

Package ‘methyAnalysis’

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Suggests IlluminaHumanMethylation450k.db, TxDb.Hsapiens.UCSC.hg19.knownGene

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Description The methyAnalysis package aims for the DNA methylation data analysis and visualization. A new class is defined to keep the chromosome location information together with the data. The current version of the package mainly focus on analyzing the Illumina Infinium methylation array data, but most methods can be generalized to other methylation array or sequencing data.

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LazyLoad yes

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R topics documented:

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annotateDMRInfo	<i>Annotate the DMR (Differentially Methylated Region)</i>
-----------------	--

Description

Annotate the DMR (Differentially Methylated Region) information

Usage

```
annotateDMRInfo(DMRInfo, annotationDatabase, CpGInfo = NULL, flankRange = 500, promoterRange = 200)
```

Arguments

DMRInfo	A GRanges object or a list of GRanges objects (sigDMRInfo and sigDataInfo), which is the return of identifySigDMR
annotationDatabase	Annotation database: a TranscriptDb package, TranscriptDb object or GRanges object.
CpGInfo	A Bed file or GRanges object, which keeps the CpG-island information
flankRange	The flank range to be added to the input GRanges object
promoterRange	Define the size of promoter range at the upstream of TSS. User can also directly provide the GRanges object
EntrezDB	The Entrez database for mapping from Entrez ID to gene symbols
as.GRanges	Whether return a GRanges object or a data.frame

Details

This function is to annotate the DMRs to the gene promoters or bodies. The annotation information is attached as additional columns of the GRanges object values.

Value

Return a GRanges object or list of GRanges when the as.GRanges is TRUE. Or else it returns a data.frame or a list of data.frame objects (sigDMRInfo and sigDataInfo). The annotation information is attached as additional columns of the GRanges object values or the data.frame.

Author(s)

Pan Du

See Also

See Also [annotateGRanges](#)

Examples

```
data(exampleMethyGenoSet)
## get sample type information
sampleType <- pData(exampleMethyGenoSet)$SampleType

## Do differential test
allResult <- detectDMR.slideWin(exampleMethyGenoSet, sampleType=sampleType, testMethod='ttest')

## Identify the DMR (Differentially Methylated Region) by setting proper parameters.
## Here we just use default ones
allDMRInfo <- identifySigDMR(allResult)

## Annotate significant DMR info
if (require(TxDb.Hsapiens.UCSC.hg19.knownGene)) {
  DMRInfo.ann <- annotateDMRInfo(allDMRInfo, 'TxDb.Hsapiens.UCSC.hg19.knownGene')
}
```

annotateGRanges	<i>Annotate a GRanges object</i>
-----------------	----------------------------------

Description

Annotate a GRanges object based on a transcription database

Usage

```
annotateGRanges(grange, annotationDatabase, CpGInfo = NULL, exons = FALSE, flankRange = 0, promoterRange = 0)
```

Arguments

grange	A GRanges object
annotationDatabase	Annotation database: a TranscriptDb package, TranscriptDb object or GRanges object.
CpGInfo	A Bed file or GRanges object, which keeps the CpG-island information
exons	Whether to annotate at the exon level. exons can be either TRUE/FALSE or a GRanges object represent the exon annotation.
flankRange	The flank range to be added to the input GRanges object
promoterRange	Define the size of promoter range at the upstream of TSS. Users can also directly provide the GRanges object
EntrezDB	The Entrez database for mapping from Entrez ID to gene symbols

Details

This function is to annotate a GRanges object to the gene promoters or bodies. The annotation information is attached as additional columns of the GRanges object values.

Value

Return an annotated GRanges object with the annotation information attached as additional columns.

Author(s)

Pan Du

See Also

See Also [annotateDMRInfo](#)

Examples

```
data(exampleMethyGenoSet)
## get sample type information
sampleType <- pData(exampleMethyGenoSet)$SampleType

## Do differential test
allResult <- detectDMR.slideWin(exampleMethyGenoSet, sampleType=sampleType, testMethod='ttest')

## Identify the DMR (Differentially Methylated Region) by setting proper parameters.
## Here we just use default ones
allDMRInfo <- identifySigDMR(allResult)
sigDMRInfo <- allDMRInfo$sigDMRInfo
class(sigDMRInfo)

## Annotate significant DMR info
if (require(TxDb.Hsapiens.UCSC.hg19.knownGene)) {
  sigDMRInfo.ann <- annotateDMRInfo(sigDMRInfo, 'TxDb.Hsapiens.UCSC.hg19.knownGene')
}
```

buildAnnotationTracks *Build annotation tracks for visualizing using Gviz package*

Description

Build annotation tracks for visualizing using Gviz package

Usage

```
buildAnnotationTracks(gene, extendRange = c(2000, 2000), includeGeneBody = TRUE, cytobandInfo = NULL)
```

Arguments

gene	An Entrez gene id or a GRanges object with length equals one
extendRange	extended range on each side of the gene
includeGeneBody	whether to include genebody of the provided gene
cytobandInfo	cytoband information
CpGInfo	CpG-island information, GRanges or bed file are supported

genomeAxis	whether to add genome axis or not
lib	gene annotation library
genome	genome version
genomicFeature	genomic features: "TranscriptDb" library or object, "Mart" object
...	other parameters used by createTranscriptTrack function

Details

This function aims to build annotation tracks to be visualized using Gviz package. If the cyto-bandInfo and CpGInfo are NULL and internet connection is available, it will download information directly from UCSC website. Set them as NAs if you want suppress this default behavior.

Value

A list of different annotation Tracks

Author(s)

Pan Du

See Also

[help](#)

Examples

```
if (require(TxDb.Hsapiens.UCSC.hg19.knownGene) && require(Gviz)) {
  annotationTracks <- buildAnnotationTracks('1826', includeGeneBody = FALSE, genomicFeature = "TxDb.Hsapiens.UC
  plotTracks(annotationTracks)
}
```

checkChrName *check chromosome names*

Description

Check chromosome names and make sure chromosome names start with "chr" (or not if addChr is FALSE)

Usage

```
checkChrName(grange, addChr = TRUE)
```

Arguments

grange	a GRanges, RangedData object, character or named vector
addChr	Whether to add "chr" in front of chromosome names

Details

Because some annotation database names the chromosomes without "chr" prefix, while many others do, it causes problems when both types of data exist in the analysis. This function aims to resolve such issues by checking chromosome names and make sure chromosome names start with "chr" (or not if addChr is FALSE).

Value

return the same type of object with chromosome names checked.

Author(s)

Pan Du

Examples

```
data(exampleMethyGenoSet)
names(locData(exampleMethyGenoSet))

tt <- checkChrName(exampleMethyGenoSet, addChr = TRUE)
names(locData(tt))
```

createTranscriptTrack *Create a transcript annotation track*

Description

Create a transcript track, which is a GeneRegionTrack object

Usage

```
createTranscriptTrack(gene, genomicFeature = "TxDb.Hsapiens.UCSC.hg19.knownGene", lib = "org.Hs.eg.db")
```

Arguments

gene	An Entrez gene ID or a GRanges object with length equals one
genomicFeature	a TranscriptDb library, TranscriptDb object, or Mart object
lib	Entrez annotation library
genome	The version of genome
extendRange	extended range on each side of the gene
includeGeneBody	whether to include the whole gene body or not
background.title	the background color of the title
...	other parameters

Details

This function is to create a GeneRegionTrack object for visualization using Gviz package.

Value

a GeneRegionTrack object

Author(s)

Pan Du

See Also

[plotTracks](#), [plotTracksWithDataTrackInfo](#), [heatmapByChromosome](#), [plotMethylationHeatmapByGene](#)

Examples

```
if (require(TxDb.Hsapiens.UCSC.hg19.knownGene) && require(Gviz)) {
  rangeTrack <- createTranscriptTrack('7157', genomicFeature = "TxDb.Hsapiens.UCSC.hg19.knownGene")
  plotTracks(rangeTrack)
}
```

detectDMR.slideWin	<i>Detect DMR (Differentially Methylated Region) using slide window smoothing</i>
--------------------	---

Description

Detect DMR (Differentially Methylated Region) using slide window smoothing

Usage

```
detectDMR.slideWin(methyGenoSet, sampleType, winSize = 250, testMethod = c("ttest", "wilcox"), p.adjust.m
```

Arguments

methyGenoSet	A MethyGenoSet object includes the methylation data information
sampleType	A vector shows the sample type information
winSize	Slide window size (half window size, bp at each side of the probe)
testMethod	test methods
p.adjust.method	p.value FDR adjust method
...	other paramters

Details

The function will check whether the data was previously smoothed. If not, slide-window smoothing will be performed first, and then followed by differential methylation tests

Value

A GRanges object with additional test information (difference, p.value, p.adjust, and etc.)

Author(s)

Pan Du

See Also[identifySigDMR](#)**Examples**

```
data(exampleMethyGenoSet)

sampleType <- pData(exampleMethyGenoSet)$SampleType

## Do differential test
allResult <- detectDMR.slideWin(exampleMethyGenoSet, sampleType=sampleType, testMethod='ttest')
head(allResult)
```

```
exampleMethyGenoSet    Example MethyGenoSet dataset
```

Description

Example MethyGenoSet dataset, which includes eight randomly picked cancer cell line samples from two tissue types. To save space, only 21 chromosome data was included.

Usage

```
data(exampleMethyGenoSet)
```

Details

Example MethyGenoSet dataset, which includes eight randomly picked cancer cell line samples from two tissue types. To save space, only 21 chromosome data was included.

Examples

```
data(exampleMethyGenoSet)
class(exampleMethyGenoSet)
sampleNames(exampleMethyGenoSet)
exampleMethyGenoSet
```

```
export.DMRInfo            Output the DMR (Differentially Methylated Region) data information
```

Description

Output the DMR (Differentially Methylated Region) data information

Usage

```
export.DMRInfo(DMRInfo.ann, methyData = NULL, savePrefix = "")
```


Arguments

DMRInfo.ann The annotated DMR information outputted by annotateDMRInfo.
 methyData Methylation data information in MethyGenoSet or MethyLumiM class
 savePrefix The prefix added to the output file names.

Details

This function basically save the annotated DMR information as text .csv files.

Value

results files.

Author(s)

Pan Du

See Also

[annotateDMRInfo](#)

Examples

```
data(exampleMethyGenoSet)

sampleType <- pData(exampleMethyGenoSet)$SampleType

## Do differential test
allResult <- detectDMR.slideWin(exampleMethyGenoSet, sampleType=sampleType, testMethod='ttest')

## Identify the DMR (Differentially Methylated Region) by setting proper parameters.
## Here we just use default ones
allDMRInfo <- identifySigDMR(allResult)

## Annotate significant DMR info
if (require(TxDb.Hsapiens.UCSC.hg19.knownGene)) {
  DMRInfo.ann <- annotateDMRInfo(allDMRInfo, 'TxDb.Hsapiens.UCSC.hg19.knownGene')
  export.DMRInfo(DMRInfo.ann, savePrefix='testExample')
}
```

export.methyGenoSet *Export a MethyGenoSet object to be visualized using external genome browser tools*

Description

Export a MethyGenoSet object to be visualized in IGV, IGB or other tools. Current version supports "gct" or "bw" formats.

Usage

```
export.methyGenoSet(methyGenoSet, file.format = c("gct", "bw"), exportValue = c("beta", "M"), savePrefix =
```

Arguments

methyGenoSet	A MethyGenoSet object.
file.format	Export file format
exportValue	Export methylation values
savePrefix	The prefix used in the output filename.

Details

An easy way to visualize DNA methylation data is to export the DNA methylation data in certain formats, and visualize these files using some external genome browser tools, like IGV (<http://www.broadinstitute.org/igv/>) and IGB (<http://bioviz.org/igb/index.html>). The current implementation of this function supports two output formats: ".gct" and ".bw" files. ".gct" includes all samples in a single file. It is only supported by IGV genome browser. The BigWig format (".bw") is a more general format supported by many visualization tools. Each BigWig file represents one single sample. So it is more flexible for the users only interested in a subset of samples.

Value

Output "gct" (for IGV) or "bw" (BigWig) files

Author(s)

Pan Du

References

IGV: <http://www.broadinstitute.org/igv/> IGB: <http://bioviz.org/igb/index.html>

Examples

```
data(exampleMethyGenoSet)
export.methyGenoSet(exampleMethyGenoSet, file.format='gct', savePrefix='test')
# export.methyGenoSet(exampleMethyGenoSet, file.format='bw', savePrefix='test')
```

getContinuousRegion	<i>Get continuous chromosome region by merging nearby or overlapping regions</i>
---------------------	--

Description

Get continuous chromosome region by merging nearby or overlapping regions

Usage

```
getContinuousRegion(detectResult, scoreColumns = NULL, scoreFuns = c(mean=mean), maxGap = 2000, min
```

Arguments

detectResult	A GRanges object (with "status" column) or a data.frame with "CHROMOSOME", "POSITION" and "status" columns
scoreColumns	The numeric score columns to be summarized in DMR
scoreFuns	A named vector of summarizing functions. The vector names will be used in the output columns
maxGap	The maximum gap allowed between two nearby probes to be considered within a same DMR
minGap	If two nearby DMRs have a gap less than or equal to the minGap, they will be merged as a single DMR

Details

The "status" column in the "detectResult" parameter is required, which is a logical vector indicating the interested probes.

Value

A GRanges object of DMR

Author(s)

Pan Du

See Also

[identifySigDMR](#)

Examples

```
data(exampleMethyGenoSet)
## get sample type information
sampleType <- pData(exampleMethyGenoSet)$SampleType

## Do differential test
allResult <- detectDMR.slideWin(exampleMethyGenoSet, sampleType=sampleType, testMethod='ttest')

## Identify the DMR (Differentially Methylated Region) by setting proper parameters.
## Here we simply using fdr.adjusted p.value cutoff 0.05 to define DMR
## "status" column is required for getContinuousRegion function.
values(allResult)$status <- values(allResult)$p.adjust < 0.05
dmrInfo <- getContinuousRegion(allResult)
```

heatmapByChromosome *heatmap with chromosome location as x axis*

Description

heatmap with chromosome location as x axis and plot together with other gene annotation information

Usage

```
heatmapByChromosome(methyGenoSet, gene, annotationTracks = NULL, otherTrackList = NULL, expProfile
```

Arguments

methyGenoSet	a GenoSet object keeping the methylation data as the "exprs" numeric matrix in the AssayData
gene	a Entrez Gene ID, or a GRanges object to define the chromosome range of the plot.
annotationTracks	A annotation tracks list returned by buildAnnotationTracks
otherTrackList	A list of other tracks supported by plotTracks function
expProfile	a data matrix with the same number of rows or columns as the columns of methyGenoSet.
expColorMap	the colormap for expression heatmap
extendRange	extended range on each side of the gene
includeGeneBody	whether to include genebody of the provided gene
sortSample	whether to sort samples or not
cytobandInfo	cytoband information
CpGInfo	CpG-island information, GRanges or bed file are supported
genomeAxis	whether to add genome axis or not
dataTrackName	the title of the data track
lib	the Entrez annotation library
genome	genome name
genomicFeature	genomic features: "TranscriptDb" library or object, "Mart" object
gradient	the gradient color used by data track heatmap
ncolor	the number of color levels
main	the title of the plot
...	other parameters used by plotTracksWithDataTrackInfo

Details

This function plots heatmap with chromosome location as x axis and together with other gene annotation information. It is adapted based on the [plotTracks](#) function in Gviz package. Users can also provide a GRanges object to specify a plot region.

Value

returns the grid viewport layout information

Author(s)

Pan Du

See Also

[plotTracks](#), [plotTracksWithDataTrackInfo](#), [plotMethylationHeatmapByGene](#)

Examples

```
data(exampleMethyGenoSet)
if (require(TxDb.Hsapiens.UCSC.hg19.knownGene) && require(Gviz)) {
  ## define data track
  exampleMethyGenoSet <- checkChrName(exampleMethyGenoSet)

  ## build annotation tracks
  selGene <- '1826'
  annotationTracks <- buildAnnotationTracks(selGene, includeGeneBody = FALSE, genomicFeature = "TxDb.Hsapiens.UCSC.hg19.knownGene")
  heatmapByChromosome(exampleMethyGenoSet, selGene, annotationTracks = annotationTracks)
}
```

identifySigDMR	<i>Identify significantly DMR (Differentially Methylated Region)</i>
----------------	--

Description

Identify significantly DMR (Differentially Methylated Region)

Usage

```
identifySigDMR(detectResult, p.adjust.method = "fdr", pValueTh = 0.01, fdrTh = pValueTh, diffTh = 1, minP
```

Arguments

detectResult	A GRanges object or a data.frame with "CHROMOSOME" and "POSITION" columns
p.adjust.method	p.value FDR adjust method
pValueTh	The threshold of p.value
fdrTh	The threshold of FDR (adjusted p.value)
diffTh	The threshold of difference between two conditions
minProbeNum	Minimum number of probes in each DMR
maxGap	The maximum gap allowed between two nearby probes to be considered within a same DMR
minGap	If two nearby DMRs have a gap less than or equal to the minGap, they will be merged as a single DMR

oppositeMethylation Whether require the averaged methylation levels in the DMR are in opposite direction

topNum Whether only returns the top number of probes (ranked by p.value)

Details

(with "status" column)

We define a differentially methylated region (DMR) as a region, in which most measured CpG-sites are differentially methylated. To identify DMRs, the function first determines the differential methylation status of each probe, then merge them as a continuous region. The `identifySigDMR` function returns a list of two GRanges objects. The `sigDMRInfo` includes the identified DMRs, and the `sigDataInfo` includes all differentially methylated probe information.

Value

A list of GRanges objects, `sigDMRInfo` and `sigDataInfo`. `sigDMRInfo` contains DMR information, while `sigDataInfo` includes the probe level information within the DMRs.

Author(s)

Pan Du

See Also

[getContinuousRegion](#), [annotateDMRInfo](#)

Examples

```
data(exampleMethyGenoSet)

sampleType <- pData(exampleMethyGenoSet)$SampleType

## Do differential test
allResult <- detectDMR.slideWin(exampleMethyGenoSet, sampleType=sampleType, testMethod='ttest')

## Identify the DMR (Differentially Methylated Region) by setting proper parameters.
## Here we just use default ones
allDMRInfo <- identifySigDMR(allResult)
```

MethyGenoSet-class	<i>Class MethyGenoSet: contain and describe Illumina Infinium methylation data in GenoSet-class</i>
--------------------	---

Description

This is a class representation for Illumina Infinium methylation microarray data. It directly extends [GenoSet](#). The purpose of this class is to make the high-density methylation microarray data [MethyLumiM-class](#) compatible with the Biocoductor infrastructure packages designed for sequencing analysis.

Extends

Directly extends class [GenoSet](#).

Creating Objects

MethyGenoSet(locData, exprs, methylated, unmethylated, detection = NULL, pData = NULL, annotation = "", universe = NULL, ...)

MethyGenoSet instances are usually created through converting from MethyLumiM object using MethyLumiM2GenoSet function or calling MethyGenoSet function as shown above. The arguments, locData, exprs, methylated and unmethylated, are required; others can be missing. Please check [GenoSet](#) for more details of other parameters.

Slots

locData: a RangedData object, inherited from [GenoSet](#)

assayData: contains equal dimensional matrices: exprs (contains the methylation M-value, same as [MethyLumiM-class](#)), methylated (contains the methylated probe intensities. Same as [MethyLumiM-class](#)), unmethylated (contains the unmethylated probe intensities. Same as [MethyLumiM-class](#)), detection (records the detection p-value of the probe. Same as [MethyLumiM-class](#)). For more details of assayData, please see [ExpressionSet](#)

featureData: See [eSet](#)

phenoData: See [eSet](#)

experimentData: See [eSet](#)

protocolData: See [eSet](#)

annotation: See [eSet](#)

.___classVersion___: See [eSet](#)

history: a data.frame recording the operation history of the MethyGenoSet object.

Methods**Class-specific methods:**

exprs(MethyGenoSet), exprs(MethyGenoSet,matrix)<-: Access and set elements named exprs in the AssayData-class slot.

methylated(MethyGenoSet), methylated(MethyGenoSet)<-: Access and set elements named methylated in the AssayData-class slot.

unmethylated(MethyGenoSet), unjmethylated(MethyGenoSet)<-: Access and set elements named unmethylated in the AssayData-class slot.

detection(MethyGenoSet), detection(MethyGenoSet)<-: Access and set elements named detection in the AssayData-class slot.

as(methyGenoSet,"MethyLumiM") Coerce objects of [MethyGenoSet-class](#) to MethyLumiM

as(genoSet,"MethyGenoSet") Coerce objects of [GenoSet-class](#) to MethyGenoSet

getHistory(MethyGenoSet): Access the operation history of MethyGenoSet object.

Derived from [GenoSet](#):

locData(MethyGenoSet): return a RangedData object, which contains the chromosome location information

Derived from [ExpressionSet](#) (For the directly inherited methods, please see [ExpressionSet](#) and [eSet](#)):

`combine(MethyGenoSet,missing)`: Combine two `MethyGenoSet` objects, including history slot.
See [eSet](#)

`exprs(MethyGenoSet)`, `exprs(MethyGenoSet,matrix)<-`: Access and set elements named `exprs` in the `AssayData`-class slot.

`object[(i,j)]`: Conduct subsetting of the data in a `MethyGenoSet` object

Standard generic methods Please check [ExpressionSet](#) and [eSet](#) for other inherited methods,

Author(s)

Pan Du

See Also

[MethyLumiM2GenoSet](#))

Examples

```
## load example data
data(exampleMethyGenoSet)
class(exampleMethyGenoSet)
```

MethyLumiM2GenoSet *Coerce objects of MethyLumiM-class to MethyGenoSet*

Description

Coerce objects of [MethyLumiM-class](#) to `MethyGenoSet`

Usage

```
MethyLumiM2GenoSet(methyLumiM, lib = "IlluminaHumanMethylation450k.db")
```

Arguments

`methyLumiM` a `MethyLumiM` object
`lib` `lib` is a annotation library

Value

a `MethyGenoSet` object

Author(s)

Pan Du

See Also

[MethyGenoSet](#)

Examples

```

if (require(IlluminaHumanMethylation450k.db)) {
  data(exampleMethyGenoSet)
  ## set as MethyLumiM object
  methyLumiM <- as(exampleMethyGenoSet, 'MethyLumiM')
  ## set back as MethyGenoSet object
  methyGenoSet <- MethyLumiM2GenoSet(methyLumiM, lib = "IlluminaHumanMethylation450k.db")
  class(methyGenoSet)
}

```

```

plotMethylationHeatmapByGene
  plot methylation heatmap by genes

```

Description

plot methylation heatmap by genes

Usage

```
plotMethylationHeatmapByGene(selGene, methyGenoSet, gene2tx = NULL, tx2exon = NULL, expression.tx =
```

Arguments

selGene	a vector of EntrezIDs or a list of gene2tx
methyGenoSet	a GenoSet object for methylation data
gene2tx	a gene to transcript mapping list, used for retrieving expression.tx data
tx2exon	a transcript to exon mapping list, used for retrieving expression.exon data
expression.tx	an ExpressionSet or data matrix for transcript expression
expression.exon	an ExpressionSet or data matrix for exon expression
phenotype	a data.frame for phenotype information
sortBy	whether to sort samples based on the mean of expression profiles, methylation cluster or NA (no sorting)
renameExon	whether to rename exons as "transcript_exon1"
showAllTx	whether to show all transcript in gene2tx or just those provided in selGene
useBetaValue	whether to use methylation Beta-value in the plot.
includeGeneBody	if FALSE, then only shows the promoter region
CpGInfo	a bed file or GRanges for CpG island information
genomicFeature	used by buildAnnotationTracks function
phenoColor	a list of colors corresponding to phenotype
th	the quantile threshold used to remove outlier, which affects the plot color ranges.
title.suffix	a string attached to the end of the title
addLegend	whether to add a legend or not

gradient	the gradient color to show the DataTrack
ncolor	the number of color levels
main	title of the plot. If it is null, then the Gene Symbol will be the plot title
newPlot	whether to create a new plot or add it to previous plot
...	other parameters used by heatmapByChromosome

Details

Function, plotMethylationHeatmapByGene, is specifically designed for the methylation data. It plots one gene or genomic range each time. Users can add phenotypes or matched gene expression data to the right panel of the plot. Figure legends can be also added. By default, the plotMethylationHeatmapByGene plots methylation Beta-values (in the range of 0 to 1) instead of M-values. Users can set useBetaValue as FALSE if they want to change to M-values.

Value

returns the grid viewport information

Author(s)

Pan Du

See Also

See also [heatmapByChromosome](#)

Examples

```
data('exampleMethyGenoSet')
if (require(TxDb.Hsapiens.UCSC.hg19.knownGene)) {
  genomicFeature <- 'TxDb.Hsapiens.UCSC.hg19.knownGene'
  selGene <- '1826'
  plotMethylationHeatmapByGene(selGene, methyGenoSet=exampleMethyGenoSet, phenotype=pData(exampleMethyGenoSet))

  ## use different color map for expression data
  es.example <- matrix(runif(ncol(exampleMethyGenoSet), max=10), nrow=1)
  rownames(es.example) <- selGene
  plotMethylationHeatmapByGene(selGene, methyGenoSet=exampleMethyGenoSet, expression.tx=es.example, genomicFeature=genomicFeature)
}
```

plotTracksWithDataTrackInfo

plot Tracks with additional DataTrack information added to the left of the plot

Description

plot Tracks with additional DataTrack information added to the left of the plot

Usage

```
plotTracksWithDataTrackInfo(trackList, labels, grange2show = NULL, dataTrackName = NULL, dataInfo = N
```

Arguments

trackList	a list of tracks supported by plotTracks function
labels	the sample labels
grange2show	a GRanges to indicate the plot range
dataTrackName	the name of the DataTrack
dataInfo	a data matrix to show the related sample information, e.g. its expression profile
dataColorMap	the color map to plot the dataInfo
dataInfoRange	the range of dataInfo to control the range of color map
labelWidth	the width of the label, which is the ratio of the entire plot width
gradient	the gradient color to show the DataTrack
ncolor	the number of color levels
main	the title of the plot
newPlot	whether to create a new plot or add it to previous plot
...	other parameters used by plotTracks

Details

This function is adapted based on the [plotTracks](#) function in Gviz package. It adds sample labels to the heatmap dataTracks.

Value

Grid viewport layout information

Author(s)

Pan Du

See Also

See Also [plotTracks](#), [heatmapByChromosome](#)

Examples

```
data(exampleMethyGenoSet)
if (require(TxDb.Hsapiens.UCSC.hg19.knownGene) && require(Gviz)) {
  ## define data track
  exampleMethyGenoSet <- checkChrName(exampleMethyGenoSet)
  dTrack <- DataTrack(range=suppressWarnings(as(locData(exampleMethyGenoSet), 'GRanges')), data=t(exprs(examp
  chromosome='chr21', type='heatmap'))

  ## build annotation tracks
  annotationTracks <- buildAnnotationTracks('1826', includeGeneBody = FALSE, genomicFeature = "TxDb.Hsapiens.UC
  trackList <- c(annotationTracks, list(dTrack))
  plotTracksWithDataTrackInfo(trackList, labels=sampleNames(exampleMethyGenoSet), grange2show = attr(annotation
  }
```

smoothMethyData *Smooth the methylation data*

Description

Smooth the methylation data by a sliding window with fixed width in bp unit

Usage

```
smoothMethyData(methyData, winSize = 250, lib = "IlluminaHumanMethylation450k.db", ...)
```

Arguments

methyData	A MethyLumiM or MethyGenoSet object
winSize	Half sliding window size in bp unit at each side of the probe
lib	Methylation annotation library
...	other parameters

Details

The function basically averages the probes within a local window (within winSize bp at each side of the probe).

Value

An object with the methylation values smoothed

Author(s)

Pan Du

See Also

[detectDMR.slideWin](#)

Examples

```
data(exampleMethyGenoSet)
smoothData <- smoothMethyData(exampleMethyGenoSet)
```

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