Package 'sesame'

June 5, 2026

Type Package

Title SEnsible Step-wise Analysis of DNA MEthylation BeadChips

Description Tools For analyzing Illumina Infinium DNA methylation arrays. SeSAMe provides utilities to support analyses of multiple generations of Infinium DNA methylation BeadChips, including preprocessing, quality control, visualization and inference. SeSAMe features accurate detection calling, intelligent inference of ethnicity, sex and advanced quality control routines.

Version 1.31.0

Depends R (>= 4.5.0), sesameData

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RoxygenNote 7.3.3

Imports graphics, BiocParallel, utils, methods, stringr, readr, tibble, MASS, wheatmap (>= 0.2.0), GenomicRanges (>= 1.61.1), IRanges, grid, preprocessCore, S4Vectors, ggplot2, BiocFileCache, Seqinfo, stats, SummarizedExperiment (>= 1.39.1), dplyr, reshape2

Suggests scales, BiocManager, GenomeInfoDb, knitr, DNAcopy, e1071, randomForest, RPMM, rmarkdown, testthat, tidyr, BiocStyle, ggrepel, grDevices, KernSmooth, pals

Encoding UTF-8

VignetteBuilder knitr

URL https://github.com/zwdzwd/sesame

BugReports https://github.com/zwdzwd/sesame/issues

biocViews DNAMethylation, MethylationArray, Preprocessing, QualityControl

Collate 'readIDAT.R' 'sex.R' 'species.R' 'QC.R' 'GEO.R' 'SigDFMethods.R' 'sesame.R' 'age.R' 'background.R' 'cell_composition.R' 'channel_inference.R' 'cnv.R' 'impute.R' 'mLiftOver.R' 'ethnicity.R' 'deidentify.R' 'detection.R' 'dm.R' 'dye_bias.R' 'feature_selection.R' 'fileSet.R' 'mask.R' 'sesameAnno.R' 'open.R' 'strain.R' 'tissue.R' 'track.R' 'match_design.R' 'utils.R' 'vcf.R' 'visualize.R' 'visualizeHelper.R' 'zzz.R' 'palgen.R'

git_url https://git.bioconductor.org/packages/sesame

git_branch devel

git_last_commit 9dcdf06

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-06-04

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Contents

`sesame-package` *Analyze DNA methylation data*

Description

SEnsible and step-wise analysis of DNA methylation data

Details

This package complements array functionalities that allow processing >10,000 samples in parallel on clusters.

Value

package

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References

Zhou W, Triche TJ, Laird PW, Shen H (2018)

See Also

Useful links:

- https://github.com/zwdzwd/sesame
- Report bugs at https://github.com/zwdzwd/sesame/issues

Examples

```
sdf <- readIDATpair(sub('_Grn.idat','',system.file(
    'extdata','4207113116_A_Grn.idat',package='sesameData')))

## The OpenSesame pipeline
betas <- openSesame(sdf)
```

`addMask` *Add probes to mask*

Description

This function essentially merge existing probe masking with new probes to mask

Usage

```
addMask(sdf, probes)
```

Arguments

`sdf`	a `SigDF`
`probes`	a vector of probe IDs or a logical vector with TRUE representing masked probes

Value

a `SigDF` with added mask

Examples

```
sdf <- sesameDataGet('EPIC.1.SigDF')
sum(sdf$mask)
sum(addMask(sdf, c("cg14057072", "cg22344912"))$mask)
```

`assemble_plots` *assemble plots*

Description

assemble plots

Usage

```
assemble_plots(
  betas,
  txns,
  probes,
  plt.txns,
  plt.mapLines,
  plt.cytoband,
  heat.height = NULL,
  mapLine.height = 0.2,
  show.probeNames = TRUE,
  show.samples.n = NULL,
  show.sampleNames = TRUE,
  sample.name.fontsize = 10,
  dmin = 0,
  dmax = 1
)
```

Arguments

`betas`	beta value
`txns`	transcripts GRanges
`probes`	probe GRanges
`plt.txns`	transcripts plot objects
`plt.mapLines`	map line plot objects
`plt.cytoband`	cytoband plot objects
`heat.height`	heatmap height (auto inferred based on rows)
`mapLine.height`	height of the map lines
`show.probeNames`	whether to show probe names
`show.samples.n`	number of samples to show (default: all)
`show.sampleNames`	whether to show sample names
`sample.name.fontsize`	sample name font size
`dmin`	data min
`dmax`	data max

Value

a grid object

betasCollapseToPfx *Collapse betas by averagng probes with common probe ID prefix*

Description

Collapse betas by averagng probes with common probe ID prefix

Usage

```
betasCollapseToPfx(betas, BPPARAM = SerialParam())
```

Arguments

betas	either a named numeric vector or a numeric matrix (row: probes, column: samples)
BPPARAM	use MulticoreParam(n) for parallel processing

Value

either named numeric vector or a numeric matrix of collapsed beta value matrix

Examples

```
## input is a matrix
m <- matrix(seq(0,1,length.out=9), nrow=3)
rownames(m) <- c("cg00004963_TC21", "cg00004963_TC22", "cg00004747_TC21")
colnames(m) <- c("A","B","C")
betasCollapseToPfx(m)

## input is a vector
m <- setNames(seq(0,1,length.out=3),
    c("cg00004963_TC21", "cg00004963_TC22", "cg00004747_TC21"))
betasCollapseToPfx(m)
```

BetaValueToMValue *Convert beta-value to M-value*

Description

Logit transform a beta value vector to M-value vector.

Usage

```
BetaValueToMValue(b)
```

Arguments

b	vector of beta values

Details

Convert beta-value to M-value (aka logit transform)

Value

a vector of M values

Examples

```
BetaValueToMValue(c(0.1, 0.5, 0.9))
```

---

binSignals *Bin signals from probe signals*

Description

require GenomicRanges

Usage

```
binSignals(probe.signals, bin.coords, probeCoords)
```

Arguments

probe.signals	probe signals
bin.coords	bin coordinates
probeCoords	probe coordinates

Value

bin signals

---

bisConversionControl *Compute internal bisulfite conversion control*

Description

Compute GCT score for internal bisulfite conversion control. The function takes a SigSet as input. The higher the GCT score, the more likely the incomplete conversion.

Usage

```
bisConversionControl(sdf, extR = NULL, extA = NULL, verbose = FALSE)
```

Arguments

sdf	a SigDF
extR	a vector of probe IDs for Infinium-I probes that extend to converted A
extA	a vector of probe IDs for Infinium-I probes that extend to original A
verbose	print more messages

Value

GCT score (the higher, the more incomplete conversion)

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
bisConversionControl(sdf)

## For more recent platforms like EPICv2, MSA:
## One need extR and extA of other arrays using the sesameAnno
## Not run:
mft = sesameAnno_buildManifestGRanges(sprintf(
  "%s/EPICv2/EPICv2.hg38.manifest.tsv.gz",
  "https://github.com/zhou-lab/InfiniumAnnotationV1/raw/main/Anno/"),
  columns="nextBase")
extR = names(mft)[!is.na(mft$nextBase) & mft$nextBase=="R"]
extA = names(mft)[!is.na(mft$nextBase) & mft$nextBase=="A"]

## End(Not run)
```

`calcEffectSize` *Compute effect size for different variables from prediction matrix*

Description

The effect size is defined by the maximum variation of a variable with all the other variables controled constant.

Usage

```
calcEffectSize(pred)
```

Arguments

`pred`	predictions

Value

a data.frame of effect sizes. Columns are different variables. Rows are different probes.

Examples

```
data <- sesameDataGet('HM450.76.TCGA.matched')
res <- DMLpredict(data$betas[1:10,], ~type, meta=data$sampleInfo)
head(calcEffectSize(res))
```

checkLevels *filter data matrix by factor completeness only works for discrete factors*

Description

filter data matrix by factor completeness only works for discrete factors

Usage

```
checkLevels(betas, fc)
```

Arguments

betas	matrix data
fc	factors, or characters

Value

a boolean vector whether there is non-NA value for each tested group for each probe

Examples

```
se0 <- sesameDataGet("MM285.10.SE.tissue")[1:100,]
se_ok <- checkLevels(SummarizedExperiment::assay(se0),
    SummarizedExperiment::colData(se0)$tissue)
sum(se_ok) # number of good probes
se1 <- se0[se_ok,]

sesameDataGet_resetEnv()
```

chipAddressToSignal *Lookup address in one sample*

Description

Lookup address and transform address to probe

Usage

```
chipAddressToSignal(dm, mft, min_beads = NULL)
```

Arguments

dm	data frame in chip address, 2 columns: cy3/Grn and cy5/Red
mft	a data frame with columns Probe_ID, M, U and col
min_beads	minimum bead counts, otherwise masked

Details

Translate data in chip address to probe address. Type I probes can be separated into Red and Grn channels. The methylated allele and unmethylated allele are at different addresses. For type II probes methylation allele and unmethylated allele are at the same address. Grn channel is for methylated allele and Red channel is for unmethylated allele. The out-of-band signals are type I probes measured using the other channel.

Value

a SigDF, indexed by probe ID address

---

cnSegmentation *Perform copy number segmentation*

Description

Perform copy number segmentation using the signals in the signal set. The function takes a `SigDF` for the target sample and a set of normal `SigDF` for the normal samples. An optional arguments specifies the version of genome build that the inference will operate on. The function outputs an object of class `CNSegment` with signals for the segments (seg.signals), the bin coordinates (bin.coords) and bin signals (bin.signals).

Usage

```
cnSegmentation(
  sdf,
  sdfs.normal = NULL,
  genomeInfo = NULL,
  probeCoords = NULL,
  tilewidth = 50000,
  verbose = FALSE,
  return.probe.signals = FALSE
)
```

Arguments

`sdf`	`SigDF`
`sdfs.normal`	a list of `SigDF`s for normalization, if not given, use the stored normal data from sesameData. However, we do recommend using a matched copy number normal dataset for normalization. assembly
`genomeInfo`	the genomeInfo files. The default is retrieved from sesameData. Alternative genomeInfo files can be found at https://github.com/zhou-lab/GenomeInfo
`probeCoords`	the probe coordinates in the corresponding genome if NULL (default), then the default genome assembly is used. Default genome is given by, e.g., sesameData_check_genome(NULL, "EPIC") For additional mapping, download the GRanges object from http://zwdzwd.github.io/InfiniumAnnotation and provide the following argument ..., probeCoords = sesameAnno_buildManifestGRanges("downloaded_file"),. to this function.
`tilewidth`	tile width for smoothing

verbose print more messages

return.probe.signals
return probe-level instead of bin-level signal

Value

an object of CNSegment

Examples

```
sesameDataCache()

## Not run:
sdfs <- sesameDataGet('EPICv2.8.SigDF')
sdf <- sdfs[["K562_206909630040_R01C01"]]
seg <- cnSegmentation(sdf)
seg <- cnSegmentation(sdf, return.probe.signals=TRUE)
visualizeSegments(seg)

## End(Not run)
```

---

compareMouseStrainReference

Compare Strain SNPs with a reference panel

Description

Compare Strain SNPs with a reference panel

Usage

```
compareMouseStrainReference(
  betas = NULL,
  show_sample_names = FALSE,
  query_width = NULL
)
```

Arguments

betas beta value vector or matrix (for multiple samples)

show_sample_names
whether to show sample name

query_width optional argument for adjusting query width

Value

grid object that contrast the target sample with pre-built mouse strain reference

Examples

```
sesameDataCache() # if not done yet
compareMouseStrainReference()
```

compareReference *Compare array data with references (e.g., tissue, cell types)*

Description

Compare array data with references (e.g., tissue, cell types)

Usage

```
compareReference(
  ref,
  betas = NULL,
  stop.points = NULL,
  query_width = 0.3,
  show_sample_names = FALSE
)
```

Arguments

ref	the reference beta values in SummarizedExperiment. One can download them from the sesameData package. See examples.
betas	matrix of betas for the target sample This argument is optional. If not given, only the reference will be shown.
stop.points	stop points for the color palette. Default to blue, yellow.
query_width	the width of the query beta value matrix
show_sample_names	whether to show sample names (default: FALSE)

Value

grid object that contrast the target sample with references.

Examples

```
sesameDataCache() # if not done yet
compareReference(sesameDataGet("MM285.tissueSignature"))
sesameDataGet_resetEnv()
```

controls *get the controls attributes*

Description

get the controls attributes

Usage

```
controls(sdf, verbose = FALSE)
```

Arguments

sdf	a SigDF
verbose	print more messages

Value

the controls data frame

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
head(controls(sdf))
```

---

convertProbeID *Convert Probe ID*

Description

Convert Probe ID

Usage

```
convertProbeID(
  x,
  target_platform,
  source_platform = NULL,
  mapping = NULL,
  target_uniq = TRUE,
  include_new = FALSE,
  include_old = FALSE,
  return_mapping = FALSE
)
```

Arguments

x	source probe IDs
target_platform	the platform to take the data to
source_platform	optional source platform
mapping	a liftOver mapping file. Typically this file contains empirical evidence whether a probe mapping is reliable. If given, probe ID-based mapping will be skipped. This is to perform more stringent probe ID mapping.
target_uniq	whether the target Probe ID should be kept unique.
include_new	if true, include mapping of added probes
include_old	if true, include mapping of deleted probes
return_mapping	return mapping table, instead of the target IDs.

Value

mapped probe IDs, or mapping table if return_mapping = T

---

createUCSCtrack *Turn beta values into a UCSC browser track*

Description

Turn beta values into a UCSC browser track

Usage

```
createUCSCtrack(betas, output = NULL, platform = "HM450", genome = "hg38")
```

Arguments

betas	a named numeric vector
output	output file name
platform	HM450, EPIC etc.
genome	hg38, mm10, ..., will infer if not given. For additional mapping, download the GRanges object from http://zwdzwd.github.io/InfiniumAnnotation and provide the following argument ..., genome = sesameAnno_buildManifestGRanges("downloaded_file"),... to this function.

Value

when output is null, return a data.frame, otherwise NULL

Examples

```
betas.tissue <- sesameDataGet('HM450.1.TCGA.PAAD')$betas
## add output to create an actual file
df <- createUCSCtrack(betas.tissue)

## to convert to bigBed
## sort -k1,1 -k2,2n output.bed >output_sorted.bed
## bedToBigBed output_sorted.bed hg38.chrom output.bb
```

---

dataFrame2sesameQC *Convert data frame to sesameQC object*

Description

The function convert a data frame back to a list of sesameQC objects

Usage

```
dataFrame2sesameQC(df)
```

Arguments

df	a publicQC data frame

Value

a list sesameQC objects

`deIdentify` *De-identify IDATs by removing SNP probes*

Description

Mask SNP probe intensity mean by zero.

Usage

```
deIdentify(path, out_path = NULL, snps = NULL, mft = NULL, randomize = FALSE)
```

Arguments

path	input IDAT file
out_path	output IDAT file
snps	SNP definition, if not given, default to SNP probes
mft	sesame-compatible manifest if non-standard
randomize	whether to randomize the SNPs. if TRUE, randomize the signal intensities. one can use set.seed to reidentify the IDAT with the secret seed (see examples). If FALSE, this sets all SNP intensities to zero.

Value

NULL, changes made to the IDAT files

Examples

```
my_secret <- 13412084
set.seed(my_secret)
temp_out <- tempfile("test")
deIdentify(system.file(
    "extdata", "4207113116_A_Grn.idat", package = "sesameData"),
     temp_out, randomize = TRUE)
unlink(temp_out)
```

detectionPnegEcdf *Detection P-value based on ECDF of negative control*

Description

The function takes a SigDF as input, computes detection p-value using negative control probes' empirical distribution and returns a new SigDF with an updated mask slot.

Usage

```
detectionPnegEcdf(sdf, return.pval = FALSE, pval.threshold = 0.05)
```

Arguments

sdf	a SigDF
return.pval	whether to return p-values, instead of a masked SigDF
pval.threshold	minimum p-value to mask

Value

a SigDF, or a p-value vector if return.pval is TRUE

Examples

```
sdf <- sesameDataGet("EPIC.1.SigDF")
sum(sdf$mask)
sum(detectionPnegEcdf(sdf)$mask)
```

diffRefSet *Restrict refset to differentially methylated probes use with care, might introduce bias*

Description

The function takes a matrix with probes on the rows and cell types on the columns and output a subset matrix and only probes that show discordant methylation levels among the cell types.

Usage

```
diffRefSet(g)
```

Arguments

g	a matrix with probes on the rows and cell types on the columns

Value

g a matrix with a subset of input probes (rows)

Examples

```
g = diffRefSet(getRefSet(platform='HM450'))
sesameDataGet_resetEnv()
```

`dmContrasts` *List all contrasts of a DMLSummary*

Description

List all contrasts of a DMLSummary

Usage

```
dmContrasts(smry)
```

Arguments

`smry`	a DMLSummary object

Value

a character vector of contrasts

Examples

```
data <- sesameDataGet('HM450.76.TCGA.matched')
smry <- DML(data$betas[1:10,], ~type, meta=data$sampleInfo)
dmContrasts(smry)

sesameDataGet_resetEnv()
```

`DML` *Test differential methylation on each locus*

Description

The function takes a beta value matrix with probes on the rows and samples on the columns. It also takes a sample information data frame (meta) and formula for testing. The function outputs a list of coefficient tables for each factor tested.

Usage

```
DML(betas, fm, meta = NULL, BPPARAM = SerialParam())
```

Arguments

betas	beta values, matrix or SummarizedExperiment rows are probes and columns are samples.
fm	formula
meta	data frame for sample information, column names are predictor variables (e.g., sex, age, treatment, tumor/normal etc) and are referenced in formula. Rows are samples. When the betas argument is a SummarizedExperiment object, this is ignored. colData(betas) will be used instead. The row order of the data frame must match the column order of the beta value matrix.
BPPARAM	number of cores for parallel processing, default to SerialParam() Use MulticoreParam(mc.cores) for parallel processing. For Windows, try DoparParam or SnowParam.

Value

a list of test summaries, summary.lm objects

Examples

```
sesameDataCache() # in case not done yet
data <- sesameDataGet('HM450.76.TCGA.matched')
smry <- DML(data$betas[1:1000,], ~type, meta=data$sampleInfo)

sesameDataGet_resetEnv()
```

DMLpredict *Predict new data from DML*

Description

This function is also important for investigating factor interactions.

Usage

```
DMLpredict(betas, fm, pred = NULL, meta = NULL, BPPARAM = SerialParam())
```

Arguments

betas	beta values, matrix or SummarizedExperiment rows are probes and columns are samples.
fm	formula
pred	new data for prediction, useful for studying effect size. This argument is a data.frame to specify new data. If the argument is NULL, all combinations of all contrasts will be used as input. It might not work if there is a continuous variable input. One may need to explicitly provide the input in a data frame.
meta	data frame for sample information, column names are predictor variables (e.g., sex, age, treatment, tumor/normal etc) and are referenced in formula. Rows are samples. When the betas argument is a SummarizedExperiment object, this is ignored. colData(betas) will be used instead.
BPPARAM	number of cores for parallel processing, default to SerialParam() Use MulticoreParam(mc.cores) for parallel processing. For Windows, try DoparParam or SnowParam.

Value

a SummarizedExperiment of predictions. The colData describes the input of the prediction.

Examples

```
data <- sesameDataGet('HM450.76.TCGA.matched')

## use all contrasts as new input
res <- DMLpredict(data$betas[1:10,], ~type, meta=data$sampleInfo)

## specify new input
res <- DMLpredict(data$betas[1:10,], ~type, meta=data$sampleInfo,
  pred = data.frame(type=c("Normal","Tumour")))

## note that the prediction needs to be a factor of the same
## level structure as the original training data.
pred = data.frame(type=factor(c("Normal"), levels=c("Normal","Tumour")))
res <- DMLpredict(data$betas[1:10,], ~type,
  meta=data$sampleInfo, pred = pred)
```

DMR *Find Differentially Methylated Region (DMR)*

Description

This subroutine uses Euclidean distance to group CpGs and then combine p-values for each segment. The function performs DML test first if cf is NULL. It groups the probe testing results into differential methylated regions in a coefficient table with additional columns designating the segment ID and statistical significance (P-value) testing the segment.

Usage

```
DMR(
  betas,
  smry,
  contrast,
  platform = NULL,
  probe.coords = NULL,
  dist.cutoff = NULL,
  seg.per.locus = 0.5
)
```

Arguments

betas	beta values for distance calculation
smry	DML
contrast	the pair-wise comparison or contrast check colnames(attr(smry, "model.matrix")) if uncertain
platform	EPIC, HM450, MM285, ...

probe.coords	GRanges object that defines CG coordinates if NULL (default), then the default genome assembly is used. Default genome is given by, e.g., sesameData_check_genome(NULL, "EPIC") For additional mapping, download the GRanges object from http://zwdzwd.github.io/InfiniumAnnotation and provide the following argument ..., probe.coords = sesameAnno_buildManifestGRanges("downloaded_file"),.. to this function.
dist.cutoff	cutoff of beta value differences for two neighboring CGs to be considered the same DMR (by default it's determined using the quantile function on seg.per.locus)
seg.per.locus	number of segments per locus higher value leads to more segments

Value

coefficient table with segment ID and segment P-value each row is a locus, multiple loci may share a segment ID if they are merged to the same segment. Records are ordered by Seg_Est.

Examples

```
sesameDataCache() # in case not done yet

data <- sesameDataGet('HM450.76.TCGA.matched')
smry <- DML(data$betas[1:1000,], ~type, meta=data$sampleInfo)
colnames(attr(smry, "model.matrix")) # pick a contrast from here
## showing on a small set of 100 CGs
merged_segs <- DMR(data$betas[1:1000,], smry, "typeTumour", platform="HM450")

sesameDataGet_resetEnv()
```

---

dyeBiasCorr *Correct dye bias in by linear scaling.*

Description

The function takes a SigDF as input and scale both the Grn and Red signal to a reference (ref) level. If the reference level is not given, it is set to the mean intensity of all the in-band signals. The function returns a SigDF with dye bias corrected.

Usage

```
dyeBiasCorr(sdf, ref = NULL)
```

Arguments

sdf	a SigDF
ref	reference signal level

Value

a normalized SigDF

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
sdf.db <- dyeBiasCorr(sdf)
```

`dyeBiasCorrMostBalanced` *Correct dye bias using most balanced sample as the reference*

Description

The function chose the reference signal level from a list of `SigDF`. The chosen sample has the smallest difference in Grn and Red signal intensity as measured using the normalization control probes. In practice, it doesn't matter which sample is chosen as long as the reference level does not deviate much. The function returns a list of `SigDF`s with dye bias corrected.

Usage

```
dyeBiasCorrMostBalanced(sdfs)
```

Arguments

`sdfs`	a list of normalized `SigDF`s

Value

a list of normalized `SigDF`s

Examples

```
sesameDataCache() # if not done yet
sdfs <- sesameDataGet('HM450.10.SigDF')[1:2]
sdfs.db <- dyeBiasCorrMostBalanced(sdfs)
```

`dyeBiasL` *Correct dye bias in by linear scaling.*

Description

The function takes a `SigDF` as input and scale both the Grn and Red signal to a reference (ref) level. If the reference level is not given, it is set to the mean intensity of all the in-band signals. The function returns a `SigDF` with dye bias corrected.

Usage

```
dyeBiasL(sdf, ref = NULL)
```

Arguments

`sdf`	a `SigDF`
`ref`	reference signal level

Value

a normalized SigDF

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
sdf.db <- dyeBiasL(sdf)
```

---

dyeBiasNL *Dye bias correction by matching green and red to mid point*

Description

This function compares the Type-I Red probes and Type-I Grn probes and generates and mapping to correct signal of the two channels to the middle. The function takes one single SigDF and returns a SigDF with dye bias corrected.

Usage

```
dyeBiasNL(sdf, mask = TRUE, verbose = FALSE)

dyeBiasCorrTypeINorm(sdf, mask = TRUE, verbose = FALSE)
```

Arguments

sdf	a SigDF
mask	include masked probes in Infinium-I probes. No big difference is noted in practice. More probes are generally better.
verbose	print more messages

Value

a SigDF after dye bias correction.

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
sdf.db <- dyeBiasNL(sdf)
sdf <- sesameDataGet('EPIC.1.SigDF')
sdf <- dyeBiasCorrTypeINorm(sdf)
```

ELBAR *ELiminate BAckground-dominated Reading (ELBAR)*

Description

ELiminate BAckground-dominated Reading (ELBAR)

Usage

```
ELBAR(
  sdf,
  return.pval = FALSE,
  pval.threshold = 0.05,
  margin = 0.05,
  capMU = 3000,
  delta.beta = 0.2,
  n.windows = 500
)
```

Arguments

sdf	a SigDF
return.pval	whether to return p-values, instead of a SigDF
pval.threshold	minimum p-value to mask
margin	the percentile margin to define envelope, the smaller the value the more aggressive the masking.
capMU	the maximum M+U to search for intermediate betas
delta.beta	maximum beta value change from sheer background-dominated readings
n.windows	number of windows for smoothing

Value

a SigDF with mask added

Examples

```
sdf <- sesameDataGet("EPIC.1.SigDF")
sum(sdf$mask)
sum(ELBAR(sdf)$mask)
```

estimateLeukocyte *Estimate leukocyte fraction using a two-component model*

Description

The method assumes only two components in the mixture: the leukocyte component and the target tissue component. The function takes the beta values matrix of the target tissue and the beta value matrix of the leukocyte. Both matrices have probes on the row and samples on the column. Row names should have probe IDs from the platform. The function outputs a single numeric describing the fraction of leukocyte.

Usage

```
estimateLeukocyte(
  betas.tissue,
  betas.leuko = NULL,
  betas.tumor = NULL,
  platform = c("EPIC", "HM450", "HM27")
)
```

Arguments

betas.tissue	tissue beta value matrix (#probes X #samples)
betas.leuko	leukocyte beta value matrix, if missing, use the SeSAMe default by infinium platform
betas.tumor	optional, tumor beta value matrix
platform	"HM450", "HM27" or "EPIC"

Value

leukocyte estimate, a numeric vector

Examples

```
betas.tissue <- sesameDataGet('HM450.1.TCGA.PAAD')$betas
estimateLeukocyte(betas.tissue)
sesameDataGet_resetEnv()
```

formatVCF *Convert SNP from Infinium array to VCF file*

Description

Convert SNP from Infinium array to VCF file

Usage

```
formatVCF(sdf, anno, vcf = NULL, genome = "hg38", verbose = FALSE)
```

Arguments

sdf	SigDF
anno	SNP variant annotation, available at https://github.com/zhou-lab/InfiniumAnnotationV1/tree/main/An EPIC.hg38.snp.tsv.gz
vcf	output VCF file path, if NULL output to console
genome	genome
verbose	print more messages

Value

VCF file. If vcf is NULL, a data.frame is output to console. The data.frame does not contain VCF headers. Note the output vcf is not sorted.

Examples

```
sesameDataCacheAll() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')

## Not run:
## download anno from
## http://zwdzwd.github.io/InfiniumAnnotation
## output to console
anno = read_tsv(sesameAnno_download("EPICv2.hg38.snp.tsv.gz"))
head(formatVCF(sdf, anno))

## End(Not run)
```

---

getAFs *Get allele frequency*

Description

Get allele frequency

Usage

```
getAFs(sdf, ...)
```

Arguments

sdf	SigDF
...	additional options to getBetas

Value

allele frequency

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
af <- getAFs(sdf)
```

getAFTypeIbySumAlleles *Get allele frequency treating type I by summing alleles*

Description

Takes a SigDF as input and returns a numeric vector containing extra allele frequencies based on Color-Channel-Switching (CCS) probes. If no CCS probes exist in the SigDF, then an numeric(0) is returned.

Usage

```
getAFTypeIbySumAlleles(sdf, known.ccs.only = TRUE)
```

Arguments

sdf	SigDF
known.ccs.only	consider only known CCS probes

Value

beta values

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
af <- getAFTypeIbySumAlleles(sdf)
```

getBetas *Get beta Values*

Description

sum.typeI is used for rescuing beta values on Color-Channel-Switching CCS probes. The function takes a SigDF and returns beta value except that Type-I in-band signal and out-of-band signal are combined. This prevents color-channel switching due to SNPs.

Usage

```
getBetas(
  sdf,
  mask = TRUE,
  sum.TypeI = FALSE,
  collapseToPfx = FALSE,
  collapseMethod = c("mean", "minPval")
)
```

Arguments

sdf	SigDF
mask	whether to use mask
sum.TypeI	whether to sum type I channels
collapseToPfx	remove replicate to prefix (e.g., cg number) and remove the suffix
collapseMethod	mean or minPval

Value

a numeric vector, beta values

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
betas <- getBetas(sdf)
```

---

getBinCoordinates *Get bin coordinates*

Description

requires GenomicRanges, IRanges

Usage

```
getBinCoordinates(seqLength, gapInfo, tilewidth = 50000, probeCoords)
```

Arguments

seqLength	chromosome information object
gapInfo	chromosome gap information
tilewidth	tile width for smoothing
probeCoords	probe coordinates

Value

bin.coords

getMask *get probe masking by mask names*

Description

get probe masking by mask names

Usage

```
getMask(platform = "EPICv2", mask_names = "recommended")
```

Arguments

platform	EPICv2, EPIC, HM450, HM27, ...
mask_names	mask names (see listAvailableMasks) by default: "recommended" see recommendedMaskNames() for detail.

Value

a vector of probe ID

Examples

```
length(getMask("MSA", "recommended"))
length(getMask("EPICv2", "recommended"))
length(getMask("EPICv2", c("recommended", "M_SNPcommon_1pt")))
length(getMask("EPICv2", "M_mapping"))
length(getMask("EPIC"))
length(getMask("HM450"))
length(getMask("MM285"))
```

getRefSet *Retrieve reference set*

Description

The function retrieves the curated reference DNA methylation status for a set of cell type names under the Infinium platform. Supported cell types include "CD4T", "CD19B", "CD56NK", "CD14Monocytes", "granulocytes", "scFat", "skin" etc. See package sesameData for more details. The function output a matrix with probes on the rows and specified cell types on the columns. 0 suggests unmethylation and 1 suggests methylation. Intermediate methylation and nonclusive calls are left with NA.

Usage

```
getRefSet(cells = NULL, platform = c("EPIC", "HM450"))
```

Arguments

cells	reference cell types
platform	EPIC or HM450

Value

g, a 0/1 matrix with probes on the rows and specified cell types on the columns.

Examples

```
betas = getRefSet('CD4T', platform='HM450')
sesameDataGet_resetEnv()
```

`imputeBetas` *Impute of missing data of specific platform*

Description

Impute of missing data of specific platform

Usage

```
imputeBetas(
  betas,
  platform = NULL,
  BPPARAM = SerialParam(),
  celltype = NULL,
  sd_max = 999
)
```

Arguments

`betas`	named vector of beta values
`platform`	platform
`BPPARAM`	use MulticoreParam(n) for parallel processing
`celltype`	celltype/tissue context of imputation, if not given, will use nearest neighbor to determine.
`sd_max`	maximum standard deviation in imputation confidence

Value

imputed data, vector or matrix

Examples

```
betas = openSesame(sesameDataGet("EPIC.1.SigDF"))
sum(is.na(betas))
betas2 = imputeBetas(betas, "EPIC")
sum(is.na(betas2))
```

`imputeBetasByGenomicNeighbors` *Impute missing data based on genomic neighbors.*

Description

Impute missing data based on genomic neighbors.

Usage

```
imputeBetasByGenomicNeighbors(
  betas,
  platform = NULL,
  BPPARAM = SerialParam(),
  max_neighbors = 3,
  max_dist = 10000
)
```

Arguments

`betas`	named vector of beta values
`platform`	platform
`BPPARAM`	use MulticoreParam(n) for parallel processing
`max_neighbors`	maximum neighbors to use for dense regions
`max_dist`	maximum distance to count as neighbor

Value

imputed data, vector or matrix

Examples

```
betas = openSesame(sesameDataGet("EPICv2.8.SigDF")[[1]])
sum(is.na(betas))
betas2 = imputeBetasByGenomicNeighbors(betas, "EPICv2")
sum(is.na(betas2))
```

`imputeBetasMatrixByMean` *Impute Missing Values with Mean This function replaces missing values (NA) in a matrix, default is row means.*

Description

Impute Missing Values with Mean This function replaces missing values (NA) in a matrix, default is row means.

Usage

```
imputeBetasMatrixByMean(mx, axis = 1)
```

Arguments

mx	A matrix
axis	A single integer. Use 1 to impute column means (default), and 2 to impute row means.

Value

A matrix with missing values imputed.

Examples

```
mx <- cbind(c(1, 2, NA, 4), c(NA, 2, 3, 4))
imputeBetasMatrixByMean(mx, axis = 1)
imputeBetasMatrixByMean(mx, axis = 2)
```

---

inferInfiniumIChannel *Infer and reset color channel for Type-I probes instead of using what is specified in manifest. The results are stored to sdf@extra$IGG and sdf@extra$IRR slot.*

Description

IGG => Type-I green that is inferred to be green IRR => Type-I red that is inferred to be red

Usage

```
inferInfiniumIChannel(
  sdf,
  switch_failed = FALSE,
  mask_failed = FALSE,
  verbose = FALSE,
  summary = FALSE
)
```

Arguments

sdf	a SigDF
switch_failed	whether to switch failed probes (default to FALSE)
mask_failed	whether to mask failed probes (default to FALSE)
verbose	whether to print correction summary
summary	return summarized numbers only.

Value

a SigDF, or numerics if summary == TRUE

Examples

```
sdf <- sesameDataGet('EPIC.1.SigDF')
inferInfiniumIChannel(sdf)
```

`inferSex` *Infer sex.*

Description

We established our sex calling based on the CpGs hypermethylated in inactive X (XiH), CpGs hypomethylated in inactive X (XiL).

Usage

```
inferSex(betas, platform = NULL)
```

Arguments

`betas`	DNA methylation beta
`platform`	EPICv2, EPIC, HM450, MM285, etc.

Details

Note genotype abnormalities such as Dnmt genotype, XXY male (Klinefelter's), 45,X female (Turner's) can confuse the model sometimes. This function works on a single sample.

Value

Inferred sex of sample

Examples

```
## EPICv2 input
betas = openSesame(sesameDataGet("EPICv2.8.SigDF")[[1]])
inferSex(betas)

## Not run:
## MM285 input
betas = openSesame(sesameDataGet("MM285.1.SigDF"))
inferSex(betas)

## EPIC input
betas = openSesame(sesameDataGet('EPIC.1.SigDF'))
inferSex(betas)

## HM450 input
betas = openSesame(sesameDataGet("HM450.10.SigDF")[[1]])
inferSex(betas)

## End(Not run)
```

`inferSpecies` *Infer Species*

Description

We infer species based on probes pvalues and alignment score. AUC was calculated for each specie, y_true is 1 or 0 for pval < threshold.pos or pval > threshold.neg, respeceively,

Usage

```
inferSpecies(
  sdf,
  topN = 1000,
  threshold.pos = 0.01,
  threshold.neg = 0.1,
  return.auc = FALSE,
  return.species = FALSE,
  verbose = FALSE
)
```

Arguments

`sdf`	a `SigDF`
`topN`	Top n positive and negative probes used to infer species. increase this number can sometimes improve accuracy (DEFAULT: 1000)
`threshold.pos`	pvalue < threshold.pos are considered positive (default: 0.01).
`threshold.neg`	pvalue > threshold.neg are considered negative (default: 0.2).
`return.auc`	return AUC calculated, override return.species
`return.species`	return a string to represent species
`verbose`	print more messaeges

Value

a SigDF

Examples

```
sdf <- sesameDataGet("MM285.1.SigDF")
sdf <- inferSpecies(sdf)

## all available species
all_species <- names(sesameDataGet(sprintf(
  "%s.addressSpecies", sdfPlatform(sdf)))$species)
```

`inferStrain` *Infer strain information for mouse array*

Description

Infer strain information for mouse array

Usage

```
inferStrain(
  sdf,
  return.strain = FALSE,
  return.probability = FALSE,
  return.pval = FALSE,
  min_frac_dt = 0.2,
  verbose = FALSE
)
```

Arguments

`sdf`	SigDF
`return.strain`	return strain name
`return.probability`	return probability vector for all strains
`return.pval`	return p-value
`min_frac_dt`	minimum fraction of detected signal (DEFAULT: 0.2) otherwise, we give up strain inference and return NA.
`verbose`	print more messages

Value

a list of best guess, p-value of the best guess and the probabilities of all strains

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('MM285.1.SigDF')
inferStrain(sdf, return.strain = TRUE)
sdf.strain <- inferStrain(sdf)
```

`inferTissue` *inferTissue infers the tissue of a single sample (as identified through the branchIDs in the row data of the reference) by reporting independent composition through cell type deconvolution.*

Description

inferTissue infers the tissue of a single sample (as identified through the branchIDs in the row data of the reference) by reporting independent composition through cell type deconvolution.

Usage

```
inferTissue(
  betas,
  reference = NULL,
  platform = NULL,
  abs_delta_beta_min = 0.3,
  auc_min = 0.99,
  coverage_min = 0.8,
  topN = 15
)
```

Arguments

`betas`	Named vector with probes and their corresponding beta value measurement
`reference`	Summarized Experiment with either hypomethylated or hypermethylated probe selection (row data), sample selection (column data), meta data, and the betas (assay)
`platform`	String representing the array type of the betas and reference
`abs_delta_beta_min`	Numerical value indicating the absolute minimum required delta beta for the probe selection criteria
`auc_min`	Numeric value corresponding to the minimum AUC value required for a probe to be considered
`coverage_min`	Numeric value corresponding to the minimum coverage requirement for a probe to be considered. Coverage is defined here as the proportion of samples without an NA value at a given probe.
`topN`	number of probes to at most use for each branch

Value

inferred tissue as a string

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet("MM285.1.SigDF")
inferTissue(getBetas(dyeBiasNL(noob(sdf))))

sesameDataGet_resetEnv()
```

initFileSet *initialize a fileSet class by allocating appropriate storage*

Description

initialize a fileSet class by allocating appropriate storage

Usage

```
initFileSet(map_path, platform, samples, probes = NULL, inc = 4)
```

Arguments

map_path	path of file to map
platform	EPIC, HM450 or HM27, consistent with sdfPlatform(sdf)
samples	sample names
probes	probe names
inc	bytes per unit data storage

Value

a sesame::fileSet object

Examples

```
fset <- initFileSet('mybetas2', 'HM27', c('s1','s2'))
```

listAvailableMasks *list existing quality masks for a SigDF*

Description

list existing quality masks for a SigDF

Usage

```
listAvailableMasks(platform, verbose = FALSE)
```

Arguments

platform	EPIC, MM285, HM450 etc
verbose	print more messages

Value

a tibble of masks

Examples

```
listAvailableMasks("EPICv2")
```

mapFileSet — *Deposit data of one sample to a fileSet (and hence to file)*

Description

Deposit data of one sample to a fileSet (and hence to file)

Usage

```
mapFileSet(fset, sample, named_values)
```

Arguments

fset	a sesame::fileSet, as obtained via readFileSet
sample	sample name as a string
named_values	value vector named by probes

Value

a sesame::fileSet

Examples

```
## create two samples
fset <- initFileSet('mybetas2', 'HM27', c('s1','s2'))

## a hypothetical numeric array (can be beta values, intensities etc)
hypothetical <- setNames(runif(fset$n), fset$probes)

## map the numeric to file
mapFileSet(fset, 's1', hypothetical)

## get data
sliceFileSet(fset, 's1', 'cg00000292')
```

mapToMammal40 — *Map the SDF (from overlap array platforms) Replicates are merged by picking the best detection*

Description

Map the SDF (from overlap array platforms) Replicates are merged by picking the best detection

Usage

```
mapToMammal40(sdf)
```

Arguments

sdf	a SigDF object

Value

a named numeric vector for beta values

Examples

```
sdf <- sesameDataGet("Mammal40.1.SigDF")
betas <- mapToMammal40(sdf[1:10,])
```

`matchDesign` *normalize Infinium I probe betas to Infinium II*

Description

This is designed to counter tail inflation in Infinium I probes.

Usage

```
matchDesign(sdf, min_dbeta = 0.3)
```

Arguments

`sdf`	SigDF
`min_dbeta`	the default algorithm perform 2-state quantile-normalization of the unmethylated and methylated modes separately. However, when the two modes are too close, we fall back to a one-mode normalization. The threshold defines the maximum inter-mode distance.

Value

SigDF

Examples

```
library(RPMM)
sdf <- sesameDataGet("MM285.1.SigDF")
sesameQC_plotBetaByDesign(sdf)
sesameQC_plotBetaByDesign(matchDesign(sdf))
```

meanIntensity *Whole-dataset-wide Mean Intensity*

Description

The function takes one single SigDF and computes mean intensity of all the in-band measurements. This includes all Type-I in-band measurements and all Type-II probe measurements. Both methylated and unmethylated alleles are considered. This function outputs a single numeric for the mean.

Usage

```
meanIntensity(sdf, mask = TRUE)
```

Arguments

sdf	a SigDF
mask	whether to mask probes using mask column

Details

Note: mean in this case is more informative than median because methylation level is mostly bimodal.

Value

mean of all intensities

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
meanIntensity(sdf)
```

medianTotalIntensity *Whole-dataset-wide Median Total Intensity (M+U)*

Description

The function takes one single SigDF and computes median intensity of M+U for each probe. This function outputs a single numeric for the median.

Usage

```
medianTotalIntensity(sdf, mask = TRUE)
```

Arguments

sdf	a SigDF
mask	whether to mask probes using mask column

Value

median of all intensities

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
medianTotalIntensity(sdf)
```

`mLiftOver` *Lift over beta values or SigDFs to another Infinium platform This function wraps ID conversion and provide optional imputation functionality.*

Description

Lift over beta values or SigDFs to another Infinium platform This function wraps ID conversion and provide optional imputation functionality.

Usage

```
mLiftOver(
  x,
  target_platform,
  source_platform = NULL,
  BPPARAM = SerialParam(),
  mapping = NULL,
  impute = FALSE,
  sd_max = 999,
  celltype = "Blood",
  ...
)
```

Arguments

`x`	either named beta value (vector or matrix), probe IDs or SigDF(s) if input is a matrix, probe IDs should be in the row names if input is a numeric vector, probe IDs should be in the vector names. If input is a character vector, the input will be considered probe IDs.
`target_platform`	the platform to take the data to
`source_platform`	optional information of the source data platform (when there might be ambiguity).
`BPPARAM`	use MulticoreParam(n) for parallel processing
`mapping`	a liftOver mapping file. Typically this file contains empirical evidence whether a probe mapping is reliable. If given, probe ID-based mapping will be skipped. This is to perform more stringent probe ID mapping.
`impute`	whether to impute or not, default is FALSE

sd_max	the maximum standard deviation for filtering low confidence imputation.
celltype	the cell type / tissue context of imputation, if not given, will use nearest neighbor to find out.
...	extra arguments, see ?convertProbeID

Value

imputed data, vector, matrix, SigDF(s)

Examples

```
## Not run:
sesameDataCache()

## lift SigDF

sdf = sesameDataGet("EPICv2.8.SigDF")[["GM12878_206909630042_R08C01"]]
dim(mLiftOver(sdf, "EPICv2"))
dim(mLiftOver(sdf, "EPIC"))
dim(mLiftOver(sdf, "HM450"))

sdfs = sesameDataGet("EPICv2.8.SigDF")[1:2]
sdfs_hm450 = mLiftOver(sdfs, "HM450")
## parallel processing
sdfs_hm450 = mLiftOver(
    sdfs, "HM450", BPPARAM=BiocParallel::MulticoreParam(2))

sdf = sesameDataGet("EPIC.5.SigDF.normal")[[1]]
dim(mLiftOver(sdf, "EPICv2"))
dim(mLiftOver(sdf, "EPIC"))
dim(mLiftOver(sdf, "HM450"))

sdf = sesameDataGet("HM450.10.SigDF")[[1]]
dim(mLiftOver(sdf, "EPICv2"))
dim(mLiftOver(sdf, "EPIC"))
dim(mLiftOver(sdf, "HM450"))

## lift beta values

betas = openSesame(sesameDataGet("EPICv2.8.SigDF")[[1]])
betas_hm450 = mLiftOver(betas, "HM450", impute=TRUE)
length(betas_hm450)
sum(is.na(betas_hm450))
betas_hm450 <- mLiftOver(betas, "HM450", impute=FALSE)
length(betas_hm450)
sum(is.na(betas_hm450))
betas_epic1 <- mLiftOver(betas, "EPIC", impute=TRUE)
length(betas_epic1)
sum(is.na(betas_epic1))
betas_epic1 <- mLiftOver(betas, "EPIC", impute=FALSE)
length(betas_epic1)
sum(is.na(betas_epic1))

betas_matrix = openSesame(sesameDataGet("EPICv2.8.SigDF")[1:4])
dim(betas_matrix)
betas_matrix_hm450 = mLiftOver(betas_matrix, "HM450", impute=T)
```

```
dim(betas_matrix_hm450)
## parallel processing
betas_matrix_hm450 = mLiftOver(betas_matrix, "HM450", impute=T,
BPPARAM=BiocParallel::MulticoreParam(4))

## use empirical evidence in mLiftOver
mapping = sesameDataGet("liftOver.EPICv2ToEPIC")
betas_matrix = openSesame(sesameDataGet("EPICv2.8.SigDF")[1:4])
dim(mLiftOver(betas_matrix, "EPIC", mapping = mapping))
## compare to without using empirical evidence
dim(mLiftOver(betas_matrix, "EPIC"))

betas <- c("cg04707299"=0.2, "cg13380562"=0.9, "cg00000103"=0.1)
head(mLiftOver(betas, "HM450", impute=TRUE))

betas <- c("cg00004963_TC21"=0, "cg00004963_TC22"=0.5, "cg00004747_TC21"=1.0)
betas_hm450 <- mLiftOver(betas, "HM450", impute=TRUE)
head(na.omit(mLiftOver(betas, "HM450", impute=FALSE)))

## lift probe IDs

cg_epic2 = names(sesameData_getManifestGRanges("EPICv2"))
head(mLiftOver(cg_epic2, "HM450"))

cg_epic2 = grep(
    "cg", names(sesameData_getManifestGRanges("EPICv2")), value=T)
head(mLiftOver(cg_epic2, "HM450"))

cg_hm450 = grep(
    "cg", names(sesameData_getManifestGRanges("HM450")), value=T)
head(mLiftOver(cg_hm450, "EPICv2"))

rs_epic2 = grep(
    "rs", names(sesameData_getManifestGRanges("EPICv2")), value=T)
head(mLiftOver(rs_epic2, "HM450", source_platform="EPICv2"))

probes_epic2 = names(sesameData_getManifestGRanges("EPICv2"))
head(mLiftOver(probes_epic2, "EPIC"))
head(mLiftOver(probes_epic2, "EPIC", target_uniq = TRUE))
head(mLiftOver(probes_epic2, "EPIC", include_new = FALSE))
head(mLiftOver(probes_epic2, "EPIC", include_old = FALSE))
head(mLiftOver(probes_epic2, "EPIC", return_mapping=TRUE))


## End(Not run)
```

`MValueToBetaValue` *Convert M-value to beta-value*

Description

Convert M-value to beta-value (aka inverse logit transform)

Usage

```
MValueToBetaValue(m)
```

Arguments

m	a vector of M values

Value

a vector of beta values

Examples

```
MValueToBetaValue(c(-3, 0, 3))
```

---

negControls *get negative control signal*

Description

get negative control signal

Usage

```
negControls(sdf)
```

Arguments

sdf	a SigDF

Value

a data frame of negative control signals

---

noMasked *remove masked probes from SigDF*

Description

remove masked probes from SigDF

Usage

```
noMasked(sdf)
```

Arguments

sdf	input SigDF object

Value

a SigDF object without masked probes

Examples

```
sesameDataCache()
sdf <- sesameDataGet("EPIC.1.SigDF")
sdf <- pOOBAH(sdf)

sdf_noMasked <- noMasked(sdf)
```

---

noob *Noob background subtraction*

Description

The function takes a SigDF and returns a modified SigDF with background subtracted. Background was modelled in a normal distribution and true signal in an exponential distribution. The Norm-Exp deconvolution is parameterized using Out-Of-Band (oob) probes. For species-specific processing, one should call inferSpecies on SigDF first. Multi-mapping probes are excluded.

Usage

```
noob(sdf, combine.neg = TRUE, offset = 15)
```

Arguments

sdf	a SigDF
combine.neg	whether to combine negative control probe.
offset	offset

Details

When combine.neg = TRUE, background will be parameterized by both negative control and out-of-band probes.

Value

a new SigDF with noob background correction

Examples

```
sdf <- sesameDataGet('EPIC.1.SigDF')
sdf.nb <- noob(sdf)
```

normControls *get normalization control signal*

Description

get normalization control signal from SigDF. The function optionally takes mean for each channel.

Usage

```
normControls(sdf, average = FALSE, verbose = FALSE)
```

Arguments

sdf	a SigDF
average	whether to average
verbose	print more messages

Value

a data frame of normalization control signals

openSesame *The openSesame pipeline*

Description

This function is a simple wrapper of noob + nonlinear dye bias correction + pOOBAH masking.

Usage

```
openSesame(
  x,
  prep = "QCDPB",
  prep_args = NULL,
  manifest = NULL,
  func = getBetas,
  BPPARAM = SerialParam(),
  platform = "",
  min_beads = 1,
  ...
)
```

Arguments

x	SigDF(s), IDAT prefix(es)
prep	preprocessing code, see ?prepSesame
prep_args	optional preprocessing argument list, see ?prepSesame
manifest	optional dynamic manifest
func	either getBetas or getAFs, if NULL, then return SigDF list
BPPARAM	get parallel with MulticoreParam(n)
platform	optional platform string
min_beads	minimum bead number, probes with R or G smaller than this threshold will be masked. If NULL, no filtering based on bead count will be applied. Default to 1.
...	parameters to getBetas

Details

Please use mask=FALSE to turn off masking.

If the input is an IDAT prefix or a SigDF, the output is the beta value numerics.

Value

a numeric vector for processed beta values

Examples

```
in_dir <- system.file("extdata", "", package = "sesameData")
betas <- openSesame(in_dir)
## or
IDATprefixes <- searchIDATprefixes(in_dir)
betas <- openSesame(IDATprefixes)
```

---

openSesameToFile *openSesame pipeline with file-backed storage*

Description

openSesame pipeline with file-backed storage

Usage

```
openSesameToFile(map_path, idat_dir, BPPARAM = SerialParam(), inc = 4)
```

Arguments

map_path	path of file to be mapped (beta values file)
idat_dir	source IDAT directory
BPPARAM	get parallel with MulticoreParam(2)
inc	bytes per item data storage. increase to 8 if precision is important. Most cases 32-bit representation is enough.

Value

a sesame::fileSet

Examples

```
openSesameToFile('mybetas',
    system.file('extdata',package='sesameData'))
```

---

palgen *Generate some additional color palettes*

Description

Generate some additional color palettes

Usage

```
palgen(pal, n = 150, space = "Lab")
```

Arguments

pal	a string for adhoc pals
n	the number of colors for interpolation
space	rgb or Lab

Value

a palette-generating function

Examples

```
library(pals)
pal.bands(palgen("whiteturbo"))
```

---

parseGEOsignalMU *Convert signal M and U to SigDF*

Description

This overcomes the issue of missing IDAT files. However, out-of-band signals will be missing or faked (sampled from a normal distribution).

Usage

```
parseGEOsignalMU(
  sigM,
  sigU,
  Probe_IDs,
  oob.mean = 500,
  oob.sd = 300,
  platform = NULL
)
```

Arguments

sigM	methylated signal, a numeric vector
sigU	unmethylated signal, a numirc vector
Probe_IDs	probe ID vector
oob.mean	assumed mean for out-of-band signals
oob.sd	assumed standard deviation for out-of-band signals
platform	platform code, will infer if not given

Value

SigDF

Examples

```
sigM <- c(11436, 6068, 2864)
sigU <- c(1476, 804, 393)
probes <- c("cg07881041", "cg23229610", "cg03513874")
sdf <- parseGEOsignalMU(sigM, sigU, probes, platform = "EPIC")
```

---

pOOBAH *Detection P-value based on ECDF of out-of-band signal*

Description

aka pOOBAH (p-vals by Out-Of-Band Array Hybridization)

Usage

```
pOOBAH(
  sdf,
  return.pval = FALSE,
  combine.neg = TRUE,
  pval.threshold = 0.05,
  verbose = FALSE
)
```

Arguments

sdf	a SigDF
return.pval	whether to return p-values, instead of a masked SigDF
combine.neg	whether to combine negative control probes with the out-of-band probes in simulating the signal background
pval.threshold	minimum p-value to mask
verbose	print more messages

Details

The function takes a SigDF as input, computes detection p-value using out-of-band probes empirical distribution and returns a new SigDF with an updated mask slot.

Value

a SigDF, or a p-value vector if return.pval is TRUE

Examples

```
sdf <- sesameDataGet("EPIC.1.SigDF")
sum(sdf$mask)
sum(pOOBAH(sdf)$mask)
```

---

predictAge *Predict age using linear models*

Description

The function takes a named numeric vector of beta values. The name attribute contains the probe ID (cg, ch or rs IDs). The function looks for overlapping probes and estimate age using different models.

Usage

```
predictAge(betas, model, na_fallback = FALSE, min_nonna = 10)
```

Arguments

betas	a probeID-named vector of beta values
model	a model object from sesameDataGet. should contain param, intercept, response2age. default to the Horvath353 model.
na_fallback	use fall back values if na
min_nonna	the minimum number of non-NA values.

Details

You can get the models such as the Horvath aging model (Horvath 2013 Genome Biology) from sesameDataGet. The function outputs a single numeric of age in years.

Here are some built-in age models: Anno/HM450/Clock_Horvath353.rds Anno/HM450/Clock_Hannum.rds Anno/HM450/Clock_SkinBlood.rds Anno/EPIC/Clock_PhenoAge.rds Anno/MM285/Clock_Zhou347.rds see vignette inferences.html#Age__Epigenetic_Clock for details

Value

age in the unit specified in the model (usually in year, but sometimes can be month, like in the mouse clocks).

Examples

```
betas <- sesameDataGet('HM450.1.TCGA.PAAD')$betas
## Not run:
## download age models from
## https://github.com/zhou-lab/InfiniumAnnotationV1/tree/main/Anno
## e.g., Anno/HM450/Clock_Horvath353.rds
predictAge(betas, model)

## End(Not run)
```

---

prefixMask *Mask SigDF by probe ID prefix*

Description

Mask SigDF by probe ID prefix

Usage

```
prefixMask(sdf, prefixes = NULL, invert = FALSE)
```

Arguments

sdf	SigDF
prefixes	prefix characters
invert	use the complement set

Value

SigDF

Examples

```
sdf <- resetMask(sesameDataGet("MM285.1.SigDF"))
sum(prefixMask(sdf, c("ctl","rs"))$mask)
sum(prefixMask(sdf, c("ctl"))$mask)
sum(prefixMask(sdf, c("ctl","rs","ch"))$mask)
```

prefixMaskButC *Mask all but C probes in SigDF*

Description

Mask all but C probes in SigDF

Usage

```
prefixMaskButC(sdf)
```

Arguments

sdf	SigDF

Value

SigDF

Examples

```
sdf <- resetMask(sesameDataGet("MM285.1.SigDF"))
sum(prefixMaskButC(sdf)$mask)
```

prefixMaskButCG *Mask all but CG probes in SigDF*

Description

Mask all but CG probes in SigDF

Usage

```
prefixMaskButCG(sdf)
```

Arguments

sdf	SigDF

Value

SigDF

Examples

```
sdf <- resetMask(sesameDataGet("MM285.1.SigDF"))
sum(prefixMaskButCG(sdf)$mask)
```

prepSesame *Apply a chain of sesame preprocessing functions in an arbitrary order*

Description

Notes on the order of operation: 1. qualityMask and inferSpecies should go before noob and pOOBAH, otherwise the background is too high because of Multi, uk and other probes 2. dyeBias correction needs to happen early 3. channel inference before dyebias 4. noob should happen last, pOOBAH before noob because noob modifies oob

Usage

```
prepSesame(sdf, prep = "QCDPB", prep_args = NULL)
```

Arguments

sdf	SigDF
prep	code that indicates preprocessing functions and their execution order (functions on the left is executed first).
prep_args	optional argument list to individual functions, e.g., prepSesame(sdf, prep_args=list(Q=list(mask_nam = "design_issue"))) sets qualityMask(sdf, mask_names = "design_issue")

Value

SigDF

Examples

```
sdf <- sesameDataGet("MM285.1.SigDF")
sdf1 <- prepSesame(sdf, "QCDPB")
```

prepSesameList *List supported prepSesame functions*

Description

List supported prepSesame functions

Usage

```
prepSesameList()
```

Value

a data frame with code, func, description

Examples

```
prepSesameList()
```

print.DMLSummary *Print DMLSummary object*

Description

Print DMLSummary object

Usage

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

Arguments

x	a DMLSummary object
...	extra parameter for print

Value

print DMLSummary result on screen

Examples

```
sesameDataCache() # in case not done yet
data <- sesameDataGet('HM450.76.TCGA.matched')
## test the first 10
smry <- DML(data$betas[1:10,], ~type, meta=data$sampleInfo)
smry

sesameDataGet_resetEnv()
```

print.fileSet *Print a fileSet*

Description

Print a fileSet

Usage

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

Arguments

x	a sesame::fileSet
...	stuff for print

Value

string representation

Examples

```
fset <- initFileSet('mybetas2', 'HM27', c('s1','s2'))
fset
```

`probeID_designType` *Extract the probe type field from probe ID This only works with the new probe ID system. See https://github.com/zhou-lab/InfiniumAnnotation for illustration*

Description

Extract the probe type field from probe ID This only works with the new probe ID system. See https://github.com/zhou-lab/InfiniumAnnotation for illustration

Usage

```
probeID_designType(Probe_ID)
```

Arguments

`Probe_ID`	Probe ID

Value

a vector of '1' and '2' suggesting Infinium-I and Infinium-II

Examples

```
probeID_designType("cg36609548_TC21")
```

`probeSuccessRate` *Whole-dataset-wide Probe Success Rate*

Description

This function calculates the probe success rate using pOOBAH detection p-values. Probes that has a detection p-value higher than a specific threshold are considered failed probes.

Usage

```
probeSuccessRate(sdf, mask = TRUE, max_pval = 0.05)
```

Arguments

`sdf`	a `SigDF`
`mask`	whether or not we count the masked probes in SigDF
`max_pval`	the maximum p-value to consider detection success

Value

a fraction number as probe success rate

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
probeSuccessRate(sdf)
```

---

qualityMask *Mask beta values by design quality*

Description

Currently quality masking only supports three platforms see also listAvailableMasks(sdfPlatform(sdf))

Usage

```
qualityMask(sdf, mask_names = "recommended", verbose = TRUE)
```

Arguments

sdf	a SigDF object
mask_names	a vector of masking groups, see listAvailableMasks use "recommended" for recommended masking. One can also combine "recommended" with other masking groups by specifying a vector, e.g., c("recommended", "M_mapping")
verbose	be verbose

Value

a filtered SigDF

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
sum(sdf$mask)
sum(qualityMask(sdf)$mask)
sum(qualityMask(sdf, mask_names = NULL)$mask)

## list available masks, the dbname column
listAvailableMasks(sdfPlatform(sdf))
listAvailableMasks("EPICv2")
```

readFileSet *Read an existing fileSet from storage*

Description

This function only reads the meta-data.

Usage

```
readFileSet(map_path)
```

Arguments

map_path	path of file to map (should contain valid _idx.rds index)

Value

a sesame::fileSet object

Examples

```
## create two samples
fset <- initFileSet('mybetas2', 'HM27', c('s1','s2'))

## a hypothetical numeric array (can be beta values, intensities etc)
hypothetical <- setNames(runif(fset$n), fset$probes)

## map the numeric to file
mapFileSet(fset, 's1', hypothetical)

## read it from file
fset <- readFileSet('mybetas2')

## get data
sliceFileSet(fset, 's1', 'cg00000292')
```

readIDATpair *Import a pair of IDATs from one sample*

Description

The function takes a prefix string that are shared with _Grn.idat and _Red.idat. The function returns a SigDF.

Usage

```
readIDATpair(
  prefix.path,
  manifest = NULL,
  platform = "",
  min_beads = NULL,
  controls = NULL,
  verbose = FALSE
)
```

Arguments

prefix.path	sample prefix without _Grn.idat and _Red.idat
manifest	optional design manifest file
platform	EPIC, HM450 and HM27 etc.
min_beads	minimum bead number, probes with R or G smaller than this threshold will be masked. If NULL, no filtering based on bead count will be applied.
controls	optional control probe manifest file
verbose	be verbose? (FALSE)

Value

a SigDF

Examples

```
sdf <- readIDATpair(sub('_Grn.idat','',system.file(
    "extdata", "4207113116_A_Grn.idat", package = "sesameData")))
```

---

recommendedMaskNames *Recommended mask names for each Infinium platform*

Description

The returned name is the db name used in KYCG.mask

Usage

```
recommendedMaskNames(platform)
```

Arguments

platform	string for platform, e.g., EPIC, EPICv2, MSA

Value

a named list of mask names

Examples

```
recommendedMaskNames("EPICv2")
recommendedMaskNames("EPIC")
```

reIdentify *Re-identify IDATs by restoring scrambled SNP intensities*

Description

This requries setting a seed with a secret number that was used to de-identify the IDAT (see example). This requires a secret number that was used to de-idenitfy the IDAT

Usage

```
reIdentify(path, out_path = NULL, snps = NULL, mft = NULL)
```

Arguments

path	input IDAT file
out_path	output IDAT file
snps	SNP definition, if not given, default to SNP probes
mft	sesame-compatible manifest if non-standard

Value

NULL, changes made to the IDAT files

Examples

```
temp_out <- tempfile("test")

set.seed(123)
reIdentify(system.file(
    "extdata", "4207113116_A_Grn.idat", package = "sesameData"), temp_out)
unlink(temp_out)
```

resetMask *Reset Masking*

Description

Reset Masking

Usage

```
resetMask(sdf, verbose = FALSE)
```

Arguments

sdf	a SigDF
verbose	print more messages

Value

a new SigDF with mask reset to all FALSE

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
sum(sdf$mask)
sdf <- addMask(sdf, c("cg14057072", "cg22344912"))
sum(sdf$mask)
sum(resetMask(sdf)$mask)
```

---

scrub *SCRUB background correction*

Description

This function takes a SigDF and returns a modified SigDF with background subtracted. scrub subtracts residual background using background median

Usage

```
scrub(sdf)
```

Arguments

sdf	a SigDF

Details

This function is meant to be used after noob.

Value

a new SigDF with noob background correction

Examples

```
sdf <- sesameDataGet('EPIC.1.SigDF')
sdf.nb <- noob(sdf)
sdf.nb.scrub <- scrub(sdf.nb)
```

scrubSoft *SCRUB background correction*

Description

This function takes a SigDF and returns a modified SigDF with background subtracted. scrubSoft subtracts residual background using a noob-like procedure.

Usage

```
scrubSoft(sdf)
```

Arguments

sdf	a SigDF

Details

This function is meant to be used after noob.

Value

a new SigDF with noob background correction

Examples

```
sdf <- sesameDataGet('EPIC.1.SigDF')
sdf.nb <- noob(sdf)
sdf.nb.scrubSoft <- scrubSoft(sdf.nb)
```

SDFcollapseToPfx *collapse to probe prefix*

Description

collapse to probe prefix

Usage

```
SDFcollapseToPfx(sdf)
```

Arguments

sdf	a SigDF object

Value

a data frame with updated Probe_ID

sdfPlatform *Convenience function to output platform attribute of SigDF*

Description

Convenience function to output platform attribute of SigDF

Usage

```
sdfPlatform(sdf, verbose = FALSE)
```

Arguments

sdf	a SigDF object
verbose	print more messages

Value

the platform string for the SigDF object

Examples

```
sesameDataCache()
sdf <- sesameDataGet('EPIC.1.SigDF')
sdfPlatform(sdf)
```

sdf_read_table *read a table file to SigDF*

Description

read a table file to SigDF

Usage

```
sdf_read_table(fname, platform = NULL, verbose = FALSE, ...)
```

Arguments

fname	file name
platform	array platform (will infer if not given)
verbose	print more information
...	additional argument to read.table

Value

read table file to SigDF

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
fname <- sprintf("%s/sigdf.txt", tempdir())
sdf_write_table(sdf, file=fname)
sdf2 <- sdf_read_table(fname)
```

---

sdf_write_table *write SigDF to table file*

Description

write SigDF to table file

Usage

```
sdf_write_table(sdf, ...)
```

Arguments

sdf	the SigDF to output
...	additional argument to write.table

Value

write SigDF to table file

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
sdf_write_table(sdf, file=sprintf("%s/sigdf.txt", tempdir()))
```

---

searchIDATprefixes *Identify IDATs from a directory*

Description

The input is the directory name as a string. The function identifies all the IDAT files under the directory. The function returns a vector of such IDAT prefixes under the directory.

Usage

```
searchIDATprefixes(dir.name, recursive = TRUE, use.basename = TRUE)
```

Arguments

dir.name	the directory containing the IDAT files.
recursive	search IDAT files recursively
use.basename	basename of each IDAT path is used as sample name This won't work in rare situation where there are duplicate IDAT files.

Value

the IDAT prefixes (a vector of character strings).

Examples

```
## only search what are directly under
IDATprefixes <- searchIDATprefixes(
    system.file("extdata", "", package = "sesameData"))

## search files recursively is by default
IDATprefixes <- searchIDATprefixes(
    system.file(package = "sesameData"), recursive=TRUE)
```

---

segmentBins *Segment bins using DNAcopy*

Description

Segment bins using DNAcopy

Usage

```
segmentBins(bin.signals, bin.coords)
```

Arguments

bin.signals	bin signals (input)
bin.coords	bin coordinates

Value

segment signal data frame

---

sesameAnno_attachManifest *Annotate a data.frame using manifest*

Description

Annotation source: https://zwdzwd.github.io/InfiniumAnnotation e.g., EPICv2.hg38.manifest

Usage

```
sesameAnno_attachManifest(
  df,
  probe_id = "Probe_ID",
  platform = NULL,
  genome = NULL
)
```

Arguments

df	input data frame with Probe_ID as a column
probe_id	the Probe_ID column name, default to "Probe_ID" or rownames
platform	which array platform, guess from probe ID if not given
genome	the genome build, use default if not given

Value

a new data.frame with manifest attached

Examples

```
## Not run:
df <- data.frame(Probe_ID = c("cg00101675_BC21", "cg00116289_BC21"))
sesameAnno_attachManifest(df)

## End(Not run)
```

---

sesameAnno_buildAddressFile

Build sesame ordering address file from tsv

Description

Build sesame ordering address file from tsv

Usage

```
sesameAnno_buildAddressFile(tsv)
```

Arguments

tsv	a platform name, a file path or a tibble/data.frame manifest file

Value

a list of ordering and controls

Examples

```
## Not run:
tsv = sesameAnno_download("HM450.hg38.manifest.tsv.gz")
addr <- sesameAnno_buildAddressFile(tsv)

## End(Not run)
```

sesameAnno_buildManifestGRanges *Build manifest GRanges from tsv*

Description

manifest tsv files can be downloaded from http://zwdzwd.github.io/InfiniumAnnotation

Usage

```
sesameAnno_buildManifestGRanges(
  tsv,
  genome = NULL,
  decoy = FALSE,
  columns = NULL
)
```

Arguments

tsv	a file path, a platform (e.g., EPIC), or a tibble/data.frame object
genome	a genome string, e.g., hg38, mm10
decoy	consider decoy sequence in chromosome order
columns	the columns to include in the GRanges

Value

GRanges

Examples

```
## Not run:
tsv = sesameAnno_download("HM450.hg38.manifest.tsv.gz")
gr <- sesameAnno_buildManifestGRanges(tsv)
## direct access
gr <- sesameAnno_buildManifestGRanges("HM450.hg38.manifest")

## End(Not run)
```

sesameAnno_download *Download SeSAMe annotation files*

Description

see also http://zwdzwd.github.io/InfiniumAnnotation

Usage

```
sesameAnno_download(url, destfile = tempfile(basename(url)))
```

Arguments

url	url or title of the annotation file
destfile	download to this file, a temp file if unspecified

Details

This function acts similarly as sesameAnno_get except that it directly download files without invoking BiocFileCache. This is needed in some situation because BiocFileCache may change the file name and downstream program may depend on the correct file names. It also lets you download files in a cleaner way without routing through BiocFileCache

Value

the path to downloaded file

Examples

```
## Not run:
## avoid testing as this function uses external host
sesameAnno_download("Test/3999492009_R01C01_Grn.idat")
sesameAnno_download("EPIC.hg38.manifest.tsv.gz")
sesameAnno_download("EPIC.hg38.snp.tsv.gz")

## End(Not run)
```

---

sesameAnno_readManifestTSV

Read manifest file to a tsv format

Description

Read manifest file to a tsv format

Usage

```
sesameAnno_readManifestTSV(tsv_fn)
```

Arguments

tsv_fn	tsv file path

Value

a manifest as a tibble

Examples

```
## Not run:
tsv = sesameAnno_download("HM450.hg38.manifest.tsv.gz")
mft <- sesameAnno_readManifestTSV(tsv)
## direct access
mft <- sesameAnno_readManifestTSV("HM450.hg38.manifest")

## End(Not run)
```

---

sesameQC-class *An S4 class to hold QC statistics*

Description

An S4 class to hold QC statistics

Value

sesameQC object

Slots

`stat` a list to store qc stats

---

sesameQCtoDF *Convert a list of sesameQC to data frame*

Description

Convert a list of sesameQC to data frame

Usage

```
sesameQCtoDF(qcs, cols = c("frac_dt_cg", "RGdistort", "RGratio"))
```

Arguments

`qcs`	sesameQCs
`cols`	QC columns, use NULL to report all

Value

a data frame

Examples

```
sdf <- sesameDataGet("EPIC.1.SigDF")
qcs <- sesameQC_calcStats(sdf, "detection")
sesameQCtoDF(qcs)
```

sesameQC_calcStats *Calculate QC statistics*

Description

It is a function to call one or multiple sesameQC_calcStats functions

Usage

```
sesameQC_calcStats(sdf, funs = NULL)
```

Arguments

sdf	a SigDF object
funs	a sesameQC_calcStats_* function or a list of them default to all functions. One can also use a string such as "detection" or c("detection", "intensity") to reduce typing

Details

currently supporting: detection, intensity, numProbes, channel, dyeBias, betas

Value

a sesameQC object

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
sesameQC_calcStats(sdf)
sesameQC_calcStats(sdf, "detection")
sesameQC_calcStats(sdf, c("detection", "channel"))
## retrieve stats as a list
sesameQC_getStats(sesameQC_calcStats(sdf, "detection"))
## or as data frames
as.data.frame(sesameQC_calcStats(sdf, "detection"))
```

sesameQC_getStats *Get stat numbers from an sesameQC object*

Description

Get stat numbers from an sesameQC object

Usage

```
sesameQC_getStats(qc, stat_names = NULL, drop = TRUE)
```

Arguments

qc	a sesameQC object
stat_names	which stat(s) to retrieve, default to all.
drop	whether to drop to a string when stats_names has only one element.

Value

a list of named stats to be retrieved

Examples

```
sdf <- sesameDataGet("EPIC.1.SigDF")
qc <- sesameQC_calcStats(sdf, "detection")
sesameQC_getStats(qc, "frac_dt")
```

---

sesameQC_plotBar *Bar plots for sesameQC*

Description

By default, it plots median_beta_cg, median_beta_ch, RGratio, RGdistort, frac_dt

Usage

```
sesameQC_plotBar(qcs, keys = NULL)
```

Arguments

qcs	a list of SigDFs
keys	optional, other key to plot, instead of the default keys can be found in the parenthesis of the print output of each sesameQC output.

Value

a bar plot comparing different QC metrics

Examples

```
sesameDataCache() # if not done yet
sdfs <- sesameDataGet("EPIC.5.SigDF.normal")[1:2]
sesameQC_plotBar(lapply(sdfs, sesameQC_calcStats, "detection"))
```

sesameQC_plotBetaByDesign *Plot betas distinguishing different Infinium chemistries*

Description

Plot betas distinguishing different Infinium chemistries

Usage

```
sesameQC_plotBetaByDesign(
  sdf,
  prep = NULL,
  legend_pos = "top",
  mar = c(3, 3, 1, 1),
  main = "",
  ...
)
```

Arguments

sdf	SigDF
prep	prep codes to step through
legend_pos	legend position (default: top)
mar	margin of layout when showing steps of prep
main	main title in plots
...	additional options to plot

Value

create a density plot

Examples

```
sdf <- sesameDataGet("EPIC.1.SigDF")
sesameQC_plotBetaByDesign(sdf, prep="DB")
```

sesameQC_plotHeatSNPs *Plot SNP heatmap*

Description

Plot SNP heatmap

Usage

```
sesameQC_plotHeatSNPs(sdfs, cluster = TRUE, filter.nonvariant = TRUE)
```

Arguments

sdfs	beta value matrix, row: probes; column: samples
cluster	show clustered heatmap
filter.nonvariant	whether to filter nonvariant (range < 0.3)

Value

a grid graphics object

Examples

```
sdfs <- sesameDataGet("EPIC.5.SigDF.normal")[1:2]
plt <- sesameQC_plotHeatSNPs(sdfs, filter.nonvariant = FALSE)
```

---

sesameQC_plotIntensVsBetas

Plot Total Signal Intensities vs Beta Values This plot is helpful in revealing the extent of signal background and dye bias.

Description

Plot Total Signal Intensities vs Beta Values This plot is helpful in revealing the extent of signal background and dye bias.

Usage

```
sesameQC_plotIntensVsBetas(
  sdf,
  mask = TRUE,
  use_max = FALSE,
  intens.range = c(5, 15),
  pal = "whiteturbo",
  ...
)
```

Arguments

sdf	a SigDF
mask	whether to remove probes that are masked
use_max	to use max(M,U) or M+U
intens.range	plot range of signal intensity
pal	color palette, whiteturbo, whiteblack, whitejet
...	additional arguments to smoothScatter

Value

create a total signal intensity vs beta value plot

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
sesameQC_plotIntensVsBetas(sdf)
```

---

sesameQC_plotRedGrnQQ *Plot red-green QQ-Plot using Infinium-I Probes*

Description

Plot red-green QQ-Plot using Infinium-I Probes

Usage

```
sesameQC_plotRedGrnQQ(sdf, main = "R-G QQ Plot", ...)
```

Arguments

sdf	a SigDF
main	plot title
...	additional options to qqplot

Value

create a qqplot

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
sesameQC_plotRedGrnQQ(sdf)
```

---

sesameQC_rankStats *This function compares the input sample with public data. Only overlapping metrics will be compared.*

Description

This function compares the input sample with public data. Only overlapping metrics will be compared.

Usage

```
sesameQC_rankStats(qc, publicQC = NULL, platform = "EPIC")
```

Arguments

qc	a sesameQC object
publicQC	public QC statistics, filtered from e.g.: EPIC.publicQC, MM285.publicQC and Mammal40.publicQC
platform	EPIC, MM285 or Mammal40, used when publicQC is not given

Value

a sesameQC

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
sesameQC_rankStats(sesameQC_calcStats(sdf, "intensity"))
```

---

sesame_checkVersion *Check SeSAMe versions*

Description

print package verison of sesame and depended packages to help troubleshoot installation issues.

Usage

```
sesame_checkVersion()
```

Value

print the version of sesame, sesameData, biocondcutor and R

Examples

```
sesame_checkVersion()
```

---

setMask *Set mask to only the probes specified*

Description

Set mask to only the probes specified

Usage

```
setMask(sdf, probes)
```

Arguments

sdf	a SigDF
probes	a vector of probe IDs or a logical vector with TRUE representing masked probes

Value

a SigDF with added mask

Examples

```
sdf <- sesameDataGet('EPIC.1.SigDF')
sum(sdf$mask)
sum(setMask(sdf, "cg14959801")$mask)
sum(setMask(sdf, c("cg14057072", "cg22344912"))$mask)
```

`SigDF` *SigDF validation from a plain data frame*

Description

SigDF validation from a plain data frame

Usage

```
SigDF(df, platform = "EPIC", ctl = NULL)
```

Arguments

`df`	a `data.frame` with Probe_ID, MG, MR, UG, UR, col and mask
`platform`	a string to specify the array platform
`ctl`	optional control probe data frame

Value

a `SigDF` object

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
```

`signalMU` *report M and U for regular probes*

Description

report M and U for regular probes

Usage

```
signalMU(sdf, mask = TRUE, MU = FALSE)
```

Arguments

`sdf`	a `SigDF`
`mask`	whether to apply mask
`MU`	add a column for M+U

Value

a data frame of M and U columns

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
head(signalMU(sdf))
```

`sliceFileSet` *Slice a fileSet with samples and probes*

Description

Slice a fileSet with samples and probes

Usage

```
sliceFileSet(fset, samples = fset$samples, probes = fset$probes, memmax = 10^5)
```

Arguments

`fset`	a sesame::fileSet, as obtained via readFileSet
`samples`	samples to query (default to all samples)
`probes`	probes to query (default to all probes)
`memmax`	maximum items to read from file to memory, to protect from accidental memory congestion.

Value

a numeric matrix of length(samples) columns and length(probes) rows

Examples

```
## create two samples
fset <- initFileSet('mybetas2', 'HM27', c('s1','s2'))

## a hypothetical numeric array (can be beta values, intensities etc)
hypothetical <- setNames(runif(fset$n), fset$probes)

## map the numeric to file
mapFileSet(fset, 's1', hypothetical)

## get data
sliceFileSet(fset, 's1', 'cg00000292')
```

summaryExtractTest *Extract slope information from DMLSummary*

Description

Extract slope information from DMLSummary

Usage

```
summaryExtractTest(smry)
```

Arguments

smry	DMLSummary from DML command

Value

a table of slope and p-value

Examples

```
sesameDataCache() # in case not done yet
data <- sesameDataGet('HM450.76.TCGA.matched')
smry <- DML(data$betas[1:10,], ~type, meta=data$sampleInfo)
slopes <- summaryExtractTest(smry)

sesameDataGet_resetEnv()
```

totalIntensities *M+U Intensities Array*

Description

The function takes one single SigDF and computes total intensity of all the in-band measurements by summing methylated and unmethylated alleles. This function outputs a single numeric for the mean.

Usage

```
totalIntensities(sdf, mask = FALSE)
```

Arguments

sdf	a SigDF
mask	whether to mask probes using mask column

Value

a vector of M+U signal for each probe

Examples

```
sesameDataCache() # if not done yet
sdf <- sesameDataGet('EPIC.1.SigDF')
intensities <- totalIntensities(sdf)
```

`twoCompsEst2` *Estimate the fraction of the 2nd component in a 2-component mixture*

Description

Estimate the fraction of the 2nd component in a 2-component mixture

Usage

```
twoCompsEst2(
  pop1,
  pop2,
  target,
  use.ave = TRUE,
  diff_1m2u = NULL,
  diff_1u2m = NULL
)
```

Arguments

`pop1`	Reference methylation level matrix for population 1
`pop2`	Reference methylation level matrix for population 2
`target`	Target methylation level matrix to be analyzed
`use.ave`	use population average in selecting differentially methylated probes
`diff_1m2u`	A vector of differentially methylated probes (methylated in population 1 but unmethylated in population 2)
`diff_1u2m`	A vector of differentially methylated probes (unmethylated in population 1 but methylated in population 2)

Value

Estimate of the 2nd component in the 2-component mixture

updateSigDF *Set color and mask using strain/species-specific manifest*

Description

also sets attr(,"species")

Usage

```
updateSigDF(sdf, species = NULL, strain = NULL, addr = NULL, verbose = FALSE)
```

Arguments

sdf	a SigDF
species	the species the sample is considered to be
strain	the strain the sample is considered to be
addr	species-specific address species, optional
verbose	print more messages

Value

a SigDF with updated color channel and mask

Examples

```
sdf <- sesameDataGet('Mammal40.1.SigDF')
sdf_mouse <- updateSigDF(sdf, species="mus_musculus")
```

visualizeGene *Visualize Gene*

Description

Visualize the beta value in heatmaps for a given gene. The function takes a gene name which is taken from the UCSC refGene. It searches all the transcripts for the given gene and optionally extend the span by certain number of base pairs. The function also takes a beta value matrix with sample names on the columns and probe names on the rows. The function can also work on different genome builds (default to hg38, can be hg19).

Usage

```
visualizeGene(
  gene_name,
  betas,
  platform = NULL,
  genome = NULL,
  upstream = 2000,
  dwstream = 2000,
  ...
)
```

Arguments

gene_name	gene name
betas	beta value matrix (row: probes, column: samples)
platform	HM450, EPIC, or MM285 (default)
genome	hg19, hg38, or mm10 (default)
upstream	distance to extend upstream
dwstream	distance to extend downstream
...	additional options, see visualizeRegion, assemble_plots

Value

None

Examples

```
betas <- sesameDataGet('HM450.76.TCGA.matched')$betas
visualizeGene('ADA', betas, 'HM450')
```

---

visualizeProbes *Visualize Region that Contains the Specified Probes*

Description

Visualize the beta value in heatmaps for the genomic region containing specified probes. The function works only if specified probes can be spanned by a single genomic region. The region can cover more probes than specified. Hence the plotting heatmap may encompass more probes. The function takes as input a string vector of probe IDs (cg/ch/rs-numbers). if draw is FALSE, the function returns the subset beta value matrix otherwise it returns the grid graphics object.

Usage

```
visualizeProbes(
  probeNames,
  betas,
  platform = NULL,
  genome = NULL,
  upstream = 1000,
  dwstream = 1000,
  ...
)
```

Arguments

probeNames	probe names
betas	beta value matrix (row: probes, column: samples)
platform	HM450, EPIC or MM285 (default)
genome	hg19, hg38 or mm10 (default)
upstream	distance to extend upstream
dwstream	distance to extend downstream
...	additional options, see visualizeRegion and assemble_plots

Value

None

Examples

```
betas <- sesameDataGet('HM450.76.TCGA.matched')$betas
visualizeProbes(c('cg22316575', 'cg16084772', 'cg20622019'), betas, 'HM450')
```

`visualizeRegion` *Visualize Region*

Description

The function takes a genomic coordinate (chromosome, start and end) and a beta value matrix (probes on the row and samples on the column). It plots the beta values as a heatmap for all probes falling into the genomic region. If 'draw=TRUE' the function returns the plotted grid graphics object. Otherwise, the selected beta value matrix is returned. 'cluster.samples=TRUE/FALSE' controls whether hierarchical clustering is applied to the subset beta value matrix.

Usage

```
visualizeRegion(
  chrm,
  beg,
  end,
  betas,
  platform = NULL,
  genome = NULL,
  draw = TRUE,
  cluster.samples = FALSE,
  na.rm = FALSE,
  nprobes.max = 1000,
  txn.types = "protein_coding",
  txn.font.size = 6,
  ...
)
```

Arguments

`chrm`	chromosome
`beg`	begin of the region
`end`	end of the region
`betas`	beta value matrix (row: probes, column: samples)
`platform`	EPIC, HM450, or MM285
`genome`	hg38, mm10, ..., will infer if not given. For additional mapping, download the GRanges object from http://zwdzwd.github.io/InfiniumAnnotation and provide the following argument ..., genome = sesameAnno_buildManifestGRanges("downloaded_file"),... to this function.
`draw`	draw figure or return betas

cluster.samples	whether to cluster samples
na.rm	remove probes with all NA.
nprobes.max	maximum number of probes to plot
txn.types	default to protein_coding, use NULL for all
txn.font.size	transcript name font size
...	additional options, see assemble_plots

Value

graphics or a matrix containing the captured beta values

Examples

```
betas <- sesameDataGet('HM450.76.TCGA.matched')$betas
visualizeRegion('chr20', 44648623, 44652152, betas, 'HM450')
```

---

visualizeSegments *Visualize segments*

Description

The function takes a CNSegment object obtained from cnSegmentation and plot the bin signals and segments (as horizontal lines).

Usage

```
visualizeSegments(seg, to.plot = NULL, genes.to.label = NULL)
```

Arguments

seg	a CNSegment object
to.plot	chromosome to plot (by default plot all chromosomes)
genes.to.label	gene(s) to label

Details

require ggplot2, scales

Value

plot graphics

Examples

```
sesameDataCache()
## Not run:
sdfs <- sesameDataGet('EPICv2.8.SigDF')
sdf <- sdfs[["K562_206909630040_R01C01"]]
seg <- cnSegmentation(sdf)
seg <- cnSegmentation(sdf, return.probe.signals=TRUE)
visualizeSegments(seg)
visualizeSegments(seg, to.plot=c("chr9","chr22"))
visualizeSegments(seg, genes.to.label=c("ABL1","BCR"))

## End(Not run)

sesameDataGet_resetEnv()
```

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