

# Package ‘sesameData’

October 2, 2025

**Type** Package

**Title** Supporting Data for SeSAmE Package

**Description** Provides supporting annotation and test data for SeSAmE package. This includes chip tango addresses, mapping information, performance annotation, and trained predictor for Infinium array data. This package provides user access to essential annotation data for working with many generations of the Infinium DNA methylation array. Current we support human array (HM27, HM450, EPIC), mouse array (MM285) and the Horvath-MethylChip40 (Mammal40) array.

**Version** 1.27.1

**License** Artistic-2.0

**Depends** R (>= 4.2.0), ExperimentHub, AnnotationHub

**Imports** utils, readr, stringr, GenomicRanges (>= 1.61.1), S4Vectors, IRanges, Seqinfo

**Suggests** BiocGenerics, GenomeInfoDb, sesame, testthat, knitr, rmarkdown

**biocViews** ExperimentData, MicroarrayData, Genome, ExperimentHub, MethylationArrayData

**URL** <https://github.com/zwdzwd/sesame>

**BugReports** <https://github.com/zwdzwd/sesame/issue>

**VignetteBuilder** knitr

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**Author** Wanding Zhou [aut, cre] (ORCID:  
<<https://orcid.org/0000-0001-9126-1932>>),  
Hui Shen [aut],  
Timothy Triche [ctb]

**Maintainer** Wanding Zhou <[zhouwanding@gmail.com](mailto:zhouwanding@gmail.com)>

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|                   |                          |
|-------------------|--------------------------|
| build_GENCODE_gtf | <i>build GENCODE gtf</i> |
|-------------------|--------------------------|

---

Description

build GENCODE gtf

Usage

build\_GENCODE\_gtf(x)

Arguments

x                      GENCODE ftp url

Value

GRangesList

---

|           |                                                  |
|-----------|--------------------------------------------------|
| df_master | <i>Master data frame for all object to cache</i> |
|-----------|--------------------------------------------------|

---

### Description

This is an internal object which will be updated on every new release library(ExperimentHub) `eh <- query(ExperimentHub(localHub=FALSE), c("sesameData", "v1.13.1")) data.frame(name=eh$title, eh=names(eh))`

### Details

Cache location is default to `/Users/zhouw3/Library/Caches/org.R-project.R/R/ExperimentHub/`

### Value

master sheet of sesameData objects

---

|        |                         |
|--------|-------------------------|
| extend | <i>Extend a GRanges</i> |
|--------|-------------------------|

---

### Description

source: <https://support.bioconductor.org/p/78652/>

### Usage

```
extend(gr, upstream = 0, downstream = 0)
```

### Arguments

|            |                               |
|------------|-------------------------------|
| gr         | a GenomicRanges::GRanges      |
| upstream   | distance to expand upstream   |
| downstream | distance to expand downstream |

### Value

a GenomicRanges::GRanges

---

```
inferPlatformFromProbeIDs
      infer platform from Probe_IDs
```

---

**Description**

infer platform from Probe\_IDs

**Usage**

```
inferPlatformFromProbeIDs(Probe_IDs, silent = FALSE)
```

**Arguments**

|           |                  |
|-----------|------------------|
| Probe_IDs | probe IDs        |
| silent    | suppress message |

**Value**

a platform code

**Examples**

```
sesameDataCache("probeIDSignature")
inferPlatformFromProbeIDs(c("cg14620903", "cg22464003"))
```

---

|                 |                   |
|-----------------|-------------------|
| sesameDataCache | Cache SeSAmE data |
|-----------------|-------------------|

---

**Description**

Cache SeSAmE data

**Usage**

```
sesameDataCache(data_titles = NULL)
```

**Arguments**

|             |                                            |
|-------------|--------------------------------------------|
| data_titles | data to cache, if not given will cache all |
|-------------|--------------------------------------------|

**Value**

TRUE

**Examples**

```
sesameDataCache("genomeInfo.hg38")
```

---

|                    |                              |
|--------------------|------------------------------|
| sesameDataCacheAll | <i>Cache all SeSAmE data</i> |
|--------------------|------------------------------|

---

**Description**

Cache all SeSAmE data

**Usage**

```
sesameDataCacheAll(data_titles = NULL)
```

**Arguments**

data\_titles      data to cache, if not given will cache all

**Value**

TRUE

**Examples**

```
sesameDataCache("genomeInfo.hg38")
```

---

|               |                        |
|---------------|------------------------|
| sesameDataGet | <i>Get SeSAmE data</i> |
|---------------|------------------------|

---

**Description**

Get SeSAmE data

**Usage**

```
sesameDataGet(title, verbose = FALSE)
```

**Arguments**

title              title of the data  
verbose            whether to output ExperimentHub message

**Value**

data object

**Examples**

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

---

```
sesameDataGet_checkEnv
```

*Check whether the title exists in cacheEnv*

---

### Description

Check whether the title exists in cacheEnv

### Usage

```
sesameDataGet_checkEnv(title)
```

### Arguments

title                      the title to check

### Value

the data associated with the title or NULL if title doesn't exist

---

```
sesameDataGet_resetEnv
```

*Empty cache environment to free memory*

---

### Description

When this function is called sesameDataGet will retrieve all data from disk again instead of using the in-memory cache, i.e., sesameData:::cacheEnv.

### Usage

```
sesameDataGet_resetEnv()
```

### Details

Note this is different from sesameDataClearHub which empties the ExperimentHub on disk.

### Value

gc() output

### Examples

```
sesameDataGet_resetEnv()
```

---

|               |                               |
|---------------|-------------------------------|
| sesameDataHas | <i>Whether sesameData has</i> |
|---------------|-------------------------------|

---

**Description**

Whether sesameData has

**Usage**

```
sesameDataHas(data_titles)
```

**Arguments**

data\_titles      data titles to check

**Value**

a boolean vector the same length as data\_titles

**Examples**

```
sesameDataHas(c("EPIC.address", "EPIC.address.Nonexist"))
```

---

|                |                             |
|----------------|-----------------------------|
| sesameDataList | <i>List all SeSAMe data</i> |
|----------------|-----------------------------|

---

**Description**

List all SeSAMe data

**Usage**

```
sesameDataList(filter = NULL, full = FALSE)
```

**Arguments**

filter              keyword to filter title, optional  
full                whether to display all columns

**Value**

all titles from SeSAMe Data

**Examples**

```
sesameDataList("KYCG")
```

---

sesameData\_annoProbes *Annotate Probes by Probe ID*

---

## Description

Columns in the manifests will be added to the annotation. Please note that if unfound, the annotation will be NA. The probe will always be kept in the output.

## Usage

```
sesameData_annoProbes(
  Probe_IDs,
  regs = NULL,
  collapse = TRUE,
  chooseOne = FALSE,
  column = NULL,
  sep = ",",
  return_ov_probes = FALSE,
  return_ov_features = FALSE,
  out_name = NULL,
  platform = NULL,
  genome = NULL,
  silent = FALSE
)
```

## Arguments

|                    |                                                                                                                                                                                                                                                                                                                                 |
|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Probe_IDs          | a character vector of probe IDs                                                                                                                                                                                                                                                                                                 |
| regs               | a GenomicRanges::GRanges object against which probes will be annotated, default to genes if not given                                                                                                                                                                                                                           |
| collapse           | whether to collapse multiple regs into one                                                                                                                                                                                                                                                                                      |
| chooseOne          | choose an arbitrary annotation if multiple exist default to FALSE. which concatenates all with ","                                                                                                                                                                                                                              |
| column             | which column in regs to annotate, if not given return all overlapping probes                                                                                                                                                                                                                                                    |
| sep                | the delimiter for collapsing                                                                                                                                                                                                                                                                                                    |
| return_ov_probes   | if TRUE will return overlapping probes in a GRanges object.                                                                                                                                                                                                                                                                     |
| return_ov_features | if TRUE will return overlapping features in a GRanges object.                                                                                                                                                                                                                                                                   |
| out_name           | column header of the annotation, use column if not given                                                                                                                                                                                                                                                                        |
| platform           | EPIC, MM285 etc. will infer from Probe_IDs if not given                                                                                                                                                                                                                                                                         |
| genome             | hg38, mm10, ... will infer if not given. For additional mapping, download the GRanges object from <a href="http://zwdzwd.github.io/InfiniumAnnotation">http://zwdzwd.github.io/InfiniumAnnotation</a> and provide the following argument ..., genome = sesameAnno_buildManifestGRanges("downloaded_file"),... to this function. |
| silent             | suppress messages                                                                                                                                                                                                                                                                                                               |

**Value**

a GRanges with annotated column If a probe has no overlap with regs, it will be included in the results with NA. But if a probe is not included in the manifest (due to mappability), it won't be included in the results.

**Examples**

```
library(GenomicRanges)
sesameDataCache(c(
  "genomeInfo.mm10", "MM285.address",
  "genomeInfo.hg38", "Mammal40.address"))

regs = sesameData_getTxnGRanges("mm10")
Probe_IDs = names(sesameData_getManifestGRanges("MM285"))
anno = sesameData_annoProbes(Probe_IDs, promoters(regs), column="gene_name")

## get all genes associated with a probe set
genes = sesameData_getTxnGRanges("hg38", merge2gene = TRUE)
anno = sesameData_annoProbes(
  c("cg14620903", "cg22464003"), genes, return_ov_features=TRUE)
```

---

sesameData\_check\_genome

*Find genome assembly version(s) supported for a platform*

---

**Description**

Find genome assembly version(s) supported for a platform

**Usage**

```
sesameData_check_genome(genome, platform)
```

**Arguments**

|          |                                     |
|----------|-------------------------------------|
| genome   | mm10, hg38, ..., or NULL            |
| platform | HM27, HM450, EPIC, EPICv2, MSA, ... |

**Value**

genome as string

**Examples**

```
sesameData_check_genome(NULL, "Mammal40")
```

sesameData\_check\_platform  
*Check platform code*

---

**Description**

Note: custome platforms lead to error here.

**Usage**

```
sesameData_check_platform(platform = NULL, probes = NULL, silent = TRUE)
```

**Arguments**

|          |                                             |
|----------|---------------------------------------------|
| platform | input platform                              |
| probes   | probes by which the platform may be guessed |
| silent   | suppress message                            |

**Value**

platform code

**Examples**

```
sesameData_check_platform("HM450")
```

---

sesameData\_getGenomeInfo  
*Get genome info files*

---

**Description**

Get genome info files

**Usage**

```
sesameData_getGenomeInfo(genome)
```

**Arguments**

|        |                                                            |
|--------|------------------------------------------------------------|
| genome | hg38, mm10, or GRanges with a metadata(genome)[["genome"]] |
|--------|------------------------------------------------------------|

**Value**

a list of genome info files

**Examples**

```
sesameDataCache("genomeInfo.hg38")  
res <- sesameData_getGenomeInfo("hg38")
```

---

```
sesameData_getManifestGRanges
  get Infinium manifest GRanges
```

---

### Description

Note that some unaligned probes are not included. For full manifest, please visit <http://zwdzwd.github.io/InfiniumAnnotation>

### Usage

```
sesameData_getManifestGRanges(platform, genome = NULL)
```

### Arguments

|          |                                                                                                                                                                                                                                                                                                                                 |
|----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| platform | Mammal40, MM285, EPIC, and HM450                                                                                                                                                                                                                                                                                                |
| genome   | hg38, mm10, ... will infer if not given. For additional mapping, download the GRanges object from <a href="http://zwdzwd.github.io/InfiniumAnnotation">http://zwdzwd.github.io/InfiniumAnnotation</a> and provide the following argument ..., genome = sesameAnno_buildManifestGRanges("downloaded_file"),... to this function. |

### Value

GRanges

### Examples

```
sesameDataCache("Mammal40.address")
res <- sesameData_getManifestGRanges("Mammal40")
```

---

```
sesameData_getProbesByGene
  Get Probes by Genes or Gene Promoters
```

---

### Description

Get probes mapped to a gene. All transcripts for the gene are considered. The function takes a gene name as appears in UCSC RefGene database. The platform and reference genome build can be changed with 'platform' and 'genome' options. The function returns a vector of probes that falls into the given gene.

### Usage

```
sesameData_getProbesByGene(
  gene_name = NULL,
  platform = NULL,
  promoter = FALSE,
  upstream = 1500,
  downstream = 1500,
  genome = NULL
)
```

**Arguments**

|            |                                                     |
|------------|-----------------------------------------------------|
| gene_name  | gene name, if NULL return all genes                 |
| platform   | EPIC or HM450                                       |
| promoter   | if TRUE, use TSS instead of the whole gene          |
| upstream   | number of bases to expand upstream of target gene   |
| downstream | number of bases to expand downstream of target gene |
| genome     | hg38 or hg19                                        |

**Value**

GRanges containing probes that fall into the given gene

**Examples**

```
## download needed data
sesameDataCache(c("Mammal40.address", "genomeInfo.hg38"))

## get all probes overlapping with DNMT3A
probes <- sesameData_getProbesByGene(
  'DNMT3A', "Mammal40", upstream=500, downstream=500)

## get the promoter-associated probes
probes <- sesameData_getProbesByGene('DNMT3A', "Mammal40", promoter = TRUE)
```

---

sesameData\_getProbesByRegion

*Get probes by genomic region*

---

**Description**

The function takes a genomic coordinate and output the a vector of probes on the specified platform that falls in the given genomic region.

**Usage**

```
sesameData_getProbesByRegion(
  regs,
  chrm = NULL,
  beg = 1,
  end = -1,
  platform = NULL,
  chrm_to_exclude = NULL,
  genome = NULL
)
```

**Arguments**

|                 |                                                                                                                                                                                                                                                                                                                                 |
|-----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| regs            | GRanges                                                                                                                                                                                                                                                                                                                         |
| chrM            | chromosome, when given regs are ignored                                                                                                                                                                                                                                                                                         |
| beg             | begin, 1 if omitted                                                                                                                                                                                                                                                                                                             |
| end             | end, chromosome end if omitted                                                                                                                                                                                                                                                                                                  |
| platform        | EPICv2, EPIC, HM450, ...                                                                                                                                                                                                                                                                                                        |
| chrM_to_exclude | chromosome to exclude.                                                                                                                                                                                                                                                                                                          |
| genome          | hg38, mm10, ... will infer if not given. For additional mapping, download the GRanges object from <a href="http://zwdzwd.github.io/InfiniumAnnotation">http://zwdzwd.github.io/InfiniumAnnotation</a> and provide the following argument ..., genome = sesameAnno_buildManifestGRanges("downloaded_file"),... to this function. |

**Value**

GRanges of selected probes

**Examples**

```
## download needed data
sesameDataCache(c("Mammal40.address", "genomeInfo.hg38"))

## get probes in a region
library(GenomicRanges)
probes = sesameData_getProbesByRegion(
  GRanges('chr5', IRanges(135313937, 135419936)), platform = 'Mammal40')

## get all probes on chromosome 5
probes = sesameData_getProbesByRegion(chrm = "chr5", platform = "Mammal40")

## get all probes on chromosome X
probes = sesameData_getProbesByRegion(chrm = 'chrX', platform = "Mammal40")

## get all probes on both chromosome X and Y
probes = sesameData_getProbesByRegion(
  chrm = c('chrX', 'chrY'), platform = "Mammal40")

## get all autosomal probes
probes = sesameData_getProbesByRegion(
  chrm_to_exclude = c("chrX", "chrY"), platform = "Mammal40")
```

---

sesameData\_getTxnGRanges

*convert GRangesList to transcript GRanges*

---

**Description**

convert GRangesList to transcript GRanges

**Usage**

```
sesameData_getTxnGRanges(genome = NULL, grl = NULL, merge2gene = FALSE)
```

**Arguments**

|            |                           |
|------------|---------------------------|
| genome     | hg38, mm10, ...           |
| grl        | GRangesList object        |
| merge2gene | merge transcript to genes |

**Value**

a GRanges object

**Examples**

```
## all mm10 transcripts
txns <- sesameData_getTxnGRanges("mm10")

## verified protein-coding transcripts
txns[(txns$transcript_type == "protein_coding" & txns$level <= 2)]

## merged to genes
sesameData_getTxnGRanges("mm10", merge2gene = TRUE)
```

---

```
sesameData_txnToGeneGRanges
```

*convert transcript GRanges to gene GRanges*

---

**Description**

convert transcript GRanges to gene GRanges

**Usage**

```
sesameData_txnToGeneGRanges(txns)
```

**Arguments**

|      |                |
|------|----------------|
| txns | GRanges object |
|------|----------------|

**Value**

a GRanges object

**Examples**

```
txns <- sesameData_getTxnGRanges("mm10")
genes <- sesameData_txnToGeneGRanges(txns)
```

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