Package 'REMP'

October 17, 2017

Type Package

Title Repetitive Element Methylation Prediction

Version 1.0.7

Description Machine learning-based tools to predict DNA methylation of locus-specific repetitive elements (RE) by learning surrounding genetic and epigenetic information. These tools provide genomewide and single-base resolution of DNA methylation prediction on RE that are difficult to measure using array-based or sequencing-based platforms, which enables epigenome-wide association study (EWAS) and differentially methylated region (DMR) analysis on RE.

License GPL-3

Depends R (>= 3.4), SummarizedExperiment(>= 1.1.6), minfi (>= 1.22.0), IlluminaHumanMethylation450kanno.ilmn12.hg19, IlluminaHumanMethylationEPICanno.ilm10b2.hg19

Imports graphics, stats, utils, methods, settings, BiocGenerics, S4Vectors, Biostrings, GenomicRanges, IRanges, BiocParallel, doParallel, parallel, foreach, caret, kernlab, ranger, BSgenome, AnnotationHub, BSgenome.Hsapiens.UCSC.hg19, org.Hs.eg.db, impute, iterators

Suggests knitr, rmarkdown, minfiDataEPIC

Collate REMParcel-class.R REMProduct-class.R generics.R REMParcel-methods.R REMProduct-methods.R options.R utils.R tools.R getGM12878.R grooMethy.R initREMP.R remp.R DemoData.R REMP-package.R

VignetteBuilder knitr

URL https://github.com/YinanZheng/REMP

BugReports https://github.com/YinanZheng/REMP/issues

LazyData true

biocViews DNAMethylation, Microarray, MethylationArray, GenePrediction, Sequencing, Alignment, Epigenetics, Normalization, Preprocessing, MultiChannel, TwoChannel, DifferentialMethylation, QualityControl, DataImport

RoxygenNote 6.0.1

NeedsCompilation no

Author Yinan Zheng [aut, cre], Lei Liu [aut],

Wei Zhang [aut],
Warren Kibbe [aut],
Lifang Hou [aut, cph]

Maintainer Yinan Zheng <y-zheng@northwestern.edu>

R topics documented:

REMP-package *Repetitive Element Methylation Prediction*

Description

Machine learning-based tools to predict DNA methylation of locus-specific repetitive elements (RE) by learning surrounding genetic and epigenetic information. These tools provide genomewide and single-base resolution of DNA methylation prediction on RE that are difficult to measure using array-based or sequencing-based platforms, which enables epigenome-wide association study (EWAS) and differentially methylated region (DMR) analysis on RE.

Overview - standard procedure

Step 1 Start out generating required dataset for prediction using `initREMP`. The datasets include RE information, RE-CpG (i.e. CpGs located in RE region) information, and gene annotation, which are maintained in a `REMParcel` object. It is recommended to save these generated data to the working directory so they can be used in the future.

Step 2 Clean Illumina methylation dataset using `grooMethy`. This function can help identify and fix abnormal values and automatically impute missing values, which are essential for downstream prediction.

Step 3 Run `remp` to predict genome-wide locus specific RE methylation.

Step 4 Use the built-in accessors and utilities in `REMProduct` object to get or refine the prediction results.

Author(s)

Yinan Zheng <y-zheng@northwestern.edu>, Lei Liu <lei.liu@northwestern.edu>, Wei Zhang <wei.zhang1@northwestern.edu>, Warren Kibbe <warren.kibbe@nih.gov>, Lifang Hou <l-hou@northwestern.ed

Maintainer: Yinan Zheng <y-zheng@northwestern.edu>

References

Zheng Y, Joyce BT, Liu L, Zhang Z, Kibbe WA, Zhang W, Hou L. Prediction of genome-wide DNA methylation in repetitive elements. Nucleic Acids Res. 2017;45(15):8697-711. PubMed PMID: 28911103; PMCID: PMC5587781. http://dx.doi.org/10.1093/nar/gkx587.

Alu.demo *Subset of Alu sequence dataset*

Description

A GRanges dataset containing 500 Alu sequences that have CpGs profiled by both Illumina 450k and EPIC array. The variables are as follows:

Usage

```
Alu.demo
```

Format

A GRanges object.

Details

- seqnames chromosome number
- ranges hg19 genomic position
- strand DNA strand
- name Alu subfamily
- score Smith Waterman (SW) alignment score
- Index internal index

Scripts for generating this object are contained in the scripts directory.

Value

A GRanges object with 500 ranges and 3 metadata columns.

Source

RepeatMasker database provided by package AnnotationHub.

fetchRefSeqGene *Get RefSeq gene database*

Description

fetchRefSeqGene is used to obtain refSeq gene database provided by AnnotationHub.

Usage

```
fetchRefSeqGene(ah, mainOnly = FALSE, verbose = FALSE)
```

Arguments

ah	An AnnotationHub object. Use AnnotationHub() to retrive information about all records in the hub.
mainOnly	Logical parameter. See details.
verbose	Logical parameter. Should the function be verbose?

Details

When mainOnly = FALSE, only the transcript location information will be returned, Otherwise, a GRangesList object containing gene regions information will be added. Gene regions include: 2000 base pair upstream of the transcript start site ($tss)), 5'UTR ($fiveUTR)), coding sequence ($cds)), exon ($exon)), and 3'UTR ($threeUTR)). The index column is an internal index that is used to facilitate data referral, which is meaningless for external use.

Value

A single GRanges (for main refgene data) object or a list incorporating both GRanges object (for main refgene data) and GRangesList object (for gene regions data).

Examples

```
ah <- AnnotationHub::AnnotationHub()
refGene <- fetchRefSeqGene(ah, mainOnly = TRUE, verbose = TRUE)
refGene
```

fetchRMSK *Get RE database from RepeatMasker*

Description

fetchRMSK is used to obtain specified RE database from RepeatMasker Database provided by AnnotationHub.

Usage

```
fetchRMSK(ah, REtype, verbose = FALSE)
```

Arguments

ah	An AnnotationHub object. Use AnnotationHub() to retrive information about all records in the hub.
REtype	Type of RE. Currently "Alu" and "L1" are supported.
verbose	Logical parameter. Should the function be verbose?

Value

A GRanges object containing RE database. 'name' column indicates the RE subfamily; 'score' column indicates the SW score; 'Index' is an internal index for RE to facilitate data referral, which is meaningless for external use.

Examples

```
ah <- AnnotationHub::AnnotationHub()
L1 <- fetchRMSK(ah, 'L1', verbose = TRUE)
L1
```

---

findRECpG *Find RE-CpG genomic location given RE ranges information*

Description

findRECpG is used to obtain RE-CpG genomic location data.

Usage

```
findRECpG(RE.hg19, REtype = c("Alu", "L1"), be = NULL, verbose = FALSE)
```

Arguments

RE.hg19	an GRanges object of RE genomic location database. This can be obtained by fetchRMSK.
REtype	Type of RE. Currently "Alu" and "L1" are supported.
be	A BiocParallel object containing back-end information that is ready for parallel computing. This can be obtained by getBackend.
verbose	logical parameter. Should the function be verbose?

Details

CpG site is defined as 5'-C-p-G-3'. It is reasonable to assume that the methylation status across all CpG/CpG dyads are concordant. Maintenance methyltransferase exhibits a preference for hemimethylated CpG/CpG dyads (methylated on one strand only). As a result, methyaltion status of CpG sites in both forward and reverse strands are usually consistent. Therefore, to accommodate the cytosine loci in both strands, the returned genomic ranges cover the 'CG' sequence with width of 2. The 'stand' information indicates the strand of the RE.

Value

A GRanges object containing identified RE-CpG genomic location data.

Examples

```
data(Alu.demo)
be <- getBackend(1, verbose = TRUE)
RE.CpG <- findRECpG(Alu.demo, 'Alu', be, verbose = TRUE)
RE.CpG
```

---

getBackend *Get BiocParallel back-end*

Description

getBackend is used to obtain BiocParallel Back-end to allow parallel computing.

Usage

```
getBackend(ncore, BPPARAM = NULL, verbose = FALSE)
```

Arguments

ncore	Number of cores to run parallel computation. By default max number of cores available in the machine will be utilized. If ncore = 1, no parallel computation is allowed.
BPPARAM	An optional BiocParallelParam instance determining the parallel back-end to be used during evaluation. If not specified, default back-end in the machine will be used.
verbose	Logical parameter. Should the function be verbose?

Value

A BiocParallel object that can be used for parallel computing.

Examples

```
# Non-parallel mode
be <- getBackend(1, verbose = TRUE)
be

# parallel mode (2 workers)
be <- getBackend(2, verbose = TRUE)
be
```

getGM12878 *Get methylation data of HapMap LCL sample GM12878 profiled by Illumina 450k array or EPIC array*

Description

getGM12878 is used to obtain public available methylation profiling data of HapMap LCL sample GM12878.

Usage

```
getGM12878(arrayType = c("450k", "EPIC"), mapGenome = FALSE)
```

Arguments

arrayType	Illumina methylation array type. Currently "450k" and "EPIC" are supported. Default = "450k".
mapGenome	Logical parameter. If TRUE, function will return a GenomicRatioSet object instead of a link{RatioSet} object.

Details

Illumina 450k data were sourced and curated from ENCODE http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeHaibMethyl450/wgEncodeHaibMethyl450Gm12878SitesRep1.bed.gz. Illumina EPIC data were obtained from data package minfiDataEPIC.

Value

A RatioSet or GenomicRatioSet containing beta value and M value of the methylation data.

Examples

```
# Get GM12878 methylation data (EPIC array)
GM12878_EPIC <- getGM12878('EPIC')
GM12878_EPIC
```

GRannot *Annotate genomic ranges data with gene region information.*

Description

GRannot is used to annotate a GRanges dataset with gene region information using refseq gene database

Usage

```
GRannot(object.GR, refgene, symbol = FALSE, verbose = FALSE)
```

Arguments

object.GR	An GRanges object of a genomic location database.
refgene	A complete refGene annotation database returned by fetchRefSeqGene (with parameter mainOnly = FALSE).
symbol	Logical parameter. Should the annotation return gene symbol?
verbose	Logical parameter. Should the function be verbose?

Details

The annotated gene region information includes: protein coding gene (InNM), noncoding RNA gene (InNR), 2000 base pair upstream of the transcript start site (InTSS), 5'UTR (In5UTR), coding sequence (InCDS), exon (InExon), and 3'UTR (In3UTR). The intergenic and intron regions can then be represented by the combination of these region data. The number shown in these columns represent the row number or 'index' column in the main refgene database obtained by fetchRefSeqGene.

Value

A GRanges or a GRangesList object containing refSeq Gene database.

Examples

```
data(Alu.demo)
ah <- AnnotationHub::AnnotationHub()
refgene.hg19 <- fetchRefSeqGene(ah, verbose = TRUE)
Alu.demo.refGene <- GRannot(Alu.demo, refgene.hg19, verbose = TRUE)
Alu.demo.refGene
```

---

grooMethy *Groom methylation data to fix potential data issues*

Description

grooMethy is used to automatically detect and fix data issues including zero beta value, missing value, and infinite value.

Usage

```
grooMethy(methyDat, impute = TRUE, imputebyrow = TRUE, mapGenome = FALSE,
  verbose = FALSE)
```

Arguments

methyDat	A RatioSet, GenomicRatioSet, DataFrame, data.table, data.frame, or matrix of Illumina methylation data.
impute	If TRUE, K-Nearest Neighbouring imputation will be applied to fill the missing values. Default = TRUE. See Details.
imputebyrow	If TRUE, missing values will be imputed using similar values in row (i.e., across samples); if FALSE, missing values will be imputed using similar values in column (i.e., across CpGs). Default is TRUE.

mapGenome	Logical parameter. If TRUE, function will return a GenomicRatioSet object instead of a RatioSet.
verbose	Logical parameter. Should the function be verbose?

Details

For methylation data in beta value, if zero value exists, the logit transformation from beta to M value will produce negative infinite value. Therefore, zero beta value will be replaced with the smallest non-zero beta value found in the dataset. grooMethy can also handle missing value (i.e. NA or NaN) using KNN imputation (see impute.knn). The infinite value will be also treated as missing value for imputation. If the original dataset is in beta value, grooMethy will first transform it to M value before imputation is carried out. If the imputed value is out of the original range (which is possible when imputebyrow = FALSE), mean value will be used instead. Warning: imputed values for multimodal distributed CpGs (across samples) may not be correct. Please check package ENmix to identify the CpGs with multimodal distribution. Please note that grooMethy is also embedded in remp so the user can run remp directly without explicitly running grooMethy.

Value

A RatioSet or GenomicRatioSet containing beta value and M value of the methylation data.

Examples

```
GM12878_450k <- getGM12878('450k') # Get GM12878 methylation data (450k array)
grooMethy(GM12878_450k, verbose = TRUE)
grooMethy(minfi::getBeta(GM12878_450k), verbose = TRUE)
```

---

initREMP *RE Annotation Database Initialization*

Description

initREMP is used to initialize annotation database for RE methylation prediction. Two major RE types in human, Alu element (Alu) and LINE-1 (L1) are available.

Usage

```
initREMP(arrayType = c("450k", "EPIC"), REtype = c("Alu", "L1"),
  RE = NULL, ncore = NULL, BPPARAM = NULL, export = FALSE,
  work.dir = tempdir(), verbose = FALSE)
```

Arguments

arrayType	Illumina methylation array type. Currently "450k" and "EPIC" are supported. Default = "450k".
REtype	Type of RE. Currently "Alu" and "L1" are supported.
RE	A GRanges object containing user-specified RE genomic location information. If NULL, the function will retrive RepeatMasker RE database from AnnotationHub (build hg19).

ncore	Number of cores to run parallel computation. By default max number of cores available in the machine will be utilized. If ncore = 1, no parallel computation is allowed.
BPPARAM	An optional BiocParallelParam instance determining the parallel back-end to be used during evaluation. If not specified, default back-end in the machine will be used.
export	Logical. Should the returned REMParcel object be saved to local machine? See Details.
work.dir	Path to the directory where the generated data will be saved. Valid when export = TRUE. If not specified and export = TRUE, temporary directory tempdir() will be used.
verbose	Logical parameter. Should the function be verbose?

Details

Currently, we support two major types of RE in human, Alu and L1. The main purpose of initREMP is to generate and annotate CpG/RE data using the refSeq Gene annotation database (provided by AnnotationHub). These annotation data are crucial to RE methylation prediction in remp. Once generated, the data can be reused in the future (data can be very large). Therefore, we recommend user to save the output from initREMP to the local machine, so that user only need to run this function once as long as there is no change to the RE database. To minimize the size of resulting data file, the generated annotation data are only for REs that contain RE-CpGs with neighboring profiled CpGs. By default, the neighboring CpGs are confined within 1200 bp flanking window. This window size can be modified using remp_options.

Value

An REMParcel object containing data needed for RE methylation prediction.

See Also

See remp for RE methylation prediction.

Examples

```
data(Alu.demo)
remparcel <- initREMP(arrayType = '450k', REtype = 'Alu', RE = Alu.demo, ncore = 1)
remparcel

# Save the data for later use
saveParcel(remparcel)
```

---

remp *Repetitive element methylation prediction*

Description

remp is used to predict genomewide methylation levels of locus-specific repetitive elements (RE). Two major RE types in human, Alu element (Alu) and LINE-1 (L1) are available.

Usage

```
remp(methyDat, REtype = c("Alu", "L1"), parcel = NULL,
  work.dir = tempdir(), groom = TRUE, win = 1000, method = c("rf",
  "svmLinear", "svmRadial", "naive"), autoTune = TRUE, param = NULL,
  seed = NULL, ncore = NULL, BPPARAM = NULL, verbose = FALSE)
```

Arguments

methyDat	A RatioSet, GenomicRatioSet, DataFrame, data.table, data.frame, or matrix of methylation dataset. See Details.
REtype	Type of RE. Currently "Alu" and "L1" are supported.
parcel	An REMParcel object containing necessary data to carry out the prediction. If NULL, the function will search the .rds data file in work.dir exported by initREMP (with export = TRUE) or saveParcel.
work.dir	Path to the directory where the annotation data generated by initREMP are saved. Valid when the argument parcel is missing. If not specified, temporary directory tempdir() will be used. If specified, the directory path has to be the same as the one specified in initREMP or in saveParcel.
groom	Should the function run grooMethy implicitly to check and fix the data? Default = TRUE. If grooMethy has been run in advance, let groom = FALSE can avoid repeated check.
win	An integer specifying window size to confine the upstream and downstream flanking region centered on the predicted CpG in RE for prediction. Default = 1000. See Details.
method	Name of model/approach for prediction. Currently "rf" (Random Forest), "svmLinear" (SVM with linear kernel), "svmRadial" (SVM with linear kernel), and "naive" (carrying over methylation values of the closest CpG site) are available. Default = "rf" (Random Forest). See Details.
autoTune	Logical parameter. If TRUE, a 3-time repeated 5-fold cross validation will be performed to determine the best model parameter. If FALSE, the param option (see below) must be specified. Default = TRUE. Auto-tune will be disabled using Random Forest. See Details.
param	A number or a vector specifying the model tuning parameter(s) (not applicable for Random Forest). For SVM, param represents 'Cost' (for linear kernel) or 'Sigma' and 'Cost' (for radial basis function kernel). This parameter is valid only when autoTune = FALSE.
seed	Random seed for Random Forest model for reproducible prediction results. Default is NULL, which generates a seed.
ncore	Number of cores to run parallel computation. By default, max number of cores available in the machine will be utilized. If ncore = 1, no parallel computation is allowed.
BPPARAM	An optional BiocParallelParam instance determining the parallel back-end to be used during evaluation. If not specified, default back-end in the machine will be used.
verbose	Logical parameter. Should the function be verbose?

Details

Before running `remp`, user should make sure the methylation data have gone through proper quality control, background correction, and normalization procedures. Both beta value and M value are allowed. Rows represents probes and columns represents samples. Please make sure to have row names that specify the Illumina probe ID (i.e. cg00000029). Parameter `win = 1000` is based on previous findings showing that neighboring CpGs are more likely to be co-modified within 1000 bp. User can specify narrower window size for slight improvement of prediction accuracy at the cost of less predicted RE. Window size greater than 1000 is not recommended as the machine learning models would not be able to learn much userful information for prediction but introduce noise. Random Forest model (`method = "rf"`) is recommented as it offers more accurate prediction and it also enables prediction reliability functionality. Prediction reliability is estimated by conditional standard deviation using Quantile Regression Forest. Please note that if parallel computing is allowed, parallel Random Forest (powered by package `ranger`) will be used automatically. The performance of Random Forest model is often relatively insensitive to the choice of `mtry`. Therefore, auto-tune will be turned off using Random Forest and `mtry` will be set to one third of the total number of predictors. For SVM, if `autoTune = TRUE`, preset tuning parameter search grid can be access and modified using `remp_options`.

Value

An `REMProduct` object containing prediction results.

See Also

See `initREMP` to prepare necessary annotation database before running `remp`.

Examples

```
# Obtain example Illumina example data (450k)
GM12878_450k <- getGM12878('450k')

# Make sure you have run 'initREMP'. See ?initREMP.

# Run prediction (grooMethy will be run implicitly)
remp.res <- remp(GM12878_450k, REtype = 'Alu', ncore = 1)
remp.res
details(remp.res)

# Extract CpG location information (inherit from class 'RangedSummarizedExperiment')
rowRanges(remp.res)

# RE annotation information
annotation(remp.res)

# Add gene annotation
remp.res <- decodeAnnot(remp.res, type = "symbol", ncore = 1)
annotation(remp.res)

# Density plot across predicted CpGs in RE
plot(remp.res)

# Trim off less reliable prediction
remp.res <- trim(remp.res)
plot(remp.res)
```

REMParcel-class *REMParcel instances*

Description

REMParcel is a container class to organize required datasets for RE methylation prediction generated from initREMP and used in remp.

Usage

```
REMParcel(REtype = "Unknown", platform = "Unknown", RefGene = GRanges(),
  RE = GRanges(), RECpG = GRanges(), ILMN = GRanges())

getRefGene(object)

getRE(object)

getRECpG(object)

getILMN(object, ...)

saveParcel(object, ...)

## S4 method for signature 'REMParcel'
saveParcel(object, work.dir = tempdir(),
  verbose = FALSE, ...)

## S4 method for signature 'REMParcel'
getRefGene(object)

## S4 method for signature 'REMParcel'
getRE(object)

## S4 method for signature 'REMParcel'
getRECpG(object)

## S4 method for signature 'REMParcel'
getILMN(object, REonly = FALSE)
```

Arguments

REtype	Type of RE ("Alu" or "L1").
platform	Illumina methylation profiling platform ("450k" or "EPIC").
RefGene	refSeq gene annotation data, which can be obtained by fetchRefSeqGene.
RE	Annotated RE genomic range data, which can be obtained by fetchRMSK and annotated by GRannot.
RECpG	Genomic range data of annotated CpG site identified in RE DNA sequence, which can be obtained by findRECpG and annotated by GRannot.
ILMN	Illumina CpG probe genomic range data.

object	A REMParcel object.
...	For saveParcel: other parameters to be passed to the saveRDS method. See saveRDS.
work.dir	For saveParcel: path to the directory where the generated data will be saved. If not specified, temporary directory tempdir() will be used.
verbose	For saveParcel: logical parameter. Should the function be verbose?
REonly	For getILMN: see Accessors.

Value

An object of class REMParcel for the constructor.

Accessors

getRefGene(object) Return RefSeq gene annotation data.

getRE(object) Return RE genomic location data for prediction (annotated by refSeq gene database).

getRECpG(object) Return RE-CpG genomic location data for prediction.

getILMN(object, REonly = FALSE) Return Illumina CpG probe genomic location data for prediction (annotated by refSeq gene database). If REonly = TRUE, only probes within RE region are returned.

Utilities

saveParcel(object, work.dir = tempdir(), verbose = FALSE, ...) Save the object to local machine.

Examples

```
showClass("REMParcel")
```

REMProduct-class *REMProduct instances*

Description

Class REMProduct is to maintain RE methylation prediction results. REMProduct inherits Bioconductor's RangedSummarizedExperiment class.

Usage

```
REMProduct(REtype = "Unknown", platform = "Unknown", win = "Unknown",
  predictModel = "Unknown", QCModel = "Unknown", rempM = NULL,
  rempB = NULL, rempQC = NULL, cpgRanges = GRanges(),
  sampleInfo = DataFrame(), REannotation = GRanges(), RECpG = GRanges(),
  regionCode = DataFrame(), refGene = GRanges(), varImp = DataFrame(),
  REStats = DataFrame(), GeneStats = DataFrame(), Seed = NULL)

rempM(object)
```

```
rempB(object)

rempQC(object)

annotation(object)

imp(object)

stats(object)

details(object)

decodeAnnot(object, ...)

trim(object, ...)

## S4 method for signature 'REMProduct'
rempM(object)

## S4 method for signature 'REMProduct'
rempB(object)

## S4 method for signature 'REMProduct'
rempQC(object)

## S4 method for signature 'REMProduct'
imp(object)

## S4 method for signature 'REMProduct'
annotation(object)

## S4 method for signature 'REMProduct'
stats(object)

## S4 method for signature 'REMProduct,missing'
plot(x, type = c("individual", "overall"), ...)

## S4 method for signature 'REMProduct'
details(object)

## S4 method for signature 'REMProduct'
decodeAnnot(object, type = c("symbol", "entrez"),
  ncore = NULL, BPPARAM = NULL)

## S4 method for signature 'REMProduct'
trim(object, threshold = 1.7, missingRate = 0.2)
```

Arguments

REtype	Type of RE ("Alu" or "L1").
platform	Illumina methylation profiling platform ("450k" or "EPIC").
win	Flanking window size of the predicting RE-CpG.

predictModel	Name of the model used for prediction.
QCModel	Name of the model used for prediction quality evaluation.
rempM	Predicted methylation level in M value.
rempB	Predicted methylation level in beta value (optional).
rempQC	Prediction quality scores, which is available only when Random Forest model is used in remp.
cpgRanges	Genomic ranges of the predicting RE-CpG.
sampleInfo	Sample information.
REannotation	Annotation data for the predicting RE.
RECpG	Annotation data for the RE-CpG profiled by Illumina platform.
regionCode	Internal index code defined in refGene for gene region indicators.
refGene	refSeq gene annotation data, which can be obtained by fetchRefSeqGene.
varImp	Importance of the predictors.
REStats	RE coverage statistics, which is internally generated in remp.
GeneStats	Gene coverage statistics, which is internally generated in remp.
Seed	Random seed for Random Forest model for reproducible prediction results.
object	A REMProduct object.
...	For plot: graphical parameters to be passed to the plot method.
x	For plot: an REMProduct object.
type	For plot and decodeAnnot: see Utilities.
ncore	For decodeAnnot: number of cores to run parallel computation. By default max number of cores available in the machine will be utilized. If ncore = 1, no parallel computation is allowed (not recommended).
BPPARAM	For decodeAnnot: an optional BiocParallelParam instance determining the parallel back-end to be used during evaluation. If not specified, default back-end in the machine will be used.
threshold	For trim: see Utilities.
missingRate	For trim: see Utilities.

Value

An object of class REMProduct for the constructor.

Accessors

rempM(object) Return M value of the prediction.

rempB(object) Return beta value of the prediction.

rempQC(object) Return prediction quality scores.

imp(object) Return relative importance of predictors.

stats(object) Return RE and gene coverage statistics.

annotation(object) Return annotation data for the predicted RE.

Utilities

`plot(x, type = c("individual", "overall"), ...)` Make a density plot of predicted methylation (beta values) in the `REMProduct` object `x`. If `type = "individual"`, density curves will be plotted for each of the samples; If `type = "overall"`, one density curve of the mean methylation level across the samples will be plotted. Default `type = "individual"`.

`details(object)` Display detailed descriptive statistics of the predicion results.

`decodeAnnot(object, type = c("symbol", "entrez")), ncore = NULL, BPPARAM = NULL` Decode the RE annotation data by Gene Symbol (when `type = "Symbol"`) or Entrez Gene (when `type = "Entrez"`).Default `type = "Symbol"`. Annotation data are provided by `org.Hs.eg.db`.

`trim(object, threshold = 1.7, missingRate = 0.2)` Any predicted CpG values with quality score < threshold (default = 1.7) will be replaced with NA. CpGs contain more than missingRate * 100 will be re-evaluated.

Examples

```
showClass("REMProduct")
```

---

remp_options *Set or get options for REMP package*

Description

Tools to manage global setting options for REMP package.

Usage

```
remp_options(...)

remp_reset()
```

Arguments

`...`	Option names to retrieve option values or `[key]=[value]` pairs to set options.

Value

`NULL`

Supported options

The following options are supported

`.default.AluFamily` A list of Alu subfamily to be included in the prediction.

`.default.L1Family` A list of L1 subfamily to be included in the prediction.

`.default.GM12878.450k.URL` URL to download GM12878 450k methylation profiling data.

`.default.AH.repeatmasker.hg19` `AnnotationHub` data ID linked to RepeatMasker database (build hg19)

`.default.AH.refgene.hg19` `AnnotationHub` data ID linked to refSeq gene database (build hg19)

`.default.TSS.upstream` Define the upstream range of transcription start site region.

`.default.TSS.downstream` Define the downstream range of transcription start site region.

`.default.max.flankWindow` Define the max size of the flanking window surrounding the predicted RE-CpG.

`.default.450k.annotation` A character string associated with the Illumina 450k array annotation dataset.

`.default.epic.annotation` A character string associated with the Illumina EPIC array annotation dataset.

`.default.genomicRegionColNames` Define the names of the genomic regions for prediction.

`.default.predictors` Define the names of predictors for RE methylation prediction.

`.default.C.svmLinear.tune` Define the default `C` (Cost) parameter for Support Vector Machine (SVM) using linear kernel.

`.default.sigma.svmRadial.tune` Define the default `sigma` parameter for SVM using Radial basis function kernel.

`.default.C.svmRadial.tune` Define the default `C` (Cost) parameter for SVM using Radial basis function kernel.

Examples

```
# Display all default settings
remp_options()

# Change default maximum flanking window size to 2000
remp_options(.default.max.flankWindow = 2000)

# Reset all options
remp_reset()
```

Index