

Package ‘AFM’

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Title Atomic Force Microscope Image Analysis

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Description

Provides Atomic Force Microscope images analysis such as Gaussian mixes identification, Power Spectral Density, roughness against lengthscale, experimental variogram and variogram models, fractal dimension and scale, 2D network analysis. The AFM images can be exported to STL format for 3D printing.

NeedsCompilation no

Repository CRAN

License AGPL-3

Encoding UTF-8

Depends R (>= 3.4)

Imports data.table(>= 1.9.6),stringr(>= 1.0.0),gstat(>= 1.0-26),fractaldim(>= 0.8-4),rgl(>= 0.96),pracma(>= 1.8.6),grid(>= 3.1.3),gridExtra(>= 2.0.0),moments(>= 0.14),ggplot2(>= 1.0.1),sp(>= 1.2-0),png(>= 0.1-7),plyr(>= 1.8.3),igraph(>= 1.0.1),methods(>= 3.1.3),shiny(>= 0.12.2),shinyjs(>= 0.4.0),scales(>= 0.4.0),dbscan(>= 0.9-8),mixtools(>= 1.0.4),fftwtools(>= 0.9-8)

Collate 'AFM3DPrinter.R' 'AFMFractalDimensionAnalyser.R'
'AFMGaussianMixAnalyser.R' 'AFMImage.R' 'AFMNetworksAnalyser.R'
'AFMPSDAnalyser.R' 'AFMVariogramAnalyser.R'
'AFMImageAnalyser.R' 'AFMReportMaker.R' 'pkgname.R'
'runAFMApp.R'

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addNode	<i>addNode</i>
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Description

add a node to an AFMImage

Usage

```
addNode(circleAFMImage, nodeDT, filterIndex)
```

Arguments

circleAFMImage	a AFMImage
nodeDT	nodeDT a data.table lon lat circleRadius
filterIndex	an integer

Value

an [AFMImage](#)

Author(s)

M.Beauvais

AFM

Atomic Force Microscopy images tools

Description

The AFM package provides statistics analysis tools for Atomic Force Microscopy image analysis.
Licence: Affero GPL v3

Details

A graphical user interface is available by using [runAFMApp](#) command.

Several high level functions are :

- create your AFM image from a list of measured heights (see example section of [AFMImage](#))
- import your image from Nanoscope Analysis (TM) tool ([importFromNanoscope](#))
- check if your sample is normally distributed and isotropic and get a pdf report ([generateCheckReport](#))
- calculate the Gaussian mixes of the heights ([performGaussianMixCalculation](#))
- perform variance (variogram), roughness against lengthscale, fractal analysis and get a pdf report ([generateReport](#))
- identify 2D networks ([getNetworkParameters](#))

Other functions are :

- check sample: for normality ([checkNormality](#)) and for isotropy ([checkIsotropy](#))
- calculate total RMS roughness: quick calculation of total root mean square roughness([totalRMSRoughness](#))
- calculate omnidirectional variogram: calculate estimated variogram ([calculateOmnidirectionalVariogram](#))
- calculate roughness against lengthscale and Power Spectrum Density (PSD): calculate roughness against length scale ([RoughnessByLengthScale](#)), PSD 1D ([PSD1DAgainstFrequency](#)) or PSD 2D ([PSD2DAgainstFrequency](#)) against frequencies
- calculate fractal dimension and scale: use ([getFractalDimensions](#)) function
- print in 3D (3D print) ([exportToSTL](#)) your AFM image

An EC2 instance is available for basic testing at the following address: <http://www.afmist.org>

Note: To use with a Brucker(TM) Atomic Force Microscope, use nanoscope analysis(TM) software and

- Use the "Flatten" function.
- Save the flattened image.
- Use the "Browse Data Files" windows, right click on image name and then Export the AFM image with the headers and the "Export> ASCII" contextual menu option.

Author(s)

M.Beauvais, J.Landoulsi, I.Liascukiene

References

Gneiting2012, Tilmann Gneiting, Hana Sevcikova and Donald B. Percival 'Estimators of Fractal Dimension: Assessing the Roughness of Time Series and Spatial Data - Statistics in statistical Science, 2012, Vol. 27, No. 2, 247-277'

Olea2006, Ricardo A. Olea "A six-step practical approach to semivariogram modeling", 2006, "Stochastic Environmental Research and Risk Assessment, Volume 20, Issue 5 , pp 307-318"

Sidick2009, Erkin Sidick "Power Spectral Density Specification and Analysis of Large Optical Surfaces", 2009, "Modeling Aspects in Optical Metrology II, Proc. of SPIE Vol. 7390 73900L-1"

See Also

[gstat](#), [fractaldim](#), [rgl](#)

Examples

```
## Not run:
library(AFM)
# Analyse the AFMImageOfRegularPeaks AFM Image from this package
data("AFMImageOfRegularPeaks")
AFMImage<-AFMImageOfRegularPeaks
# exportDirectory="C:/Users/my_windows_login" or exportDirectory="/home/ubuntu"
exportDirectory=tempdir()
AFMImage@fullfilename<-paste(exportDirectory,"AFMImageOfRegularPeaks.txt",sep="/")

# Start to check if your sample is normally distributed and isotropic.
generateCheckReport(AFMImage)

# If the sample is normally distributed and isotropic, generate a full report
generateReport(AFMImage)

## End(Not run)
```

AFMImage-class

AFM image class

Description

A S4 class to store and manipulate images from Atomic Force Microscopes.

Usage

```

AFMImage(
  data,
  samplesperline,
  lines,
  hscansize,
  vscansize,
  scansize,
  fullfilename
)

## S4 method for signature 'AFMImage'
initialize(
  .Object,
  data,
  samplesperline,
  lines,
  hscansize,
  vscansize,
  scansize,
  fullfilename
)

AFMImage(
  data,
  samplesperline,
  lines,
  hscansize,
  vscansize,
  scansize,
  fullfilename
)

```

Arguments

data	(\$x,\$y,\$h): a data.table storing the coordinates of the sample and the measured heights
samplesperline	number of samples per line (e.g.: 512)
lines	number of line (e.g.: 512)
hscansize	horizontal size of scan usually in nanometer (e.g.: hscansize=1000 for a scan size of 1000 nm)
vscansize	vertical size of scan usually in nanometer (e.g.: vscansize=1000 for a scan size of 1000 nm)
scansize	if hscansize equals vscansize, scansize is the size of scan usually in nanometer (e.g.: scansize=1000 for a scan size of 1000 nm)
fullfilename	directory and filename on the disk (e.g.: /users/ubuntu/flatten-image.txt)
.Object	an AFMImage object

Slots

data ($\$x, \$y, \$h$): a `data.table` storing the coordinates of the sample and the measured heights
samplesperline number of samples per line (e.g.: 512)
lines number of line (e.g.: 512)
hscansize horizontal size of scan usually in nanometer (e.g.: `hscansize=1000` for a scan size of 1000 nm)
vscansize vertical size of scan usually in nanometer (e.g.: `vscansize=1000` for a scan size of 1000 nm)
scansize if `hscansize` equals `vscansize`, `scansize` is the size of scan usually in nanometer (e.g.: `scansize=1000` for a scan size of 1000 nm)
fullfilename directory and filename on the disk (e.g.: `/users/ubuntu/flatten-image.txt`)

Author(s)

M.Beauvais

Examples

```

## Not run:
library(AFM)
library(data.table)

# create a 128 pixels by 128 pixels AFM image
Lines=128
Samplesperline=128
fullfilename="RandomFakeAFMImage"
# the size of scan is 128 nm
ScanSize=128
# the heights is a normal distribution in nanometers
nm<-c(rnorm(128*128, mean=0, sd=1 ))

scanby<-ScanSize/Samplesperline
endScan<-ScanSize*(1-1/Samplesperline)
RandomFakeAFMImage<-AFMImage(
  data = data.table(x = rep(seq(0,endScan, by= scanby), times = Lines),
                    y = rep(seq(0,endScan, by= scanby), each = Samplesperline),
                    h = nm),
  samplesperline = Samplesperline, lines = Lines,
  vscansize = ScanSize, hscansize = ScanSize, scansize = ScanSize,
  fullfilename = fullfilename )

## End(Not run)

```

AFMImage3DModelAnalysis-class

AFM image Power Spectrum Density analysis class

Description

AFMImage3DModelAnalysis

Slots

f1 a face of the 3D model

f2 a face of the 3D model

f3 a face of the 3D model

f4 a face of the 3D model

Author(s)

M.Beauvais

AFMImageAnalyser-class

AFM image analyser class

Description

A S4 class to handle the analysis of one AFM Image.

Usage

AFMImageAnalyser(AFMImage)

AFMImageAnalyser(AFMImage)

Arguments

AFMImage an AFMImage

Slots

AFMImage [AFMImage](#) to be analysed
 variogramAnalysis [AFMImageVariogramAnalysis](#)
 psdAnalysis [AFMImagePSDAnalysis](#)
 fdAnalysis [AFMImageFractalDimensionsAnalysis](#)
 gaussianMixAnalysis [AFMImageGaussianMixAnalysis](#)
 networksAnalysis [AFMImageNetworksAnalysis](#)
 mean the mean of heights of the [AFMImage](#)
 variance the variance of heights of the [AFMImage](#)
 TotalRrms the total Root Mean Square Roughness of the [AFMImage](#) calculated from variance
 Ra mean roughness or mean of absolute values of heights
 fullfilename to be removed ?
 updateProgress a function to update a graphical user interface

Author(s)

M.Beauvais

AFMImageCollagenNetwork
AFM image sample

Description

A real dataset containing an [AFMImage](#) of a collagen network. The image is made of 192*192 samples of a 1500 nm * 1500 nm surface. samplesperline=192 lines=192 hscansize=1500 vscansize=1500

AFMImageFractalDimensionMethod-class
AFM image fractal dimension method class

Description

AFMImageFractalDimensionMethod stores calculation from one fractal dimension method

Usage

```

AFMImageFractalDimensionMethod(fd_method, fd, fd_scale)

## S4 method for signature 'AFMImageFractalDimensionMethod'
initialize(.Object, fd_method, fd, fd_scale)

AFMImageFractalDimensionMethod(fd_method, fd, fd_scale)

```

Arguments

fd_method	Two dimensional function names used to evaluate the fractal dimension and fractal scale
fd	the value of the fractal dimension
fd_scale	the value of the fractal scale
.Object	an AFMImageFractalDimensionMethod object

Slots

fd_method	Two dimensional function names used to evaluate the fractal dimension and fractal scale
fd	the value of the fractal dimension
fd_scale	the value of the fractal scale

Author(s)

M.Beauvais

See Also

[fractaldim](#)

AFMImageFractalDimensionsAnalysis-class
AFM image fractal dimensions analysis class

Description

A S4 class to handle the fractal dimension calculation with several fractal dimension methods

Usage

```
AFMImageFractalDimensionsAnalysis()

## S4 method for signature 'AFMImageFractalDimensionsAnalysis'
initialize(.Object, fractalDimensionMethods, csvFullfilename)

AFMImageFractalDimensionsAnalysis()

fractalDimensionMethods(object)

## S4 method for signature 'AFMImageFractalDimensionsAnalysis'
fractalDimensionMethods(object)
```

Arguments

.Object an AFMImageFractalDimensionsAnalysis Class
 fractalDimensionMethods
 a list of [AFMImageFractalDimensionMethod](#)
 csvFullfilename
 To be removed ?
 object a [AFMImageFractalDimensionsAnalysis](#)

Slots

fractalDimensionMethods a list of [AFMImageFractalDimensionMethod](#)
 csvFullfilename To be removed ?
 updateProgress a function to update a graphical user interface

Author(s)

M.Beauvais

AFMImageGaussianMixAnalysis-class

AFM image Gaussian Mix analysis class

Description

AFMImageGaussianMixAnalysis handles an [AFMImage](#) Gaussian mix of heights analysis

Usage

```
AFMImageGaussianMixAnalysis()

## S4 method for signature 'AFMImageGaussianMixAnalysis'
initialize(.Object)

AFMImageGaussianMixAnalysis()

summaryMixture(object)

## S4 method for signature 'AFMImageGaussianMixAnalysis'
summaryMixture(object)

eachComponentsCounts(object)

## S4 method for signature 'AFMImageGaussianMixAnalysis'
eachComponentsCounts(object)
```

```

tcdfsEcdfsCheck(object)

densityCurvesAllHeights(object)

## S4 method for signature 'AFMImageGaussianMixAnalysis'
densityCurvesAllHeights(object)

tcdfsEcdfsCheck(object)

## S4 method for signature 'AFMImageGaussianMixAnalysis'
tcdfsEcdfsCheck(object)

gaussianMix(object)

## S4 method for signature 'AFMImageGaussianMixAnalysis'
gaussianMix(object)

minGaussianMix(object)

## S4 method for signature 'AFMImageGaussianMixAnalysis'
minGaussianMix(object)

maxGaussianMix(object)

## S4 method for signature 'AFMImageGaussianMixAnalysis'
maxGaussianMix(object)

epsilonGaussianMix(object)

## S4 method for signature 'AFMImageGaussianMixAnalysis'
epsilonGaussianMix(object)

```

Arguments

```

.Object      an AFMImageGaussianMixAnalysis object
object      a AFMImageGaussianMixAnalysis

```

Slots

```

minGaussianMix  the minimum number of components to calculate
maxGaussianMix  the maximum number of components to calculate
epsilonGaussianMix  the convergence criterion
gaussianMix     a data.table to store the calculated Gaussian mixes
summaryMixture  a data.table to summarise the mixtures
tcdfsEcdfsCheck  an array to store the points to draw tcdfs ecdfs check
densityCurvesAllHeights  an array to store the points to draw the density curves
eachComponentsCounts  an array to store the points to draw counts of each components

```

updateProgress a function to update a graphical user interface

Author(s)

M.Beauvais

AFMImageNetworksAnalysis-class

AFM image networks analysis class

Description

A S4 class to handle the networks calculation

Usage

```
AFMImageNetworksAnalysis()
```

```
## S4 method for signature 'AFMImageNetworksAnalysis'
```

```
initialize(  
  .Object,  
  vertexHashsize,  
  binaryAFMImage,  
  binaryAFMImageWithCircles,  
  circlesTable,  
  edgesTable,  
  fusionedNodesCorrespondance,  
  fusionedNodesEdgesTable,  
  isolatedNodesList,  
  heightNetworkslider,  
  filterNetworksliderMin,  
  filterNetworksliderMax,  
  smallBranchesTreatment,  
  originalGraph,  
  skeletonGraph,  
  shortestPaths,  
  networksCharacteristics,  
  holes,  
  holesCharacteristics,  
  graphEvcnt,  
  graphBetweenness,  
  libVersion  
)
```

```
AFMImageNetworksAnalysis()
```

Arguments

.Object	an AFMImageNetworksAnalysis Class
vertexHashsize	hash to transform coordinates to vertexId
binaryAFMImage	the AFMImage after transformation before analysis
binaryAFMImageWithCircles	the AFMImage after transformation with the spotted circles
circlesTable	a data.table of identified circles
edgesTable	a data.table of edges
fusionedNodesCorrespondance	a data.table of correspon
fusionedNodesEdgesTable	a data.table of correspondance between intial node and fusioned node
isolatedNodesList	a data.table of isolated nodes
heightNetworkslider	used multiplier of heights to facilitate analysis
filterNetworksliderMin	used filter minimum value to facilitate analysis
filterNetworksliderMax	used filter maximum value to facilitate analysis
smallBranchesTreatment	boolean - smallest circle used or not
originalGraph	a list of igraph
skeletonGraph	a list of igraph
shortestPaths	a data.table of shortest path
networksCharacteristics	a data.table to store the skeleton graph characteristics
holes	a data.table to store the cluster number of each point
holesCharacteristics	a data.table to summarize the data about holes
graphEvcnt	an array to store Evcnt
graphBetweenness	an array to store the graph betweenness
libVersion	version of the AFM library used to perform the analysis

Slots

vertexHashsize	hash to transform coordinates to vertexId
binaryAFMImage	the AFMImage after transformation before analysis
binaryAFMImageWithCircles	the AFMImage after transformation with the spotted circles
circlesTable	a data.table of identified circles
edgesTable	a data.table of edges

fusedNodesCorrespondance a data.table of correspondance between initial node and fused node
 fusedNodesEdgesTable a data.table of nodes fused because of intersecting
 isolatedNodesTable a data.table of isolated nodes
 heightNetworkslider used multiplier of heights to facilitate analysis
 filterNetworksliderMin used filter minimum value to facilitate analysis
 filterNetworksliderMax used filter maximum value to facilitate analysis
 smallBranchesTreatment boolean - smallest circle used or not
 originalGraph a list of [igraph](#)
 skeletonGraph a list of [igraph](#)
 shortestPaths a data.table of shortest paths
 networksCharacteristics a data.table to store the skeleton graph characteristics
 graphEvent an array to store Event
 graphBetweenness an array to store the graph betweenness
 libVersion version of the AFM library used to perform the analysis
 updateProgress a function to update a graphical user interface

Author(s)

M.Beauvais

AFMImageOfAluminiumInterface
AFM image sample

Description

A real dataset containing an [AFMImage](#) of an Aluminium interface. The image is made of 512*512 samples of a 1000 nm * 1000 nm surface. samplesperline=512 lines=512 hscansize=1000 vscansize=1000

Author(s)

J.Landoulsi, I.Liascukiene

AFMImageOfNormallyDistributedHeights
AFM image sample

Description

A fake dataset containing a manually generated [AFMImage](#) (a normal distribution of heights). The image is made of 128*128 samples of a 128 nm * 128 nm surface. samplesperline= 128 lines= 128 hscansize= 128 vscansize= 128

AFMImageOfOnePeak *AFM image sample*

Description

A fake dataset containing a manually generated [AFMImage](#) (one peak positioned on the surface). The image is made of 128*128 samples of a 128 nm * 128 nm surface. samplesperline= 128 lines= 128 hscansize= 128 vscansize= 128

AFMImageOfRegularPeaks
AFM image sample

Description

A fake dataset containing a manually generated [AFMImage](#) (peaks regularly positioned on the surface). The image is made of 128*128 samples of a 128 nm * 128 nm surface. samplesperline= 128 lines= 128 hscansize= 128 vscansize= 128

AFMImagePSDAnalysis-class
AFM image Power Spectrum Density analysis class

Description

AFMImagePSDAnalysis handles an [AFMImage](#) roughness against lengthscale analysis

Usage

```
AFMImagePSDAnalysis()  
  
## S4 method for signature 'AFMImagePSDAnalysis'  
initialize(.Object)  
  
AFMImagePSDAnalysis()  
  
psd1d_breaks(object)  
  
## S4 method for signature 'AFMImagePSDAnalysis'  
psd1d_breaks(object)  
  
psd2d_maxHighLengthScale(object)
```

```

## S4 method for signature 'AFMImagePSDAnalysis'
psd2d_maxHighLengthScale(object)

psd2d_truncHighLengthScale(object)

## S4 method for signature 'AFMImagePSDAnalysis'
psd2d_truncHighLengthScale(object)

psd1d(object)

## S4 method for signature 'AFMImagePSDAnalysis'
psd1d(object)

psd2d(object)

## S4 method for signature 'AFMImagePSDAnalysis'
psd2d(object)

roughnessAgainstLengthscale(object)

## S4 method for signature 'AFMImagePSDAnalysis'
roughnessAgainstLengthscale(object)

intersections(object)

## S4 method for signature 'AFMImagePSDAnalysis'
intersections(object)

```

Arguments

.Object an AFMImagePSDAnalysis object
object a [AFMImagePSDAnalysis](#)

Slots

roughnessAgainstLengthscale a data.table to store the roughness against lengthscale data
intersections a list to store the lengthscales values as the intersections between slopes and the sill in roughness against lengthscale graph
updateProgress a function to update a graphical user interface

Author(s)

M.Beauvais

AFMImagePSDSlopesAnalysis-class
AFM Image psd slope analysis

Description

AFMImagePSDSlopesAnalysis stores the analysis of the second slope in roughness against lengthscale

Usage

```
AFMImagePSDSlopesAnalysis()  
  
## S4 method for signature 'AFMImagePSDSlopesAnalysis'  
initialize(.Object)  
  
AFMImagePSDSlopesAnalysis()
```

Arguments

.Object an AFMImagePSDSlopesAnalysis object

Slots

lc to be removed ?
wsat to be removed ?
slope to be removed ?
yintersept to be removed ?

Author(s)

M.Beauvais

AFMImageVariogramAnalysis-class
AFM image variogram analysis class

Description

AFMImageVariogramAnalysis manages the variogram analysis of an [AFMImage](#)

Usage

```

AFMImageVariogramAnalysis(sampleFitPercentage)

## S4 method for signature 'AFMImageVariogramAnalysis'
initialize(.Object, sampleFitPercentage, updateProgress)

AFMImageVariogramAnalysis(sampleFitPercentage)

variogramModels(object)

## S4 method for signature 'AFMImageVariogramAnalysis'
variogramModels(object)

omnidirectionalVariogram(object)

## S4 method for signature 'AFMImageVariogramAnalysis'
omnidirectionalVariogram(object)

directionalVariograms(object)

## S4 method for signature 'AFMImageVariogramAnalysis'
directionalVariograms(object)

variogramSlopeAnalysis(object)

## S4 method for signature 'AFMImageVariogramAnalysis'
variogramSlopeAnalysis(object)

```

Arguments

sampleFitPercentage	a sample size as a percentage (e.g. "5" for 5 percents) of random points in the AFMImage . These points will be used to fit the variogram models.
.Object	an AFMImageVariogramAnalysis class
updateProgress	a function to update a graphical user interface
object	a AFMImageVariogramAnalysis object

Slots

width	(optional) a distance step for the calculation of the variograms (e.g.: width= integer of (scan Size divided by number of lines)= ceil(1000 / 512) for AFMImageOfAluminiumInterface
omnidirectionalVariogram	a data.table to store the omnidirectional variogram
variogramSlopeAnalysis	a AFMImageVariogramAnalysis to analyse slope in log log omnidirectional semivariogram
directionalVariograms	a data.table to store the directional variograms
sampleFitPercentage	a sample size as a percentage of random points in the AFMImage . These points will be used to fit the variogram models.

chosenFitSample the chosen random points of the [AFMImage](#) to perform the fitting of the variogram models.

cuts the cuts for splot of the [AFMImage](#). The same cuts will be used for the predicted [AFMImage](#) variogramModels A list of [AFMImageVariogramModel](#) containing the various evaluated variogram models.

fullfilename to be removed ?

updateProgress a function to update a graphical user interface

Author(s)

M.Beauvais

AFMImageVariogramModel-class

AFM Image Variogram Model class

Description

AFMImageVariogramModel stores the evaluation of one experimental variogram model

Usage

```
AFMImageVariogramModel()
```

```
## S4 method for signature 'AFMImageVariogramModel'
initialize(
  .Object,
  model,
  fit.v = data.table(),
  mykrige,
  res = data.table(),
  cor,
  press,
  sill,
  imageFullfilename
)
```

```
AFMImageVariogramModel()
```

Arguments

.Object	an AFMImageVariogramModel object
model	the variogram model name
fit.v	the values from the fit.variogram function in the gstat package
mykrige	the values from the krige function in the gstat library

res a data.table to store: (cor) the correlation between the predicted sample and the real sample (press) the sum of the square of the differences between real and predicted values for each point of the sample

cor to be removed ?

press to be removed ?

sill to be removed ?

imageFullfilename
to be removed ?

Slots

model the variogram model name

fit.v the values from the `fit.variogram` function in the `gstat` package

mykrige the values from the `krige` function in the `gstat` library

res a data.table to store: (cor) the correlation between the predicted sample and the real sample (press) the sum of the square of the differences between real and predicted values for each point of the sample

cor to be removed ?

press to be removed ?

sill to be removed ?

imageFullfilename to be removed ?

Author(s)

M.Beauvais

analyse

Analyse an AFMImage

Description

A function to wrap all the analysis of an `AFMImage`

- variogram analysis including evaluation of basic variogram models with sill and range calculation
- power spectrum density analysis including roughness against lengthscale calculation
- fractal dimension analysis including fractal dimensions calculation
- basic roughness parameters analysis such as mean, variance, Rrms, Ra

Usage

`analyse(AFMImageAnalyser)`

Arguments

AFMImageAnalyser
 a [AFMImageAnalyser](#) to manage and store image analysis

Value

an [AFMImageAnalyser](#) containing all the analysis

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)

data(AFMImageOfAluminiumInterface)
AFMImage<-extractAFMImage(AFMImageOfAluminiumInterface, 0, 0, 32)
AFMImageAnalyser<-new("AFMImageAnalyser", AFMImage= AFMImage, fullfilename = AFMImage@fullfilename)
AFMImageAnalyser<-analyse(AFMImageAnalyser)
print(AFMImageAnalyser@fdAnalysis)

## End(Not run)
```

AreNodesConnected	<i>check if nodes represented by circles are connected. The function defines all the possible segments between the circles and check if at least one segment exists.</i>
-------------------	--

Description

check if nodes represented by circles are connected. The function defines all the possible segments between the circles and check if at least one segment exists.

Usage

```
AreNodesConnected(binaryAFMImage, center1, radius1, center2, radius2)
```

Arguments

binaryAFMImage	a binary AFMImage from Atomic Force Microscopy
center1	the center of the circle with center\$lon as the x coordinates and center\$lat as the y coordinates
radius1	the radius of the circle
center2	the center of the circle with center\$lon as the x coordinates and center\$lat as the y coordinates
radius2	the radius of the circle

Value

TRUE if the nodes are connected

Author(s)

M.Beauvais

calculate3DModel	<i>Calculate the 3D model for 3D printing</i>
------------------	---

Description

calculate3DModel update [AFMImage3DModelAnalysis](#)

Usage

```
calculate3DModel(AFMImage3DModelAnalysis, AFMImage)

## S4 method for signature 'AFMImage3DModelAnalysis'
calculate3DModel(AFMImage3DModelAnalysis, AFMImage)
```

Arguments

AFMImage3DModelAnalysis
 n [AFMImage3DModelAnalysis](#) to store the setup and results of PSD analysis

AFMImage
 an [AFMImage](#) from Atomic Force Microscopy

Author(s)

M.Beauvais

calculateDirectionalVariograms	<i>Calculate experimental directional semi-variograms</i>
--------------------------------	---

Description

calculate four experimental directional variograms of an [AFMImage](#) with the [variogram](#) function of the gstat package. The directional semi-variogram can be used to check the isotropy of the sample. Note: The sample will be isotropic if the slopes of the four variograms are similar.

Usage

```
calculateDirectionalVariograms(AFMImageVariogramAnalysis, AFMImage)
```


Arguments

AFMImageVariogramAnalysis
 an [AFMImageVariogramAnalysis](#) to manage and store the result of variogram analysis

AFMImage
 an [AFMImage](#) from Atomic Force Microscopy

Details

calculateDirectionalVariograms returns the directional variograms

Value

Four directional variograms

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
library(ggplot2)

data(AFMImageOfRegularPeaks)
variogramAnalysis<-AFMImageVariogramAnalysis(sampleFitPercentage=3.43/100)
varios<-AFM::calculateDirectionalVariograms(AFMImage= AFMImageOfRegularPeaks,
                                             AFMImageVariogramAnalysis= variogramAnalysis)

dist<-gamma<-NULL
p <- ggplot(varios, aes(x=dist, y=gamma,
                       color= as.factor(dir.hor),
                       shape=as.factor(dir.hor)))

p <- p + expand_limits(y = 0)
p <- p + geom_point()
p <- p + geom_line()
p <- p + ylab("semivariance (nm^2)")
p <- p + xlab("distance (nm)")
p <- p + ggtitle("Directional")
p

## End(Not run)
```

calculateGaussianMixture

Calculate Gaussian Mixture with two components from the AFM Image.

Description

calculateGaussianMixture return a data.table containing the result of the Gaussian Mixture and result of the test

Usage

```
calculateGaussianMixture(AFMImage)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Author(s)

M.Beauvais

Examples

```
## Not run:  
library(AFM)  
data(AFMImageOfNetworks)  
mixtureCharacteristics<-calculateGaussianMixture(AFMImageOfNetworks)  
print(mixtureCharacteristics)  
  
## End(Not run)
```

```
calculateHolesCharacteristics  
                          get the networks parameters
```

Description

Calculate the holes characteristics

Usage

```
calculateHolesCharacteristics(AFMImageNetworksAnalysis)
```

Arguments

AFMImageNetworksAnalysis
 a [AFMImageNetworksAnalysis](#)

Value

a data.table with all the parameters

Author(s)

M.Beauvais

calculateIgraph *Calculate iGraph from AFMImage*

Description

calculateIgraph return

Usage

```
calculateIgraph(AFMImage, AFMImageNetworksAnalysis)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy
AFMImageNetworksAnalysis an [AFMImageNetworksAnalysis](#) from Atomic Force Microscopy

Author(s)

M.Beauvais

calculateNetworkParameters
get the networks parameters

Description

Calculate and return the networks parameters

Usage

```
calculateNetworkParameters(AFMImageNetworksAnalysis, AFMImage)
```

Arguments

AFMImageNetworksAnalysis a [AFMImageNetworksAnalysis](#)
AFMImage a [AFMImage](#)

Value

a data.table with all the parameters

Author(s)

M.Beauvais

calculateNetworks *Calculate networks on the surface*

Description

calculateNetworks update [AFMImageNetworksAnalysis](#)

Usage

```
calculateNetworks(AFMImageNetworksAnalysis, AFMImage)
```

```
## S4 method for signature 'AFMImageNetworksAnalysis'  
calculateNetworks(AFMImageNetworksAnalysis, AFMImage)
```

Arguments

AFMImageNetworksAnalysis
 n [AFMImageNetworksAnalysis](#) to store the results of networks analysis

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Author(s)

M.Beauvais

calculateNetworkSkeleton
 calculateNetworkSkeleton

Description

calculateNetworkSkeleton return

Usage

```
calculateNetworkSkeleton(AFMImage, AFMImageNetworksAnalysis)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

AFMImageNetworksAnalysis
 an [AFMImageNetworksAnalysis](#) from Atomic Force Microscopy

Author(s)

M.Beauvais

 calculateOmnidirectionalVariogram

Calculate experimental omnidirectional semi-variogram

Description

calculateOmnidirectionalVariogram returns the semivariance calculated for all the directions calculate the experimental omnidirectional variogram of an [AFMImage](#) with the [variogram](#) function of the `gstat` package. The experimental semi-variogram is used to fit (find the best sill and range) the theoretical variogram models. With 512*512 images, it takes several minutes to calculate.

Usage

```
calculateOmnidirectionalVariogram(AFMImageVariogramAnalysis, AFMImage)
```

Arguments

`AFMImageVariogramAnalysis` an [AFMImageVariogramAnalysis](#) to manage and store the result of variogram analysis

`AFMImage` an [AFMImage](#) from Atomic Force Microscopy

Value

the semivariance calculated in all the directions

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
library(ggplot2)

data(AFMImageOfRegularPeaks)
variogramAnalysis<-AFMImageVariogramAnalysis(sampleFitPercentage=3.43/100)
avario<-AFM::calculateOmnidirectionalVariogram(AFMImageVariogramAnalysis= variogramAnalysis,
                                              AFMImage= AFMImageOfRegularPeaks)

dist<-gamma<-NULL
p <- ggplot(avario, aes(x=dist, y=gamma))
p <- p + geom_point()
p <- p + geom_line()
p <- p + ylab("semivariance")
p <- p + xlab("distance (nm)")
p <- p + ggtitle("Experimental semivariogram")
p

## End(Not run)
```

calculatePhysicalDistanceFromPath

calculate the physical distances between nodes

Description

calculate the physical distances between nodes

Usage

```
calculatePhysicalDistanceFromPath(pathVidVector, hscale, vscale)
```

Arguments

pathVidVector a network path
hscale the hscale of the [AFMImage](#) from Atomic Force Microscopy
vscale the vscale of the [AFMImage](#) from Atomic Force Microscopy

Value

the physical distance the extrmitities of the path

Author(s)

M.Beauvais

calculateShortestPaths

calculate the shortest path between adjacent nodes

Description

Calculate the shortest path between all nodes of degree different to 2 that are connected with nodes of degree equal to 2 Calculate the distance between the above nodes.

Usage

```
calculateShortestPaths(..., AFMImageNetworksAnalysis)
```

Arguments

... cl: a cluster object from the parallel package
AFMImageNetworksAnalysis
a [AFMImageNetworksAnalysis](#)

Author(s)

M.Beauvais

canBeRemoved	<i>canBeRemoved</i>
--------------	---------------------

Description

canBeRemoved return

Usage

```
canBeRemoved(vertexId, g, allVertices, DEGREE_LIMIT_FOR_CANDIDATE_VERTICE)
```

Arguments

vertexId	a vertex id
g	a igraph
allVertices	list of all vertices
DEGREE_LIMIT_FOR_CANDIDATE_VERTICE	degree

Author(s)

M.Beauvais

checkIsotropy	<i>Check the isotropy of a sample</i>
---------------	---------------------------------------

Description

checkIsotropy is used to check the isotropy of an [AFMImage](#). A directional variogram is calculated for various directions. If the variogram is very similar for all the directions then the sample is isotropic.

Usage

```
checkIsotropy(AFMImage, AFMImageAnalyser)
```

Arguments

AFMImage	an AFMImage to be analysed
AFMImageAnalyser	an AFMImageAnalyser to perform the analysis

Value

an [AFMImageAnalyser](#) containing the directional variograms

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
library(ggplot2)

data(AFMImageOfAluminiumInterface)
AFMImage<-extractAFMImage(AFMImageOfAluminiumInterface, 0, 0, 32)
AFMImageAnalyser<-new("AFMImageAnalyser", AFMImage= AFMImage, fullfilename = AFMImage@fullfilename)
AFMImageAnalyser<-checkIsotropy(AFMImage,AFMImageAnalyser)
varios<-AFMImageAnalyser@variogramAnalysis@directionalVariograms
p2 <- ggplot(varios, aes(x=dist, y=gamma,
                        color= as.factor(dir.hor), shape=as.factor(dir.hor)))

p2 <- p2 + expand_limits(y = 0)
p2 <- p2 + geom_point()
p2 <- p2 + geom_line()
p2 <- p2 + ylab("semivariance (nm^2)")
p2 <- p2 + xlab("distance (nm)")
p2 <- p2 + ggtitle("Directional")
p2

## End(Not run)
```

 checkNormality

Check visually of the normality of the sample

Description

checkNormality performs a visual check to know if the distribution of heights of an [AFMImage](#) follows a normal distribution. The function displays Quantile/Quantile and distribution plots.

Usage

```
checkNormality(..., AFMImage)
```

Arguments

... pngfullfilename (optional): directory and filename to save the visual check to png or pdffullfilename(optional): directory and filename to save the visual check to pdf

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Author(s)

M.Beauvais

References

Olea2006, Ricardo A. Olea "A six-step practical approach to semivariogram modeling", 2006, "Stochastic Environmental Research and Risk Assessment, Volume 20, Issue 5 , pp 307-318"

Examples

```
## Not run:
library(AFM)

# display Quantile/Quantile and distribution plots.
data(AFMImageOfNormallyDistributedHeights)
checkNormality(AFMImage= AFMImageOfNormallyDistributedHeights)

# display and save on disk Quantile/Quantile and distribution plots.
data(AFMImageOfNormallyDistributedHeights)
checkNormality(AFMImage= AFMImageOfNormallyDistributedHeights,
               pngfullfilename=paste(tempdir(), "checkNormality.png", sep="/"))

## End(Not run)
```

createGraph

create the igraph weighted graph from the nodes and edges

Description

create the igraph weighted graph from the nodes and edges

Usage

```
createGraph(AFMImageNetworksAnalysis)
```

Arguments

```
AFMImageNetworksAnalysis
  a AFMImageNetworksAnalysis
```

Author(s)

M.Beauvais

displayColoredNetworkWithVerticesSize
displayColoredNetworkWithVerticesSize

Description

display network

Usage

displayColoredNetworkWithVerticesSize(AFMImageNetworksAnalysis, fullfilename)

Arguments

AFMImageNetworksAnalysis
a [AFMImageNetworksAnalysis](#)
fullfilename a directory plus filename for export

Author(s)

M.Beauvais

displaygridIgraphPlot *display the network of nodes and edges*

Description

display the network of nodes and edges

Usage

displaygridIgraphPlot(AFMImageNetworksAnalysis)

Arguments

AFMImageNetworksAnalysis
an [AFMImageNetworksAnalysis](#)

Author(s)

M.Beauvais

displaygridIgraphPlotFromEdges
display the network of nodes and edges

Description

display the network of nodes and edges

Usage

displaygridIgraphPlotFromEdges(AFMImage, edges, isolates)

Arguments

AFMImage	an AFMImage from Atomic Force Microscopy
edges	list of edges
isolates	list of isolated edges

Author(s)

M.Beauvais

displayHolesIn3D *Display a 3D image of the holes in an AFMImage and store it on disk.*

Description

Display a 3D image of the holes in an AFMImage and store it on disk if fullfilename variable is set. It uses the [rgl](#) package.

Usage

displayHolesIn3D(AFMImage, width, fullfilename, changeViewpoint, noLight)

Arguments

AFMImage	the AFM image to be displayed in three dimensions.
width	(optional) width of the image. Default is 512 pixels. Note: width can't be superior to screen resolution.
fullfilename	(optional) the directory and filename to save the png of the 3D image. If this variable is missing, the function will not save on disk the 3D image.
changeViewpoint	(optional) if TRUE, the viewpoint is changed. Default is TRUE.
noLight	if TRUE, the lighth is set off

Author(s)

M.Beauvais

displayIn3D	<i>Display a 3D image of an AFMImage and store it on disk.</i>
-------------	--

Description

Display a 3D image of an AFMImage and store it on disk if fullfilename variable is set. It uses the [rgl](#) package.

Usage

```
displayIn3D(AFMImage, width, fullfilename, changeViewpoint, noLight)
```

Arguments

AFMImage	the AFM image to be displayed in three dimensions.
width	(optional) width of the image. Default is 512 pixels. Note: width can't be superior to screen resolution.
fullfilename	(optional) the directory and filename to save the png of the 3D image. If this variable is missing, the function will not save on disk the 3D image.
changeViewpoint	(optional) if TRUE, the viewpoint is changed. Default is TRUE.
noLight	if TRUE, the lighth is set off

Author(s)

M.Beauvais

dnormalmix	<i>dnormalmix density of a mixture of normals</i>
------------	---

Description

dnormalmix density of a mixture of normals

Usage

```
dnormalmix(x, mixture, log = FALSE)
```

Arguments

x	a vector of quantiles
mixture	a gaussian mixture
log	perform a log transformation of the result

```
evaluateVariogramModels
```

```
evaluateVariogramModels method to evaluate the basic variogram models
```

Description

evaluateVariogramModels method to evaluate the basic variogram models available in the [gstat](#) package. A [AFMImageVariogramAnalysis](#) method to handle the variogram analysis of an [AFMImage](#). The variogram models used can be seen with the `show.vgms()` function from the [gstat](#) package.

Usage

```
evaluateVariogramModels(AFMImageVariogramAnalysis, AFMImage)

## S4 method for signature 'AFMImageVariogramAnalysis'
evaluateVariogramModels(AFMImageVariogramAnalysis, AFMImage)
```

Arguments

```
AFMImageVariogramAnalysis  an object
AFMImage                    an AFMImage
```

Examples

```
## Not run:
library(AFM)

data("AFMImageOfRegularPeaks")
# take an extract of the image to fasten the calculation
AFMImage<-extractAFMImage(AFMImageOfRegularPeaks, 40, 40, 32)
# e.g. AFMImage@fullfilename<-"/users/ubuntu/AFMImageOfRegularPeaks-extract.txt"
AFMImage@fullfilename<-paste(tempdir(), "AFMImageOfRegularPeaks-extract.txt", sep="/")

AFMImageAnalyser<-AFMImageAnalyser(AFMImage)

# Variogram analysis
sampleFitPercentage<-3.43/100
variogramAnalysis<-AFMImageVariogramAnalysis(sampleFitPercentage)
variogramAnalysis@omnidirectionalVariogram<-
  AFM:::calculateOmnidirectionalVariogram(AFMImage=AFMImage,
                                          AFMImageVariogramAnalysis=variogramAnalysis)
variogramAnalysis@directionalVariograms<-
  AFM:::calculateDirectionalVariograms(AFMImage=AFMImage,
                                        AFMImageVariogramAnalysis=variogramAnalysis)

# manage model evaluations
AFMImageVariogram<-variogramAnalysis@omnidirectionalVariogram
```

```

class(AFMImageVariogram)=c("gstatVariogram","data.frame")
variogramAnalysis<-evaluateVariogramModels(variogramAnalysis, AFMImage)

mergedDT<-getDTModelEvaluation(variogramAnalysis)
mergedDT
sillRangeDT<-getDTModelSillRange(variogramAnalysis)
sillRangeDT

## End(Not run)

```

existsEdge	<i>Does an edge exist ?</i>
------------	-----------------------------

Description

existsEdge return TRUE if an edge exists for this vertex id

Usage

```
existsEdge(AFMImage, vertexId)
```

Arguments

AFMImage	an AFMImage from Atomic Force Microscopy
vertexId	the vertex id

Author(s)

M.Beauvais

existsSegment	<i>existsSegment checks if a segment exists in an AFMImage; check if all the heights at the segment coordinates are different to zero.</i>
---------------	--

Description

existsSegment return a boolean

Usage

```
existsSegment(AFMImage, segment)
```

Arguments

AFMImage	a AFMImage from Atomic Force Microscopy or a binary AFMImage
segment	a data.table coming from the <code>getBresenham2Dsegment</code> - x and y should start from 1,1 #TODO Segment class

Value

TRUE if all the heights of the segment are different from zero

Author(s)

M.Beauvais

exportToSTL

Export an AFM Image as a STL format file.

Description

Export an [AFMImage](#) as a STL format file thanks to the [rgl](#) package. The STL file can be used as an input for a 3D printing software tool.

exportToSTL is compatible with slicr (<http://slic3r.org>) version 1.2.9 (GPL v3 licence). In order to 3D print the AFM Image with slic3r, do as following:

- Use "File> Repair STL file..." menu option to create a file with the obj extension.
- Use "Add" button below the menu to display your AFM Image on the print board
- Right click on your AFM image. Use "Scale> uniformly" option, Set "15"

Usage

```
exportToSTL(AFMImage3DModelAnalysis, AFMImage, stlfullfilename)
```

Arguments

AFMImage3DModelAnalysis

an [AFMImage3DModelAnalysis](#)

AFMImage

an [AFMImage](#) from Atomic Force Microscopy

stlfullfilename

directory and filename to save as a stl file

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
data("AFMImageOfRegularPeaks")
AFMImage<-AFMImageOfRegularPeaks
# calculate the 3D model : surface and the faces
AFMImage3DModelAnalysis<-new ("AFMImage3DModelAnalysis")
AFMImage3DModelAnalysis<-calculate3DModel(AFMImage3DModelAnalysis= AFMImage3DModelAnalysis,
```

```
AFMImage= AFMImage)
# export the 3D model to file
exportDirectory=tempdir()
print(paste("saving model in ", exportDirectory))
exportToSTL(AFMImage3DModelAnalysis=AFMImage3DModelAnalysis,
            AFMImage=AFMImage,
            stlfilename=paste(exportDirectory, "myFile.stl", sep="/"))

## End(Not run)
```

extractAFMImage *Extract a portion of an AFM image.*

Description

The extract will be a square of the specified size. If the size is too large for the original [AFMImage](#), only the biggest valid size will be kept.

Usage

```
extractAFMImage(AFMImage, cornerX, cornerY, size)
```

Arguments

AFMImage	an AFMImage from Atomic Force Microscopy
cornerX	horizontal coordinates of the extract
cornerY	vertical coordinates of the extract
size	square size of the extract in number of pixels

Details

extractAFMImage returns an extract of the AFMImage

Value

a new [AFMImage](#) sample

Author(s)

M.Beauvais

Examples

```
## Not run:
data(AFMImageOfAluminiumInterface)
anAFMImageExtract<-extractAFMImage(AFMImageOfAluminiumInterface,15,15,256)

## End(Not run)
```

filterAFMImage	<i>filter the heights of an AFMImage with a minimum and a maximum value</i>
----------------	---

Description

filterAFMImage returns a filtered AFMImage

Usage

```
filterAFMImage(AFMImage, Min, Max)
```

Arguments

AFMImage	an AFMImage from Atomic Force Microscopy
Min	the minimum height value to keep
Max	the maximum height value to keep

Value

an [AFMImage](#)

Author(s)

M.Beauvais

fusionCloseNodes	<i>fusion the nodes that are intersecting</i>
------------------	---

Description

manage the fusion of nodes which circles intersect keep all the circles, manage a fusion table node id / fusion id

Usage

```
fusionCloseNodes(AFMImageNetworksAnalysis)
```

Arguments

AFMImageNetworksAnalysis	the AFMImageNetworksAnalysis instance
--------------------------	---------------------------------------

Value

a list of edges with fused nodes

Author(s)

M.Beauvais

`generateAFMImageReport`*Generate an analysis report from an AFMImageAnalyser object*

Description`generateAFMImageReport` generates a report from an `AFMImageAnalyser` object**Usage**`generateAFMImageReport(AFMImageAnalyser, reportFullfilename, isCheckReport)`**Arguments**`AFMImageAnalyser`an [AFMImageAnalyser](#) to be used to produce report`reportFullfilename`

location on disk where to save the generated report

`isCheckReport`

TRUE to generate a check report must be generated, FALSE to generate a full report

Author(s)

M.Beauvais

`generateCheckReport`*Generate a check report for one AFMImage*

DescriptionGenerate a check report in pdf format in order to analyse the distribution and the isotropy of heights of the [AFMImage](#).**Usage**`generateCheckReport(AFMImage)`**Arguments**`AFMImage`an [AFMImage](#) imported from Nanoscope Analysis(TM) with `importFromNanoscope` or created manually [AFMImage](#)

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)

# Analyse the AFMImageOfRegularPeaks AFMImage sample from this package
data("AFMImageOfRegularPeaks")
AFMImage<-AFMImageOfRegularPeaks
# exportDirectory="C:/Users/my_windows_login" or exportDirectory="/home/ubuntu"
exportDirectory=tempdir()
AFMImage@fullfilename<-paste(exportDirectory,"AFMImageOfRegularPeaks.txt",sep="/")

# Start to check if your sample is normally distributed and isotropic.
generateCheckReport(AFMImage)
# If the sample is normally distributed and isotropic, generate a full report
generateReport(AFMImage)

# Analyse your own AFM image from nanoscope analysis (TM) software tool
anotherAFMImage<-importFromNanoscope("c:/users/me/myimage.txt")
# Start to check if your sample is normally distributed and isotropic.
generateCheckReport(anotherAFMImage)
# If your sample is normally distributed and isotropic, generate a full report
generateReport(anotherAFMImage)

## End(Not run)
```

```
generatePolygonEnvelope
      generatePolygonEnvelope
```

Description

generate a convex polygon from circles

Usage

generatePolygonEnvelope(AFMImageNetworksAnalysis, centers, radius)

Arguments

AFMImageNetworksAnalysis	a AFMImageNetworksAnalysis
centers	a matrix ?
radius	a vector of radius

Value

a polygon

Author(s)

M.Beauvais

generateReport

Generate an analysis report for one AFMImage

Description

A function to analyse an [AFMImage](#) and save on disk the analysis. The analysis are saved in outputs directory located in the image directory. All the rdata and image files in the reportDirectory directory are loaded to generate one report for one [AFMImage](#).

Usage

```
generateReport(AFMImage)
```

Arguments

AFMImage an [AFMImage](#) to be analysed

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)

# Analyse the AFMImageOfRegularPeaks AFMImage sample from this package
data("AFMImageOfRegularPeaks")
AFMImage<-AFMImageOfRegularPeaks

# exportDirectory="C:/Users/my_windows_login" or exportDirectory="/home/ubuntu"
exportDirectory=tempdir()
AFMImage@fullfilename<-paste(exportDirectory,"AFMImageOfRegularPeaks.txt",sep="/")

# Start to check if your sample is normally distributed and isotropic.
generateCheckReport(AFMImage)
# If the sample is normally distributed and isotropic, generate a full report
generateReport(AFMImage)

# Analyse your own AFM image from nanoscope analysis (TM) software tool
anotherAFMImage<-importFromNanoscope("c:/users/my_windows_login/myimage.txt")
```

```
# Start to check if your sample is normally distributed and isotropic.
  generateCheckReport(anotherAFMImage)
# If your sample is normally distributed and isotropic, generate a full report
  generateReport(anotherAFMImage)

## End(Not run)
```

```
generateReportFromNanoscopeImageDirectory
  Generate a pdf report for all AFM images in a directory
```

Description

A function to generate a pdf report for each [AFMImage](#) in a directory. Images should be in export Nanoscope format as the [importFromNanoscope](#) function will be used.

Usage

```
generateReportFromNanoscopeImageDirectory(imageDirectory, imageNumber)
```

Arguments

`imageDirectory` a directory where are located image as Nanoscope export format

`imageNumber` (optional) an image number in the directory. If it is set only the selected image will be processed.

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
# A report will be generated for all the images in imageDirectory directory
# imageDirectory="c:/images"
imageDirectory=tempdir()
exit<-generateReportFromNanoscopeImageDirectory(imageDirectory)

# A report will be generated for the fifth image in the imageDirectory directory
exit<-generateReportFromNanoscopeImageDirectory(imageDirectory,5)

## End(Not run)
```

get3DImageFullfilename
get 3D image full filename

Description

get 3D image full filename

Usage

```
get3DImageFullfilename(exportDirectory, imageName)
```

Arguments

exportDirectory a directory to export image
imageName the image name

Author(s)

M.Beauvais

getAllPointsToRemove *getAllPointsToRemove*

Description

get the points inside envelope

Usage

```
getAllPointsToRemove(AFMImageNetworksAnalysis, envelope)
```

Arguments

AFMImageNetworksAnalysis
 a [AFMImageNetworksAnalysis](#)
envelope an envelope of points ?

Value

a data.table of points

Author(s)

M.Beauvais

getAngle *calculate the angle between two vectors*

Description

calculate the angle between two vectors

Usage

```
getAngle(x, y)
```

Arguments

x	a vector
y	a vector

Value

the angle between the vectors

Author(s)

M.Beauvais

getAutoIntersectionForOmnidirectionalVariogram
Calculate slopes and intersections in variogram
getAutoIntersectionForOmnidirectionalVariogram *returns*
the slope in the omnidirectional variograms

Description

Calculate slopes and intersections in variogram getAutoIntersectionForOmnidirectionalVariogram returns the slope in the omnidirectional variograms

Usage

```
getAutoIntersectionForOmnidirectionalVariogram(AFMImageAnalyser)
```

Arguments

AFMImageAnalyser
 an [AFMImageAnalyser](#)

Value

an [omniVariogramSlopeAnalysis](#)

Author(s)

M.Beauvais

`getAutoIntersectionForRoughnessAgainstLengthscale`
get the intersection between tangente and plateau

Description

`getAutoIntersectionForRoughnessAgainstLengthscale` get the intersection between tangente and plateau

Usage

```
getAutoIntersectionForRoughnessAgainstLengthscale(  
    AFMImageAnalyser,  
    second_slope = FALSE  
)
```

Arguments

`AFMImageAnalyser` an [AFMImageAnalyser](#) to get Roughness against lengthscale calculation

`second_slope` a boolean to manage first or second slope in the roughness against lengthscale curve

Value

a [AFMImagePSDSlopesAnalysis](#)

Author(s)

M.Beauvais

`getAutomaticWidthForVariogramCalculation`
calculate a width to be used for experimental variogram calculation

Description

calculate a width to be used for experimental variogram calculation in order to generate a line instead of a cloud of points. If the chosen width is too small, the experimental variogram will be a cloud of points instead of a line.

Usage

```
getAutomaticWidthForVariogramCalculation(AFMImage)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Details

getAutomaticWidthForVariogramCalculation returns the width to be used for variogram calculation

Value

the smallest width to be used for variogram calculation

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)

data(AFMImageOfAluminiumInterface)
print(getAutomaticWidthForVariogramCalculation(AFMImageOfAluminiumInterface))

## End(Not run)
```

getBresenham2DSegment *get a segment of points thanks to Bresenham line algorithm*

Description

getBresenham2DSegment return the Bresenham segment in 2D from extremities coordinates

Usage

```
getBresenham2DSegment(x1, y1, x2, y2)
```

Arguments

x1	abscissa coordinates of the first point
y1	ordinate coordinates of the first point
x2	abscissa coordinates of the second point
y2	ordinate coordinates of the second point

Value

a `data.table` of points - `data.table(x, y)`

Author(s)

M.Beauvais

`getCircleSpatialPoints`

get the spatial points on the circle including the center of the circle

Description

get the spatial points on the circle including the center of the circle

Usage

```
getCircleSpatialPoints(binaryAFMImage, center, circleRadius)
```

Arguments

`binaryAFMImage` a binary [AFMImage](#) from Atomic Force Microscopy

`center` the center of the circle with `center$lon` as the x coordinates and `center$lat` as the y coordinates

`circleRadius` the radius of the circle

Value

a [SpatialPoints](#) object of all the points of the circle including the center of the circle

Author(s)

M.Beauvais

`getCoordinatesFromVertexId`
Get x,y coordinates from vertex id

Description

`getCoordinatesFromVertexId` return a list x,y coordinates

Usage

`getCoordinatesFromVertexId(vId)`

Arguments

`vId` the vertex id

Author(s)

M.Beauvais

`getDTModelEvaluation` *getDTModelEvaluation method*

Description

`getDTModelEvaluation` method

Usage

```
getDTModelEvaluation(AFMImageVariogramAnalysis)

## S4 method for signature 'AFMImageVariogramAnalysis'
getDTModelEvaluation(AFMImageVariogramAnalysis)
```

Arguments

`AFMImageVariogramAnalysis`
an `AFMImageVariogramAnalysis` object

getDTModelSillRange *getDTModelSillRange method*

Description

getDTModelSillRange method

Usage

```
getDTModelSillRange(AFMImageVariogramAnalysis)
```

```
## S4 method for signature 'AFMImageVariogramAnalysis'
getDTModelSillRange(AFMImageVariogramAnalysis)
```

Arguments

AFMImageVariogramAnalysis
 an AFMImageVariogramAnalysis object

getFractalDimensions *Calculate 2D fractal dimensions and scales of an AFM Image*

Description

getFractalDimensions calculates fractal dimensions and scales of an [AFMImage](#) with the `fd.estim.method` from the [fractalDIM](#) package.

Usage

```
getFractalDimensions(AFMImage, AFMImageFractalDimensionsAnalysis)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy
 AFMImageFractalDimensionsAnalysis
 an [AFMImageFractalDimensionsAnalysis](#) to store the results of the fractal analysis

Value

a list of [AFMImageFractalDimensionMethod](#) objects with the calculated fractal dimensions and scales

Author(s)

M.Beauvais

References

Gneiting2012, Tilmann Gneiting, Hana Sevcikova and Donald B. Percival 'Estimators of Fractal Dimension: Assessing the Roughness of Time Series and Spatial Data - Statistics in statistical Science, 2012, Vol. 27, No. 2, 247-277'

See Also

[fractaldim](#)

Examples

```
## Not run:  
library(AFM)  
data(AFMImageOfAluminiumInterface)  
print(getFractalDimensions(AFMImageOfAluminiumInterface))  
  
## End(Not run)
```

getHolesStatistics *calculate statistics about holes in a binary image*

Description

getHolesStatistics returns a binary AFMImage

Usage

```
getHolesStatistics(AFMImage)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Value

an [AFMImage](#)

Author(s)

M.Beauvais

Examples

```

## Not run:
library(AFM)

data(AFMImageOfAluminiumInterface)
newAFMImage<-copy(AFMImageOfAluminiumInterface)
displayIn3D(newAFMImage,noLight=TRUE)
newAFMImage<-multiplyHeightsAFMImage(newAFMImage, multiplier=2)
displayIn3D(newAFMImage,noLight=TRUE)
newAFMImage<-filterAFMImage(newAFMImage, Min=140, Max=300)
displayIn3D(newAFMImage,noLight=TRUE)
newAFMImage<-makeBinaryAFMImage(newAFMImage)
displayIn3D(newAFMImage,noLight=TRUE)

holesStats<-getHolesStatistics(newAFMImage)
print(holesStats)

## End(Not run)

```

```

getIntersectionForRoughnessAgainstLengthscale
      get the intersection between tangente and plateau

```

Description

[getIntersectionForRoughnessAgainstLengthscale](#) get the intersection between tangente and plateau

Usage

```

getIntersectionForRoughnessAgainstLengthscale(
  AFMImageAnalyser,
  minValue,
  maxValue,
  second_slope = FALSE
)

```

Arguments

AFMImageAnalyser	an AFMImageAnalyser to get Roughness against lengthscale calculation
minValue	index of the lowest point to be used for the tangent
maxValue	index of the highest point to be used for the tangent
second_slope	a boolean to manage first or second slope in the roughness against lengthscale curve

Value

a [AFMImagePSDSlopesAnalysis](#)

Author(s)

M.Beauvais

`getIntersectionPointWithBorder`
getIntersectionPointWithBorder to be described

Description

`getIntersectionPointWithBorder` return a `data.table`

Usage

`getIntersectionPointWithBorder(AFMImage, center, r, deg)`

Arguments

<code>AFMImage</code>	a AFMImage from Atomic Force Microscopy
<code>center</code>	center
<code>r</code>	radius
<code>deg</code>	degree

Author(s)

M.Beauvais

`getListOfDiameters` *getListOfDiameters*

Description

`getListOfDiameters` return

Usage

`getListOfDiameters(g)`

Arguments

<code>g</code>	list of igraph networks
----------------	-------------------------

Author(s)

M.Beauvais

```
getLogLogOmnidirectionalSlopeGraph
```

*Get the graph of the Log Log omnidirection variogram
getLogLogOmnidirectionalSlopeGraph returns Get the graph
of the Log Log omnidirectional variogram*

Description

Get the graph of the Log Log omnidirection variogram getLogLogOmnidirectionalSlopeGraph returns Get the graph of the Log Log omnidirectional variogram

Usage

```
getLogLogOmnidirectionalSlopeGraph(AFMImageAnalyser, withFratcalSlope = FALSE)
```

Arguments

AFMImageAnalyser

an [AFMImageAnalyser](#)

withFratcalSlope

a boolean to indicate if the graph should contain a line representating the slope for the calculation of the fractal index and topothesy

Value

a ggplot2 graph

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
library(ggplot2)

data(AFMImageOfRegularPeaks)

AFMImageAnalyser = new("AFMImageAnalyser",
  fullfilename="/home/ubuntu/AFMImageOfRegularPeaks-Analyser.txt")
variogramAnalysis<-AFMImageVariogramAnalysis(sampleFitPercentage=3.43/100)
AFMImageAnalyser@variogramAnalysis<-variogramAnalysis
AFMImageAnalyser@variogramAnalysis@omnidirectionalVariogram<-
  calculateOmnidirectionalVariogram(AFMImage= AFMImageOfRegularPeaks,
    AFMImageVariogramAnalysis= variogramAnalysis)
p<-getLogLogOmnidirectionalSlopeGraph(AFMImageAnalyser, withFratcalSlope=TRUE)
p

## End(Not run)
```

```
getMaxCircleMatrix    getMaxCircleMatrix
```

Description

for each pixel of the image, if the pixel is not empty try to place one circle start with biggest circle as soon as a circle is found the circle, the pixel is associated with with the circle radius

Usage

```
getMaxCircleMatrix(..., newCircleAFMImage, CIRCLE_RADIUS_INIT)
```

Arguments

```
...          cl: a cluster object from the parallel package
newCircleAFMImage
              a AFMImage
CIRCLE_RADIUS_INIT
              CIRCLE_RADIUS_INIT
```

Value

res a matrix

Author(s)

M.Beauvais

```
getNetworkGridLayout #' @export getCoordinatesFromVertexId2<-function(AFMImage,
vId) vertexId<-as.numeric(vId) y<-floor(vertexId/HASHSIZE)
x<-vertexId-y*HASHSIZE return(data.table(vId=vId, co-
ords.x1=x,coords.x2=y)) Get getNetworkGridLayout
```

Description

getNetworkGridLayout return a list x,y coordinates

Usage

```
getNetworkGridLayout(AFMImage, vId)
```

Arguments

```
AFMImage      an AFMImage from Atomic Force Microscopy
vId           the vertex id
```

Author(s)

M.Beauvais

 getNetworkParameters *Get Network parameters*

Description

Get basic network parameters : Total root mean square Roughness or Total Rrms or totalRM-SRoughness_TotalRrms
 Mean roughness or Ra or MeanRoughness_Ra

Usage

```
getNetworkParameters(AFMImageNetworksAnalysis, AFMImage)
```

```
## S4 method for signature 'AFMImageNetworksAnalysis'  
getNetworkParameters(AFMImageNetworksAnalysis, AFMImage)
```

Arguments

```
AFMImageNetworksAnalysis  
    an AFMImageNetworksAnalysis  
AFMImage  
    an AFMImage
```

Details

getNetworkParameters returns a data.table of network parameters

Value

a data.table of network parameters:

- totalNumberOfNodes the total number of nodes with degree different of 2
- totalNumberOfNodesWithDegreeTwoOrMore the total number of nodes with degree 2 or more
- totalNumberOfNodesWithDegreeOne the total number of nodes with degree one
- numberOfNodesPerArea the total number of nodes with degree different of 2 per area
- numberOfNodesPerSurfaceArea the total number of nodes with degree different of 2 per surface area
- MeanPhysicalDistanceBetweenNodes the mean physical distance between nodes of degree different of two

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
library(parallel)

data(AFMImageCollagenNetwork)
AFMImage<-AFMImageCollagenNetwork
AFMIA = new("AFMImageNetworksAnalysis")
AFMIA@heightNetworkslider=10
AFMIA@filterNetworksliderMin=150
AFMIA@filterNetworksliderMax=300
AFMIA@smallBranchesTreatment=TRUE
c1Exist<-TRUE
c1 <- makeCluster(2,outfile="")
AFMIA<-transformAFMImageForNetworkAnalysis(AFMImageNetworksAnalysis=AFMIA,AFMImage= AFMImage)
AFMIA<-identifyNodesAndEdges(c1=c1,AFMImageNetworksAnalysis= AFMIA,maxHeight= 300)
AFMIA<-identifyEdgesFromCircles(c1=c1,AFMImageNetworksAnalysis= AFMIA, MAX_DISTANCE = 75)
AFMIA<-identifyIsolatedNodes(AFMIA)
AFMIA<-createGraph(AFMIA)
AFMIA<-calculateShortestPaths(c1=c1, AFMImageNetworksAnalysis=AFMIA)
AFMIA<-calculateNetworkParameters(AFMImageNetworksAnalysis=AFMIA, AFMImage=AFMImage)
AFMIA<-calculateHolesCharacteristics(AFMImageNetworksAnalysis=AFMIA)
stopCluster(c1)

## End(Not run)
```

getNyquistSpatialFrequency

Get the Nyquist spatial frequency

Description

Get the Nyquist spatial frequency of an [AFMImage](#) calculated as following:
0.5 multiplied by the minimum between the horizontal scansize divided by the number of samples per line and the vertical scansize divided by the number of lines

Usage

```
getNyquistSpatialFrequency(AFMImage)
```

```
## S4 method for signature 'AFMImage'
getNyquistSpatialFrequency(AFMImage)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Details

getNyquistSpatialFrequency returns the Nyquist spatial frequency as a numeric

Value

the Nyquist spatial frequency of the [AFMImage](#)

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)

data(AFMImageOfNormallyDistributedHeights)
NyquistSpatialFrequency<-getNyquistSpatialFrequency(AFMImageOfNormallyDistributedHeights)
print(NyquistSpatialFrequency)

## End(Not run)
```

getPaddedAFMImage *Get a zero padded AFMImage*

Description

Get a zero padded [AFMImage](#) useful in Power Spectral Density analysis. The original [AFMImage](#) is padded with zero in order to get a larger square [AFMImage](#) which size is a power of 2.

Usage

```
getPaddedAFMImage(AFMImage)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Value

a zero-padded [AFMImage](#) with a filename equals to the original filename pasted with padded-to-"ScanSize".txt

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)

data(AFMImageOfNormallyDistributedHeights)
paddedAFMImage<-getPaddedAFMImage(AFMImageOfNormallyDistributedHeights)
displayIn3D(AFMImage= paddedAFMImage, width= 1024,noLight=TRUE)

## End(Not run)
```

getRoughnessParameters

Get Roughness parameters

Description

Get basic roughness parameters as amplitude parameters: Total root mean square Roughness or Total Rrms or totalRMSRoughness_TotalRrms
Mean roughness or Ra or MeanRoughness_Ra

Usage

```
getRoughnessParameters(AFMImage)

## S4 method for signature 'AFMImage'
getRoughnessParameters(AFMImage)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Details

getRoughnessParameters returns a data.table of roughness parameters

Value

a data.table of roughness parameters:

- totalRMSRoughness_TotalRrms the total RMS Roughness as the square root of the variance of heights
- MeanRoughness_Ra the average roughness as the mean of absolute value of heights

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)

data(AFMImageOfAluminiumInterface)
roughnessParameters<-getRoughnessParameters(AFMImageOfAluminiumInterface)
print(roughnessParameters)

## End(Not run)
```

getSpplotFromAFMImage *Get an AFMImage as a Lattice (trellis) plot*

Description

get a Lattice (trellis) plot of an [AFMImage](#) using the [spplot](#) method of the [sp](#) package. This function is used to evaluate visually the quality of the predicted surface when a variogram model is used.

Usage

```
getSpplotFromAFMImage(AFMImage, expectedWidth, expectHeight, withoutLegend)
```

Arguments

AFMImage	an AFMImage from Atomic Force Microscopy
expectedWidth	(optional) expected width of the saved image. Default is 400px.
expectHeight	(optional) expected height of the saved image. Default is 300px.
withoutLegend	(optional) set at FALSE, the cuts legend will be included in the plot. Default is FALSE.

Details

getSpplotFromAFMImage get a Lattice (trellis) plot of an [AFMImage](#) on disk

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)

data(AFMImageOfAluminiumInterface)
p<-getSpplotFromAFMImage(AFMImageOfAluminiumInterface, 800,800, TRUE)
print(p)

## End(Not run)
```

`getSurroundingVertexesList`
Get surrounding vertices from x,y coordinates

Description

`getSurroundingVertexesList` return the vertexId

Usage

`getSurroundingVertexesList(AFMImage, x, y)`

Arguments

AFMImage	an AFMImage from Atomic Force Microscopy
x	coordinates in x axis
y	coordinates in y axis

Author(s)

M.Beauvais

`getTopologyAFMImage` *Calculate topology image (TBC)*

Description

`getTopologyAFMImage` return the global topological distance

Usage

`getTopologyAFMImage(BinaryAFMImage, AFMImageNetworksAnalysis)`

Arguments

BinaryAFMImage	an AFMImage from Atomic Force Microscopy in a binary format 0 or 1 values for heights
AFMImageNetworksAnalysis	an AFMImageNetworksAnalysis from Atomic Force Microscopy

Author(s)

M.Beauvais

getTriangle	<i>get a triangle starting from center, two segments of length r with angles deg1 and deg2</i>
-------------	--

Description

getTriangle return a data.table points of a triangle

Usage

```
getTriangle(AFMImage, center, r, deg1, deg2)
```

Arguments

AFMImage	a AFMImage from Atomic Force Microscopy
center	center
r	length of segment
deg1	angle 1
deg2	angel 2

Author(s)

M.Beauvais

getVertexId	<i>Get vertex id from x,y coordinates</i>
-------------	---

Description

getVertexId return the vertexId

Usage

```
getVertexId(AFMImage, x, y)
```

Arguments

AFMImage	an AFMImage from Atomic Force Microscopy
x	coordinates in x axis
y	coordinates in y axis

Author(s)

M.Beauvais

gridIgraphPlot	<i>gridIgraphPlot</i>
----------------	-----------------------

Description

gridIgraphPlot return TRUE if vertex is adjacent to a better vertex

Usage

```
gridIgraphPlot(AFMImage, g)
```

Arguments

AFMImage	an AFMImage from Atomic Force Microscopy
g	the networks

Author(s)

M.Beauvais

identifyEdgesFromCircles	<i>display the network of nodes and edges</i>
--------------------------	---

Description

display the network of nodes and edges

Usage

```
identifyEdgesFromCircles(..., AFMImageNetworksAnalysis, MAX_DISTANCE = 40)
```

Arguments

...	cl: a cluster object from the parallel package
AFMImageNetworksAnalysis	a AFMImageNetworksAnalysis
MAX_DISTANCE	the maximum distance between nodes to check if nodes are connected. Default value is 40.

Author(s)

M.Beauvais

identifyIsolatedNodes *identify isolated nodes comparing the list of edges and the list of nodes*

Description

identify isolated nodes comparing the list of edges and the list of nodes

Usage

```
identifyIsolatedNodes(AFMImageNetworksAnalysis)
```

Arguments

AFMImageNetworksAnalysis
the AFMImageNetworksAnalysis instance

Value

the updated instance of AFMImageNetworksAnalysis

Author(s)

M.Beauvais

identifyMaxCircleRadius
identifyMaxCircleRadius

Description

identifyMaxCircleRadius

Usage

```
identifyMaxCircleRadius(  
  i,  
  allXY,  
  newCircleAFMImage,  
  binaryAFMImageMatrix,  
  maxCircleRadiusMatrix,  
  circleRadius,  
  circlenm  
)
```

Arguments

i an integer
 allXY combinations of ?
 newCircleAFMImage
 a [AFMImage](#)
 binaryAFMImageMatrix
 a [AFMImage](#)
 maxCircleRadiusMatrix
 a matrix
 circleRadius a vector of radius ?
 circlem a ?

Value

a data table with x,y,radius columns

Author(s)

M.Beauvais

identifyNodesAndEdges *identifyNodesAndEdges*

Description

find nodes and edges

Usage

identifyNodesAndEdges(..., AFMImageNetworksAnalysis, maxHeight)

Arguments

... cl: a cluster object from the parallel package
 AFMImageNetworksAnalysis
 a [AFMImageNetworksAnalysis](#)
 maxHeight a double for filtering the heights - upper to this height the heights are set to zero

Value

AFMImageNetworksAnalysis a [AFMImageNetworksAnalysis](#)

Author(s)

M.Beauvais

```
identifyNodesWithCircles
```

identify largest circles in binary image

Description

identifyNodesWithCircles return TRUE if vertex is adjacent to a better vertex

Usage

```
identifyNodesWithCircles(..., AFMImageNetworksAnalysis)
```

Arguments

... cl: a cluster object from the parallel package
 AFMImageNetworksAnalysis
 a [AFMImageNetworksAnalysis](#)

Value

AFMImageNetworksAnalysis the [AFMImageNetworksAnalysis](#) instance

Author(s)

M.Beauvais

```
importFromNanoscope Import data from nanoscope analysis(tm) tool
```

Description

The imported file should contain a header and list of heights The header should contain the following fields:

- Lines: number of scanned lines (e.g. 512)
- Sampslines: number of scan per line (e.g. 512)
- ScanSize: the sample size (e.g. 1000nm) the extension nm is mandatory and will be removed

Usage

```
importFromNanoscope(fullfilename)
```

Arguments

fullfilename a concatenated string of the directory and filename exported with Nanoscope analysis(TM) software

Details

importFromNanoscope returns an [AFMImage](#)

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)

fullfilename<-" /user/ubuntu/NanoscopeFlattenExportedFile.txt"
myAFMimage<-importFromNanoscope(fullfilename)
displayIn3D(myAFMimage, width=1024, noLight=TRUE))

## End(Not run)
```

initialize,AFMImageAnalyser-method

Constructor method of AFMImageAnalyser Class.

Description

Constructor method of AFMImageAnalyser Class.

Usage

```
## S4 method for signature 'AFMImageAnalyser'
initialize(
  .Object,
  AFMImage,
  variogramAnalysis,
  psdAnalysis,
  fdAnalysis,
  gaussianMixAnalysis,
  networksAnalysis,
  threeDimensionAnalysis,
  mean,
  variance,
  TotalRrms,
  Ra,
  fullfilename
)
```

Arguments

.Object	an AFMImageAnalyser object
AFMImage	an AFMImage
variogramAnalysis	AFMImageVariogramAnalysis
psdAnalysis	AFMImagePSDAnalysis
fdAnalysis	AFMImageFractalDimensionsAnalysis
gaussianMixAnalysis	AFMImageGaussianMixAnalysis
networksAnalysis	AFMImageNetworksAnalysis
threeDimensionAnalysis	AFMImage3DModelAnalysis
mean	the mean of heights of the AFMImage
variance	the variance of heights of the AFMImage
TotalRrms	the total Root Mean Square Roughness of the AFMImage calculated from variance
Ra	mean roughness or mean of absolute values of heights
fullfilename	to be removed?

invertBinaryAFMImage *invert a binary AFMImage*

Description

invertBinaryAFMImage returns a binary AFMImage

Usage

```
invertBinaryAFMImage(AFMImage)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Value

an [AFMImage](#)

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
data(AFMImageOfAluminiumInterface)
newAFMImage<-copy(AFMImageOfAluminiumInterface)
displayIn3D(newAFMImage,noLight=TRUE)
newAFMImage<-multiplyHeightsAFMImage(newAFMImage, multiplier=2)
displayIn3D(newAFMImage,noLight=TRUE)
newAFMImage<-filterAFMImage(newAFMImage, Min=140, Max=300)
displayIn3D(newAFMImage,noLight=TRUE)
newAFMImage<-makeBinaryAFMImage(newAFMImage)
displayIn3D(newAFMImage,noLight=TRUE)
newAFMImage<-invertBinaryAFMImage(newAFMImage)
displayIn3D(newAFMImage,noLight=TRUE)

## End(Not run)
```

isAdjacentToBetterVertex

isAdjacentToBetterVertex

Description

isAdjacentToBetterVertex return TRUE if vertex is adjacent to a better vertex

Usage

```
isAdjacentToBetterVertex(AFMImage, x, y)
```

Arguments

AFMImage	an AFMImage from Atomic Force Microscopy
x	coordinates in x axis
y	coordinates in y axis

Author(s)

M.Beauvais

isAngleBetweenEdgesAlwaysSuperiorToMinAngle

check if all the angles between one edge and a list of edges is superior to a specified value.

Description

check if all the angles between one edge and a list of edges is superior to a specified value.

Usage

```
isAngleBetweenEdgesAlwaysSuperiorToMinAngle(
  binaryAFMImage,
  edge1,
  edges2,
  minAngle
)
```

Arguments

binaryAFMImage	a binary AFMImage from Atomic Force Microscopy
edge1	one edge
edges2	list of edges
minAngle	the minimum angle value

Value

TRUE if all the angle are superior to the specified value

Author(s)

M.Beauvais

isBinary

has the AFM Image heights of 0 or 1

Description

isBinary returns TRUE is the heights of the AFMImage is 0 or 1

Usage

```
isBinary(AFMImage)
```


Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Value

a boolean

Author(s)

M.Beauvais

loglike.normalmix *loglike sum of density of a mixture of normals*

Description

loglike sum of density of a mixture of normals

Usage

```
loglike.normalmix(x, mixture)
```

Arguments

x a vector of quantiles
mixture a gaussian mixture

makeBinaryAFMImage *make a binary AFMImage setting all the heights different to 0 to 1.*

Description

makeBinaryAFMImage returns a binary AFMImage

Usage

```
makeBinaryAFMImage(AFImage)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Value

an [AFMImage](#)

Author(s)

M.Beauvais

multiplyHeightsAFMImage

multiply the heights of an AFMImage

Description

multiplyHeightsAFMImage returns a simplified AFMImage

Usage

```
multiplyHeightsAFMImage(AFMImage, multiplier)
```

Arguments

AFMImage	an AFMImage from Atomic Force Microscopy
multiplier	the number to multiply the heights with

Value

an [AFMImage](#)

Author(s)

M.Beauvais

Examples

```
## Not run:  
data(AFMImageOfAluminiumInterface)  
newAFMImage<-multiplyHeightsAFMImage(AFMImageOfAluminiumInterface,10)  
displayIn3D(newAFMImage,noLight=TRUE)  
  
## End(Not run)
```

omniVariogramSlopeAnalysis-class

AFM Image log-log experimental variogram slope analysis

Description

omniVariogramSlopeAnalysis stores the analysis of the second slope in roughness against lengthscale

Usage

```
omniVariogramSlopeAnalysis()  
  
## S4 method for signature 'omniVariogramSlopeAnalysis'  
initialize(.Object)  
  
omniVariogramSlopeAnalysis()
```

Arguments

.Object an omniVariogramSlopeAnalysis object

Slots

intersection_sill to be removed ?
sill to be removed ?
slope to be removed ?
yintersept to be removed ?

Author(s)

M.Beauvais

performAllPSDCalculation
Perform all the calculation for PSD exploitation

Description

[performAllPSDCalculation](#) perform all the calculation for PSD exploitation

Usage

```
performAllPSDCalculation(AFMImagePSDAnalysis, AFMImage)
```

Arguments

AFMImagePSDAnalysis
 an [AFMImagePSDAnalysis](#) to manage and store the results of PSD analysis
AFMImage an [AFMImage](#) from Atomic Force Microscopy

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)

data(AFMImageOfNormallyDistributedHeights)

newAFMImage<-AFMImageOfNormallyDistributedHeights
newAFMImage@fullfilename<-"C:/Users/one/AFMImageOfNormallyDistributedHeights.txt"
psdAnalysis<-AFMImagePSDAnalysis()
# Create a closure to update progress
psdAnalysis@updateProgress<- function(value = NULL, detail = NULL, message = NULL) {
  if (exists("progressPSD")){
    if (!is.null(message)) {
      progressPSD$set(message = message, value = 0)
    }else{
      progressPSD$set(value = value, detail = detail)
    }
  }
}
psdAnalysis@psd1d_breaks<-2^3
psdAnalysis@psd2d_truncHighLengthScale<-TRUE
psdAnalysis<-performAllPSDCalculation(AFMImagePSDAnalysis= psdAnalysis, AFMImage= newAFMImage)
print("done psdAnalysis")

## End(Not run)
```

```
performGaussianMixCalculation
```

Perform the calculation for the Gaussian mixes

Description

[performGaussianMixCalculation](#) perform all the calculation for PSD exploitation

Usage

```
performGaussianMixCalculation(AFMImageGaussianMixAnalysis, AFMImage)
```

Arguments

AFMImageGaussianMixAnalysis

an [AFMImageGaussianMixAnalysis](#) to manage and store the results of PSD analysis

AFMImage

an [AFMImage](#) from Atomic Force Microscopy

Author(s)

M.Beauvais

Examples

```

## Not run:
library(AFM)

data(AFMImageCollagenNetwork)

AFMImage<-AFMImageCollagenNetwork
AFMImage@fullfilename<-"/Users/one/AFMImageCollagenNetwork.txt"
gMixAnalysis<-AFMImageGaussianMixAnalysis()
# from two components
gMixAnalysis@minGaussianMix<-2
# to four components
gMixAnalysis@maxGaussianMix<-4
# convergence criteria
gMixAnalysis@epsilonGaussianMix<-1e-4
# Create a closure to update progress
gMixAnalysis@updateProgress<- function(value = NULL, detail = NULL, message = NULL) {
  if (exists("progressGaussianMix")){
    if (!is.null(message)) {
      progressGaussianMix$set(message = message, value = 0)
    }else{
      progressGaussianMix$set(value = value, detail = detail)
    }
  }
}
gMixAnalysis<-performGaussianMixCalculation(AFMImageGaussianMixAnalysis= gMixAnalysis, AFMImage)
print("done performGaussianMixCalculation")

## End(Not run)

```

pnormmix

pnormmix distribution of a mixture of normals

Description

pnormmix distribution of a mixture of normals

Usage

```
pnormmix(q, mixture)
```

Arguments

q	a vector of quantiles
mixture	a gaussian mixture

```
printVariogramModelEvaluations
    printVariogramModelEvaluations
```

Description

printVariogramModelEvaluations generates a graphic element containing the evaluation of all variogram models

Usage

```
printVariogramModelEvaluations(
    AFMImageAnalyser,
    sampleDT,
    numberOfModelsPerPage
)
```

Arguments

AFMImageAnalyser an [AFMImageAnalyser](#) to be used to produce report

sampleDT a data.table containing the evaluation information

numberOfModelsPerPage numeric to specify the number of model evaluations per pages

Author(s)

M.Beauvais

PSD1DAgainstFrequency *Calculate the 1D Power Spectral Density; returns a data table of PSD 1D and PSD 2D values against spatial frequencies. As mentionned in Sidick2009, this function calculates the PSD against spatial frequencies in 1D from [PSD2DAgainstFrequency](#) by using breaks in the log space to sum PSD 2D and frequency values.*

Description

Calculate the 1D Power Spectral Density; returns a data table of PSD 1D and PSD 2D values against spatial frequencies.

As mentionned in Sidick2009, this function calculates the PSD against spatial frequencies in 1D from [PSD2DAgainstFrequency](#) by using breaks in the log space to sum PSD 2D and frequency values.

Usage

```
PSD1DAgainstFrequency(AFMImage, AFMImagePSDAnalysis)

## S4 method for signature 'AFMImage'
PSD1DAgainstFrequency(AFMImage, AFMImagePSDAnalysis)
```

Arguments

```
AFMImage          an AFMImage to be analysed
AFMImagePSDAnalysis
                   n AFMImagePSDAnalysis to store the setup and results of PSD analysis
```

Value

PSD1DAgainstFrequency returns a data table of frequencies and PSD values

- freq: the considered frequency
- PSD: the considered PSD value
- type: PSD-1D
- fullfilename: directory and filename on the disk

Examples

```
## Not run:
library(AFM)
library(ggplot2)
library(ply)
library(scales)
data("AFMImageOfNormallyDistributedHeights")
newAFMImage<-AFMImageOfNormallyDistributedHeights
newAFMImage@fullfilename<-"C:/Users/one/AFMImageOfNormallyDistributedHeights.txt"
psdAnalysis<-AFMImagePSDAnalysis()
# Create a closure to update progress
psdAnalysis@updateProgress<- function(value = NULL, detail = NULL, message = NULL) {
  if (exists("progressPSD")){
    if (!is.null(message)) {
      progressPSD$set(message = message, value = 0)
    }else{
      progressPSD$set(value = value, detail = detail)
    }
  }
}
psdAnalysis@psd1d_breaks<-2^3
psdAnalysis@psd2d_truncHighLengthScale<-TRUE
psdAnalysis<-performAllPSDCalculation(AFMImagePSDAnalysis= psdAnalysis, AFMImage= newAFMImage)
datap<-psdAnalysis@psd1d
p <- ggplot(data=datap)
p <- p + geom_point(aes(freq, PSD, color=type),data=datap[datap$type %in% c("PSD-2D")])
p <- p + geom_line(aes(freq, PSD, color=type),data=datap[datap$type %in% c("PSD-1D")],size=1.1)
p <- p + scale_x_log10()
```

```
p <- p + scale_y_log10()
p <- p + ylab("PSD (nm^4)")
p <- p + xlab("Frequency (nm^-1)")
p

## End(Not run)
```

PSD2DAgainstFrequency *Calculate the 2D Power Spectral Density*

Description

PSD2DAgainstFrequency returns a data table of PSD 2D values against spatial frequencies

Usage

```
PSD2DAgainstFrequency(AFMImage, AFMImagePSDAnalysis)

## S4 method for signature 'AFMImage,AFMImagePSDAnalysis'
PSD2DAgainstFrequency(AFMImage, AFMImagePSDAnalysis)
```

Arguments

AFMImage an AFMImage to be analysed
AFMImagePSDAnalysis an AFMImagePSDAnalysis to store PSD analysis results

Value

PSD2DAgainstFrequency returns a data table of frequencies and PSD values

- freq: the considered frequency
- PSD: the considered PSD value
- type: PSD-2D
- fullfilename: directory and filename on the disk

References

Sidick2009, Erkin Sidick "Power Spectral Density Specification and Analysis of Large Optical Surfaces", 2009, "Modeling Aspects in Optical Metrology II, Proc. of SPIE Vol. 7390 73900L-1"

Examples

```
## Not run:
library(AFM)
library(ggplot2)
library(plyr)

# Calculate Power Spectrum Density in 2D against frequency
data("AFMImageOfNormallyDistributedHeights")
oneAFMImage<-AFMImageOfNormallyDistributedHeights
psd2d<-PSD2DAgainstFrequency(oneAFMImage)
p <- ggplot(data=psd2d)
p <- p + geom_point(aes(freq, PSD, color=type),subset = .(type %in% c("PSD-2D")))
p <- p + geom_line(aes(freq, PSD, color=type),subset = .(type %in% c("PSD-1D")),size=1.1)
p <- p + scale_x_log10()
p <- p + scale_y_log10()
p <- p + ylab("PSD (nm^4)")
p <- p + xlab("Frequency (nm^-1)")
p <- p + ggtitle(basename(oneAFMImage@fullfilename))
p

## End(Not run)
```

putAnalysisOnDisk

Export all data from an analysis of an AFM Image as rdata file

Description

A function to export to all the data from all analysis of an [AFMImage](#) and put them on disk as rdata file

Usage

```
putAnalysisOnDisk(AFMImageAnalyser, AFMImage)
```

```
## S4 method for signature 'AFMImageAnalyser'
putAnalysisOnDisk(AFMImageAnalyser, AFMImage)
```

Arguments

AFMImageAnalyser
an [AFMImageAnalyser](#)

AFMImage
an [AFMImage](#)

Author(s)

M.Beauvais

```
putImagesFromAnalysisOnDisk
    Put the images from all analysis on disk
```

Description

A function to put on disk all the images from variogram, PSD Analysis of an [AFMImage](#) An AFM Image 3D representation is saved on disk thanks to the [rgl](#) package. On Unix system, it is necessary to have a X server connection to be able to use the [rgl](#) package.

Usage

```
putImagesFromAnalysisOnDisk(AFMImageAnalyser, AFMImage, exportDirectory)
```

Arguments

```
AFMImageAnalyser    an AFMImageAnalyser
AFMImage            an AFMImage
exportDirectory     where the images will be stored
```

Author(s)

M.Beauvais

```
removeLongestEdge    removeLongestEdge
```

Description

Find and remove the longest edge if it is unique

Usage

```
removeLongestEdge(k, res, sides, myRes, vertex1)
```

Arguments

```
k                an integer
res              res ?
sides           data.table
myRes          data.table?
vertex1        a vertex ?
```

Value

a data.table with from, to

Author(s)

M.Beauvais

removeNode

removeNode

Description

remove a node from an AFMImage

Usage

```
removeNode(circleAFMImage, nodeDT)
```

Arguments

circleAFMImage a [AFMImage](#)
 nodeDT a data.table lon lat circleRadius

Value

an [AFMImage](#)

Author(s)

M.Beauvais

RoughnessByLengthScale

Calculate the roughness of the sample against length scale

Description

The calculation of the roughness against lengthscale is performed through a FFT 2D calculation, PSD 2D calculation and a meshgrid of frequencies. RoughnessByLengthScale returns a data.table of roughnesses against length scales

Usage

```
RoughnessByLengthScale(AFMImage, AFMImagePSDAnalysis)
```

```
## S4 method for signature 'AFMImage'
```

```
RoughnessByLengthScale(AFMImage, AFMImagePSDAnalysis)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy
 AFMImagePSDAnalysis
 n AFMImagePSDAnalysis to store the setup and results of PSD analysis

Value

a data table of length scale (r) and roughness values (roughness)

- roughness: roughnesses
- r: length scales
- filename: fullfilename slot of the AFMImage

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
library(ggplot2)

data("AFMImageOfNormallyDistributedHeights")
oneAFMImage<-AFMImageOfNormallyDistributedHeights
AFMImagePSDAnalysis<-AFMImagePSDAnalysis()
data<-RoughnessByLengthScale(oneAFMImage, AFMImagePSDAnalysis)
r<-roughness<-filename<-NULL
p1 <- ggplot(data, aes(x=r, y=roughness, colour= basename(filename)))
p1 <- p1 + geom_point()
p1 <- p1 + geom_line()
p1 <- p1 + ylab("roughness (nm)")
p1 <- p1 + xlab("lengthscale (nm)")
p1

## End(Not run)
```

runAFMApp

Launch the AFM shiny application

Description

Launch the AFM shiny graphical interface to access most of the functionalities of the AFM library

Usage

```
runAFMApp()
```

Author(s)

M.Beauvais

Examples

```
## Not run:  
install.packages("AFM")  
AFM::runAFMApp()  
  
## End(Not run)
```

sampleAFMImage *Get a sample of an AFM image.*

Description

Random selection of heights to keep in an [AFMImage](#). This function can be used to calculate quickly an approximated variogram of a large image.

Usage

```
sampleAFMImage(AFMImage, percentage)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy
percentage percentage of heights to keep

Details

sampleAFMImage returns a sample of the AFMImage to boost calculation time of variogram

Value

a sample of an [AFMImage](#)

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
library(ggplot2)

data(AFMImageOfAluminiumInterface)
anAFMImageSample<-sampleAFMImage(AFMImageOfAluminiumInterface,15)
variogramAnalysis<-AFMImageVariogramAnalysis(sampleFitPercentage=3.43)
avario<-AFM::calculateOmnidirectionalVariogram(AFMImage= anAFMImageSample,
                                               AFMImageVariogramAnalysis= variogramAnalysis)

dist<-gamma<-NULL
p1 <- ggplot(avario, aes(x=dist, y=gamma))
p1 <- p1 + geom_point()
p1 <- p1 + geom_line()
p1 <- p1 + ylab("semivariance")
p1 <- p1 + xlab("distance (nm)")
p1 <- p1 + ggtitle("Approximation of variogram thanks to sampling")
p1

## End(Not run)
```

saveOnDisk

Save an AFM image on disk.

Description

The function saves the an [AFMImage](#) as a rdata file. It uses the fullfilename param of the [AFMImage](#) and add "AFMImage.rda" extension to save the rdata file on disk.

Usage

```
saveOnDisk(AFMImage, exportDirectory)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

exportDirectory an optional argument to change the directory where the rdata file will be stored on disk

Details

saveOnDisk save on disk an [AFMImage](#) as rdata file

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)

data(AFMImageOfAluminiumInterface)
# save the rdata file of the AFMImage in the tempdir() directory;
# select another directory to save it permanently on your hard drive
saveOnDisk(AFMImageOfAluminiumInterface, tempdir())

## End(Not run)
```

```
saveOnDiskIntersectionForRoughnessAgainstLengthscale
```

save an image of the roughness against lengthscale calculations

Description

`saveOnDiskIntersectionForRoughnessAgainstLengthscale` save an image of the roughness against lengthscale calculations

Usage

```
saveOnDiskIntersectionForRoughnessAgainstLengthscale(
  AFMImageAnalyser,
  exportDirectory
)
```

Arguments

`AFMImageAnalyser`
an [AFMImageAnalyser](#) to get Roughness against lengthscale calculation

`exportDirectory`
a directory on the file system

Author(s)

M.Beauvais

`saveSpplotFromAFMImage`*Save on disk an AFMImage as a Lattice (trellis) plot*

Description

save a Lattice (trellis) plot of an [AFMImage](#) using the `spplot` method of the `sp` package. This function is used to evaluate visually the quality of the predicted surface when a variogram model is used.

Usage

```
saveSpplotFromAFMImage(  
  AFMImage,  
  fullfilename,  
  expectedWidth,  
  expectHeight,  
  withoutLegend  
)
```

Arguments

<code>AFMImage</code>	an AFMImage from Atomic Force Microscopy
<code>fullfilename</code>	directory and filename to save to png
<code>expectedWidth</code>	(optional) expected width of the saved image. Default is 400px.
<code>expectHeight</code>	(optional) expected height of the saved image. Default is 300px.
<code>withoutLegend</code>	(optional) set at FALSE, the cuts legend will be included in the plot. Default is FALSE.

Details

`saveSpplotFromAFMImage` save a a Lattice (trellis) plot of an [AFMImage](#) on disk

Author(s)

M.Beauvais

Examples

```
## Not run:  
library(AFM)  
  
data(AFMImageOfAluminiumInterface)  
saveSpplotFromAFMImage(AFMImageOfAluminiumInterface,  
  paste(tempdir(), "myFileWithoutLegend.png", sep="/"), 800,800, TRUE)  
saveSpplotFromAFMImage(AFMImageOfAluminiumInterface,  
  paste(tempdir(), "myFileWithLegend.png", sep="/"), 800,800, FALSE)
```



```
## End(Not run)
```

shiftedPSDuv	<i>Calculate the shifted PSD matrix</i>
--------------	---

Description

shiftedPSDuv returns the Power Spectral Density matrix in the frequency space from shifted FFT 2D

Usage

```
shiftedPSDuv(AFMImage)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Value

$(1/NM^2) * \text{abs}(\text{shiftedFFT2Ddata})^2$ with N the number of lines of the sample and M the number of samples per line of the sample

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
library(ggplot2)

data(AFMImageOfRegularPeaks)
AFMImage<-AFMImageOfRegularPeaks
nMheightsData= matrix(AFMImage@data$h, nrow=AFMImage@samplesperline)
shiftedPSDuv<-shiftedPSDuv(AFMImage)
a=AFMImage@scansize
b=AFMImage@scansize

M=AFMImage@sampsline
N=AFMImage@lines
NM=N*M # pixels^2
MN = M*N
A=a*b
ab=a*b

dx=a/M
dy=b/N
```

```

um = seq( (1-(M+1)/2)/(M*dx), (M-(M+1)/2)/(M*dx), by=1/(M*dx))
vn = seq( (1-(N+1)/2)/(N*dy), (N-(N+1)/2)/(N*dy), by=1/(N*dy))
x = rep(um, times = AFMImage@lines)
y = rep(vn, each = AFMImage@sampslines)
z = as.vector(shiftedPSDuv)

data<-data.frame(x=x, y=y, z=z)

p5 <- qplot(x, y, data=data, colour=log10(z))
p5 <- p5 + scale_colour_gradientn(colours = rainbow(7))
p5 <- p5 + ylab("v")
p5 <- p5 + xlab("u")
title<-paste("shifted PSD of", basename(AFMImage@fullfilename))
p5 <- p5 + ggtitle(title)
# Hide all the horizontal gridlines
p5 <- p5 + theme(panel.grid.minor.x=element_blank(), panel.grid.major.x=element_blank())
# Hide all the vertical gridlines
p5 <- p5 + theme(panel.grid.minor.y=element_blank(), panel.grid.major.y=element_blank())
p5 <- p5 + theme(panel.background = element_rect(fill = 'white', colour = 'black'))
p5

## End(Not run)

```

 shiftFFT2D

Shift the quadrants of the FFT 2D

Description

shiftFFT2D returns the FFT 2D matrix shifted to put zero frequencies in the middle.

Usage

```
shiftFFT2D(fft2data)
```

Arguments

fft2data the FFT 2D of the AFM image

Value

The shifted matrix

Author(s)

M.Beauvais

Examples

```
## Not run:
library(AFM)
library(fftwtools)

data(AFMImageOfNormallyDistributedHeights)
AFMImage<-AFMImageOfNormallyDistributedHeights
nMheightsData= matrix(AFMImage@data$h, nrow=AFMImage@samplesperline)
shiftedFFT2D<-shiftFFT2D(fftwtools::fftw2d(nMheightsData))

## End(Not run)
```

simplifyAFMImage	<i>simplify an AFM image.</i>
------------------	-------------------------------

Description

The simplification is taking a very simple gridded sample of the image. It can be useful to speed up display.

Usage

```
simplifyAFMImage(AFMImage, newSamplesperline, newLines)
```

Arguments

AFMImage	an AFMImage from Atomic Force Microscopy
newSamplesperline	the new number of samplesperline of the AFMImage
newLines	the new number of lines of the AFMImage

Details

simplifyAFMImage returns a simplified AFMImage

Value

a new simplified [AFMImage](#)

Author(s)

M.Beauvais

Examples

```
## Not run:
data(AFMImageOfAluminiumInterface)
anAFMImageExtract<-simplifyAFMImage(AFMImageOfAluminiumInterface,16,16)

## End(Not run)
```

simplifyNetwork	<i>simplifyNetwork</i>
-----------------	------------------------

Description

simplify the network keeping only the important edges

Usage

```
simplifyNetwork(..., allVertices, allEdges)
```

Arguments

...	cl: a cluster object from the parallel package
allVertices	a data.table of vertices
allEdges	a data.table of edges

Value

a data.table of edges

Author(s)

M.Beauvais

thinImage	<i>thin an Image in matrix format</i>
-----------	---------------------------------------

Description

thin an Image in matrix format

Usage

```
thinImage(imageMatrix)
```

Arguments

imageMatrix a matrix of an AFM image

Author(s)

M.Beauvais

totalRMSRoughness *Calculate the total Root Mean Square Roughness (Rrms total)*

Description

totalRMSRoughness returns the total RMS roughness calculated from the variance of heights

Usage

```
totalRMSRoughness(AFMImage)
```

Arguments

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Value

a numeric as the square root of the variance of heights

Author(s)

M.Beauvais

Examples

```
## Not run:  
library(AFM)  
  
data(AFMImageOfAluminiumInterface)  
totalRMSRoughness<-totalRMSRoughness(AFMImageOfAluminiumInterface)  
print(totalRMSRoughness)  
  
## End(Not run)
```

```
transformAFMImageForNetworkAnalysis
```

Multiply, filter the heights and make a binary AFMImage from the transformed AFMImage

Description

transformAFMImageForNetworkAnalysis update [AFMImageNetworksAnalysis](#) making a binary AFMImage

Usage

```
transformAFMImageForNetworkAnalysis(AFMImageNetworksAnalysis, AFMImage)
```

```
## S4 method for signature 'AFMImageNetworksAnalysis'
transformAFMImageForNetworkAnalysis(AFMImageNetworksAnalysis, AFMImage)
```

Arguments

AFMImageNetworksAnalysis
 n [AFMImageNetworksAnalysis](#) to store the results of the transformation

AFMImage an [AFMImage](#) from Atomic Force Microscopy

Author(s)

M.Beauvais

```
updateProgress                  updateProgress
```

Description

is a function used by a GUI such as shiny GUI

Usage

```
updateProgress(AFMImageVariogramAnalysis, value, detail, message)
```

Arguments

AFMImageVariogramAnalysis
 an [AFMImageVariogramAnalysis](#)

value shiny progress bar value

detail shiny progress bar detail

message shiny progress bar message

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