage::bwlabel, [79](#)
- EImage::bwlabel(), [83](#)
- EImage::clahe(), [135](#)
- EImage::closing(), [135](#)
- EImage::dilate(), [135](#)
- EImage::erode(), [135](#)
- EImage::gblur(), [135](#)
- EImage::Image(), [20](#)
- EImage::makeBrush(), [50](#), [61](#), [140](#)
- EImage::medianFilter(), [135](#)
- EImage::opening(), [135](#)
- EImage::resize(), [135](#)
- EImage::watershed, [79](#)
- EImage::watershed(), [65](#), [83](#), [142](#)
- efourier, [24](#)
- efourier(), [8](#), [12](#), [13](#), [17](#), [22](#), [25–29](#)
- efourier_coefs, [25](#)
- efourier_error, [26](#)
- efourier_error(), [14](#)
- efourier_inv, [27](#)
- efourier_norm, [28](#)
- efourier_norm(), [13](#), [25](#), [28](#)
- efourier_power, [29](#)
- efourier_power(), [14](#)
- efourier_shape, [30](#)
- ellipse, [32](#)

- file_dir (utils_file), [110](#)
- file_extension (utils_file), [110](#)
- file_name (utils_file), [110](#)

- get_biplot (utils_pca), 119
- get_biplot(), 106, 120
- get_measures (utils_measures), 113
- get_measures(), 11
- get_pliman_viewer, 33
- get_pliman_viewer(), 6, 16, 21, 34, 43, 48, 51, 56, 67, 72, 78, 86, 94, 108, 122, 139
- get_wd_here (utils_wd), 141
- get_wd_here(), 141
- getwd(), 112
- ggplot_color, 33
- graphics::barplot(), 120
- graphics::lines(), 130
- graphics::plot.window(), 95
- graphics::points(), 130
- graphics::polygon(), 130
- graphics::text(), 115
- grDevices::colors(), 38, 102

- image_align, 34
- image_align(), 101
- image_autocrop (utils_transform), 134
- image_autocrop(), 139
- image_binary, 35
- image_binary(), 10, 53, 85, 87, 117, 140
- image_blur (utils_transform), 134
- image_closing (utils_transform), 134
- image_combine, 37
- image_combine(), 85, 113
- image_contrast (utils_transform), 134
- image_create, 38
- image_crop (utils_transform), 134
- image_crop(), 101
- image_dilate (utils_transform), 134
- image_dimension (utils_transform), 134
- image_erode (utils_transform), 134
- image_expand, 39
- image_expand(), 52
- image_export (utils_image), 112
- image_filter (utils_transform), 134
- image_filter(), 8, 17, 45, 64, 70, 76, 85, 118, 139
- image_horizontal (utils_transform), 134
- image_hreflect (utils_transform), 134
- image_import (utils_image), 112
- image_index, 40
- image_index(), 8, 17, 35, 44, 45, 65, 69, 72, 75, 79, 84, 87, 94, 95, 139
- image_opening (utils_transform), 134
- image_palette (palettes), 89
- image_pliman (utils_image), 112
- image_prepare_mv, 43
- image_prepare_mv(), 16, 18, 72
- image_resize (utils_transform), 134
- image_rotate (utils_transform), 134
- image_rotate(), 34
- image_segment, 44
- image_segment_iter (image_segment), 44
- image_segment_kmeans, 47
- image_segment_manual, 48
- image_segment_mask, 49
- image_shp, 50
- image_shp(), 17, 71, 86, 87, 93
- image_skeleton (utils_transform), 134
- image_skeleton(), 74
- image_square, 52
- image_square(), 75, 78
- image_thinning (utils_transform), 134
- image_thinning_guo_hall, 52
- image_to_mat, 53
- image_trim (utils_transform), 134
- image_trim(), 139, 140
- image_vertical (utils_transform), 134
- image_view, 54
- image_vreflect (utils_transform), 134

- landmarks, 55
- landmarks(), 24, 57, 58
- landmarks_add, 56
- landmarks_angle, 57
- landmarks_dist, 58
- landmarks_regradi, 59
- landmarks_regradi(), 24, 57
- leading_zeros, 60

- make_brush, 61
- make_brush(), 49
- make_mask, 62
- make_mask(), 49
- manipulate_files (utils_file), 110
- mapedit::editMap(), 55
- mapview::mapview(), 55
- max_list (utils_stats), 134
- mean_list (utils_stats), 134
- measure_disease, 63, 73
- measure_disease(), 68, 70, 71, 73, 103
- measure_disease_byl, 68

- measure_disease_iter (measure_disease), 63
- measure_disease_shp, 71
- min_list (utils_stats), 134
- npixels (utils_dpi), 108
- npixels(), 108
- object_contour, 100
- object_contour (utils_objects), 116
- object_contour(), 24, 32, 57, 59, 98
- object_coord (utils_objects), 116
- object_coord(), 118
- object_edge, 73
- object_edge(), 7, 12, 17
- object_export, 74
- object_export_shp, 77
- object_id (utils_objects), 116
- object_id(), 117
- object_isolate (utils_objects), 116
- object_label, 79
- object_map, 81
- object_mark, 82
- object_rgb, 83
- object_split, 84
- object_split(), 68, 74
- object_split_shp, 86
- object_split_shp(), 18, 77
- object_to_color, 87
- open_wd (utils_wd), 141
- open_wd(), 141
- open_wd_here (utils_wd), 141
- open_wd_here(), 141
- otsu, 88
- palettes, 89
- pca (utils_pca), 119
- pca(), 105, 106
- pick_coords (utils_pick), 121
- pick_count (utils_pick), 121
- pick_palette (utils_pick), 121
- pick_palette(), 6, 67
- pick_rgb (utils_pick), 121
- pipe, 90
- pixel_index, 91
- pixels_to_cm (utils_dpi), 108
- pixels_to_cm(), 108, 109
- pliman_images, 92
- pliman_indexes (utils_file), 110
- pliman_indexes(), 6, 35, 40, 45, 79, 87
- pliman_indexes_eq (utils_file), 110
- pliman_indexes_eq(), 8, 17
- pliman_viewer, 93
- plot.anal_obj (analyze_objects), 4
- plot.anal_obj(), 4
- plot.image_index (image_index), 40
- plot.image_shp, 93
- plot.pca (utils_pca), 119
- plot_contour (utils_polygon_plot), 129
- plot_ellipse (utils_polygon_plot), 129
- plot_index, 94
- plot_index(), 41, 42
- plot_index_shp, 95
- plot_lw, 97
- plot_lw(), 10
- plot_mass (utils_polygon_plot), 129
- plot_measures (utils_measures), 113
- plot_polygon (utils_polygon_plot), 129
- png(), 103
- poly_align (utils_polygon), 123
- poly_align(), 12, 24
- poly_angles (utils_polygon), 123
- poly_apex_base_angle, 98
- poly_apex_base_angle(), 12
- poly_area (utils_polygon), 123
- poly_caliper (utils_polygon), 123
- poly_caliper(), 12
- poly_centdist (utils_polygon), 123
- poly_center (utils_polygon), 123
- poly_center(), 24
- poly_check (utils_polygon), 123
- poly_circularity (utils_polygon), 123
- poly_circularity_haralick (utils_polygon), 123
- poly_circularity_norm (utils_polygon), 123
- poly_close (utils_polygon), 123
- poly_convexity (utils_polygon), 123
- poly_distpts (utils_polygon), 123
- poly_eccentricity (utils_polygon), 123
- poly_elongation (utils_polygon), 123
- poly_flip_x (utils_polygon), 123
- poly_flip_y (utils_polygon), 123
- poly_is_closed (utils_polygon), 123
- poly_jitter (utils_polygon), 123
- poly_limits (utils_polygon), 123
- poly_lw (utils_polygon), 123

poly_mass (utils_polygon), 123
poly_measures (utils_polygon), 123
poly_pcv, 99
poly_perimeter (utils_polygon), 123
poly_rotate (utils_polygon), 123
poly_sample (utils_polygon), 123
poly_sample_prop (utils_polygon), 123
poly_slide (utils_polygon), 123
poly_smooth (utils_polygon), 123
poly_smooth(), 24, 57, 99
poly_solidity (utils_polygon), 123
poly_spline (utils_polygon), 123
poly_unclose (utils_polygon), 123
poly_width_at, 100
prepare_to_shp, 101

random_color, 102
remove_rownames (utils_rows_cols), 130
rgb_to_hsb (utils_colorspace), 107
rgb_to_lab (utils_colorspace), 107
rgb_to_srgb (utils_colorspace), 107
round_cols (utils_rows_cols), 130
rownames_to_column (utils_rows_cols),
130

sad, 103
sad(), 103
sd_list (utils_stats), 134
separate_col, 104
set_pliman_viewer, 105
set_pliman_viewer(), 16, 21, 34, 43, 48, 51,
56, 67, 72, 78, 87, 95, 109, 122, 139
set_wd_here (utils_wd), 141
set_wd_here(), 141
stats::prcomp(), 119
summary_index, 105

utils_colorspace, 107
utils_dpi, 108
utils_file, 110
utils_image, 112
utils_measures, 113
utils_objects, 116
utils_pca, 119
utils_pick, 121
utils_polygon, 123
utils_polygon_plot, 129
utils_rows_cols, 130
utils_shapes, 131
utils_stats, 134
utils_transform, 134
utils_wd, 141
watershed2, 142