Package ‘skewr’

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

Version  1.34.0

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

License  GPL-2

LazyData  true

biocViews  DNAMethylation, TwoChannel, Preprocessing, QualityControl

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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`
**getMethyLumiSet**

### Examples

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

### Description

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

### Usage

```r
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.
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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>MethyLumiSet</td>
<td>A MethyLumiSet object</td>
</tr>
<tr>
<td>allele</td>
<td>Should parameter estimation be done on the methylated or unmethylated signal intensities</td>
</tr>
<tr>
<td>type</td>
<td>Use the signal intensities for which probe type</td>
</tr>
<tr>
<td>snps</td>
<td>logical; should the rs probes be included in the dataset. The default is TRUE</td>
</tr>
<tr>
<td>idmr</td>
<td>logical; should the probes of imprinted gene loci be included in the dataset. The default is TRUE</td>
</tr>
<tr>
<td>ch</td>
<td>logical; should the ch probes be included in the dataset. The default is FALSE</td>
</tr>
</tbody>
</table>
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

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

```r
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

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

```r
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 subtraction 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.
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)
subsetProbes

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 contain 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 is FALSE

Value

A matrix

Author(s)

Ryan Putney <ryanputney@gmail.com>

References


See Also

getSNparams

Examples

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