

# Package: SuperpixelImageSegmentation (via r-universe)

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**Type** Package

**Title** Superpixel Image Segmentation

**Version** 1.0.5

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**BugReports** <https://github.com/mlampros/SuperpixelImageSegmentation/issues>

**URL** <https://github.com/mlampros/SuperpixelImageSegmentation>

**Description** Image Segmentation using Superpixels, Affinity Propagation and Kmeans Clustering. The R code is based primarily on the article ``Image Segmentation using SLIC Superpixels and Affinity Propagation Clustering, Bao Zhou, International Journal of Science and Research (IJSR), 2013" <<https://www.ijsr.net/archive/v4i4/SUB152869.pdf>>.

**License** GPL-3

**Encoding** UTF-8

**Depends** R(>= 3.2)

**Imports** Rcpp (>= 0.12.10), R6, OpenImageR, grDevices, lattice

**LinkingTo** Rcpp, RcppArmadillo (>= 0.9.1), ClusterR, OpenImageR

**Suggests** testthat, covr, knitr, rmarkdown

**RoxygenNote** 7.1.2

**NeedsCompilation** yes

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### Description

Segmentation of images based on Superpixels, Affinity propagation and Kmeans clustering

Segmentation of images based on Superpixels, Affinity propagation and Kmeans clustering

### Usage

```
# init <- Image_Segmentation$new()
```

### Details

*sim\_wL*, *sim\_wA*, *sim\_wB* are the weights of the three channels. They keep balance so as to be consistent with human perception.

The quantity *colorradius* adjusts the number of clusters, and if its value is low, the number of targets would increase, which leads to more detailed segmentation results.

If the *adjust\_centroids\_and\_return\_masks* parameter is set to FALSE then the output *kmeans\_image\_data* will be an RGB image, otherwise it will be a black-and-white image.

*colour\_type* parameter: RGB (Red-Green-Blue), LAB (Lightness, A-colour-dimension, B-colour-dimension) or HSV (Hue, Saturation, Value) colour.

Higher resolution images give better results.

The *affinity propagation* algorithm is used here with default parameter values.

By setting the *sim\_normalize* parameter to TRUE, the affinity propagation algorithm requires less iterations to complete. However, the *colorradius* parameter does not have an effect if the similarity matrix is normalized.

Regarding the *use\_median* parameter in the Rcpp I use the following steps: *1st.* I compute the superpixels and extract the labels, *2nd.* each superpixel label consists of multiple pixels and for these superpixels I have to compute a dissimilarity matrix therefore each superpixel must correspond to a single value, *3rd.* to come to this single value for each superpixel the R user has the option to either use the 'mean' or the 'median of multiple image pixels (per superpixel)

—————kmeans initializers—————

**optimal\_init** : this initializer adds rows of the data incrementally, while checking that they do not already exist in the centroid-matrix

**quantile\_init** : initialization of centroids by using the cumulative distance between observations and by removing potential duplicates

**kmeans++** : kmeans++ initialization. Reference : <http://theory.stanford.edu/~sergei/papers/kMeansPP-soda.pdf> AND <http://stackoverflow.com/questions/5466323/how-exactly-does-k-means-work>

**random** : random selection of data rows as initial centroids

**Methods**

Image\_Segmentation\$new()  
——

spixel\_segmentation()  
——

spixel\_masks\_show()  
——

spixel\_clusters\_show()  
——

**Methods****Public methods:**

- [Image\\_Segmentation\\$new\(\)](#)
- [Image\\_Segmentation\\$spixel\\_segmentation\(\)](#)
- [Image\\_Segmentation\\$spixel\\_masks\\_show\(\)](#)
- [Image\\_Segmentation\\$spixel\\_clusters\\_show\(\)](#)
- [Image\\_Segmentation\\$clone\(\)](#)

**Method new():**

*Usage:*

```
Image_Segmentation$new()
```

**Method spixel\_segmentation():**

*Usage:*

```
Image_Segmentation$spixel_segmentation(  
  input_image,  
  method = "slic",  
  superpixel = 200,  
  kmeans_method = "",  
  AP_data = FALSE,  
  use_median = TRUE,  
  minib_kmeans_batch = 10,  
  minib_kmeans_init_fraction = 0.5,  
  kmeans_num_init = 3,  
  kmeans_max_iters = 100,  
  kmeans_initializer = "kmeans++",  
  colour_type = "RGB",  
  compactness_factor = 20,  
  adjust_centroids_and_return_masks = FALSE,  
  return_labels_2_dimensionsional = FALSE,  
  sim_normalize = FALSE,  
  sim_wL = 3,  
  sim_wA = 10,
```

```

sim_wB = 10,
sim_color_radius = 20,
ap_maxits = 1000,
ap_convits = 100,
ap_dampfact = 0.9,
ap_nonoise = 0,
verbose = FALSE
)

```

*Arguments:*

`input_image` a 3-dimensional input image (the range of the pixel values should be preferably in the range 0 to 255)

`method` a character string specifying the superpixel method. It can be either "slic" or "slicc"

`superpixel` a numeric value specifying the number of superpixels

`kmeans_method` a character string specifying the kmeans method. If not empty ("") then it can be either "kmeans" or "mini\_batch\_kmeans"

`AP_data` a boolean. If TRUE then the affinity propagation image data will be computed and returned

`use_median` a boolean. If TRUE then the median will be used rather than the mean value for the inner computations (see the details section for more information)

`minib_kmeans_batch` the size of the mini batches

`minib_kmeans_init_fraction` percentage of data to use for the initialization centroids (applies if initializer is *kmeans++* or *optimal\_init*). Should be a float number between 0.0 and 1.0.

`kmeans_num_init` number of times the algorithm will be run with different centroid seeds

`kmeans_max_iters` the maximum number of clustering iterations

`kmeans_initializer` the method of initialization. One of, *optimal\_init*, *quantile\_init*, *kmeans++* and *random*. See details for more information

`colour_type` a character string specifying the colour type. It can be one of "RGB", "LAB" or "HSV"

`compactness_factor` a numeric value specifying the compactness parameter in case that *method* is "slic"

`adjust_centroids_and_return_masks` a boolean. If TRUE and the *kmeans\_method* parameter is NOT empty ("") then the centroids will be adjusted and image-masks will be returned. This will allow me to plot the masks using the *spixel\_masks\_show* method.

`return_labels_2_dimensional` a boolean. If TRUE then a matrix of labels based on the output superpixels in combination with the Affinity Propagation clusters will be returned

`sim_normalize` a boolean. If TRUE then the constructed similarity matrix will be normalised to have unit p-norm (see the armadillo documentation for more details)

`sim_wL` a numeric value specifying the weight for the "L" channel of the image (see the details section for more information)

`sim_wA` a numeric value specifying the weight for the "A" channel of the image (see the details section for more information)

`sim_wB` a numeric value specifying the weight for the "B" channel of the image (see the details section for more information)

`sim_color_radius` a numeric value specifying the *colorradius* (see the details section for more information)

`ap_maxits` a numeric value specifying the maximum number of iterations for the Affinity Propagation Clustering (defaults to 1000)

`ap_convits` a numeric value. If the estimated exemplars stay fixed for `convits` iterations, the affinity propagation algorithm terminates early (defaults to 100)

`ap_dampfact` a float number specifying the update equation damping level in [0.5, 1). Higher values correspond to heavy damping, which may be needed if oscillations occur in the Affinity Propagation Clustering (defaults to 0.9)

`ap_nonoise` a float number. The affinity propagation algorithm adds a small amount of noise to *data* to prevent degenerate cases; this disables that.

`verbose` a boolean. If TRUE then information will be printed in the console (`spixel_masks_show` method)

**Method** `spixel_masks_show()`:

*Usage:*

```
Image_Segmentation$spixel_masks_show(
  delay_display_seconds = 3,
  display_all = FALSE,
  margin_btwn_plots = 0.15,
  verbose = FALSE
)
```

*Arguments:*

`delay_display_seconds` a numeric value specifying the seconds to delay the display of the next image (It displays the images consecutively). This parameter applies only if the *display\_all* is set to FALSE (`spixel_masks_show` method)

`display_all` a boolean. If TRUE then all images will be displayed in a grid (`spixel_masks_show` method)

`margin_btwn_plots` a float number specifying the margins between the plots if the *display\_all* parameter is set to TRUE (`spixel_masks_show` method)

`verbose` a boolean. If TRUE then information will be printed in the console (`spixel_masks_show` method)

**Method** `spixel_clusters_show()`:

*Usage:*

```
Image_Segmentation$spixel_clusters_show(
  spix_labels,
  color_palette = grDevices::rainbow,
  parameter_list_png = NULL
)
```

*Arguments:*

`spix_labels` a matrix. I can retrieve the "spix\_labels" parameter by setting the "return\_labels\_2\_dimensional" parameter to TRUE in the "spixel\_segmentation" method (`spixel_clusters_show` method)

`color_palette` one of the color palettes. Use `?grDevices::topo.colors` to see the available color palettes

`parameter_list_png` either NULL or a list of parameters passed to the `?grDevices::png` function, such as `list(filename = 'img.png', width = 100, height = 100, units = "px", pointsize = 12, bg = "white", type = "quartz")`

**Method** clone(): The objects of this class are cloneable with this method.

*Usage:*

```
Image_Segmentation$clone(deep = FALSE)
```

*Arguments:*

deep Whether to make a deep clone.

## References

<https://www.ijsr.net/archive/v4i4/SUB152869.pdf> , "Image Segmentation using SLIC Superpixels and Affinity Propagation Clustering", Bao Zhou, 2013, International Journal of Science and Research (IJSR)

## Examples

```
library(SuperpixelImageSegmentation)

path = system.file("images", "BSR_bsds500_image.jpg", package = "SuperpixelImageSegmentation")

im = OpenImageR::readImage(path)

init = Image_Segmentation$new()

num_spix = 10          # for illustration purposes
# num_spix = 600      # recommended number of superpixels

spx = init$spixel_segmentation(input_image = im,
                               superpixel = num_spix,
                               AP_data = TRUE,
                               use_median = TRUE,
                               return_labels_2_dimensional = TRUE,
                               sim_color_radius = 10)

#.....
# plot the superpixel labels
#.....

plt = init$spixel_clusters_show(spix_labels = spx$spix_labels,
                               color_palette = grDevices::rainbow,
                               parameter_list_png = NULL)

# plt

#.....
# create a binary image for a specified cluster label
#.....

pix_values = spx$spix_labels

target_cluster = 3          # determine clusters visually ('plt' variable)
```

```
pix_values[pix_values != target_cluster] = 0    # set all other values to 0 (background)
pix_values[pix_values == target_cluster] = 1    # set the target_cluster to 1 (binary image)

# OpenImageR::imageShow(pix_values)
```

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