

# Package ‘CRImage’

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**Type** Package

**Title** CRImage a package to classify cells and calculate tumour cellularity

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**Description** CRImage provides functionality to process and analyze images, in particular to classify cells in biological images. Furthermore, in the context of tumor images, it provides functionality to calculate tumour cellularity.

**License** Artistic-2.0

**LazyLoad** yes

**Imports** MASS, e1071, foreach, sgeostat

**Depends** EBImage, DNAcopy, aCGH

**Collate** plotCorrectedCN.R correctCopyNumber.R writeDensityImage.R  
convertRGBToHSV.R convertHSVToRGB.R imageCompression.R  
createBinaryImage.R colorCorrection.R searchStructures.R  
segmentStructures.R classifyStructures.R numberOfNeighbors.R  
segmentCytoplasm.R segmentImage.R createClassifier.R  
kernelSmoother.R paintCells.R classifyCells.R  
determineCellularity.R calculateCellularity.R findSlices.R  
parseFinalScan.R classificationAperio.R processAperio.R  
Phansalkar\_threshold.R SauvolaThreshold.R  
calculateMeanStdTarget.R convertLABToRGB.R convertRGBToLAB.R  
localORThreshold.R oregonThreshold.R localThreshold.R  
calculateOtsu.R classifyPen.R getImageDistance.R hist3d.R  
labelCells.R plotImage.R

**biocViews** CellBiology, Classification

**NeedsCompilation** no

## R topics documented:

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CRImage-package	<i>CRImage is a package to analyze images and classify cells.</i>
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## Description

CRImage allows classification of cells in biological images. It offers methods to segment cells or cell nuclei in biological images for example HE stained images. It offers methods to create a classifier and to classify cells in these images. Furthermore it allows the calculation of tumour cellularity for large microscope images.

CRImage makes use of the image processing package EBImage, which uses the 'ImageMagick' library for image I/O operations and the 'GTK' library to display images.

## Details

Package:	CRImage
Type:	Package
Version:	1.0
Date:	2010-04-27
License:	LGPL Version 2 or later
LazyLoad:	yes

## Package content

Image processing methods:

- calculateThreshold

- `segmentImage`

Classification:

- `createTrainingSet`
- `createClassifier`
- `classifyCells`

Tumour cellularity

- `calculateCellularity`
- `processAperio`

### **Author(s)**

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### **Examples**

```
example(segmentImage)
example(createClassifier)
example(classifyImage)
```

---

`calculateCellularity`    *Calculation of tumour cellularity*

---

### **Description**

The function calculates the tumour cellularity of an image by counting tumour and non tumour cells.

### **Usage**

```
calculateCellularity(filename="", image=NA, classifier=NULL, cancerIdentifier=NA, KS=FALSE, maxShape=
```

**Arguments**

filename	A path to an image file.
image	If filename is undefined, an Image object
classifier	A SVM object, created with createClassifier or directly with the package e1071
cancerIdentifier	A string which describes, how the cancer class is named.
KS	Apply kernel smoother?
maxShape	Maximum size of cell nuclei
minShape	Minimum size of cell nuclei
failureRegion	minimum size of failure regions
colors	Colors to paint the classes
threshold	Which threshold should be uses, "otsu" or "phansalkar"
classesToExclude	Should a class be excluded from cellularity calculation?
numWindows	Number of windows for the threshold.
classifyStructures	Use hierarchical classification. If yes a pixel classifier has to be defined.
pixelClassifier	A SVM to classify pixel based on their color values. Needed if hierarchical classification should be applied.
ksToExclude	These classes are excluded from kernel smoothing.
densityToExclude	This class is excluded from cellularity calculation.
numDensityWindows	Number of windows for the density plot.

**Details**

The method calculates tumour cellularity of an image. The cells of the image are classified and the cellularity is:  $\text{numTumourCells}/\text{numPixel}$ . Furthermore the number of cells of the different classes are counted. A heatmap of cellularity is created. The image is divided in 16 subwindows and cellularity is calculated for every subwindow. Green in the heatmaps indicates strong cellularity, white low cellularity.

**Value**

A list containing	
cellularity values	a vector, the n first values indicate the n numbers of cells in the n classes, the n + 1th value indicates the tumour cellularity, The n + 2th value is the ratio of tumour cells by all cells
cancerHeatmap	Heatmap of cancer density

**Author(s)**

Henrik Failmezger, failmezger@mpipz.mpg.de

## Examples

```
t = system.file("extdata", "trainingData.txt", package="CRImage")
#read training data
trainingData=read.table(t,header=TRUE)
#create classifier
classifier=createClassifier(trainingData)[[1]]
#calculation of cellularity
f = system.file("extdata", "exImg.jpg", package="CRImage")
exImg=readImage(f)
cellularity=calculateCellularity(classifier=classifier, filename=f,KS=TRUE,maxShape=800,minShape=40, failure=
```

---

calculateMeanStdTarget

*Calculates Mean and Standard deviation of an image*

---

## Description

Mean and SD calculation

## Usage

```
calculateMeanStdTarget(imgT)
```

## Arguments

imgT            the Image to calculate.

## Details

Mean and SD

## Value

Vector with mean and standard deviation.

## Author(s)

Henrik Failmezger, failmezger@cip.ifl.lmu.de

## Examples

```
#read the target image
f1= system.file("extdata", "exImg2.jpg", package="CRImage")
targetImage=readImage(f1)
#read the image whose color values should be adapted
f2= system.file("extdata", "exImg3.jpg", package="CRImage")
imgToConvert=readImage(f2)
#calculate mean and standard deviation of target color channels
mst=calculateMeanStdTarget(targetImage)
# create a white pixel mask
```

```
whitePixelMask=imgToConvert[:,1]>0.85 & imgToConvert[:,2]>0.85 & imgToConvert[:,3]>0.85
#adapt color channels of image
imgCorrected=colorCorrection(imgToConvert,mst,whitePixelMask)
```

---

calculateOtsu	<i>Does Otsu thresholding</i>
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### Description

The function applies Otsu thresholding on the image.

### Usage

```
calculateOtsu(allGreyValues)
```

### Arguments

allGreyValues    Vector of grey values.

### Details

The function calculates a value which separates the grey value histogram the best in foreground and background.

### Value

the threshold

### Author(s)

Henrik Failmezger, failmezger@cip.ifi.lmu.de

### References

Nobuyuki Otsu: A threshold selection method from grey level histograms. In: IEEE Transactions on Systems, Man, and Cybernetics. New York 9.1979, S.62-66. ISSN 1083-4419

### See Also

calculateThreshold localOtsuThreshold

### Examples

```
f1= system.file("extdata", "exImg2.jpg", package="CRImage")
print(f1)
img=readImage(f1)
print(img)
#convert to grayscale
imgG=EBImage::channel(img, 'grey')
#threshold value
t=calculateOtsu(as.vector(imgG))
```

---

classifyCells	<i>A function to classify cells</i>
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---

### Description

The function classifies cells and paints the different class types in the image.

### Usage

```
classifyCells(classifier,filename="",image=NA,segmentedImage=NA,featuresObjects=NA,paint=TRUE,KS
```

### Arguments

classifier	A Support Vector Machine created by createClassifier or directly by the package e1071
filename	A path to an image file.
image	An 'Image' object or an array.
segmentedImage	An 'Image' object or an array. The corresponding segmented image (created by segmentImage)
featuresObjects	Cell feature file of the segmentedImage (created by segmentImage)
paint	If true, the classified cells are painted with different colors in the image
KS	Use Kernel Smoother in classification?
cancerIdentifier	A string which describes, how the cancer class is named.
maxShape	Maximum size of cell nuclei
minShape	Minimum size of cell nuclei
failureRegion	minimum size of failure regions
colors	Colors to paint the classes
classesToExclude	Which class should be excluded?
threshold	Which thresholding method should be used, "otsu" or "phansalkar"
numWindows	Number of windows to use for thresholding.
structures	If the image is already segmented, structures can be inserted to enable hierarchical classification.
classifyStructures	Use hierarchical classification. If yes a pixel classifier has to be defined.
pixelClassifier	A SVM to classify pixel based on their color values. Needed if hierarchical classification should be applied.
ksToExclude	These classes are excluded from kernel smoothing.

### Details

The kernels smoother improves the classification for cells which are likely to occur in clusters, like tumour cells. The kernel smoothing method can only be applied for two classes. If there are more classes only the normal svm without kernel smoothing is applied. Different classes are labeled with different colors in the image.

**Value**

A list with

comp1	classes
comp2	Classes, painted in the image, if paint was true

**Author(s)**

Henrik Failmezger, failmezger@mpipz.mpg.de

**Examples**

```
t = system.file("extdata", "trainingData.txt", package="CRImage")
#read training data
trainingData=read.table(t,header=TRUE)
#create classifier
classifier=createClassifier(trainingData)[[1]]
#classify cells
f = system.file("extdata", "exImg.jpg", package="CRImage")
classesValues=classifyCells(classifier, filename=f, KS=TRUE, maxShape=800, minShape=40, failureRegion=2000)
```

---

colorCorrection	<i>Color transfer between images.</i>
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---

**Description**

The colors of one image are adapted to the colors of a target image.

**Usage**

```
colorCorrection(img0, meanStdTarget, whiteMask = c())
```

**Arguments**

img0	The image who's colors should be adapted
meanStdTarget	Array with mean and standard deviation of the target image.
whiteMask	Boolean mask of white pixel in the image. These pixels are excluded from color correction.

**Details**

Mean and standard deviation of the target image can be calculated using the function calculate-MeanStdTarget.

**Value**

The image with adapted colors.

**Author(s)**

Henrik Failmezger, failmezger@cip.ifl.lmu.de



## References

Reinhard, E.; Adhikhmin, M.; Gooch, B.; Shirley, P.; , "Color transfer between images," Computer Graphics and Applications, IEEE , vol.21, no.5, pp.34-41, Sep/Oct 2001 doi: 10.1109/38.946629 URL: <http://ieeexplore.ieee.org/stamp/stamp.jsp?tp=&arnumber=946629&isnumber=20481>

## See Also

calculateMeanStandardTarget

## Examples

```
#read the target image
f1= system.file("extdata", "exImg2.jpg", package="CRImage")
targetImage=readImage(f1)
#read the image whose color values should be adapted
f2= system.file("extdata", "exImg3.jpg", package="CRImage")
imgToConvert=readImage(f2)
#calculate mean and standard deviation of target color channels
mst=calculateMeanStdTarget(targetImage)
# create a white pixel mask
whitePixelMask=imgToConvert[:,1]>0.85 & imgToConvert[:,2]>0.85 & imgToConvert[:,3]>0.85
#adapt color channels of image
imgCorrected=colorCorrection(imgToConvert,mst,whitePixelMask)
```

---

convertHSVToRGB

*Conversion from HSV color space to RGB color space*

---

## Description

The function converts images in the HSV colour space to the RGB colour space.

## Usage

```
convertHSVToRGB(imgHSV)
```

## Arguments

imgHSV            An 'Image' object or an array in the HSV colour space.

## Details

Standard colour space conversion.

## Value

An array in the RGB colour space.

## Author(s)

Henrik Failmezger, failmezger@cip.ifl.lmu.de

**See Also**

convertRGBToHSV convertRGBToLAB convertLABToRGB

**Examples**

```
f= system.file("extdata", "exImg.jpg", package="CRImage")
img=readImage(f)
#conversion to RGB color space
imgRGB=convertHSVToRGB(img)
```

---

convertLABToRGB

*Conversion of LAB colour space to RGB colour space*

---

**Description**

Color space conversion.

**Usage**

```
convertLABToRGB(imgLAB)
```

**Arguments**

imgLAB            LAB channel vectors.

**Details**

Color space conversion

**Value**

RGB channel vectors.

**Author(s)**

Henrik Failmezger, failmezger@cip.ifl.lmu.de

**Examples**

```
f= system.file("extdata", "exImg.jpg", package="CRImage")
img=readImage(f)
#conversion to HSV color space
imgRGB=convertLABToRGB(img)
```

---

convertRGBToHSV	<i>Conversion from RGB color space to HSV color space</i>
-----------------	---

---

**Description**

The RGB Image is converted to an HSV image.

**Usage**

```
convertRGBToHSV(img)
```

**Arguments**

img	The RGB image
-----	---------------

**Details**

The entries of the array are Hue, Saturation and Value.

**Value**

The image in HSV color space.

**Author(s)**

Henrik Failmezger, failmezger@cip.ifi.lmu.de

**See Also**

convertHSVToRGB convertRGBToLAB convertLABToRGB

**Examples**

```
f= system.file("extdata", "exImg.jpg", package="CRImage")
img=readImage(f)
#conversion to HSV color space
imgHSV=convertRGBToHSV(img)
```

---

convertRGBToLAB	<i>Converts RGB to LAB color space.</i>
-----------------	---

---

**Description**

Conversion of Color spaces.

**Usage**

```
convertRGBToLAB(imgT)
```

**Arguments**

imgT	The RGB image.
------	----------------

**Details**

Color space conversion

**Value**

The image in LAB color space.

**Author(s)**

Henrik Failmezger, failmezger@cip.ifi.lmu.de

**Examples**

```
f= system.file("extdata", "exImg.jpg", package="CRImage")
img=readImage(f)
#conversion to LAB color space
imgLAB=convertRGBToLAB(img)
```

---

correctCopyNumber      *Allelic Copy Number correction for cellularity*

---

**Description**

This function segments copy number and corrects log-ratios (LRR) and beta allele frequencies (BAF) values for cellularity.

**Usage**

```
correctCopyNumber(arr="Sample1", chr=NULL, p=NULL, z=NULL, min.value=-5)
```

**Arguments**

arr	Name of the array.
chr	Chromosome to run. If NULL, all chromosomes are run.
p	Percentage of tumoural cells.
z	Copy Number Data. Must be a dataframe with the following columns: Name (id of the probe), Chr (chromosome), Pos (position), LRR (log ratios) and BAF (beta allele frequencies).
min.value	Value assigned to the probes that have 0 copies after correction.

**Details**

The data.frame z must contain only SNP probes, that is probes with both LRR and BAF values. It is recommended that all replicated probes are merged so the positions are unique. This function calls DNACopy to segment the LRR and then correct the segmented profiles for normal contamination according to the method described in the reference below (see for details).

**Value**

A list with 2 components:

- y a data.frame with as many rows as probes containing the following variables: Chrom (chromosome), Pos (position), Orig.LRR (LRR before correction) Orig.BAF (BAF before correction), Corr.LRR (LRR after cellularity correction) and Corr.BAF (BAF after correction)
- seg a data.frame with the segmented data. Contains the following columns: ID (name of the array), chrom (chromosome), loc.start (start of the region), loc.end (end of the region), num.mark (number of probes in the region), seg.mean (LRR of the region), BAF (BAF of the regions), num.BAF (number of SNP probes in the region), Sa (estimated absolute copy number for the first allele), Sb (estimated absolute copy number for the first allele), LRR.tum (corrected LRR for the region), BAF.tum (corrected BAF for the region).

**Note**

Includes an adaptation of aCGH mergeLevels function to fix a problem with ansari.test.

**Author(s)**

Oscar M. Rueda, rueda.om@gmail.com

**References**

Yuan, Y et al. Quantitative image analysis of cellular heterogeneity in primary breast tumors enriches genomic assays. In prep.

**Examples**

```
LRR <- c(rnorm(100, 0, 1), rnorm(10, -2, 1), rnorm(20, 3, 1),
        rnorm(100, 0, 1))
BAF <- c(rnorm(100, 0.5, 0.1), rnorm(5, 0.2, 0.01), rnorm(5, 0.8, 0.01), rnorm(10, 0.25, 0.1), rnorm(10, 0.75,
        rnorm(100, 0.5, 0.1))

Pos <- sample(x=1:500, size=230, replace=TRUE)
Pos <- cumsum(Pos)
Chrom <- rep(1, length(LRR))
z <- data.frame(Name=1:length(LRR), Chrom=Chrom, Pos=Pos, LRR=LRR, BAF=BAF)
res <- correctCopyNumber(arr="Sample1", chr=1, p=0.75, z=z)
```

---

createBinaryImage      *Thresholding*

---

**Description**

Creates a binary image from a grayscale image by thresholding.

**Usage**

```
createBinaryImage(imgG, img=NULL, method="otsu", threshold=NULL, numWindows=1, whitePixelMask=c())
```

**Arguments**

img	An Image object or an array.
imgG	The grey valued Image object.
method	Either "otsu" or "phansalkar"
threshold	Fixed threshold
numWindows	Number of windows to use for threshold calculation.
whitePixelMask	Boolean mask of white pixels, if they should be excluded from thresholding

**Details**

The function returns the binary image resulting from the thresholding. If threshold is defined, all pixels smaller than this value will be fixed to 1 all other values will be set to 0. If threshold is undefined, the thresholding value is calculated automatically using 'otsu' or 'phansalkar' thresholding.

The function 'otsu' does Otsu thresholding on the grey level histograms of the image. The function 'phansalkar' does thresholding using the mean and standard deviation of a specified window. The thresholding is done on the RGB as well as the LAP color space and the results are ORed. The window size is dim(img)/numWindows. White pixel can be excluded from thresholding (e.g. if white is background) by defining a whitePixelMask

**Value**

The binary image.

**Author(s)**

Henrik Failmezger, failmezger@lmb.uni-muenchen.de

**References**

Neerad Phansalkar, Sumit More, Ashish Sabale, Dr. Madhuri Joshi, "Adaptive Local Thresholding for Detection of Nuclei in Diversly Stained Cytology Images," 2011 IEEE International Conference in Communications and Signal Processing (ICCSP), pp. 218, 10 Feb. 2011

Nobuyuki Otsu: A threshold selection method from grey level histograms. In: IEEE Transactions on Systems, Man, and Cybernetics. New York 9.1979, S.62-66. ISSN 1083-4419

**Examples**

```
f= system.file("extdata", "exImg.jpg", package="CRImage")
img=readImage(f)
#conversion to grayscale
imgG=EBImage::channel(img, "gray")
imgB=createBinaryImage(imgG, img=img, method="otsu", numWindows=4)
#white pixel mask
whitePixelMask=img[,1]>0.85 & img[,2]>0.85 & img[,3]>0.85
#exclude white pixels from thresholding
imgB=createBinaryImage(imgG, img=img, method="otsu", numWindows=4, whitePixelMask)
#phansalkar threshold
imgB=createBinaryImage(imgG, img=img, method="phansalkar", numWindows=4)
```

---

createClassifier	<i>Construction of a classifier</i>
------------------	-------------------------------------

---

**Description**

Creates a classifier for a training set.

**Usage**

```
createClassifier(trainingData, cross = FALSE)
```

**Arguments**

trainingData	A table, created by segmentImage with manually added classes.
cross	Does 10-fold cross validation to test the classifiers performance.

**Details**

Topological features include the density of cells and the size of the surrounding cytoplasm of a cell. These features depend on the size of the image. If training image and the image to classify have different size, these features can fool the classification and should not be enabled.

**Value**

A List containing:

classifier	The classifier
performance	cross validation performance

**Author(s)**

Henrik Failmezger, failmezger@mpipz.mpg.de

**See Also**

'createTrainingSet', 'classifyCells'

**Examples**

```
f = system.file("extdata", "trainingData.txt", package="CRImage")
#read training data
trainingData=read.table(f,header=TRUE)
#create classifier
classifier=createClassifier(trainingData)[[1]]
```

---

 labelCells

*Interactive Session for cell labeling*


---

### Description

The functions creates an interactive session in order to label cells with their classes. The labeled cells can be used as training set for the classifier. Note!! This is until now only tested for MacOSX.

### Usage

```
labelCells(img, segmentedImage, classes, classColours, nblocks = 3, labeledPoints = NULL, filename
```

### Arguments

img	The image.
segmentedImage	The segmented image.
classes	The possible class labels.
classColours	The colors for the class labels.
nblocks	The image can be separated in several blocks, as zooming is not possible.
labeledPoints	Labeled cells from a previous training session.
filename	The table of labeled cells is saved at this location.
filenameImage	The image with the labeled cells is saved at this location.
transformCoordinates	deprecated

### Details

Use the keys: a: In order to add a label to a cell. d: In order to delete a label from a cell. c: To switch between classes. q: To quit the interactive session. r: To refresh the session (labeled cells will be shown after refreshing)

### Value

A table with columns: index: the index of the cell in the segmented image. x: x-coordinate of the cell y: y-coordinate of the cell classCell: Label of the cell xLocal: Local x coordinate in the subimage(block) yLocal: Local y coordinate in the subimage(block) block: Block number in which the cell arises.

### Author(s)

Henrik Failmezger

### Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
```



---

plotCorrectedCN	<i>Plot CN profiles corrected for cellularity</i>
-----------------	---

---

### Description

This function takes the result of a call to `correctCopyNumber` and plots the results.

### Usage

```
plotCorrectedCN(CN, chr=NULL)
```

### Arguments

CN	object result of a call to <code>correctCopyNumber</code> .
chr	chromosome to plot.

### Details

A panel with four plots is created. The top panel shows LRR (with DNAcopy segmentation overlaid) and BAF before correction and the bottom panel shows the plots after correction.

### Value

No value is returned.

### Author(s)

Oscar M. Rueda, [rueda.om@gmail.com](mailto:rueda.om@gmail.com)

### References

Yuan, Y et al. Quantitative image analysis of cellular heterogeneity in primary breast tumors enriches genomic assays. In prep.

### Examples

```
LRR <- c(rnorm(100, 0, 1), rnorm(10, -2, 1), rnorm(20, 3, 1),
        rnorm(100, 0, 1))
BAF <- c(rnorm(100, 0.5, 0.1), rnorm(5, 0.2, 0.01), rnorm(5, 0.8, 0.01), rnorm(10, 0.25, 0.1), rnorm(10, 0.75,
        rnorm(100, 0.5, 0.1))

Pos <- sample(x=1:500, size=230, replace=TRUE)
Pos <- cumsum(Pos)
Chrom <- rep(1, length(LRR))
z <- data.frame(Name=1:length(LRR), Chrom=Chrom, Pos=Pos, LRR=LRR, BAF=BAF)
res <- correctCopyNumber(arr="Sample1", chr=1, p=0.75, z=z)
plotCorrectedCN(res, chr=1)
```

---

 processAperio

*Cellularity Calculation of Aperio TX Scanner*


---

**Description**

Procession of Aperio TX Slides.

**Usage**

```
processAperio(classifier=classifier,inputFolder=inputFolder,outputFolder=outputFolder,identifier
```

**Arguments**

classifier	The classifier.
inputFolder	The path to the image folder.
outputFolder	The path to the output folder.
identifier	The identifier of the files ("Ss" or "Da")
numSlides	The number of sections in the image.
cancerIdentifier	The identifier of the cancer class
classOther	deprecated
maxShape	Maximum size of cell nuclei
minShape	Minimum size of cell nuclei
failureRegion	minimum size of failure regions
slideToProcess	Set this parameter if only a certain slide should be processed
KS	Apply Kernel Smoother?
colors	Colors to paint the classes
classesToExclude	Which class should be excluded?
threshold	Which thresholding method should be used, "otsu" or "phansalkar" possible
numWindows	Number of windows to use for thresholding.
colorCorrection	deprecated
classifyStructures	Use hierarchical classification. If yes a pixel classifier has to be defined.
ksToExclude	These classes are excluded from kernel smoothing.
pixelClassifier	A SVM to classify pixel based on their color values. Needed if hierarchical classification should be applied.
densityToExclude	This class is excluded from cellularity calculation.
numDensityWindows	Number of windows for the density plot.

resizeFactor	Specifies the size of the cell density image. If this variable is not defined, the size of the thumbnail is used for the cell density image, else the size is calculated by $\text{size}(\text{thumbnail}) * \text{resizeFactor}$ . The thumbnail is the small overview image, created by the Aperio software.
plotCellTypeDensity	Plot the density of different cell types?
greyscaleImage	Color channel of the RGB image that should be used for thresholding
penClassifier	Classifier to exclude low quality images (will be part of next release)
referenceHist	Colour Histogram of a reference image that can be used to calculate the quality of the recent image. (will be part of next release)
fontSize	will be part of next release

### Details

The function processes images of Aperio TX scanners. The images have to be saved in the CWS format.

### Value

Four folders are created in the output folder.

Files	Cellularity values and cell numbers are saved in the file
classifiedImage	Subimages with labeled tumour and non tumour cells
tumourDensity	Cancer heatmaps for every subimage
cellCoordinates	Coordinates and cell class for every cell in the subimage
resizeFactor	Size of the cellularity density image, calculated by $\text{size}(\text{thumbnail}) * \text{resizeFactor}$ . Whereas the thumbnail is the small overview image produced by Aperio.

### Author(s)

Henrik Failmezger, failmezger@mpipz.mpg.de

### Examples

```
#t = system.file("extdata", "trainingData.txt", package="CRImage")
#read training data
#trainingData=read.table(t,header=TRUE)
#create classifier
#classifier=createClassifier(trainingData,topo=FALSE)[[1]]
#classify aperio
#f = system.file("extdata", package="CRImage")
#f=file.path(f,"8905")
#dir.create("AperioOutput")
#takes long time!

f = system.file("extdata", package="CRImage")
fc=file.path(f,"testClassifier")
load(fc)
fp=file.path(f,"pixelClassifier")
load(fp)
pixelClassifier=model
```

```
pathToImage=file.path(f,"8905")  
pathToOutput="" #specify an output folder here  
#processAperio(classifier=classifier,inputFolder=pathToImage,outputFolder=pathToOutput,identifier="Da",num
```

---

SauvolaThreshold      *Do Sauvola thresholding*

---

### Description

Thresholding method using mean and standard deviation.

### Usage

```
SauvolaThreshold(allGreyValues)
```

### Arguments

allGreyValues    Vector of gray values.

### Details

A threshold for the gray values is returned

### Value

The threshold.

### Author(s)

Henrik Failmezger, failmezger@cip.ifi.lmu.de

### References

J. Sauvola, M. Pietikainen, "Adaptive Document Image Binarization," Pattern Recognition, vol. 33, 225-236, 2000

### See Also

createBinaryImage

### Examples

```
f1= system.file("extdata", "exImg2.jpg", package="CRImage")  
print(f1)  
img=readImage(f1)  
print(img)  
#convert to grayscale  
imgG=EBImage::channel(img, 'grey')  
#threshold value  
t=SauvolaThreshold(as.vector(imgG))
```

---

segmentImage	<i>Segmentation of an image</i>
--------------	---------------------------------

---

### Description

The function segments cells or cell nuclei in the image.

### Usage

```
segmentImage(filename="", image=NA, maxShape=NA, minShape=NA, failureRegion=NA, threshold="otsu", numW
```

### Arguments

filename	A path to an image
image	An 'image' object, if no filename is specified.
maxShape	Maximum size of cell nuclei
minShape	Minimum size of cell nuclei
failureRegion	minimum size of failure regions
threshold	Thresholding method, "otsu" or "phansalkar"
numWindows	Number of windows to use for thresholding.
colorCorrection	deprecated
classifyStructures	Segment structures in the image, if yes a pixel classifier has to be defined
pixelClassifier	A SVM which classifies RGB color values in foreground and background.
greyscaleImage	Channel of the RGB image, to use for thresholding, if 0 use a joined greyscale image.
penClassifier	Classifier to exclude low quality images(will be part of next release)
referenceHist	Color histogram of a reference image, that can be used to estimate the quality of the recent image (will be part of next release)

### Details

The image is converted to greyscale and thresholded. Clutter is deleted using morphological operations. Clustered objects are separated using watershed algorithm. Segmented Cell nuclei, which exceed the maximum size are thresholded and segmented again. Cell nuclei which fall below the minimum size are deleted. Dark regions which exceed the parameter failureRegion are considered as artefacts and deleted. If the parameters are not defined, the operations will not be executed. Features are generated for every segmented object.

### Value

A list is returned containing

image	The original image
segmented image	The segmented image

**Author(s)**

Henrik Failmezger, failmezger@cip.ifi.lmu.de

**References**

EImage, '<http://www.bioconductor.org/packages/release/bioc/html/EImage.html>'

**Examples**

```
#segment image
#f = system.file('extdata' , 'exImg.jpg', package='CRImage')
#segmentationValues=segmentImage(f,maxShape=800,minShape=40,failureRegion=2000,threshold="otsu",numWindows=
#image=segmentationValues[[1]]
#segmentedImage=segmentationValues[[2]]
#imageFeatures=segmentationValues[[3]]
```

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