

# Package ‘sesame’

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**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.

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**License** MIT + file LICENSE

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<i>sesame-package</i>	<i>Analyze DNA methylation data</i>
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---

## 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.

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## 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)
```

---

aggregateTestEnrichments  
*Aggregate test enrichment results*

---

**Description**

Aggregate test enrichment results

**Usage**

```
aggregateTestEnrichments(result_list, column = "estimate", return_df = FALSE)
```

**Arguments**

result\_list        a list of results from testEnrichment  
column            the column name to aggregate (Default: estimate)  
return\_df        whether to return a merged data frame

**Value**

a matrix for all results

**Examples**

```
## pick some big TFBS-overlapping CpG groups
cg_lists <- KYCG_getDBs("MM285.TFBS")
queries <- cg_lists[(sapply(cg_lists, length) > 40000)]
result_list <- lapply(queries, testEnrichment, "MM285.chromHMM")
mtx <- aggregateTestEnrichments(result_list)
```

---

assemble_plots	<i>assemble_plots</i>
----------------	-----------------------

---

**Description**

assemble plots

**Usage**

```
assemble_plots(
  betas,
  txns,
  probes,
  plt.txns,
  plt.mapLines,
  plt.cytoband,
  heat.height = NULL,
  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)  
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

---

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	<i>Bin signals from probe signals</i>
------------	---------------------------------------

---

**Description**

require GenomicRanges

**Usage**

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

**Arguments**

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

**Value**

bin signals

---

bisConversionControl	<i>Compute internal bisulfite conversion control</i>
----------------------	--

---

**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, verbose = FALSE)
```

**Arguments**

sdf	a SigDF
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)
```

---

checkLevels	<i>filter data matrix by factor completeness only works for discrete factors</i>
-------------	--

---

**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	<i>Lookup address in one sample</i>
---------------------	-------------------------------------

---

**Description**

Lookup address and transform address to probe

**Usage**

```
chipAddressToSignal(dm, mft)
```

**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

**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	<i>Perform copy number segmentation</i>
----------------	---

---

**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, verbose = FALSE)
```

**Arguments**

sdf	SigDF
sdfs.normal	a list of SigDFs 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.
verbose	print more messages

**Value**

an object of CNSegment

**Examples**

```
sesameDataCache()

## sdf <- sesameDataGet('EPIC.1.SigDF')
## sdfs.normal <- sesameDataGet('EPIC.5.SigDF.normal')
## seg <- cnSegmentation(sdf, sdfs.normal)
```

---

compareDatabaseSetOverlap

*calculates the pairwise overlap between given list of database sets using a distance metric.*

---

### Description

calculates the pairwise overlap between given list of database sets using a distance metric.

### Usage

```
compareDatabaseSetOverlap(databases = NA, metric = "Jaccard")
```

### Arguments

databases	List of vectors corresponding to the database sets of interest with associated meta data as an attribute to each element. Optional. (Default: NA)
metric	String representing the similarity metric to use. Optional. (Default: "Jaccard").

### Value

An upper triangular matrix containing a metric (Jaccard) comparing the pairwise distances between database sets.

---

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()
```

---

```
compareMouseTissueReference
```

*Compare mouse array data with mouse tissue references*

---

**Description**

Compare mouse array data with mouse tissue references

**Usage**

```
compareMouseTissueReference(  
  betas = NULL,  
  color = "blueYellow",  
  query_width = 0.3  
)
```

**Arguments**

betas	matrix of betas for the target sample
color	either blueYellow or fullJet
query_width	the width of the query beta value matrix

**Value**

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

**Examples**

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

---

createDBNetwork            *createGeneNetwork creates database network using the Jaccard index.*

---

**Description**

createGeneNetwork creates database network using the Jaccard index.

**Usage**

```
createDBNetwork(databases)
```

**Arguments**

databases                Vector of probes corresponding to a single database set of interest.

**Value**

ggplot lollipop plot

---

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, hg19 etc.

### 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

**Examples**

```
df <- sesameDataGet("MM285.publicQC")
qcs <- dataFrame2sesameQC(df[1:2,])
```

---

dbStats	<i>dbStats builds dataset for a given betas matrix composed of engineered features from the given database sets</i>
---------	---

---

**Description**

dbStats builds dataset for a given betas matrix composed of engineered features from the given database sets

**Usage**

```
dbStats(betas, databases, fun = mean, na.rm = TRUE, n_min = NULL, f_min = 0.1)
```

**Arguments**

betas	matrix of beta values where probes are on the rows and samples are on the columns
databases	List of vectors corresponding to probe locations for which the features will be extracted
fun	aggregation function, default to mean
na.rm	whether to remove NA
n_min	min number of non-NA for aggregation function to apply, overrides f_min
f_min	min fraction of non-NA for aggregation function to apply

**Value**

matrix with samples on the rows and database set on the columns

**Examples**

```
library(SummarizedExperiment)
se <- sesameDataGet('MM285.467.SE.tissue20Kprobes')
head(dbStats(assay(se), "MM285.probeType")[,1:3])
sesameDataGet_resetEnv()
```



---

deIdentify	<i>De-identify IDATs by removing SNP probes</i>
------------	---

---

**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)
```

---

detectionIB	<i>Mask detection by intermediate beta values</i>
-------------	---

---

**Description**

Mask detection by intermediate beta values

**Usage**

```
detectionIB(
  sdf,
  return.pval = FALSE,
  pval.threshold = 0.05,
  capMU = 3000,
  window = 100
)
```

**Arguments**

sdf	a SigDF
return.pval	whether to return p-values, instead of a SigDF
pval.threshold	minimum p-value to mask
capMU	the maximum M+U to search for intermediate betas
window	window size for smoothing and beta fraction calc.

**Value**

a SigDF with mask added

**Examples**

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

---

detectionPnegEcdf	<i>Detection P-value based on ECDF of negative control</i>
-------------------	--

---

**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	<i>Restrict refset to differentially methylated probes use with care, might introduce bias</i>
------------	--

---

**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	<i>List all contrasts of a DMLSummary</i>
-------------	---

---

**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	<i>Test differential methylation on each locus</i>
-----	--

---

**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, mc.cores = 1)
```

**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.
mc.cores	number of cores for parallel processing

**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()
```

---

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,
  genome = 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, ...
genome	hg38, hg19, mm10, ...
dist.cutoff	distance cutoff (default to use dist.cutoff.quantile)
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[1:100,], smry, "typeTumour")

sesameDataGet_resetEnv()
```

---

dyeBiasCorr	<i>Correct dye bias in by linear scaling.</i>
-------------	---

---

**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 SigDFs with dye bias corrected.

**Usage**

```
dyeBiasCorrMostBalanced(sdfs)
```

**Arguments**

sdfs            a list of normalized SigDFs

**Value**

a list of normalized SigDFs

**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)
```

---

estimateCellComposition

*Estimate cell composition using reference*

---

**Description**

This is a reference-based cell composition estimation. The function takes a reference methylation status matrix (rows for probes and columns for cell types, can be obtained by getRefSet function) and a query beta value measurement. The length of the target beta values should be the same as the number of rows of the reference matrix. The method assumes one unknown component. It outputs a list containing the estimated cell fraction, the error of optimization and methylation status of the unknown component.

**Usage**

```
estimateCellComposition(g, q, refine = TRUE, dichotomize = FALSE, ...)
```

**Arguments**

g	reference methylation
q	target measurement: length(q) == nrow(g)
refine	to refine estimate, takes longer
dichotomize	to dichotomize query beta value before estimate, this relieves unclean background subtraction
...	extra parameters for optimization, this includes temp - annealing temperature (0.5) maxIter - maximum iteration to stop after converge (1000) delta - delta score to reset counter (0.0001) verbose - output debug info (FALSE)

**Value**

a list of fraction, min error and unknown component methylation state

---

estimateLeukocyte	<i>Estimate leukocyte fraction using a two-component model</i>
-------------------	--

---

**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	<i>Convert SNP from Infinium array to VCF file</i>
-----------	--

---

### Description

Convert SNP from Infinium array to VCF file

### Usage

```
formatVCF(  
  sdf,  
  vcf = NULL,  
  genome = "hg19",  
  annoS = NULL,  
  annoI = NULL,  
  verbose = FALSE  
)
```

### Arguments

sdf	SigDF
vcf	output VCF file path, if NULL output to console
genome	genome
annoS	SNP variant annotation, download if not given
annoI	Infinium-I variant annotation, download if not given hg19 and hg38 in human
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 vcf is not sorted. You can sort with `awk '$1 ~ /^#/ print $0;next print $0 | "sort -k1,1 -k2,2n"'`

### Examples

```
sesameDataCacheAll() # if not done yet  
sdf <- sesameDataGet('EPIC.1.SigDF')  
  
## output to console  
head(formatVCF(sdf))
```

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)
```

**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

**Value**

a numeric vector, beta values

**Examples**

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

---

getBinCoordinates	<i>Get bin coordinates</i>
-------------------	----------------------------

---

**Description**

requires GenomicRanges, IRanges

**Usage**

```
getBinCoordinates(seqLength, gapInfo, probe.coords)
```

**Arguments**

seqLength	chromosome information object
gapInfo	chromosome gap information
probe.coords	probe coordinates

**Value**

bin.coords

---

getRefSet	<i>Retrieve reference set</i>
-----------	-------------------------------

---

**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()
```

---

getSexInfo

*Get sex-related information*


---

**Description**

The function takes a SigDF and returns a vector of three numerics: the median intensity of chrY probes; the median intensity of chrX probes; and fraction of intermediate chrX probes. chrX and chrY probes excludes pseudo-autosomal probes.

**Usage**

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

**Arguments**

sdf	a SigDF
verbose	print more messages

**Value**

medianY and medianX, fraction of XCI, methylated and unmethylated X probes, median intensities of auto-chromosomes.

**Examples**

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

---

inferEthnicity

*Infer Ethnicity*


---

**Description**

This function uses both the built-in rsprobes as well as the type I Color-Channel-Switching probes to infer ethnicity.

**Usage**

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

**Arguments**

sdf                    a SigDF  
 verbose                print more messages

**Details**

s better be background subtracted and dyebias corrected for best accuracy  
 Please note: the betas should come from SigDF \*without\* channel inference.

**Value**

string of ethnicity

**Examples**

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

---

`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,
  verbose = FALSE,
  summary = FALSE
)
```

**Arguments**

sdf                    a SigDF  
 switch\_failed        whether to switch 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	<i>Infer Sex</i>
----------	------------------

---

**Description**

Infer Sex

**Usage**

```
inferSex(x, platform = NULL, verbose = FALSE)
```

**Arguments**

x	either a raw SigDF or a beta value vector named by probe ID SigDF is preferred over beta values.
platform	Only MM285, EPIC and HM450 are supported.
verbose	print more messages

**Value**

'F' or 'M' We established our sex calling based on the CpGs hypermethylated in inactive X (XiH), CpGs hypomethylated in inactive X (XiL) and signal intensity ratio of Y-chromosome over autosomes. Currently human inference uses a random forest and mouse inference uses a support vector machine.

The function checks the sample quality. If the sample is of poor quality the inference return NA.

Note many factors 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.

**Examples**

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

---

inferSexKaryotypes      *Infer Sex Karyotype*

---

### Description

The function takes a SigDF and infers the sex chromosome Karyotype and presence/absence of X-chromosome inactivation (XCI). chrX, chrY and XCI are inferred relatively independently. This function gives a more detailed look of potential sex chromosome aberrations.

### Usage

```
inferSexKaryotypes(sdf)
```

### Arguments

sdf                      a SigDF

### Value

Karyotype string, with XCI

### Examples

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

---

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 messages

**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	<i>Infer strain information for mouse array</i>
-------------	---

---

**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	<i>inferTissue1 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.</i>
-------------	---

---

**Description**

inferTissue1 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	<i>initialize a fileSet class by allocating appropriate storage</i>
-------------	---

---

**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'))
```

---

KYCG_annoProbes	<i>Annotate Probe IDs using KYCG databases</i>
-----------------	--

---

**Description**

see sesameData\_annoProbes if you'd like to annotate by genomic coordinates (in GRanges)

**Usage**

```
KYCG_annoProbes(
  query,
  databases,
  db_names = NULL,
  platform = NULL,
  sep = ",",
  indicator = FALSE,
  silent = FALSE
)
```

**Arguments**

query	probe IDs in a character vector
databases	character or actual database (i.e. list of probe IDs)
db_names	specific database (default to all databases)
platform	EPIC, MM285 etc. will infer from probe IDs if not given
sep	delimiter used in paste
indicator	return the indicator matrix instead of a concatenated annotation (in the case of have multiple annotations)
silent	suppress message

**Value**

named annotation vector, or indicator matrix

**Examples**

```
query <- names(sesameData_getManifestGRanges("MM285"))
anno <- KYCG_annoProbes(query, "designGroup", silent = TRUE)
```

---

KYCG_buildGeneDBs	<i>build gene-probe association database</i>
-------------------	--

---

**Description**

build gene-probe association database

**Usage**

```
KYCG_buildGeneDBs(  
  query = NULL,  
  platform = NULL,  
  max_distance = 10000,  
  silent = FALSE  
)
```

**Arguments**

query	the query probe list. If NULL, use all the probes on the platform
platform	HM450, EPIC, MM285, Mammal40, will infer from query if not given
max_distance	probe-gene distance for association
silent	suppress messages

**Value**

gene databases

**Examples**

```
query <- c("cg04707299", "cg13380562", "cg00480749")  
dbs <- KYCG_buildGeneDBs(query, platform = "EPIC")  
testEnrichment(query, dbs, platform = "EPIC")
```

---

KYCG_getDBs	<i>Get databases by full or partial names of the database group(s)</i>
-------------	--

---

**Description**

Get databases by full or partial names of the database group(s)

**Usage**

```
KYCG_getDBs(
  group_nms,
  db_names = NULL,
  platform = NULL,
  summary = FALSE,
  allow_multi = FALSE,
  type = NULL,
  silent = FALSE
)
```

**Arguments**

group_nms	database group names
db_names	name of the database, fetch only the given databases
platform	EPIC, HM450, MM285, ... If given, will restrict to that platform.
summary	return a summary of database instead of db itself
allow_multi	allow multiple groups to be returned for
type	numerical, categorical, default: all
silent	no messages each query.

**Value**

a list of databases, return NULL if no database is found

**Examples**

```
dbs <- KYCG_getDBs("MM285.chromHMM")
dbs <- KYCG_getDBs(c("MM285.chromHMM", "MM285.probeType"))
```

---

KYCG_listDBGroups	<i>List database group names</i>
-------------------	----------------------------------

---

**Description**

List database group names

**Usage**

```
KYCG_listDBGroups(filter = NULL, type = NULL)
```

**Arguments**

filter	keywords for filtering
type	categorical, numerical (default: all)



**Value**

a list of db group names

**Examples**

```
head(KYCG_listDBGroups("chromHMM"))
```

---

KYCG\_plotBar *Bar plot to show most enriched CG groups from testEnrichment*

---

**Description**

The input data frame should have an "estimate" and a "FDR" columns.

**Usage**

```
KYCG_plotBar(df, n_min = 10, n_max = 30, max_fdr = 0.05, min_cap = -5)
```

**Arguments**

df	KYCG result data frame
n_min	minimum number of databases to report
n_max	maximum number of databases to report
max_fdr	maximum FDR
min_cap	the minimum log2(OR), value below this are capped

**Details**

Top CG groups are determined by estimate (descending order).

**Value**

grid plot object

**Examples**

```
KYCG_plotBar(data.frame(
  estimate=runif(10,0,10), FDR=runif(10,0,1), nD=10,
  overlap=as.integer(runif(10,0,30)), group="g", dbname=seq_len(10)))
```

---

`KYCG_plotDot`*Dot plot to show most enriched CG groups from testEnrichment*

---

**Description**

The input data frame should have an "estimate" and a "FDR" columns.

**Usage**

```
KYCG_plotDot(df, n_min = 10, n_max = 30, max_fdr = 0.05)
```

**Arguments**

<code>df</code>	KYCG result data frame
<code>n_min</code>	minimum number of databases to report
<code>n_max</code>	maximum number of databases to report
<code>max_fdr</code>	maximum FDR

**Details**

Top CG groups are determined by estimate (descending order).

**Value**

grid plot object

**Examples**

```
KYCG_plotDot(data.frame(
  estimate=runif(10,0,10), FDR=runif(10,0,1), nD=runif(10,10,20),
  overlap=as.integer(runif(10,0,30)), group="g", dbname=seq_len(10)))
```

---

`KYCG_plotEnrichAll`*plot enrichment test result*

---

**Description**

plot enrichment test result

**Usage**

```
KYCG_plotEnrichAll(df, fdr_max = 25, n_label = 15, min_estimate = 0)
```

**Arguments**

df	test enrichment result data frame
fdr_max	maximum fdr for capping
n_label	number of database to label
min_estimate	minimum estimate

**Value**

grid object

**Examples**

```
query <- KYCG_getDBs("MM285.designGroup")[[ "PGCMeth" ]]
res <- testEnrichment(query)
KYCG_plotEnrichAll(res)
```

---

KYCG\_plotLollipop *creates a lollipop plot of log(estimate) given data with fields estimate.*

---

**Description**

creates a lollipop plot of log(estimate) given data with fields estimate.

**Usage**

```
KYCG_plotLollipop(df, label_column = "dbname", n = 20)
```

**Arguments**

df	DataFrame where each row is a database name with its estimate.
label_column	column in df to be used as the label (default: dbname)
n	Integer representing the number of top enrichments to report. Optional. (Default: 10)

**Value**

ggplot lollipop plot

**Examples**

```
KYCG_plotLollipop(data.frame(
  estimate=runif(10,0,10), FDR=runif(10,0,1), nD=runif(10,10,20),
  overlap=as.integer(runif(10,0,30)), group="g",
  dbname=as.character(seq_len(10))))
```

---

KYCG_plotManhattan	<i>KYCG_plotManhattan makes a manhattan plot to summarize EWAS results</i>
--------------------	--

---

### Description

KYCG\_plotManhattan makes a manhattan plot to summarize EWAS results

### Usage

```
KYCG_plotManhattan(
  vals,
  platform = NULL,
  gr = NULL,
  genome = NULL,
  title = NULL,
  label_min = 100,
  col = c("wheat1", "sienna3"),
  ylabel = "Value"
)
```

### Arguments

vals	named vector of values (P,Q etc), vector name is Probe ID.
platform	String corresponding to the type of platform to use for retrieving GRanges coordinates of probes. Either MM285, EPIC, HM450, or HM27. If it is not provided, it will be inferred from the query set probeIDs (Default: NA).
gr	GRanges object containing genomic coordinates of probes. If not provided, GRanges for provided or inferred platform will be retrieved
genome	genome build
title	title for plot
label_min	Threshold above which data points will be labelled with Probe ID
col	color
ylabel	y-axis label

### Value

a ggplot object

### Examples

```
## see vignette for examples
sesameDataGet_resetEnv()
```

---

KYCG_plotMeta	<i>Plot meta gene or other meta genomic features</i>
---------------	--

---

**Description**

Plot meta gene or other meta genomic features

**Usage**

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

**Arguments**

betas	a named numeric vector or a matrix (row: probes; column: samples)
platform	if not given and x is a SigDF, will be inferred the meta features

**Value**

a grid plot object

**Examples**

```
sdf <- sesameDataGet("EPIC.1.SigDF")
KYCG_plotMeta(getBetas(sdf))
```

---

KYCG_plotMetaEnrichment	<i>Plot meta gene or other meta genomic features</i>
-------------------------	--

---

**Description**

Plot meta gene or other meta genomic features

**Usage**

```
KYCG_plotMetaEnrichment(result_list)
```

**Arguments**

result_list	one or a list of testEnrichment
-------------	---------------------------------

**Value**

a grid plot object

**Examples**

```
cg_lists <- KYCG_getDBs("MM285.TFBS")
queries <- cg_lists[(sapply(cg_lists, length) > 40000)]
result_list <- lapply(queries, testEnrichment,
  "MM285.metagene", silent=TRUE)

KYCG_plotMetaEnrichment(result_list)
```

---

KYCG\_plotPointRange *Plot point range for a list of enrichment testing results against the same set of databases*

---

**Description**

Plot point range for a list of enrichment testing results against the same set of databases

**Usage**

```
KYCG_plotPointRange(result_list)
```

**Arguments**

result\_list a list of testEnrichment resultsx

**Value**

grid plot object

**Examples**

```
## pick some big TFBS-overlapping CpG groups
cg_lists <- KYCG_getDBs("MM285.TFBS")
queries <- cg_lists[(sapply(cg_lists, length) > 40000)]
result_list <- lapply(queries, testEnrichment, "MM285.chromHMM")
KYCG_plotPointRange(result_list)
```

---

KYCG\_plotVolcano      *creates a volcano plot of  $-\log_2(p.value)$  and  $\log(estimate)$  given data with fields estimate and p.value.*

---

**Description**

creates a volcano plot of  $-\log_2(p.value)$  and  $\log(estimate)$  given data with fields estimate and p.value.

**Usage**

```
KYCG_plotVolcano(data, label_column = "dbname", alpha = 0.05)
```

**Arguments**

data	DataFrame where each field is a database name with two fields for the estimate and p.value.
label_column	column in df to be used as the label (default: dbname)
alpha	Float representing the cut-off alpha value for the plot. Optional. (Default: 0.05)

**Value**

ggplot volcano plot

**Examples**

```
KYCG_plotVolcano(data.frame(
  estimate=runif(10,0,10), FDR=runif(10,0,1), nD=runif(10,10,20),
  overlap=as.integer(runif(10,0,30)), group="g", dbname=seq_len(10)))
```

---

KYCG\_plotWaterfall      *create a waterfall plot of  $\log(estimate)$  given test enrichment*

---

**Description**

create a waterfall plot of  $\log(estimate)$  given test enrichment

**Usage**

```
KYCG_plotWaterfall(df, label_column = "dbname")
```

**Arguments**

df	data frame where each row is a database with test enrichment result
label_column	column in df to be used as the label (default: dbname)

**Value**

grid

**Examples**

```
library(SummarizedExperiment)
df <- rowData(sesameDataGet('MM285.tissueSignature'))
query <- df$Probe_ID[df$branch == "fetal_brain" & df$type == "Hypo"]
results <- testEnrichment(query, "TFBS")
KYCG_plotWaterfall(results)
```

---

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("EPIC")
```



---

mapFileSet	<i>Deposit data of one sample to a fileSet (and hence to file)</i>
------------	--

---

**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	<i>Map the SDF (from overlap array platforms) Replicates are merged by picking the best detection</i>
---------------	---

---

**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	<i>normalize Infinium I probe betas to Infinium II</i>
-------------	--

---

**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	<i>Whole-dataset-wide Mean Intensity</i>
---------------	--

---

**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	<i>Whole-dataset-wide Median Total Intensity (M+U)</i>
----------------------	--

---

**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)
```

---

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	<i>get negative control signal</i>
-------------	------------------------------------

---

**Description**

get negative control signal

**Usage**

```
negControls(sdf)
```

**Arguments**

sdf                    a SigDF

**Value**

a data frame of negative control signals

---

noMasked	<i>remove masked probes from SigDF</i>
----------	--

---

**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 <- p00BAH(sdf)  
  
sdf_noMasked <- noMasked(sdf)
```

---

noob	<i>Noob background subtraction</i>
------	------------------------------------

---

### 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	<i>get normalization control signal</i>
--------------	---

---

### 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	<i>The openSesame pipeline</i>
------------	--------------------------------

---

**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 = "",
  ...
)
```

**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
...	parameters to getBetas

**Details**

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**

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

---

openSesameToFile	<i>openSesame pipeline with file-backed storage</i>
------------------	---

---

**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	<i>Generate some additional color palettes</i>
--------	--

---

**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	<i>Convert signal M and U to SigDF</i>
------------------	--

---

**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 numeric 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-val 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$mask)
sum(p00BAH(sdf)$mask)
```

---

predictAgeHorvath353 *Horvath 353 age predictor*

---

**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 Horvath aging model (Horvath 2013 Genome Biology). The function outputs a single numeric of age in years.

**Usage**

```
predictAgeHorvath353(betas)
```

**Arguments**

betas            a probeID-named vector of beta values

**Value**

age in years

**Examples**

```
betas <- sesameDataGet('HM450.1.TCGA.PAAD')$betas
predictAgeHorvath353(betas)
sesameDataGet_resetEnv()
```

---

predictAgeSkinBlood     *Horvath Skin and Blood age predictor*

---

**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 Horvath aging model (Horvath et al. 2018 Aging, 391 probes). The function outputs a single numeric of age in years.

**Usage**

```
predictAgeSkinBlood(betas)
```

**Arguments**

betas                    a probeID-named vector of beta values

**Value**

age in years

**Examples**

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

---

predictMouseAgeInMonth  
                          *Mouse age predictor*

---

**Description**

The function takes a named numeric vector of beta values. The name attribute contains the probe ID. The function looks for overlapping probes and estimate age using an aging model built from 321 MM285 probes. The function outputs a single numeric of age in months. The clock is most accurate with the sesame preprocessing.

**Usage**

```
predictMouseAgeInMonth(betas, na_fallback = TRUE)
```

**Arguments**

betas            a probeID-named vector of beta values  
na\_fallback    use the fallback default for NAs.

**Value**

age in month

**Examples**

```
betas <- SummarizedExperiment::assay(sesameDataGet('MM285.10.SE.tissue'))[,1]
predictMouseAgeInMonth(betas)
sesameDataGet_resetEnv()
```

---

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_names = "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	<i>Extract the probe type field from probe ID This only works with the new probe ID system. See <a href="https://github.com/zhou-lab/InfiniumAnnotation">https://github.com/zhou-lab/InfiniumAnnotation</a> for illustration</i>
--------------------	--

---

**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	<i>Whole-dataset-wide Probe Success Rate</i>
------------------	--

---

### 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	<i>Mask beta values by design quality</i>
-------------	---

---

### Description

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

### Usage

```
qualityMask(sdf, mask_names = "recommended", prefixes = NULL, verbose = FALSE)
```

### Arguments

sdf	a SigDF object
mask_names	mask names, default to "recommended", can be a vector of multiple masks, e.g., c("design_issue", "multi"), NULL to skip
prefixes	mask by probe ID prefixes, e.g., cg
verbose	print more messages

**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, prefixes = "rs")$mask)

## list available masks, the mask_name column
listAvailableMasks(sdfPlatform(sdf))
```

---

readFileSet	<i>Read an existing fileSet from storage</i>
-------------	--

---

**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	<i>Import a pair of IDATs from one sample</i>
--------------	---

---

### 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,  
  platform = "",  
  manifest = NULL,  
  controls = NULL,  
  verbose = FALSE  
)
```

### Arguments

<code>prefix.path</code>	sample prefix without <code>_Grn.idat</code> and <code>_Red.idat</code>
<code>platform</code>	EPIC, HM450 and HM27 etc.
<code>manifest</code>	optional design manifest file
<code>controls</code>	optional control probe manifest file
<code>verbose</code>	be verbose? (FALSE)

### Value

a `SigDF`

### Examples

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

---

reIdentify	<i>Re-identify IDATs by restoring scrambled SNP intensities</i>
------------	---

---

**Description**

This requires 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-identify 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	<i>Reset Masking</i>
-----------	----------------------

---

**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	<i>SCRUB background correction</i>
-------	------------------------------------

---

**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	<i>SCRUB background correction</i>
-----------	------------------------------------

---

**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	<i>collapse to probe prefix</i>
------------------	---------------------------------

---

**Description**

collapse to probe prefix

**Usage**

```
SDFcollapseToPfx(sdf)
```

**Arguments**

sdf                    a SigDF object

**Value**

a data frame with updated Probe\_ID

---

sdfPlatform	<i>Convenience function to output platform attribute of SigDF</i>
-------------	---

---

**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	<i>read a table file to SigDF</i>
----------------	-----------------------------------

---

**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	<i>write SigDF to table file</i>
-----------------	----------------------------------

---

**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_download	<i>Download additional annotation files</i>
---------------------	---

---

**Description**

From the Infinium annotation website associated github repo e.g., <https://github.com/zhou-lab/InfiniumAnnotationV1>

**Usage**

```
sesameAnno_download(title, dest_dir, version = anno_base_default_version)
```

**Arguments**

title	title of the annotation file
dest_dir	download to this directory
version	version number

**Details**

The default version number should always work. One need to refer to the actual repo to see which one of the other versions also work.

See also <http://zwdzwd.github.io/InfiniumAnnotation>

**Value**

annotation file

**Examples**

```
## avoid testing as this function uses external host
if (FALSE) {
  sesameAnno_download("Test/3999492009_R01C01_Grn.idat", tempdir())
}
```

---

sesameAnno_get	<i>Retrieve additional annotation Rds data</i>
----------------	--

---

**Description**

From the Infinium annotation website associated github repo e.g., <https://github.com/zhou-lab/InfiniumAnnotationV1>

**Usage**

```
sesameAnno_get(title, version = anno_base_default_version, dest_dir = NULL)
```

**Arguments**

title	title of the annotation file
version	version number
dest_dir	if not NULL, download to this directory

**Details**

The default version number should always work. One need to refer to the actual repo to see which one of the other versions also work.

See also <http://zwdzwd.github.io/InfiniumAnnotation>

**Value**

annotation file

**Examples**

```
## avoided testing as this function uses external host
if (FALSE) {
  annoI <- anno_get("Anno/EPIC/EPIC.hg19.typeI_overlap_b151.rds")
}
```

---

sesameAnno_getManifestDF	<i>download Infinium manifest from Github repositories</i>
--------------------------	--

---

**Description**

download Infinium manifest from Github repositories

**Usage**

```
sesameAnno_getManifestDF(  
  platform,  
  genome = NULL,  
  version = anno_base_default_version  
)
```

**Arguments**

platform	Mammal40, MM285, EPIC, and HM450
genome	hg38, mm10 etc.
version	release version, default is the latest

**Value**

tibble

**Examples**

```
## avoid testing since it depends on external host  
if (FALSE) {  
  mft <- sesameAnno_getManifestDF("Mammal40")  
}
```

---

sesameData\_getAnno     *retrieve additional annotation files*

---

**Description**

retrieve additional annotation files

**Usage**

```
sesameData_getAnno(title, version = anno_base_default_version, dest_dir = NULL)
```

**Arguments**

title	title of the annotation file
version	version number
dest_dir	if not NULL, download to this directory

**Value**

annotation file

**Examples**

```
cat("Deprecated!")
```

---

sesameQC-class	<i>An S4 class to hold QC statistics</i>
----------------	--

---

**Description**

An S4 class to hold QC statistics

**Slots**

stat a list to store qc stats

---

sesameQC_calcStats	<i>Calculate QC statistics</i>
--------------------	--------------------------------

---

**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),  
  ...  
)
```

**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
...	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"))
```

---

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	<i>report M and U for regular probes</i>
----------	--

---

**Description**

report M and U for regular probes

**Usage**

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

**Arguments**

sdf	a SigDF
mask	whether to apply mask

**Value**

a data frame of M and U columns

**Examples**

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

---

sliceFileSet	<i>Slice a fileSet with samples and probes</i>
--------------	--

---

**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	<i>Extract slope information from DMLSummary</i>
--------------------	--

---

**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()
```

---

testEnrichment	<i>testEnrichment tests for the enrichment of set of probes (query set) in a number of features (database sets).</i>
----------------	--

---

### Description

testEnrichment tests for the enrichment of set of probes (query set) in a number of features (database sets).

### Usage

```
testEnrichment(
  query,
  databases = NULL,
  universe = NULL,
  alternative = "greater",
  platform = NULL,
  silent = FALSE
)
```

### Arguments

query	Vector of probes of interest (e.g., significant probes)
databases	List of vectors corresponding to the database sets of interest with associated meta data as an attribute to each element. Optional. (Default: NA)
universe	Vector of probes in the universe set containing all of the probes to be considered in the test. If it is not provided, it will be inferred from the provided platform. (Default: NA).
alternative	"two.sided", "greater", or "less"
platform	String corresponding to the type of platform to use. Either MM285, EPIC, HM450, or HM27. If it is not provided, it will be inferred from the query set probeIDs (Default: NA).
silent	output message? (Default: FALSE)

### Value

One list containing features corresponding the test estimate, p-value, and type of test.

### Examples

```
library(SummarizedExperiment)
df <- rowData(sesameDataGet('MM285.tissueSignature'))
query <- df$Probe_ID[df$branch == "B_cell"]
res <- testEnrichment(query, "chromHMM")
sesameDataGet_resetEnv()
```

---

testEnrichmentFisher *testEnrichmentFisher uses Fisher's exact test to estimate the association between two categorical variables.*

---

### Description

Estimates log2 Odds ratio

### Usage

```
testEnrichmentFisher(query, database, universe, alternative = "greater")
```

### Arguments

query	Vector of probes of interest (e.g., significant probes)
database	Vectors corresponding to the database set of interest with associated meta data as an attribute to each element.
universe	Vector of probes in the universe set containing all of
alternative	greater or two.sided (default: greater) the probes to be considered in the test. (Default: NULL)

### Value

A DataFrame with the estimate/statistic, p-value, and name of test for the given results.

---

testEnrichmentGSEA *testEnrichmentGSEA uses the GSEA test to estimate the association of a categorical variable against a continuous variable.*

---

### Description

estimate represent enrichment score and negative estimate indicate a test for depletion

### Usage

```
testEnrichmentGSEA(
  query,
  databases = NULL,
  platform = NULL,
  silent = FALSE,
  precise = FALSE
)
```



**Arguments**

query	query, if numerical, expect categorical database, if categorical expect numerical database
databases	database, numerical or categorical, but needs to be different from query
platform	EPIC, MM285, ..., infer if not given
silent	suppress message (default: FALSE)
precise	whether to compute precise p-value (up to numerical limit) of interest.

**Value**

A DataFrame with the estimate/statistic, p-value, and name of test for the given results.

**Examples**

```
query <- KYCG_getDBs("KYCG.MM285.designGroup")[["TSS"]]
res <- testEnrichmentGSEA(query, "MM285.seqContextN")
```

---

testEnrichmentSpearman

*testEnrichmentSpearman uses the Spearman statistical test to estimate the association between two continuous variables.*

---

**Description**

testEnrichmentSpearman uses the Spearman statistical test to estimate the association between two continuous variables.

**Usage**

```
testEnrichmentSpearman(query, database)
```

**Arguments**

query	Vector of probes of interest (e.g., significant probes)
database	List of vectors corresponding to the database set of interest with associated meta data as an attribute to each element.

**Value**

A DataFrame with the estimate/statistic, p-value, and name of test for the given results.

---

totalIntensities	<i>M+U Intensities Array</i>
------------------	------------------------------

---

### 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	<i>Estimate the fraction of the 2nd component in a 2-component mixture</i>
--------------	--

---

### 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	<i>Set color and mask using strain/species-specific manifest</i>
-------------	--

---

**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,  
  dwestream = 2000,  
  ...  
)
```

### Arguments

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

### 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,  
  dstream = 1000,  
  ...  
)
```

### Arguments

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

### Value

None

### Examples

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

---

visualizeRegion	<i>Visualize Region</i>
-----------------	-------------------------

---

### 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, hg19, or mm10
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)
```

**Arguments**

seg	a CNSegment object
to.plot	chromosome to plot (by default plot all chromosomes)

**Details**

require ggplot2, scales

**Value**

plot graphics

**Examples**

```
sesameDataCache()
## sdf <- sesameDataGet('EPIC.1.SigDF')
## sdf.normal <- sesameDataGet('EPIC.5.SigDF.normal')
## seg <- cnSegmentation(sdf, sdf.normal)
## visualizeSegments(seg)

sesameDataGet_resetEnv()
```

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