

Package ‘funtooNorm’

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Type Package

Title Normalization Procedure for Infinium HumanMethylation450 BeadChip Kit

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Author Celia Greenwood <celia.greenwood@mcgill.ca>, Stepan Grinek
<stepan.grinek@ladydavis.ca>

Maintainer Raphael Poujol <raphael.poujol@umontreal.ca>

Description Provides a function to normalize Illumina Infinium Human
Methylation 450 BeadChip (Illumina 450K), correcting for tissue and/or cell
type.

License GPL-3

Imports pls,
matrixStats,
minfi

Suggests BiocStyle,
minfiData

Depends R(>= 3.2)

LazyData true

biocViews DNAMethylation, Preprocessing, Normalization

RoxygenNote 5.0.1

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agreement	<i>Function to measure intra-replicate agreement in methylation data.</i>
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Description

Function to measure intra-replicate agreement in methylation data.

Usage

```
agreement(Beta, individualID)
```

Arguments

`individualID` : a vector where 2 replicates have the exact same value for two technical replicate. Order of samples should nmatch the samples (columns) in `Beta`

`Matrix` with beta-values, rows corresponding to probes, columns corresponding to samples.

Details

We expect that the values returned by the agreement function after normalization by `funtooNorm` to be smaller than before.

Value

The average value of the square distance between replicates: a measure of agreement between replicates in methylation data.

fromGenStudFiles	<i>create a sample set from GenomeStudio files</i>
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Description

create a sample set from GenomeStudio files

Usage

```
fromGenStudFiles(controlProbeFile, signalFile, cell_type)
```

Arguments

`controlProbeFile` file exported from GenomeStudio

`signalFile` file exported from GenomeStudio with the exact same samples

`cell_type` this vector should have names matching all the sample in the files from genome studios, and at least 2 different cell types.

Value

a SampleSet object

Examples

```
myNewSampleSet <- fromRGChannelSet("ControlProbeProfile.txt",
  "SignalIntensity.txt", cell_type)
```

fromRGChannelSet	<i>create a SampleSet from RGSet from minfi package</i>
------------------	---

Description

create a SampleSet from RGSet from minfi package

Usage

```
fromRGChannelSet(myRGChannelSet)
```

Arguments

```
myRGChannelSet,
  from mini package, should contain a cell_type vector in it s phenotypes data
  pData
```

Value

a SampleSet object

Examples

```
myNewSampleSet <- fromRGChannelSet(objectOfTypeRGChannelSet)
```

funtooNorm	<i>funtooNorm</i>
------------	-------------------

Description

The funtooNorm Package provides a normalization method for data arising from the Illumina Infinium Human Methylation 450 BeadChip (Illumina 450K), including explicit considerations of differences between tissues or cell types. This method should only be used when the data set contains samples from multiple different tissues or cell types.

Details

Package:	funtooNorm
Type:	Package
Version:	0.99.3
Date:	2016-03-28
License:	GPL-3

funtooNorm	<i>This function apply the normalization method central to the package on each signal</i>
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Description

This function apply the normalization method central to the package on each signal

Usage

```
funtooNorm(object, type.fits = "PCR", ncmp = 4, force = FALSE)
```

Arguments

object	of type SampleSet
type.fits	can be "PCR" or "PLS" (default "PCR")
ncmp	number of component use for anaysis (default 4)
force	set it to TRUE in order to re-compute the normalisation whent it is already done

Value

a SampleSet containing the normalised signal

Examples

```
mySampleSet <- funtooNorm(mySampleSet)
```

getLogSigA	<i>internal function to get the signal A</i>
------------	--

Description

internal function to get the signal A

Usage

```
getLogSigA(signal)
```

Arguments

signal

Value

all signal A in the good order

getLogSigB	<i>internal function to get the signal B</i>
------------	--

Description

internal function to get the signal B

Usage

```
getLogSigB(signal)
```

Arguments

signal

Value

all signal B in the good order

getNormBeta	<i>compute the beta value after normalization for each position and each sample</i>
-------------	---

Description

compute the beta value after normalization for each position and each sample

Usage

```
getNormBeta(object, offset = 100)
```

Arguments

object	of type SampleSet
offset	default is 100 as Illumina standard

Value

a matrix containing beta after normalization value for each CpG position and each samples

Examples

```
myNormBetaMatrix <- getNormBeta(mySampleSet)
```

getNormM	<i>compute the M value after normalization for each position and each sample</i>
----------	--

Description

compute the M value after normalization for each position and each sample
 compute the beta value after normalization for each position and each sample

Usage

```
getNormM(object, offset = 100)

getNormM(object, offset = 100)
```

Arguments

object	of type SampleSet
offset	default is 100 as Illumina standard
object	of type SampleSet
offset	default is 100 as Illumina standard

Value

a matrix containing M after normalization value for each position and each samples $\log(\text{Meth}/\text{Unmeth})$
 a matrix containing M after normalization value for each position and each samples

getRawBeta	<i>compute the beta value of the raw signal for each position and each sample</i>
------------	---

Description

compute the beta value of the raw signal for each position and each sample

Usage

```
getRawBeta(object, offset = 100)
```

Arguments

object	of type SampleSet
offset	default is 100 as Illumina standard

Value

a matrix containing beta value for each position and each samples

Examples

```
myRawBetaMatrix <- getRawBeta(mySampleSet)
```

```
getSampleSetAnnotation
```

Get the SampleSet Annotation in the same order as the beta matrix

Description

Get the SampleSet Annotation in the same order as the beta matrix

Usage

```
getSampleSetAnnotation()
```

Arguments

object of type SampleSet

Value

annotation

Examples

```
getSampleSetAnnotation(mySampleSet)
```

```
getSnpM
```

compute the M value after normalization for each SNP position and each sample

Description

compute the M value after normalization for each SNP position and each sample

Usage

```
getSnpM(object)
```

Arguments

object of type SampleSet
offset default is 100 as Illumina standard

Value

a matrix containing M after normalization value for each SNP of the chip and each sample $\log(\text{Meth}/\text{Unmeth})$

```
plotValidationGraph
```

Plot a series of graphs with different numbers of components for each signal

Description

Plot a series of graphs with different numbers of components for each signal

Usage

```
plotValidationGraph(object, type.fits = "PCR", file = "")
```

Arguments

object	of type SampleSet
type.fits	can be "PCR" or "PLS" (default "PCR")
file	if not empty will write a pdf at this place

Examples

```
plotValidationGraph(mySampleSet, file="myPlots.pdf")
```

```
print.SampleSet
```

Print information about the SampleSet

Description

Print information about the SampleSet

Usage

```
## S3 method for class 'SampleSet '  
print(object)
```

Arguments

object	of type SampleSet
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Examples

```
mySampleSet
```

SampleSet-class	<i>SampleSet are S3 objects define for the purpose of runing funtooNorm algorithm, they are list containing signal data and different variables usefull for funtooNorm. The data is separated into the 3 probes type, having 2 channels (methylated and unmethylated ie : A and B. We then define then the 6 (2*3) labels: AIGrn BIGrn AIRed BIRed AII BII</i>
-----------------	--

Description

SampleSet are S3 objects define for the purpose of runing funtooNorm algorithm, they are list containing signal data and different variables usefull for funtooNorm. The data is separated into the 3 probes type, having 2 channels (methylated and unmethylated ie : A and B. We then define then the 6 (2*3) labels: AIGrn BIGrn AIRed BIRed AII BII

Value

a SampleSet object

Slots

type character: is 'minfi' or 'GenomeStudio'
 sampleNames character vector: contain the list of sample names in order used
 sampleSize numeric: the number of samples
 nPos numeric: the number of positions in the ILLUMINA chip
 cell_type list: list matching each sample to define the categories
 qntllist numeric: vector of ordered quantiles
 quantiles numeric: list of 6 auqntiles tables for 6 type of signals
 ctl.covmat numeric: covariance matrix for the model fit
 signal numeric: list of 6 signal tables the 6 type of signals

Examples

```
showClass("SampleSet")
```

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