Package: methimpute (via r-universe)

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`methimpute-package` *methIMPUTE: Imputation-guided methylation status calling for WGBS-seq*

Description

methimpute is an R-package for methylation status calling in Whole-Genome Bisulfite-sequencing (WGBS-seq) data. Its powerful Hidden Markov model implementation enables imputation of methylation status calls for cytosines without any coverage.

Details

Please read the vignette for a tutorial on how to use this package. You can do this by typing `browseVignettes("methimpute")`. Here is an overview of all `plotting` functions.

Author(s)

Aaron Taudt

`arabidopsis_chromosomes` *Chromosome lengths for Arabidopsis*

Description

A data.frame with chromosome lengths for Arabidopsis.

Format

A data.frame.

Examples

```
data(arabidopsis_chromosomes)
print(arabidopsis_chromosomes)
```

`arabidopsis_genes` *Gene coordinates for Arabidopsis (chr1)*

Description

A `GRanges-class` object for demonstration purposes in examples of package **methimpute**. The object contains gene coordinates of chr1 from Arabidopsis.

Format

A `GRanges-class` object.

Examples

```
data(arabidopsis_genes)
print(arabidopsis_genes)
```

arabidopsis_TEs *Transposable element coordinates for Arabidopsis (chr1)*

Description

A GRanges-class object for demonstration purposes in examples of package **methimpute**. The object contains transposable element coordinates of chr1 from Arabidopsis.

Format

A GRanges-class object.

Examples

```
data(arabidopsis_TEs)
print(arabidopsis_TEs)
```

arabidopsis_toydata *Toy data for Arabidopsis (200.000bp of chr1)*

Description

A methimputeData object for demonstration purposes in examples of package **methimpute**. The object contains the first 200.000 cytosines of chr1 from Arabidopsis.

Format

A methimputeData object.

Examples

```
data(arabidopsis_toydata)
print(arabidopsis_toydata)
```

binning *Methimpute binning functions*

Description

This page provides an overview of all **methimpute** binning functions.

Usage

```
binCounts(data, binsize)

binPositions(data, binsize)

binMethylome(data, binsize, contexts = "total", columns.average = NULL)
```

Arguments

data	A GRanges-class object with metadata columns 'context' and 'counts' (which is a matrix with columns 'methylated' and 'total').
binsize	The window size used for binning.
contexts	A character vector with contexts for which the binning will be done.
columns.average	A character vector with names of columns in data that should be averaged in bins.

Value

A GRanges-class object for binCounts and binPostions. A list() of GRanges-class objects for binMethylome.

Functions

- binCounts: Get the aggregated number of counts in each bin (no context).
- binPositions: Get the number of cytosines in each bin (total and per context).
- binMethylome: Get number of cytosines and aggregated counts for the specified contexts.

Examples

```
## Get some toy data
file <- system.file("data","arabidopsis_toydata.RData",
                    package="methimpute")
data <- get(load(file))
print(data)
## Bin the data in various ways
binCounts(data, binsize=1000)
binPositions(data, binsize=1000)
binMethylome(data, binsize=1000, contexts=c("total", "CG"),
```

```
                columns.average=NULL)
```

`binomialTestMethylation` *Call methylation status*

Description

Call methylation status of cytosines (or bins) with a binomial test.

Usage

```
binomialTestMethylation(data, conversion.rate, min.coverage = 3,
  p.threshold = 0.05)
```

Arguments

`data`	A `methimputeData` object.
`conversion.rate`	A conversion rate between 0 and 1.
`min.coverage`	Minimum coverage to consider for the binomial test.
`p.threshold`	Significance threshold between 0 and 1.

Details

The function uses a binomial test with the specified `conversion.rate`. P-values are then multiple testing corrected with the Benjamini & Yekutieli procedure. Methylated positions are selected with the `p.threshold`.

Value

A vector with methylation statuses.

Examples

```
## Get some toy data
file <- system.file("data","arabidopsis_toydata.RData", package="methimpute")
data <- get(load(file))
data$binomial <- binomialTestMethylation(data, conversion.rate=0.998)
```

`callMethylation` *Call methylation status*

Description

Call methylation status of cytosines (or bins) with a Hidden Markov Model.

Usage

```
callMethylation(data, fit.on.chrom = NULL, transDist = Inf, eps = 1,
  max.time = Inf, max.iter = Inf, count.cutoff = 500,
  verbosity = 1, num.threads = 2 + include.intermediate,
  initial.params = NULL, include.intermediate = FALSE,
  update = "independent", min.reads = 0)
```

Arguments

`data`	A `methimputeData` object.
`fit.on.chrom`	A character vector specifying the chromosomes on which the HMM will be fitted.
`transDist`	The decaying constant for the distance-dependent transition matrix. Either a single numeric or a named numeric vector, where the vector names correspond to the transition contexts. Such a vector can be obtained from `estimateTransDist`.
`eps`	Convergence threshold for the Baum-Welch algorithm.
`max.time`	Maximum running time in seconds for the Baum-Welch algorithm.
`max.iter`	Maximum number of iterations for the Baum-Welch algorithm.
`count.cutoff`	A cutoff for the counts to remove artificially high counts from mapping artifacts. Set to `Inf` to disable this filtering (not recommended).
`verbosity`	An integer from 1 to 5 specifying the verbosity of the fitting procedure. Values > 1 are only for debugging.
`num.threads`	Number of CPU to use for the computation. Parallelization is implemented on the number of states, which is 2 or 3, so setting `num.threads > 3` will not give additional performance increase.
`initial.params`	A `methimputeBinomialHMM` object. This parameter is useful to continue the fitting procedure for a `methimputeBinomialHMM` object.
`include.intermediate`	A logical specifying wheter or not the intermediate component should be included in the HMM.
`update`	One of `c("independent", "constrained")`. If `update="independent"` probability parameters for the binomial test will be updated independently. If `update="constrained"` the probability parameter of the intermediate component will be constrained to the mean of the unmethylated and the methylated component.
`min.reads`	The minimum number of reads that a position must have to contribute in the Baum-Welch fitting procedure.

Details

The Hidden Markov model uses a binomial test for the emission densities. Transition probabilities are modeled with a distance dependent decay, specified by the parameter `transDist`.

Value

A `methimputeBinomialHMM` object.

Examples

```
## Get some toy data
file <- system.file("data","arabidopsis_toydata.RData", package="methimpute")
data <- get(load(file))
print(data)
model <- callMethylation(data)
print(model)
```

---

callMethylationSeparate

Call methylation status

Description

Call methylation status of cytosines (or bins) with a separate Hidden Markov Model for each context.

Usage

```
callMethylationSeparate(data, fit.on.chrom = NULL, transDist = Inf,
  eps = 1, max.time = Inf, max.iter = Inf, count.cutoff = 500,
  verbosity = 1, num.threads = 2 + include.intermediate,
  initial.params = NULL, include.intermediate = FALSE,
  update = "independent", min.reads = 0)
```

Arguments

`data`	A `methimputeData` object.
`fit.on.chrom`	A character vector specifying the chromosomes on which the HMM will be fitted.
`transDist`	The decaying constant for the distance-dependent transition matrix. Either a single numeric or a named numeric vector, where the vector names correspond to the transition contexts. Such a vector can be obtained from `estimateTransDist`.
`eps`	Convergence threshold for the Baum-Welch algorithm.
`max.time`	Maximum running time in seconds for the Baum-Welch algorithm.
`max.iter`	Maximum number of iterations for the Baum-Welch algorithm.

count.cutoff	A cutoff for the counts to remove artificially high counts from mapping artifacts. Set to Inf to disable this filtering (not recommended).
verbosity	An integer from 1 to 5 specifying the verbosity of the fitting procedure. Values > 1 are only for debugging.
num.threads	Number of CPU to use for the computation. Parallelization is implemented on the number of states, which is 2 or 3, so setting num.threads > 3 will not give additional performance increase.
initial.params	A methimputeBinomialHMM object. This parameter is useful to continue the fitting procedure for a methimputeBinomialHMM object.
include.intermediate	A logical specifying wheter or not the intermediate component should be included in the HMM.
update	One of c("independent", "constrained"). If update="independent" probability parameters for the binomial test will be updated independently. If update="constrained" the probability parameter of the intermediate component will be constrained to the mean of the unmethylated and the methylated component.
min.reads	The minimum number of reads that a position must have to contribute in the Baum-Welch fitting procedure.

Details

The Hidden Markov model uses a binomial test for the emission densities. Transition probabilities are modeled with a distance dependent decay, specified by the parameter transDist.

Value

A methimputeBinomialHMM object.

Examples

```
## Get some toy data
file <- system.file("data","arabidopsis_toydata.RData", package="methimpute")
data <- get(load(file))
print(data)
model <- callMethylationSeparate(data)
print(model)
```

---

collapseBins *Collapse consecutive bins*

Description

The function will collapse consecutive bins which have, for example, the same combinatorial state.

Usage

```
collapseBins(data, column2collapseBy = NULL, columns2sumUp = NULL,
  columns2average = NULL, columns2getMax = NULL, columns2drop = NULL)
```

Arguments

`data`	A data.frame containing the genomic coordinates in the first three columns.
`column2collapseBy`	The number of the column which will be used to collapse all other inputs. If a set of consecutive bins has the same value in this column, they will be aggregated into one bin with adjusted genomic coordinates.
`columns2sumUp`	Column numbers that will be summed during the aggregation process.
`columns2average`	Column numbers that will be averaged during the aggregation process.
`columns2getMax`	Column numbers where the maximum will be chosen during the aggregation process.
`columns2drop`	Column numbers that will be dropped after the aggregation process.

Details

The following tables illustrate the principle of the collapsing:

Input data:

seqnames	start	end	column2collapseBy	moreColumns	columns2sumUp
chr1	0	199	2	1 10	1 3
chr1	200	399	2	2 11	0 3
chr1	400	599	2	3 12	1 3
chr1	600	799	1	4 13	0 3
chr1	800	999	1	5 14	1 3

Output data:

seqnames	start	end	column2collapseBy	moreColumns	columns2sumUp
chr1	0	599	2	1 10	2 9
chr1	600	999	1	4 13	1 6

Value

A data.frame.

Author(s)

Aaron Taudt

Examples

```
## Load example data
## Get an example multiHMM
data(arabidopsis_toydata)
df <- as.data.frame(arabidopsis_toydata)
shortdf <- collapseBins(df, column2collapseBy='context', columns2sumUp='width', columns2average=7:8)
```

`distanceCorrelation` *Distance correlation*

Description

Compute the distance correlation from a `methimputeData` object.

Usage

```
distanceCorrelation(data, distances = 0:50, separate.contexts = FALSE)
```

Arguments

`data`	A `methimputeData` object.
`distances`	An integer vector specifying the distances for which the correlation will be calculated.
`separate.contexts`	A logical indicating whether contexts are treated separately. If set to `TRUE`, correlations will only be calculated between cytosines of the same context.

Value

A list() with an array containing the correlation values and the corresponding `ggplot`.

Examples

```
## Get some toy data
file <- system.file("data","arabidopsis_toydata.RData",
                    package="methimpute")
data <- get(load(file))
distcor <- distanceCorrelation(data)
print(distcor$plot)
```

estimateTransDist transDist *parameter*

Description

Obtain an estimate for the transDist parameter (used in function callMethylation) by fitting an exponential function to the supplied correlations (from distanceCorrelation).

Usage

```
estimateTransDist(distcor, skip = 2, plot.parameters = TRUE)
```

Arguments

distcor	The output produced by distanceCorrelation.
skip	Skip the first n cytosines for the fitting. This can be necessary to avoid periodicity artifacts due to the context definition.
plot.parameters	Whether to plot fitted parameters on to the plot or not.

Value

A list() with fitted transDist parameters and the corresponding ggplot.

Examples

```
## Get some toy data
file <- system.file("data","arabidopsis_toydata.RData",
                    package="methimpute")
data <- get(load(file))
distcor <- distanceCorrelation(data)
fit <- estimateTransDist(distcor)
print(fit)
```

exportMethylome *Export a methylome*

Description

Export a methylome as a TSV file.

Usage

```
exportMethylome(model, filename)
```

Arguments

model	A methimputeBinomialHMM object.
filename	The name of the file to be exported.

Value

NULL

Examples

```
## Not run:
## Get some toy data
file <- system.file("data","arabidopsis_toydata.RData", package="methimpute")
data <- get(load(file))
print(data)
model <- callMethylation(data, max.iter=10)
exportMethylome(model, filename = tempfile())

## End(Not run)
```

---

extractCytosinesFromFASTA

Extract cytosine coordinates

Description

Extract cytosine coordinates and context information from a FASTA file. Cytosines in ambiguous reference contexts are not reported.

Usage

```
extractCytosinesFromFASTA(file, contexts = c("CG", "CHG", "CHH"),
  anchor.C = NULL)
```

Arguments

file	A character with the file name.
contexts	The contexts that should be extracted. If the contexts are named, the returned object will use those names for the contexts.
anchor.C	A named vector with positions of the anchoring C in the contexts. This is necessary to distinguish contexts such as C*C*CG (anchor.C = 2) and *C*CCG (anchor.C = 1). Names must match the contexts. If unspecified, the first C within each context will be taken as anchor.

Value

A GRanges-class object with coordinates of extracted cytosines and meta-data column 'context'.

Examples

```
## Read a non-compressed FASTA files:
filepath <- system.file("extdata", "arabidopsis_sequence.fa.gz", package="methimpute")

## Only CG context
cytosines <- extractCytosinesFromFASTA(filepath, contexts = 'CG')
table(cytosines$context)

## Split CG context into subcontexts
cytosines <- extractCytosinesFromFASTA(filepath,
               contexts = c('DCG', 'CCG'),
               anchor.C = c(DCG=2, CCG=2))
table(cytosines$context)

## With contexts that differ only by anchor
cytosines <- extractCytosinesFromFASTA(filepath,
               contexts = c('DCG', 'CCG', 'CCG', 'CWG', 'CHH'),
               anchor.C = c(DCG=2, CCG=2, CCG=1, CWG=1, CHH=1))
table(cytosines$context)

## With named contexts
contexts <- c(CG='DCG', CG='CCG', CHG='CCG', CHG='CWG', CHH='CHH')
cytosines <- extractCytosinesFromFASTA(filepath,
               contexts = contexts,
               anchor.C = c(DCG=2, CCG=2, CCG=1, CWG=1, CHH=1))
table(cytosines$context)
```

---

getDistinctColors *Get distinct colors*

Description

Get a set of distinct colors selected from `colors`.

Usage

```
getDistinctColors(n, start.color = "blue4", exclude.colors = c("white",
  "black", "gray", "grey", "\\<yellow\\>", "yellow1", "lemonchiffon"),
  exclude.brightness.above = 1, exclude.rgb.above = 210)
```

Arguments

`n`	Number of colors to select. If `n` is a character vector, `length(n)` will be taken as the number of colors and the colors will be named by `n`.
`start.color`	Color to start the selection process from.
`exclude.colors`	Character vector with colors that should not be used.

`exclude.brightness.above`
: Exclude colors where the 'brightness' value in HSV space is above. This is useful to obtain a matt palette.

`exclude.rgb.above`
: Exclude colors where all RGB values are above. This is useful to exclude whitish colors.

Details

The function computes the euclidian distance between all `colors` and iteratively selects those that have the furthest closes distance to the set of already selected colors.

Value

A character vector with colors.

Author(s)

Aaron Taudt

Examples

```
cols <- getDistinctColors(5)
pie(rep(1,5), labels=cols, col=cols)
```

---

getPosteriors *Get original posteriors*

Description

Transform the 'posteriorMeth', 'posteriorMax', and 'status' columns into original posteriors from the HMM.

Usage

```
getPosteriors(data)
```

Arguments

`data`	The `$data` entry from a `methimputeBinomialHMM` object.

Value

A matrix with posteriors.

getStateColors *Get state colors*

Description

Get the colors that are used for plotting.

Usage

```
getStateColors(states = NULL)
```

Arguments

states	A character vector.

Value

A character vector with colors.

See Also

plotting

Examples

```
cols <- getStateColors()
pie(1:length(cols), col=cols, labels=names(cols))
```

import *Methimpute data import*

Description

This page provides an overview of all **methimpute** data import functions.

Usage

```
importBSMAP(file, chrom.lengths = NULL, skip = 1, contexts = c(CG =
  "NNCGN", CHG = "NNCHG", CHH = "NNCHH"))

importMethylpy(file, chrom.lengths = NULL, skip = 1, contexts = c(CG
  = "CGN", CHG = "CHG", CHH = "CHH"))

importBSSeeker(file, chrom.lengths = NULL, skip = 0)

importBismark(file, chrom.lengths = NULL, skip = 0)
```

Arguments

file	The file to import.
chrom.lengths	A data.frame with chromosome names in the first, and chromosome lengths in the second column. Only chromosomes named in here will be returned. Alternatively a tab-separated file with such a data.frame (with headers).
skip	The number of lines to skip. Usually 1 if the file contains a header and 0 otherwise.
contexts	A character vector of the contexts that are to be assigned. Since some programs report 5-letter contexts, this parameter can be used to obtain a reduced number of contexts. Will yield contexts CG, CHG, CHH by default. Set contexts=NULL to obtain all available contexts.

Value

A methimputeData object.

Functions

- importBSMAP: Import a BSMAP methylation extractor file.
- importMethylpy: Import a Methylpy methylation extractor file.
- importBSSeeker: Import a BSSeeker methylation extractor file.
- importBismark: Import a Bismark methylation extractor file.

Examples

```
## Get an example file in BSSeeker format
file <- system.file("extdata","arabidopsis_bsseeker.txt.gz", package="methimpute")
data(arabidopsis_chromosomes)
bsseeker.data <- importBSSeeker(file, chrom.lengths=arabidopsis_chromosomes)

## Get an example file in Bismark format
file <- system.file("extdata","arabidopsis_bismark.txt", package="methimpute")
data(arabidopsis_chromosomes)
arabidopsis_chromosomes$chromosome <- sub('chr', '', arabidopsis_chromosomes$chromosome)
bismark.data <- importBismark(file, chrom.lengths=arabidopsis_chromosomes)

## Get an example file in BSMAP format
file <- system.file("extdata","arabidopsis_BSMAP.txt", package="methimpute")
data(arabidopsis_chromosomes)
bsmap.data <- importBSMAP(file, chrom.lengths=arabidopsis_chromosomes)

## Get an example file in Methylpy format
file <- system.file("extdata","arabidopsis_methylpy.txt", package="methimpute")
data(arabidopsis_chromosomes)
arabidopsis_chromosomes$chromosome <- sub('chr', '', arabidopsis_chromosomes$chromosome)
methylpy.data <- importMethylpy(file, chrom.lengths=arabidopsis_chromosomes)
```

importRene *Import a Rene methylation extractor file*

Description

Import a Rene methylation extractor file into a GRanges-class object.

Usage

```
importRene(file, chrom.lengths = NULL, skip = 1)
```

Arguments

file	The file to import.
chrom.lengths	A data.frame with chromosome names in the first, and chromosome lengths in the second column. Only chromosomes named in here will be returned. Alternatively a tab-separated file with such a data.frame (with headers).
skip	The number of lines to skip. Usually 1 if the file contains a header and 0 otherwise.

Value

A methimputeData object.

Examples

```
## Get an example file in Rene format
file <- system.file("extdata","arabidopsis_rene.txt", package="methimpute")
data(arabidopsis_chromosomes)
rene.data <- methimpute:::importRene(file, chrom.lengths=arabidopsis_chromosomes)
```

inflateMethylome *Inflate an imported methylation extractor file*

Description

Inflate an imported methylation extractor file to contain all cytosine positions. This is useful to obtain a full methylome, including non-covered cytosines, because most methylation extractor programs only report covered cytosines.

Usage

```
inflateMethylome(methylome, methylome.full)
```

Arguments

methylome	A GRanges-class with methylation counts.
methylome.full	A GRanges-class with positions for all cytosines or a file with such an object.

Value

The methylome.full object with added metadata column 'counts'.

Examples

```
## Get an example file in BSSeeker format
file <- system.file("extdata","arabidopsis_bsseeker.txt.gz", package="methimpute")
bsseeker.data <- importBSSeeker(file)
bsseeker.data

## Inflate to full methylome (including non-covered sites)
data(arabidopsis_toydata)
full.methylome <- inflateMethylome(bsseeker.data, arabidopsis_toydata)
full.methylome
```

---

loadFromFiles *Load* **methimpute** *objects from file*

Description

Wrapper to load **methimpute** objects from file and check the class of the loaded objects.

Usage

```
loadFromFiles(files, check.class = c("GRanges", "methimputeBinomialHMM"))
```

Arguments

files	A list of GRanges-class or methimputeBinomialHMM objects or a character vector with files that contain such objects.
check.class	Any combination of c('GRanges', 'methimputeBinomialHMM'). If any of the loaded objects does not belong to the specified class, an error is thrown.

Value

A list of GRanges-class or methimputeBinomialHMM objects.

Examples

```
## Get some files that you want to load
file <- system.file("data","arabidopsis_toydata.RData",
                    package="methimpute")
## Load and print
data <- loadFromFiles(file)
print(data)
```

`methimpute-objects` *methimpute objects*

Description

methimpute defines several objects.

- `methimputeData`: Returned by `importBSSeeker`, `importBismark` and `inflateMethylome`.
- `methimputeBinomialHMM`: Returned by `callMethylation`.

`methimputeBinomialHMM` *methimputeBinomialHMM*

Description

The `methimputeBinomialHMM` is a list() which contains various entries (see Value section). The main entry of this object is `$data`, which contains the methylation status calls and posterior values. See Details for a description of all columns.

Details

The `$data` entry in this object contains the following columns:

- context The sequence context of the cytosine.
- counts Counts for methylated and total number of reads at each position.
- distance The distance in base-pairs from the previous to the current cytosine.
- transitionContext Transition context in the form "previous-current".
- posteriorMax Maximum posterior value of the methylation status call, can be interpreted as the confidence in the call.
- posteriorMeth Posterior value of the "methylated" component.
- posteriorUnmeth Posterior value of the "unmethylated" component.
- status Methylation status.
- rc.meth.lvl Recalibrated methylation level, calculated as `r$data$rc.meth.lvl = r$data$params$emissionParams$U * r$data$posteriorUnmeth + r$params$emissionParams$Methylated[data$context,] * r$data$posteriorMeth`, where `r` is the `methimputeBinomialHMM` object.

Value

A list() with the following entries:

convergenceInfo	A list() with information about the convergence of the model fitting procedure.
params	A list() with fitted and non-fitted model parameters.
params.initial	A list() with initial values for the model parameters.
data	A GRanges-class with cytosine positions and methylation status calls.
segments	The data entry where coordinates of consecutive cytosines with the same methylation status have been merged.

See Also

methimpute-objects

---

methimputeData *methimputeData*

Description

A GRanges-class object containing cytosine coordinates with meta-data columns 'context' and 'counts'.

See Also

methimpute-objects

---

parameterScan *Perform a parameter scan*

Description

Perform a parameter scan for an arbitrary parameter.

Usage

```
parameterScan(f, param, values, ...)
```

Arguments

f	A function for which to perform the scan.
param	A character with the parameter for which to perform the scan.
values	A vector with parameter values for which to perform the scan.
...	Other parameters passed through to f.

Value

A data.frame with loglikelihood values.

`plotting` *Methimpute plotting functions*

Description

This page provides an overview of all **methimpute** plotting functions.

Usage

```
plotHistogram(model, total.counts, binwidth = 1)

plotScatter(model, datapoints = 1000)

plotTransitionProbs(model)

plotConvergence(model)

plotEnrichment(model, annotation, windowsize = 100, insidewindows = 20,
  range = 1000, category.column = NULL, plot = TRUE,
  df.list = NULL)

plotPosteriorDistance(model, datapoints = 1e+06, binwidth = 5,
  max.coverage.y = 0, min.coverage.x = 3, xmax = 200,
  xbreaks.interval = xmax/10, cutoffs = NULL)
```

Arguments

`model`	A `methimputeBinomialHMM` object.
`total.counts`	The number of total counts for which the histogram is to be plotted.
`binwidth`	The bin width for the histogram/boxplot.
`datapoints`	The number of randomly selected datapoints for the plot.
`annotation`	A `GRanges-class` object with coordinates for the annotation.
`windowsize`	Resolution in base-pairs for the curve upstream and downstream of the annotation.
`insidewindows`	Number of data points for the curve inside the annotation.
`range`	Distance upstream and downstream for which the enrichment profile is calculated.
`category.column`	The name of a column in `data` that will be used for facetting of the plot.
`plot`	Logical indicating whether a plot or the underlying data.frame is to be returned.

df.list	A list() of data.frames, output from plotEnrichment(..., plot=FALSE). If specified, option data will be ignored.
max.coverage.y	Maximum coverage for positions on the y-axis.
min.coverage.x	Minimum coverage for positions on the x-axis.
xmax	Upper limit for the x-axis.
xbreaks.interval	Interval for breaks on the x-axis.
cutoffs	A vector with values that are plotted as horizontal lines. The names of the vector must match the context levels in data$context.

Value

A ggplot object.

Functions

- plotHistogram: Plot a histogram of count values and fitted distributions.
- plotScatter: Plot a scatter plot of read counts colored by methylation status.
- plotTransitionProbs: Plot a heatmap of transition probabilities.
- plotConvergence: Plot the convergence of the probability parameters.
- plotEnrichment: Plot an enrichment profile around an annotation.
- plotPosteriorDistance: Maximum posterior vs. distance to nearest covered cytosine.

Examples

```
## Get some toy data
file <- system.file("data","arabidopsis_toydata.RData",
                    package="methimpute")
data <- get(load(file))
print(data)
model <- callMethylation(data)
## Make nice plots
plotHistogram(model, total.counts=5)
plotScatter(model)
plotTransitionProbs(model)
plotConvergence(model)
plotPosteriorDistance(model$data)

## Get annotation data and make an enrichment profile
# Note that this looks a bit ugly because our toy data
# has only 200000 datapoints.
data(arabidopsis_genes)
plotEnrichment(model, annotation=arabidopsis_genes)
```

print.methimputeBinomialHMM *Print model object*

Description

Print model object

Usage

```
## S3 method for class 'methimputeBinomialHMM'
print(x, ...)
```

Arguments

x	A methimputeBinomialHMM object.
...	Ignored.

Value

An invisible NULL.

transCoord *Transform genomic coordinates*

Description

Add two columns with transformed genomic coordinates to the GRanges-class object. This is useful for making genomewide plots.

Usage

```
transCoord(gr)
```

Arguments

gr	A GRanges-class object.

Value

The input GRanges-class with two additional metadata columns 'start.genome' and 'end.genome'.

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