analyseCGH

GLAD analysis

Description

Glad Analysis of 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.
Other daglad parameters.

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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See Also
getModel

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=
amplicon=2.1, deletion=-3.5, deltaN=0.15, forceGL=c(-0.2,0.2), param=c(d=2),
...)

Arguments
quartetInfo  a data frame containing all the raw quartet intensities plus their 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 iterations 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 frequency (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`

Other daglad parameters.

Note

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Examples

```r
## 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,"/data/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.nsp package
headdetails <- readCelHeader(filename[1])
pkname <- cleanPlatformName(headdetails["chiptype"])
snpInfo <- getSnpInfo(pkname)

## 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)
```
## ITALICS normalization

```r
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

```r
plotProfile(profilSNPHind, Smoothing="Smoothing", Bkp=TRUE)
```

## End(Not run)

---

### Description

Estimation of the quartet effect based on several normal sample chips

### Usage

```r
trainITALICS (dir, amplicon=2.1, deletion=-3.5, deltaN=0.15, forceGL=c(-0.2,0.2), param=c(d=2), nbsigma=1, ...)
```

### Arguments

- **dir**: The directory containing the normal sample chips. All these 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 recommend 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 recommend 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
- Other daglad parameters.

### Note

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

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
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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getCorrection  

**Description**
This function computes the corrected intensity.

**Usage**
```r
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**
People interested in tools dealing with array CGH analysis and DNA copy number analysis can visit our web-page [http://bioinfo.curie.fr](http://bioinfo.curie.fr).

**Author(s)**
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gEffet  

**Description**
This function retrieves the estimated biological effect.

**Usage**
```r
gEffet(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)
**getModel**

**Description**

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

**Usage**

```r
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**

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

**Author(s)**

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**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**  
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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addInfo  

**add info to quartet annotation**  

**Description**  
This function merges information obtained 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 additional information it must contain a fsetid and fid column

**Value**  
a data.frame similar to the quartetInfo item of quartet plus additional column
fromQuartetToSnp

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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---

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. 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

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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fromSnpToQuartet

Function to get from SNP to quartet

Description

This function puts 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 their 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 additional column: "Smoothing" corresponding to the estimated smoothing value.

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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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 or a data frame containing SNPs position along the genome

Note

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

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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)
**readQuartetCopyNb**

**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](http://bioinfo.curie.fr).

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**Source**

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---

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

**Description**

This function reads the cel files and returns 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

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.

**Note**

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