Package 'ITALICS'

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Suggests pd.mapping50k.hind240, pd.mapping250k.sty, pd.mapping250k.nsp

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Description A Method to normalize of Affymetrix GeneChip Human Mapping 100K and 500K set

License GPL-2

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`addInfo` *add info to quartet annotation*

Description

This function merge information obtain from the getQuartet function and a given table

Usage

```
addInfo(quartet, dat)
```

Arguments

`quartet`	list obtain through the getQuartet Function
`dat`	a data.frame with additionnal information it must contain a fsetid and fid column

Value

a data.frame similar to the quartetInfo item of quartet plus additionnal column

Note

People interested in tools dealing with array CGH analysis and DNA copy number analysis can visit our web-page `http://bioinfo.curie.fr`.

Author(s)

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Source

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`analyseCGH` *GLAD analysis*

Description

Glad Analysis ot the genomic profile

Usage

```
analyseCGH(data, amplicon, deletion, deltaN, forceGL, param, nbsigma, ...)
```

Arguments

`data`	A data frame containing SNP's intensity, chromosome and position on the genome. data must have a Chr, X and LogRatio columns
`amplicon`	see the amplicon parameter in the daglad function
`deletion`	see the deletion parameter in the daglad function
`deltaN`	see the deltaN parameter in the daglad function
`forceGL`	see the forceGL parameter in the daglad function
`param`	see the param parameter in the daglad function
`nbsigma`	see the nbsigma parameter in the daglad function
`...`	Other daglad parameters.

Value

An object of class profileCGH

Note

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Author(s)

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`fromQuartetToSnp` *Compute the copy number of each SNP from its quartets intensities*

Description

This function removes the LogRatio column of the snpInfo data.frame. Then compute the copy number of each SNP having its quartet intensities. And return the snpInfo data.frame with the newly computed LogRatio.

Usage

```
fromQuartetToSnp(quartetInfo, snpInfo, cIntensity="quartetLogRatio", nLog=1)
```

Arguments

`quartetInfo`	A table containing the quartet intensities and other quartet information. It must have a column called : fsetid.
`snpInfo`	A table containing snp information.
`cIntensity`	A vector containing the names of the quartet information to be aggregate. For example quartetLogRatio.
`nLog`	The position of the field which will be named LogRatio in the snpInfo data.frame. For example if cIntensity = c("a", "b") and you want b to be considered as the LogRatio you should set nLog=2

Value

return the data.frame snpInfo with additionnal columns.

Note

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Author(s)

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Source

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`fromSnpToQuartet` *Function to get from snp to quartet*

Description

This function put the smoothing value of each SNP in front of its corresponding quartet in the quartetInfo data.frame.

Usage

```
fromSnpToQuartet(quartetInfo, profilSNP)
```

Arguments

`quartetInfo`	a data frame containing all the quartet values plus there GC content, fragment length and GC content and Quartet effect
`profilSNP`	a data frame, corresponding to the profileValues argument of a profilCGH object (see GLAD)

Value

return the data.frame quartetInfo with an additionnal column: "Smoothing" corresponding to the estimated smoothing value.

Note

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Author(s)

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getConfDat *Elimination of badly predicted probes*

Description

This function eliminate badly predicted probes using a regression table and an estimated model given by the function `getModel` or `getBestBICModelLight`. Then it computes the corrected intensity.

Usage

```
getConfDat(confidence, quartetInfo, model)
```

Arguments

`confidence`	The confidence interval : 0.95
`quartetInfo`	A Regression table containing the variables in the model
`model`	The class lm object given by the function `getModel`

Value

A data frame with the corrected intensity. Only goodly predicted probes are taken into account. SNP's with more than 8 badly predicted probes get a NA.

Note

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Author(s)

Guillem Rigaill, <italics@curie.fr>.

Source

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getCorrection *Correction*

Description

This function computes the corrected intensity.

Usage

```
getCorrection(effet, model, regTab)
```

Arguments

effet	The name of the biological effect
model	The class lm object given by the getModel function
regTab	The regression table used to estimate the linear model, and containing the variables in the model

Note

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Author(s)

Guillem Rigaill, <italics@curie.fr>.

Source

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getEffet *Effet*

Description

This function retrieves the estimated biological effect

Usage

```
getEffet(effet, model, regTab)
```

Arguments

effet	The name of the biological effect
model	The class lm object given by the getModel function
regTab	The regression table used to estimate the linear model, and containing the variables in the model

Note

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Author(s)

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getModel *Regression Model*

Description

Computes the linear regression model and and return an object of class lm.

Usage

```
getModel(formule, response, regTab)
```

Arguments

formule	A symbolic description of the term of the model. It is a string
response	The parameter you want to explain (the response) : the SNP "LogRatio". Y is a string
regTab	A Regression table containing the variables in the model

Note

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Author(s)

Guillem Rigaill, <italics@curie.fr>.

Source

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`getQuartet` *Function to retrieve the information of each quartet*

Description

This function retrieve information of each quartet. This function use the pd.mapping50k.xba240, pd.mapping50k.hind240, pd.mapping250k.sty and pd.mapping250k.nsp package.

Usage

```
getQuartet(pkgname, snpInfo)
```

Arguments

`pkgname`	the chip type pd.mapping50k.xba240, pd.mapping50k.hind240, pd.mapping250k.sty or pd.mapping250k.nsp
`snpInfo`	a data frame containing SNPs position along the genome

Value

return a list with two fields. fid : containing the position of each quartet on the CEL file. quartetInfo : a data fame containing the columns : fsetid, fid, FL (fragment length) and GC (content of the quartet)

Note

People interested in tools dealing with array CGH analysis and DNA copy number analysis can visit our web-page http://bioinfo.curie.fr.

Author(s)

Guillem Rigaill, <italics@curie.fr>.

Source

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`getResidu` *Correction*

Description

This function retrieves the residual values

Usage

```
getResidu(model)
```

Arguments

`model`	The class lm object given by the `getModel` function

Note

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Author(s)

Guillem Rigaill, <italics@curie.fr>.

Source

Institut Curie, <italics@curie.fr>.

`getSnpInfo` *Function to retrieve the chromosome and the position of each SNP on a given Affymetrix SNP array*

Description

This function retrieve the chromosome and position in bp of each SNP of a given Affymetrix SNP array. This function use the pd.mapping50k.xba240, pd.mapping50k.hind240, pd.mapping250k.sty and pd.mapping250k.nsp package.

Usage

```
getSnpInfo(pkgname)
```

Arguments

`pkgname`	the chip type pd.mapping50k.xba240, pd.mapping50k.hind240, pd.mapping250k.sty or pd.mapping250k.nsp

Value

Return a data.frame with five columns : fsetid, dbsnp_rs_id, Chr, X and fragment_length corresponding to the fsetid, the rs_id, the chromosome, the position on the chromosome and the PCR amplified fragment length respectively.

Note

People interested in tools dealing with array CGH analysis and DNA copy number analysis can visit our web-page http://bioinfo.curie.fr.

Author(s)

Guillem Rigaill, <italics@curie.fr>.

Source

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ITALICS *Affymetrix SNP chip normalization*

Description

Normalize and analyse Affymetrix SNP array 100K and 500K set (see the vignette)

Usage

```
ITALICS(quartetInfo, snpInfo, confidence=0.95, iteration=2,
   formule="Smoothing+QuartetEffect+FL+I(FL^2)+I(FL^3)+GC+I(GC^2)+I(GC^3)", prc=0.3,
   amplicon=2.1, deletion=-3.5, deltaN=0.15, forceGL=c(-0.2,0.2), param=c(d=2), nbsigma=1, ... )
```

Arguments

quartetInfo	a data frame containing all the raw quartet intensities plus there GC content, fragment length, and Quartet effect
snpInfo	a data frame containing SNPs position along the genome and raw copy number
confidence	The confidence interval. After the last bias estimation step, quartets outside this confidence interval are flagged. The lower confidence is, the more quartets will be flagged. See also the parameter prc.
iteration	The number of iteration you d'like to do
formule	A symbolic description of the term of the model. The default value of formule means that we want correct the observed quartetLogRatio using the estimated copy number (Smoothing), the Quartet Effect, the quartet Fragment Length (FL) and the quartet GC content.

prc	prc is a frequence (between 0 and 1). After the final iteration of ITALICS, badly predicted probes are flagged (see also the parameter confidence). Only SNPs having more than prc of their probes non-flagged are kept for the final GLAD analysis. The higher prc is, the more SNPs are removed before the final GLAD analysis.
amplicon	see the amplicon parameter in the daglad function
deletion	see the deletion parameter in the daglad function
deltaN	see the deltaN parameter in the daglad function
forceGL	see the forceGL parameter in the daglad function
param	see the param parameter in the daglad function
nbsigma	see the nbsigma parameter in the daglad function
...	Other daglad parameters.

Details

The function ITALICS implements the methodology which is described in the article : ITALICS: an algorithm for normalization and DNA copy number calling for Affymetrix SNP arrays (Rigaill et al., Bioinformatics Advance Access published on February 5, 2008).

The principle of the ITALICS algorithm: ITALICS, is a normalization method that estimates both the biological and the non-relevant effects in an alternate and iterative way to accurately remove the non-relevant effects.

ITALICS deals with known systematic sources of variation such as the GC-content of the quartets, the PCR amplified fragment length and the GC-content of the PCR amplified fragment . It also takes into account the quartet effect which corresponds to the fact that some quartets systematically have a small intensity while others tend to have a high intensity. ITALICS is also able to correct spatial artifacts which sometimes arise on Affymetrix SNP arrays 100K and 500K set.

Value

Return an object of class profileCGH

Note

People interested in tools dealing with array CGH analysis and DNA copy number analysis can visit our web-page http://bioinfo.curie.fr.

Author(s)

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Examples

```
## Not run:
## step to get the path of the HF0844_Hind.CEL file
ITALICSDataPATH <- attr(as.environment(match("package:ITALICSData",search())),"path")
filename <- paste(ITALICSDataPATH,"/extdata/HF0844_Hind.CEL", sep="")
quartetEffectFile <- paste(ITALICSDataPATH,"/data/Hind.QuartetEffect.csv", sep="")

## load quartet effect
quartetEffect <- read.table(quartetEffectFile, sep=";", header=TRUE)

## load annotation using the pd.mapping50k.xba24 or pd.mapping50k.hind240 or  pd.mapping250k.sty or pd.mapping250k
headdetails <- readCelHeader(filename[1])
pkgname <- cleanPlatformName(headdetails[["chiptype"]])
snpInfo <- getSnpInfo(pkgname)
quartet <- getQuartet(pkgname, snpInfo)

## read cel files and format data
tmpExprs <- readCelIntensities(filename, indices=quartet$fid)
quartet$quartetInfo$quartetLogRatio <- readQuartetCopyNb(tmpExprs)
quartet$quartetInfo <- addInfo(quartet, quartetEffect)
snpInfo <- fromQuartetToSnp(cIntensity="quartetLogRatio", quartetInfo=quartet$quartetInfo, snpInfo=snpInfo)


## ITALICS normalization
profilSNPHind <- ITALICS(quartet$quartetInfo, snpInfo,
    formule="Smoothing+QuartetEffect+FL+I(FL^2)+I(FL^3)+GC+I(GC^2)+I(GC^3)")

## plot the profile
data(cytoband)
plotProfile(profilSNPHind, Smoothing="Smoothing", Bkp=TRUE, cytoband = cytoband)

## End(Not run)
```

---

readQuartetCopyNb *Read PM probes of selected quartets and compute the quartet intensity*

Description

This function read the cel files and return the raw-value of each quartet = mean of allele A and B

Usage

```
readQuartetCopyNb(tmpExprs)
```

Arguments

tmpExprs	A vector of the perfect match intensity of allele A and B of the quartets. This vector should be sorted in a specific order. See the example given in the help of the ITALICS function.

Value

return a vector with the raw-value of each quartet

Note

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Author(s)

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Source

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`trainITALICS` *ITALICS training*

Description

Estimation of the quartet effect based on several normal sample chips

Usage

```
trainITALICS (dir,  amplicon=2.1, deletion=-3.5, deltaN=0.15, forceGL=c(-0.2,0.2), param=c(d=2), nbsig
```

Arguments

`dir`	The directory containing the normal sample chips. All theses chips should be of the same type hind, xba, nsp or sty. Only .CEL files be considered
`amplicon`	see the amplicon parameter in the daglad function
`deletion`	see the deletion parameter in the daglad function
`deltaN`	see the deltaN parameter in the daglad function
`forceGL`	see the forceGL parameter in the daglad function
`param`	see the param parameter in the daglad function
`nbsigma`	see the nbsigma parameter in the daglad function
`...`	Other daglad parameters.

Details

The ITALICS function take into account a quartet effect which is computed on a reference data set of normal women samples. The ITALICSData provide quartetEffect for the Xba, Hind, Sty and Nsp chip computed on our own reference data set.

We recommand that you use your own reference data set to compute the quartet Effect by using the trainITALICS function. ITALICS reference data should contain only woman normal samples. Furthermore we recommand that you check that none of these chip have obvious spatial artifact. To so read the cel files using the read.affybatch (form the affy package). Then use the image function on the obtain affybatch object.

Value

a data.frame with two column fsetid and quartetEffect

Note

People interested in tools dealing with array CGH analysis and DNA copy number analysis can visit our web-page http://bioinfo.curie.fr.

Author(s)

Guillem Rigaill, <italics@curie.fr>.

Source

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