Package 'skewr'

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Title Visualize Intensities Produced by Illumina's Human Methylation 450k BeadChip

Version 1.44.0

Description The skewr package is a tool for visualizing the output of the Illumina Human Methylation 450k BeadChip to aid in quality control. It creates a panel of nine plots. Six of the plots represent the density of either the methylated intensity or the unmethylated intensity given by one of three subsets of the 485,577 total probes. These subsets include Type I-red, Type I-green, and Type II.The remaining three distributions give the density of the Beta-values for these same three subsets. Each of the nine plots optionally displays the distributions of the ``rs'' SNP probes and the probes associated with imprinted genes as series of 'tick' marks located above the x-axis.

Depends R (>= 3.1.1), methylumi, wateRmelon, mixsmsn, IlluminaHumanMethylation450kmanifest

Imports minfi, S4Vectors (>= 0.19.1), RColorBrewer

Suggests GEOquery, knitr, minfiData

VignetteBuilder knitr

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`getBarcodes` *Get barcodes from idat file names*

Description

A convenience function for retrieving simple barcodes from idat file names.

Usage

```
getBarcodes(path = getwd(), recurse = FALSE)
```

Arguments

`path`	The path or a character vector to the directory or directories in which to find the idat files.
`recurse`	logical; should the function check subdirectories to derive barcodes from any found idat files. The default is `FALSE`.

Details

Barcodes will be generated by all found idats in path(s). The default path is the current working directory.

Value

A character vector of barcodes.

Author(s)

Ryan Putney <ryanputney@gmail.com>

See Also

`getMethyLumiSet`

Examples

```
if(require(minfiData)){
  path <- system.file("extdata/5723646052", package="minfiData")
  barcodes <- getBarcodes(path = path)
}
```

---

getMethyLumiSet *Read idat files and create a* MethyLumiSet *object*

Description

This a wrapper function for methylumIDAT that does not require a vector of barcodes to be provided.

Usage

```
getMethyLumiSet(path = getwd(), barcodes = NULL,
                norm = c("none", "illumina", "SWAN", "dasen"),
                bg.corr = TRUE)
```

Arguments

path	The path to the directory containing the idat files.
barcodes	A vector of barcodes specifying which idat's to read.
norm	Should normalization be done on the resulting MethyLumiSet. The default is "none"
bg.corr	logical; if TRUE, an Illumina style background subtraction will be performed only if norm is set to 'illumina'. Otherwise, it is ignored. If background subtraction without any normalization is desired, the preprocess method must be used.

Details

If only path is provided, all idat's found in the given folder will be pulled. If only barcodes is given, corresponding idat's will be pulled from the current working directory. Both path and barcodes may be passed for finer control. The default is to pull all idat's found in the current working directory.

Value

A MethyLumiSet object

Note

One would probably not normally want to use the preprocess option at this stage. It is more likely that a MethyLumiSet of the raw data will be desired. Then the preprocess method may be used to normalize the raw data or use background subtraction only on the raw data. See the vignette for example workflow.

Author(s)

Ryan Putney <ryanputney@gmail.com>

References

Davis S, Du P, Bilke S, Triche T, Jr. and Bootwalla M (2014). methylumi: Handle Illumina methylation data. R package version 2.12.0.

See Also

getBarcodes, preprocess

Examples

```
if(require('minfiData')) {
  path <- system.file("extdata/5723646052", package="minfiData")
  barcodes <- getBarcodes(path = path)
  methylumiset.raw <- getMethyLumiSet(path = path, barcodes = barcodes[1])
}
```

---

getSNparams *Estimate parameters for finite mixture of Skew-Normal distributions*

Description

Utilizes smsn.mix from the mixsmsn package to find the parameters for a finite mixture of skew normal distributions to model the overall distribution of signal intensities for a subset of probes on the Illumina Infinium HumanMethylation450. The probes may be subset by type and methylated or unmethylated. It can also be specified whether the SNP(rs), imprinted(idmr), or ch probes should be included or filtered out prior to parameter estimation.

Usage

```
getSNparams(MethyLumiSet, allele = c('M', 'U'),
            type = c('I-red', 'I-green', 'II'),
            snps = TRUE, idmr = TRUE, ch = FALSE)
```

Arguments

MethyLumiSet	A MethyLumiSet object
allele	Should parameter estimation be done on the methylated or unmethylated signal intensities
type	Use the signal intensities for which probe type
snps	logical; should the rs probes be included in the dataset. The default is TRUE
idmr	logical; should the probes of imprinted gene loci be included in the dataset. The default is TRUE
ch	logical; should the ch probes be included in the dataset. The default is FALSE

Value

A Skew.normal object as returned by smsn.mix from the mixsmsn package with the means and modes of the components added.

Author(s)

Ryan Putney <ryanputney@gmail.com>

References

Pidsley R, Wong CCY, Volta M, Lunnon K, Mill J, Schalwyk LC(2013). A data-driven approach to preprocessing Illumina 450k methylation array data. BMC Genomics, 14:293.

Prates MO, Cabral CRB, Lachos VH (2013).mixsmsn: Fitting Finite Mixture of Scale Mixture of Skew-Normal Distributions. Journal of Statistical Software, 54(12), 1-20. http://www.jstatsoft.org/v54/i12/

See Also

subsetProbes

Examples

```
if(require('wateRmelon')) {
  data(melon)
  mixes.raw.meth.II <- getSNparams(melon[,1], 'M', 'II')
}
```

---

panelPlots — *Plot the distributions of the probe intensities and the components of the skew-normal mixture model*

Description

Creates a panel of nine plots. Six of the plots represent the density of either the methylated intensity or the unmethylated intensity given by one of three subsets of the 485,577 total probes. These subsets include Type I-red, Type I-green, and Type II.The remaining three distributions give the density of the beta-values for these same three subsets. Each of the nine plots optionally displays the distributions of the "rs" SNP probes and the probes associated with imprinted genes(Pidsley,2013) as a series of 'tick' marks located above the x-axis.

Usage

```
panelPlots(MethyLumiSet, typeIRedModels, typeIGreenModels, typeIIModels,
           plot = c("panel", "frames"), samp.num = NULL, frame.nums = 1:9,
           norm = "", idmr = TRUE, snps = TRUE)
```

Arguments

MethyLumiSet	The MethyLumiSet object from which the mixture models were derived
typeIRedModels	A list of the Type I-red mixture models listed in the following order: methylated models followed by unmethylated models
typeIGreenModels	A list of the Type I-green mixture models listed in the following order: methylated models followed by unmethylated models
typeIIModels	A list of the Type II mixture models listed in the following order: methylated models followed by unmethylated models
plot	Should the output consist of panel plots–one panel per sample or a single panel if samp.num is specified; or should the function output separate plots corresponding to the frames, given by frame.nums, for a single sample. The default is "panel". If set to "frames", samp.num must be specified
samp.num	If plotting for a single sample is desired, for which sample. The number given simply refers to the MethyLumiSet column that corresponds to the sample of interest
frame.nums	if plot is set to "frame", then frame.nums is a vector that specifies which frames of the panel to plot. The default is to plot all nine frames. The frames are numbered from 1 to 9 in column-major order starting with the top left. For example, to plot the four corners, use frame.nums=c(1,3,7,9)
norm	A character string which will be displayed as part of the main title for each plot. Useful in indicated which normalization method was used for the modeled and plotted data
idmr	logical; should the intensities of the idmr probes be plotted as a series of tick-marks above the x-axis. The default is TRUE
snps	logical; should the intensities of the rs probes be plotted as a series of tick-marks above the x-axis. The default is TRUE

Value

No return value. Only plots are generated.

Note

Please refer to the vignette for an example workflow.

Author(s)

Ryan Putney <ryanputney@gmail.com>

References

Prates MO, Cabral CRB, Lachos VH (2013).mixsmsn: Fitting Finite Mixture of Scale Mixture of Skew-Normal Distributions. Journal of Statistical Software, 54(12), 1-20. http://www.jstatsoft.org/v54/i12/

See Also

getSNparams

Examples

```
if(require('minfiData')) {
  path <- system.file("extdata/5723646052", package="minfiData")
  methylumiset.raw <- getMethyLumiSet(path = path)
  mixes.raw.meth.I.red <- getSNparams(methylumiset.raw, 'M', 'I-red')
  mixes.raw.meth.I.green <- getSNparams(methylumiset.raw, 'M', 'I-green')
  mixes.raw.meth.II <- getSNparams(methylumiset.raw, 'M', 'II')
  mixes.raw.unmeth.I.red <- getSNparams(methylumiset.raw, 'U', 'I-red')
  mixes.raw.unmeth.I.green <- getSNparams(methylumiset.raw, 'U', 'I-green')
  mixes.raw.unmeth.II <- getSNparams(methylumiset.raw, 'U', 'II')
  mixes.I.red <- list(mixes.raw.meth.I.red, mixes.raw.unmeth.I.red)
  mixes.I.green <- list(mixes.raw.meth.I.green, mixes.raw.unmeth.I.green)
  mixes.II <- list(mixes.raw.meth.II, mixes.raw.unmeth.II)
  panelPlots(methylumiset.raw, mixes.I.red, mixes.I.green, mixes.II)
}
```

---

preprocess *Normalize a MethyLumiSet object using some popular choices*

Description

This is a wrapper function that allows normalizing of a MethyLumiSet using either a BeadStudio approximation, SWAN, or dasen. If desired, background correction only may be performed on the raw data.

Usage

```
preprocess(MethyLumiSet, norm = c("none", "illumina", "SWAN", "dasen"),
           bg.corr = TRUE)
```

Arguments

MethyLumiSet	A MethyLumiSet object
norm	The normalization method to be used
bg.corr	If TRUE, background subtarction using negative controls is performed. Ignored unless norm equals 'illumina' or 'none'

Details

Both Illumina style normalization via controls and the background correct method are handled by methylumi. The SWAN and dasen normalization methods are both performed by wateRmelon

Value

A MethyLumiSet

Author(s)

Ryan Putney <ryanputney@gmail.com>

References

Davis S, Du P, Bilke S, Triche T, Jr. and Bootwalla M (2014). methylumi: Handle Illumina methylation data. R package version 2.12.0.

Maksimovic J, Gordon L, Oshlack A (2012). SWAN: Subset Quantile Within-Array Normalization for Illumina Infinium HumanMethylation450 BeadChips. Genome Biology, 13:R44.

Pidsley R, Wong CCY, Volta M, Lunnon K, Mill J, Schalwyk LC(2013). A data-driven approach to preprocessing Illumina 450k methylation array data. BMC Genomics, 14:293.

Schalkwyk LC, Pidsley R, Wong CC, Touleimat N, Defrance M, Teschendorff A and Maksimovic J (2013). wateRmelon: Illumina 450 methylation array normalization and metrics. R package version 1.5.1.

See Also

getMethyLumiSet

Examples

```
if(require('wateRmelon')) {
  data(melon)
  melon.dasen <- preprocess(melon, norm = 'dasen')
}
```

---

subsetProbes *Conveniently subset probes by type and retrieve the methylated or unmethylated intensities*

Description

Thus function accepts a MethyLumiSet object generated by methylumi or a MethylSet object generated by minfi. It will subset the probes by type–"I-red", "I-green", or "II"–and return a matrix of the methylated, "M", or unmethylated, "U" signal intensities. It is also possible to include or filter out probes according to whether they are CpG sites(cg), SNPs(rs), imprinted(idmr) gene sites, or non-CpG loci(ch).

Usage

```
subsetProbes(object, allele = c("M", "U"),
             type = c("I-red", "I-green", "II"),
             cg = TRUE, snps = TRUE, idmr = TRUE, ch = FALSE)
```

Arguments

object	A MethyLumiSet or MethylSet object
allele	Should methylated or unmethylated data for the probes be returned.
type	May be "I-red", "I-green", or "II".
cg	Logical; Should the returned dataset contain the CpG probes. The default is TRUE
snps	Logical; Should the returned dataset conain the rs probes. The default is TRUE
idmr	Logical; should the returned dataset include probes that interrogate imprinted gene sites as given by Pidsley et al.(2013). The default is TRUE
ch	Logical; should the returned dataset include the non-CpG (ch) probes. The default if FALSE

Value

A matrix

Author(s)

Ryan Putney <ryanputney@gmail.com>

References

Pidsley R, Wong CCY, Volta M, Lunnon K, Mill J, Schalwyk LC(2013). A data-driven approach to preprocessing Illumina 450k methylation array data. BMC Genomics, 14:293.

See Also

getSNparams

Examples

```
if(require('wateRmelon')) {
  data(melon)
  melon.meth.II <- subsetProbes(melon, 'M', 'II')
}
```

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