

# Package ‘methimpute’

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**Type** Package

**Title** Imputation-guided re-construction of complete methylomes from WGBS data

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**Description**

This package implements functions for calling methylation for all cytosines in the genome.

**Depends** R (>= 3.4.0), GenomicRanges, ggplot2

**Imports** Rcpp (>= 0.12.4.5), methods, utils, grDevices, stats, GenomeInfoDb, IRanges, Biostrings, reshape2, minpack.lm, data.table

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methimpute-package	<i>methIMPUTE: Imputation-guided methylation status calling for WGBS-seq</i>
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## 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

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

### Value

A `GRanges-class` object for `binCounts` and `binPositions`. 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

<code>data</code>	A <code>methimputeData</code> object.
<code>conversion.rate</code>	A conversion rate between 0 and 1.
<code>min.coverage</code>	Minimum coverage to consider for the binomial test.
<code>p.threshold</code>	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	<i>Call methylation status</i>
-----------------	--------------------------------

---

**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 <a href="#">methimputeData</a> 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 <a href="#">estimateTransDist</a> .
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 <a href="#">methimputeBinomialHMM</a> object. This parameter is useful to continue the fitting procedure for a <a href="#">methimputeBinomialHMM</a> object.
include.intermediate	A logical specifying whether 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

<code>data</code>	A <code>methimputeData</code> object.
<code>fit.on.chrom</code>	A character vector specifying the chromosomes on which the HMM will be fitted.
<code>transDist</code>	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 <code>estimateTransDist</code> .
<code>eps</code>	Convergence threshold for the Baum-Welch algorithm.
<code>max.time</code>	Maximum running time in seconds for the Baum-Welch algorithm.
<code>max.iter</code>	Maximum number of iterations for the Baum-Welch algorithm.
<code>count.cutoff</code>	A cutoff for the counts to remove artificially high counts from mapping artifacts. Set to <code>Inf</code> 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 <code>methimputeBinomialHMM</code> object. This parameter is useful to continue the fitting procedure for a <code>methimputeBinomialHMM</code> object.
include.intermediate	A logical specifying wheter or not the intermediate component should be included in the HMM.
update	One of <code>c("independent", "constrained")</code> . If <code>update="independent"</code> probability parameters for the binomial test will be updated independently. If <code>update="constrained"</code> 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**

<code>data</code>	A data.frame containing the genomic coordinates in the first three columns.
<code>column2collapseBy</code>	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.
<code>columns2sumUp</code>	Column numbers that will be summed during the aggregation process.
<code>columns2average</code>	Column numbers that will be averaged during the aggregation process.
<code>columns2getMax</code>	Column numbers where the maximum will be chosen during the aggregation process.
<code>columns2drop</code>	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 <a href="#">distanceCorrelation</a> .
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	<i>Export a methylome</i>
-----------------	---------------------------

---

**Description**

Export a methylome as a TSV file.

**Usage**

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

**Arguments**

model	A <a href="#">methimputeBinomialHMM</a> 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	<i>Get original posteriors</i>
---------------	--------------------------------

---

**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	<i>Get state colors</i>
----------------	-------------------------

---

**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	<i>Methimpute data import</i>
--------	-------------------------------

---

## 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 Methylypy format
file <- system.file("extdata", "arabidopsis_methylypy.txt", package="methimpute")
data(arabidopsis_chromosomes)
arabidopsis_chromosomes$chromosome <- sub('chr', '', arabidopsis_chromosomes$chromosome)
methylypy.data <- importMethylypy(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	<i>Inflate an imported methylation extractor file</i>
------------------	---

---

### 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	<i>Load <b>methimpute</b> objects from file</i>
---------------	---

---

### 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$emissionParams * r\data$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 <a href="#">GRanges-class</a> 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	<i>methimputeData</i>
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---

**Description**

A [GRanges-class](#) object containing cytosine coordinates with meta-data columns 'context' and 'counts'.

**See Also**

[methimpute-objects](#)

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parameterScan	<i>Perform a parameter scan</i>
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---

**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.

**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**

<code>model</code>	A <a href="#">methimputeBinomialHMM</a> object.
<code>total.counts</code>	The number of total counts for which the histogram is to be plotted.
<code>binwidth</code>	The bin width for the histogram/boxplot.
<code>datapoints</code>	The number of randomly selected datapoints for the plot.
<code>annotation</code>	A <a href="#">GRanges-class</a> object with coordinates for the annotation.
<code>windowsize</code>	Resolution in base-pairs for the curve upstream and downstream of the annotation.
<code>insidewindows</code>	Number of data points for the curve inside the annotation.
<code>range</code>	Distance upstream and downstream for which the enrichment profile is calculated.
<code>category.column</code>	The name of a column in data that will be used for facetting of the plot.
<code>plot</code>	Logical indicating whether a plot or the underlying data.frame is to be returned.
<code>df.list</code>	A <code>list()</code> of data.frames, output from <code>plotEnrichment(...,plot=FALSE)</code> . If specified, option data will be ignored.
<code>max.coverage.y</code>	Maximum coverage for positions on the y-axis.
<code>min.coverage.x</code>	Minimum coverage for positions on the x-axis.
<code>xmax</code>	Upper limit for the x-axis.
<code>xbreaks.interval</code>	Interval for breaks on the x-axis.
<code>cutoffs</code>	A vector with values that are plotted as horizontal lines. The names of the vector must match the context levels in <code>data\$context</code> .

**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**

<code>x</code>	A <code>methimputeBinomialHMM</code> object.
<code>...</code>	Ignored.

**Value**

An invisible NULL.

---

transCoord	<i>Transform genomic coordinates</i>
------------	--------------------------------------

---

**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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