Package ‘recountmethylation’

April 9, 2024

Version 1.12.0
Title Access and analyze public DNA methylation array data compilations
Description Resources for cross-study analyses of public DNA methylation array data from NCBI GEO repo, produced using Illumina's Infinium HumanMethylation450K (HM450K) and MethylationEPIC (EPIC) platforms. Provided functions enable download, summary, and filtering of large compilation files. Vignettes detail background about file formats, example analyses, and more. Note the disclaimer on package load and consult the main manuscripts for further info.
License Artistic-2.0
Encoding UTF-8
URL https://github.com/metamaden/recountmethylation
BugReports https://github.com/metamaden/recountmethylation/issues
LazyData FALSE
Depends R (>= 4.1)
Imports minfi, HDF5Array, rhdf5, S4Vectors, utils, methods, RCurl, R.utils, BiocFileCache, basilisk, reticulate, DelayedMatrixStats
Suggests minfiData, minfiDataEPIC, knitr, testthat, ggplot2, gridExtra, rmarkdown, BiocStyle, GenomicRanges, limma, ExperimentHub, AnnotationHub
VignetteBuilder knitr
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Description

Get background signal for BeadArray metric calculations.
Get the Biotin staining Red BeadArray metric.
Get the Biotin staining Green BeadArray metric.
Get the Non-polymorphic Red BeadArray metric.
Get the Non-polymorphic Green BeadArray metric.
Get the Bisulfite Conversion I Red BeadArray metric.
Get the Restoration BeadArray metric.
Get the Specificity I Red BeadArray metric.
Get the Specificity I Green BeadArray metric.
Get the Specificity II Green BeadArray metric.
Get the Extension Red BeadArray metric.
Get the Extension Green BeadArray metric.
Get the Hybridication (high vs. medium) BeadArray metric.
Get the Hybridication (medium vs. low) BeadArray metric.
Get the Target Removal 1 BeadArray metric.
Get the Target Removal 2 BeadArray metric.
Get the Bisulfite Conversion I Green BeadArray metric.
Get the Bisulfite Conversion II BeadArray metric.

Usage

ba.background(cdf, ct = "Extension")

ba.biotinstaining.red(
    rs,
    biotin.baseline,
    rm,
    cdf,
    mnum = 1,
    mtot = 17,
    cnamei = "biotin.stain.red",
    ct = "Biotin|DNP"
)

ba.biotinstaining.grn(
    gs,
    biotin.baseline,
    rm,
    cdf,
    mnum = 2,
    mtot = 17,
    cnamei = "biotin.stain.grn",
    ct = "Biotin|DNP"
)

ba.nonpolymorphic.red(
    rs,
    rm,
    cdf,
mnum = 3,
mtot = 17,
cnamei = "nonpolymorphic.red",
ct = "NP"
)

ba.nonpolymorphic.grn(
    gs,
    rm,
    cdf,
    mnum = 4,
    mtot = 17,
    cnamei = "nonpolymorphic.grn",
    ct = "NP"
)

ba.bisulfiteconv1.red(
    rs,
    rm,
    cdf,
    mnum = 5,
    mtot = 17,
    cnamei = "bisulfite.conv1.red",
    ct = "Conversion I-
"
)

ba.restoration(
    gs,
    rm,
    cdf,
    addr.bkg,
    baseline = 3000,
    mnum = 6,
    mtot = 17,
    cnamei = "restoration.grn",
    ct = "RESTORATION"
)

ba.specificity1.red(
    rs,
    rm,
    cdf,
    mnum = 7,
    mtot = 17,
    cnamei = "specificityI.red"
)

ba.specificity1.grn(
    gs,
    rm,
    cdf,
    mnum = 8,
    mtot = 17,
    cnamei = "specificityII.grn",
    ct = "SPECIFICITY II"
)

ba.background
gs, rm, cdf, mnum = 8, mtot = 17, cnamei = "specificityI.grn"
)

ba.specificity2(
    rs, gs, rm, cdf, mnum = 9, mtot = 17, cnamei = "specificityII", ct = "Specificity 2"
)

ba.extension.red(
    rs, rm, cdf, mnum = 10, mtot = 17, cnamei = "extension.red", ct = "Extension.*"
)

ba.extension.grn(
    gs, rm, cdf, mnum = 11, mtot = 17, cnamei = "extension.grn", ct = "Extension.*"
)

ba.hybridization.hi.vs.med(
    gs, rm, cdf, mnum = 12, mtot = 17, cnamei = "hyb.hi.med", ct = "High|Medium"
)
ba.hijridization.med.vs.low(
    gs,
    rm,
    cdf,
    mnum = 13,
    mtot = 17,
    cnamei = "hyb.med.low",
    ct = "Low|Medium"
)

ba.targetremoval1(
    gs,
    rm,
    cdf,
    baseline = 3000,
    mnum = 14,
    mtot = 17,
    cnamei = "target.removal1",
    ct = "Extension|Target Removal 1"
)

ba.targetremoval2(
    gs,
    rm,
    cdf,
    baseline = 3000,
    mnum = 15,
    mtot = 17,
    cnamei = "target.removal2",
    ct = "Extension|Target Removal 2"
)

ba.bisulfiteconv1.grn(
    gs,
    rm,
    cdf,
    mnum = 16,
    mtot = 17,
    cnamei = "bisulfite.conv1.grn",
    ct = "Conversion I-"
)

ba.bisulfiteconv2(
    rs,
    gs,
    rm,
    cdf,
```r
mnum = 17,
mtot = 17,
cnamei = "bisulfite.conv2",
ct = "Conversion II-"
)
```

### Arguments

- **cdf**: Control probe data frame (required).
- **ct**: Column name/metric title (character, required).
- **rs**: Red signal matrix (required).
- **biotin.baseline**: Baseline signal for the biotin stain assay (required).
- **rm**: Results matrix containing control metrics (required).
- **mnum**: Metric number out of total (numeric).
- **mtot**: Total metrics to be calculated (numeric, 17).
- **cnamei**: Column name (character, required).
- **gs**: Green signal matrix (required).
- **addr.bkg**: Background signal probe address (required).
- **baseline**: Baseline measure for signals (integer, 3000).

### Description

Get the BeadArray control metrics from HM450K platform red/grn signals.

### Usage

```r
bactrl(cdf = NULL,
baset = "reduced",
rg = NULL,
rs = NULL,
gs = NULL,
baseline = 3000,
biotin.baseline = 1)
```
Arguments

cdf  Control probe annotations (optional, NULL, data.frame, cols = properties, rows = probes).

baset  Either the most informative BeadArray metrics (a.k.a. "reduced" set, 5 metrics, recommended), or the full set of 17 metrics ("all").

rg  An RGChannelSet object (optional, NULL).

rs  Red signal data (optional, NULL, data.frame, columns are probes, rows are samples, column names are addresses, rownames are samples/GSM IDs).

gs  Green signal data (optional, NULL, data.frame, columns are probes, rows are samples, column names are addresses, rownames are samples/GSM IDs).

baseline  Baseline measure for signals (integer, 3000).

biotin.baseline  Baseline to use for biotin controls (integer, 1).

Details

This function calculates the BeadArray quality metrics based on Illumina’s documentation and previous work (see references). Based on previous work, this function can calculate the full set of 17 metrics (e.g. baset = 'all'), or the reduced set of 5 metrics (e.g. baset = 'reduced'), where the latter is recommended for most purposes. For additional details, consult the BeadArray metrics vignette in this package.

Value

Matrix of BeadArray signal values

References


See Also

bathresh

Examples

dir <- system.file("extdata", "bactrl", package = "recountmethylation")
rgf <- get(load(file.path(dir, "rgf-cgctrl-test_hm450k-minfidata.rda")))
mba <- bactrl(rg = rgf)
bathresh

\textit{Get BeadArray control outcomes from a matrix of metric signals}

\textbf{Description}

Get Illumina’s prescribed minimum quality thresholds for BeadArray metrics.

\textbf{Usage}

\begin{verbatim}
bathresh()
\end{verbatim}

\textbf{Value}

Data frame of minimum BeadArray quality thresholds.

\textbf{References}


\textbf{See Also}

bactrl

\textbf{Examples}

\begin{verbatim}
dfthresh <- bathresh()
\end{verbatim}

data_mdpost

\textit{Retrieve all available sample metadata from an HDF5 database.}

\textbf{Description}

Retrieve all available sample metadata in a dataset from an HDF5 database. Returns data in metadata dataset "dsn" contained in an h5 file located at path "dbn."

\textbf{Usage}

\begin{verbatim}
data_mdpost(dbn = "remethdb2.h5", dsn = "mdpost")
\end{verbatim}

\textbf{Arguments}

\begin{verbatim}
dbn Path to h5 HDF5 database file.
dsn Name or group path to HDF5 dataset containing the sample metadata and learned annotations.
\end{verbatim}
gds_idat2rg

Value
data.frame of available sample metadata.

See Also
hread()

Examples

path <- system.file("extdata", "h5test", package = "recountmethylation")
fn <- list.files(path)
dbpath <- file.path(path, fn)
mdp <- data_mdpost(dbn = dbpath, dsn = "mdpost")
dim(mdp) # [1] 2 19

Description

Queries and downloads GSM IDAT files in GEO Data Sets db, then returns the assay data as an
"RGChannelSet", calling gds_idatquery() then minfi::read.metharray().

Usage

gds_idat2rg(
  gsmvi,
  rmdl = TRUE,
  ext = "gz",
  dfp = "/idats/",
  silent = TRUE
)

Arguments
gsmvi A vector of GSM IDs (alphanumeric character strings).
rmdl Whether to remove downloaded IDAT files when finished (default TRUE).
ext Extension for downloaded files (default "gz").
dfp Destination for IDAT downloads.
silent Whether to suppress warnings on download removal (default TRUE).

Value

An RGChannelSet object.
See Also
gds_idatquery(), read.metharray()

Examples

gsmvi <- c("GSM2465267", "GSM2814572")
fpather <- file.path(tempdir(), "gds_idat2rg_example")
rg <- try(gds_idat2rg(gsmvi, dfp = fpath))

Value
Lists the basename paths and filenames of IDATs downloaded.
Access database files.

Description

Combines download and load functions for databases. If the "namematch" argument isn't provided, the latest available file is downloaded. All files include metadata for the available samples.

There are 6 functions. Functions with "h5se" access HDF5-SummarizedExperiment files, and "h5" functions access HDF5 databases. The 4 h5se functions are "rg" (RGChannelSet), "gm" (MethylSet), "gr" (GenomicRatioSet), and "test" (data for 2 samples from "gr"). The 2 h5 functions are "rg" (red and green signal datasets), and "test" (data for 2 samples from "rg"). See vignette for details about file types and classes.

Usage

```r
getdb_h5se_test(
  platform = NULL,
  dfp = NULL,
  namematch = "remethdb-h5se_gr-test.*",
  verbose = FALSE
)

getdb_h5_test(
  platform = NULL,
  namematch = "remethdb-h5_rg-test_.*",
  dfp = NULL,
  verbose = FALSE
)

getdb_h5se_gr(
  platform = c("hm450k", "epic"),
  dfp = NULL,
  namematch = "remethdb_h5se-gr_.*",
  verbose = FALSE
)

getdb_h5se_gm(
  platform = c("hm450k", "epic"),
  dfp = NULL,
  namematch = "remethdb_h5se-gm_.*",
  verbose = FALSE
)

getdb_h5se_rg(
  platform = c("hm450k", "epic"),
  dfp = NULL,
  namematch = "remethdb_h5se-rg_.*",
  verbose = FALSE
)
```
getrg

getrg = "remethdb-h5se_rg_.*",
verbose = FALSE
)

getdb_h5_rg(
    platform = c("hm450k", "epic"),
dfp = NULL,
namematch = "remethdb-h5_rg_.*",
verbose = FALSE
)

Arguments

platform Valid supported DNAm array platform type. Currently either "epic" for EPIC/HM850K,
or "hm450k" for HM450K.

dfp Folder to search for database file (optional, if NULL then searches cache dir
specified by BiocFileCache).

namematch Filename pattern to match when searching for database (see defaults).

verbose Whether to return verbose messages (default FALSE).

Value

Either a SummarizedExperiment object for h5se functions, or a file path for h5 functions.

See Also

get_rmdl()  

Examples

h5 <- getdb_h5_test(dfp = tempdir())

getrg

Query and store data from h5 file signal tables

Description

Queries signal datasets in an h5 HDF5 database file. Handles identity queries to rows (GSM IDs)
or columns (bead addresses). Returns query matches either as a list of datasets or a single RGChannelSet, with option to include sample metadata.
Usage

call <- function(dbn, 
            gsmv = NULL, 
            cgv = NULL, 
            data.type = c("se"), 
            dsv = c("redsignal", "greensignal"), 
            all.gsm = FALSE, 
            all.cg = TRUE, 
            metadata = TRUE, 
            md.dsn = "mdpost", 
            verbose = FALSE)

Arguments

dbn Name of the HDF5 database file.
gsmv Vector valid GSM IDs (rows) to query, either NULL or vector of length > 2 valid 
GSM IDs, or "all.gsm" should be TRUE.
cgv Vector of valid bead addresses (columns) to query in the signal datasets (default NULL).
data.type Format for returned query matches, either as datasets "df" or RGChannelSet "se" 
object.
dsv Vector of raw signal datasets or group paths to query, including both the red 
channel 'redsignal' and green channel 'greensignal' datasets.
all.gsm Whether to query all available GSM IDs.
all.cg Whether to query all available CpG probe addresses.
metadata Whether to access available postprocessed metadata for queried samples.
md.dsn Name of metadata dataset in h5 file.
verbose Whether to post status messages.

Value

Returns either an RGChannelSet or list of data.frame objects from dataset query matches.

See Also

rgse()

Examples

path <- system.file("extdata", "h5test", package = "recountmethylation")
fn <- list.files(path)
dbpath <- file.path(path, fn)
rg <- getrg(dbn = dbpath, all.gsm = TRUE, metadata = FALSE)
dim(rg) # [1] 11162 2
get_crossreactive_cpgs

class(rg)
  # [1] "RGChannelSet"
  # attr(, "package")
  # [1] "minfi"

describe(get_crossreactive_cpgs)
get_crossreactive_cpgs

Description

Get cross-reactive CpG probe IDs for Illumina BeadArray platforms.

Usage

get_crossreactive_cpgs(probeset = "all")

Arguments

probeset Specify the set of probes to filter ("all", "hm450k", "epic", "chen", "pidsley", "illumina").

Details

Prior work showed significant cross-reactivity at subsets of CpG probes on Illumina’s BeadArray platforms, including HM450K and EPIC. This was primarily due to the probe sequence, as the targeted 50-bp sequence can be either too short or too degenerate to bind a particular DNA region with high specificity. This can cause cross-reaction with off-target DNA locations, including at entirely different chromosomes than the target sequence. Consult the individual publication sources for details about the identification and consequences of cross-reactive CpG probes.

You can retrieve a cross-reactive probe set in a variety of ways. For instance, declare the publication source with either "chen" (for Chen et al 2013), "pidsley" (for Pidsley et al 2016), or "illumina" (for official Illumina documentation), or declare the platform category as either "all" (both HM450K and EPIC), "hm450k", or "epic".

Value

Vector of cross-reactive CpG probe IDs.

References

get_fh

See Also

bactrl, get_qcsignal

Examples

length(get_crossreactive_cpgs("all"))    # 46324
length(get_crossreactive_cpgs("hm450k")) # 30540
length(get_crossreactive_cpgs("epic"))   # 43410
length(get_crossreactive_cpgs("chen"))   # 29233
length(get_crossreactive_cpgs("pidsley")) # 43254
length(get_crossreactive_cpgs("illumina")) # 1031

Description

Get the hashed features for a data table. Uses reticulate package to call the Python script to do feature hashing on a table of data. It is assumed the input table has sample data in rows, with probe data in columns. The input data table should have row names but not column names.

Usage

get_fh(csv_savepath, csv_openpath, ndim = 1000, lstart = 1)

Arguments

csv_savepath   Name/path of hashed features table to write (required, string, writes new csv where rows = samples, cols = hashed features).
csv_openpath   Name/path of table to hash (required, string, assumes a csv where rows = samples, cols = probes).
ndim           Number of hashed features (integer, 1000).
lstart         Line index to start on (0-based for Python, required, int, 0).

Value

Path to new hashed features table.

Examples

# get example bval csv
# of_fpath <- system.file("extdata", "fhtest",
# package = "recountmethylation")
# of_fpath <- file.path(of_fpath, "tbval_test.csv")
# write new hashed features results
# get_fh(csv_savepath = "bval_fn.csv", csv_openpath = of_fpath, ndim = 100)
Description

Get the medians of the log2-transformed M and U signals. This function uses the DelayedMatrixStats implementations of colMedians for rapid calculations on DelayedArray-formatted matrices.

Usage

get_qcsignal(se = NULL, mm = NULL, mu = NULL, sample_idv = NULL)

Arguments

- **se**: Valid SummarizedExperiment object, such as a MethylSet or similar object for which getMeth() and getUnmeth() methods are defined (optional).
- **mm**: Matrix of methylated/M signals (optional, not required if se provided).
- **mu**: Matrix of unmethylated/U signals (optional, not required if se provided).
- **sample_idv**: Vector of sample IDs to label rows in the returned data frame (optional, uses mm colnames instead if not provided).

Details

Calculates the log2 of median signal for methylated/M and unmethylated/U signals separately.

Value

Data frame of signal summaries.

See Also

bactrl

Examples

```r
library(minfiData)
data(MsetEx)
se <- MsetEx
class(se)
# [1] "MethylSet"
# attr(,"package")
# [1] "minfi"
ms <- get_qcsignal(se)
```
get_rmdl  Get DNA methylation assay data.

Description

Uses RCurl to download the latest HDF5-SummarizedExperiment or HDF5 database compilation files objects from the server. Calls servermatrix and performs various quality checks to validate files and downloads. This function is wrapped in the getdb() set of functions (type '?getdb' for details).

Usage

get_rmdl(
    which.class = c("rg", "gm", "gr", "test"),
    which.type = c("h5se", "h5"),
    which.platform = c("hm450k", "epic"),
    fn = NULL,
    dfp = "downloads",
    url = "https://methylation.recount.bio/",
    show.files = FALSE,
    download = TRUE,
    sslver = FALSE,
    verbose = TRUE
)

Arguments

- **which.class**: Either "rg", "gm", "gr", or "test" for RGChannelSet, MethylSet, GenomicRatioSet, or 2-sample subset.
- **which.type**: Either "h5se" for an HDF5-SummarizedExperiment or "h5" for an HDF5 database.
- **which.platform**: Supported DNA methylation array platform type. Currently supports either "epic" for EPIC/HM850K, or "hm450k" for HM450K.
- **fn**: Name of file on server to download (optional, default NULL).
- **dfp**: Download destination directory (default "downloads").
- **url**: The server URL to locate files for download.
- **show.files**: Whether to print server file data to console (default FALSE).
- **download**: Whether to download (TRUE) or return queried filename (FALSE).
- **sslver**: Whether to use server certificate check (default FALSE).
- **verbose**: Whether to return verbose messages (default TRUE).

Value

New filepath to dir containing the downloaded data.
get_servermatrix

See Also

servermatrix(), getURL(), loadHDF5SummarizedExperiment(), h5ls()

Examples

# prints file info from server:
path <- try(get_rmdl(which.class = "test", which.type = "h5se",
show.files = TRUE, download = FALSE))

---

get_servermatrix  get_servermatrix

Description

Get a matrix of server files. If the RCurl call fails, a matrix is loaded from the stored package files at 'sm_path'.

Usage

get_servermatrix(
  dn = NULL,
  sslver = FALSE,
  printmatrix = TRUE,
  url = "https://methylation.recount.bio/",
  verbose = FALSE,
  sm_path = system.file("extdata", "servermatrix_rda", package = "recountmethylation")
)

Arguments

dn
sslver
printmatrix
url
verbose
sm_path

Server data returned from RCurl (default NULL).
Whether to use SSL certificate authentication for server connection (default FALSE).
Whether to print the data matrix to console (default TRUE).
Server website url (default "https://methylation.recount.bio/").
Whether to show verbose messages (default FALSE).
Path to the servermatrix_rda dir containing the stored servermatrix files (default: system.file...).

Value

Matrix of server files and file metadata

See Also

servermatrix, get_rmdl, smfilt
hread

*Query and store an HDF5 dataset on row and column indices.*

**Description**

Connect to an HDF5 database h5 file with rhdf5::h5read(). Returns the subsetted data.

**Usage**

```r
hread(ri, ci, dsn = "redsignal", dbn = "remethdb2.h5")
```

**Arguments**

- **ri**: Row indices in dataset.
- **ci**: Column indices in dataset.
- **dsn**: Name of dataset or group of dataset to connect with.
- **dbn**: Path to h5 database file.

**Value**

HDF5 database connection object.

**Examples**

```r
# Get tests data pointer
path <- system.file("extdata", "h5test", package = "recountmethylation")
fn <- list.files(path)
dbpath <- file.path(path, fn)
# red signal, first 2 assay addr, 3 samples
reds <- hread(1:2, 1:3, d = "redsignal", dbn = dbpath)
dim(reds) # [1] 2 3
```
make_si

Description

Make search index from table of hashed features. Additional details about the hnswlib search index parameters (e.g. ‘space_val’, ‘efc_val’, ‘m_val’, and ‘ef_val’) can be found in the Python package docstrings and ReadMe.

Usage

make_si(
    fh_csv_fpath,
    si_fname = "new_search_index.pickle",
    si_dict_fname = "new_index_dict.pickle",
    threads = 4,
    space_val = "l2",
    efc_val = 2000,
    m_val = 1000,
    ef_val = 2000
)

Arguments

fh_csv_fpath  Name/path of csv (e.g. a table of hashed features) containing data for the index (required, string, "bvaltest.csv", where rows = samples, cols = features).

si_fname      Name of new search index file to save (required, string, "new_search_index.pickle")

si_dict_fname Name of new index dictionary, with string labels, to save (required, string, "new_index_dict.pickle").

threads       Number of threads for processing new index (required, int, 4).

space_val     Space value for new search index (required, valid string, l2").

efc_val       EFC value for the index (required, int, 2000).

m_val         M value for the index (required, int, 1000).

ef_val        EF value for the index (required, int, 2000).

Value

Boolean, TRUE if new search index and dictionary created, FALSE if creating the new search index and dictionary files failed, otherwise NULL.

Examples

# fh_csv_fpath <- system.file("extdata", "fhtest",
# package = "recountmethylation")
# fh_csv_fpath <- file.path(fh_csv_fpath, "bval_fn.csv")
# make_si(fh_csv_fpath)
matchds_1to2

**Match two datasets on rows and columns**

**Description**

Match 2 datasets using the character vectors of row or column names. This is used to assemble an "RGChannelSet" from a query to an h5 dataset.

**Usage**

```r
matchds_1to2(
  ds1,
  ds2,
  mi1 = c("rows", "columns"),
  mi2 = c("rows", "columns"),
  subset.match = FALSE
)
```

**Arguments**

- `ds1` First dataset to match
- `ds2` Second dataset to match
- `mi1` Match index of ds1 (either "rows" or "columns")
- `mi2` Match index of ds2 (either "rows" or "columns")
- `subset.match` If index lengths don’t match, match on the common subset instead

**Value**

A list of the matched datasets.

**Examples**

```r
# get 2 data matrices
ds1 <- matrix(seq(1, 10, 1), nrow = 5)
ds2 <- matrix(seq(11, 20, 1), nrow = 5)
rownames(ds1) <- rownames(ds2) <- paste0("row", seq(1, 5, 1))
colnames(ds1) <- colnames(ds2) <- paste0("col", c(1, 2))
ds2 <- ds2[rev(seq(1, 5, 1)), c(2, 1)]
# match row and column names
lmatched <- matchds_1to2(ds1, ds2, mi1 = "rows", mi2 = "rows")
lmatched <- matchds_1to2(lmatched[[1]], lmatched[[2]], mi1 = "columns",
  mi2 = "columns")
# check matches
dslm <- lmatched[[1]]
dsm2 <- lmatched[[2]]
identical(rownames(dslm), rownames(dsm2))
identical(colnames(dslm), colnames(dsm2))
```
Description

Query an HNSW search index. Does K Nearest Neighbors lookup on a previously saved search index object, returning the K nearest neighbors of the queried sample(s). The `query_si()` function returns verbose output, which can be silenced with `suppressMessages()`.

Usage

```r
query_si(
  sample_idv,
  fh_csv_fpath,
  si_fname = "new_search_index",
  si_fpath = ".",
  lkval = c(1, 2)
)
```

Arguments

- **sample_idv**: Vector of valid sample IDs, or GSM IDs, which are included in the rownames of the hashed features table at `fh_csv_fpath` (required, vector of char strings).
- **fh_csv_fpath**: Path to the hashed features table, which includes rownames corresponding to sample ID strings in the `sample_idv` vector (required, char).
- **si_fname**: Base filename of the search index object, used to find the search index and index dict files, which are expected to be located at `si_fpath` (required, char).
- **si_fpath**: Path to the directory containing the search index and index dict files (required, char).
- **lkval**: Vector of K nearest neighbors to return per query (optional, int, c(1,2)).

Value

Nearest neighbors results of search index query.

Examples

```r
# file paths
# fh table
# fh_csv_fname <- system.file("extdata", "fhtest",
# package = "recountmethylation")
# fh_csv_fname <- file.path(fh_csv_fname, "bval_fh10.csv")
# si dict
# index_dict_fname <- system.file("extdata", "sitest",
# package = "recountmethylation")
# index_dict_fname <- file.path(index_dict_fname, "new_index_dict.pickle")
```
# set sample ids to query
# sample_idv <- c("GSM1038308.1548799666.hlink.GSM1038308_5958154021_R01C01", 
# "GSM1038309.1548799666.hlink.GSM1038309_5958154021_R02C01")
# set a list of k nearest neighbors to query
# lkval <- c(1,2,3)

# get query results as a data frame (with verbose results messaging)
# dfk <- query_si(sample_idv = sample_idv, lkval = lkval,
# # fh_csv_fname = "bval_fn.csv",
# # index_dict_fname = "new_index_dict.pickle")
# returns:
# Starting basilisk process...
# Defining the virtual env dependencies...
# Running virtual environment setup...
# Sourcing Python functions...
# Querying the search index...
# Getting hashed features data for samples...
# Getting index data for sample:
# GSM1038308.1548799666.hlink.GSM1038308_5958154021_R01C01'
# Getting index data for sample:
# GSM1038309.1548799666.hlink.GSM1038309_5958154021_R02C01'
# Beginning queries of k neighbors from lk...
# ii = 0 , ki = 1
# Loading search index...
# Querying 2 elements in data with k = 1 nearest neighbors...
# Query completed, time: 0.0007359981536865234
# Applying labels to query results...
# Returning data (sample id, k index, and distance)...
# ii = 1 , ki = 2
# Loading search index...
# Querying 2 elements in data with k = 2 nearest neighbors...
# Query completed, time: 0.0006208419799804688
# Applying labels to query results...
# Returning data (sample id, k index, and distance)...
# ii = 2 , ki = 3
# Provided k '3' > n si samples, skipping...
# Returning query results...

rgse

Form an RGChannelSet from a list containing signal data matrices

**Description**

Forms an RGChannelSet from signal data list. This is called by certain queries to h5 files.

**Usage**

rgse(ldat, verbose = FALSE)
servermatrix

Arguments

1. **ldat**
   - List of raw signal data query results. Must include 2 data.frame objects named "redsignal" and "greensignal."

2. **verbose**
   - Whether to post status messages.

Value

Returns a RGChannelSet object from raw signal dataset queries.

See Also

getrg(), RGChannelSet()

Examples

```r
path <- system.file("extdata", "h5test", package = "recountmethylation")
fn <- list.files(path)
dbpath <- file.path(path, fn)
rg <- getrg(dbn = dbpath, all.gsm = TRUE, metadata = FALSE)
dim(rg) # [1] 11162 2
class(rg)
# [1] "RGChannelSet"
# attr(,"package")
# [1] "minfi"
```

servermatrix servermatrix

Description

Called by get_rmdl() to get a matrix of database files and file info from the server. Verifies valid versions and timestamps in filenames, and that h5se directories contain both an assays and an se.rds file.

Usage

```r
servermatrix(
  dn = NULL,
  sslver = FALSE,
  printmatrix = TRUE,
  url = "https://methylation.recount.bio/",
  verbose = FALSE
)
```
**setup_sienv**

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>dn</code></td>
<td>Server data returned from RCurl (default NULL).</td>
</tr>
<tr>
<td><code>sslver</code></td>
<td>Whether to use SSL certificate authentication for server connection (default FALSE).</td>
</tr>
<tr>
<td><code>printmatrix</code></td>
<td>Whether to print the data matrix to console (default TRUE).</td>
</tr>
<tr>
<td><code>url</code></td>
<td>Server website url (default &quot;<a href="https://methylation.recount.bio/">https://methylation.recount.bio/</a>&quot;).</td>
</tr>
<tr>
<td><code>verbose</code></td>
<td>Whether to show verbose messages (default FALSE).</td>
</tr>
</tbody>
</table>

**Value**

Matrix of server files and file metadata

**See Also**

get_rmdl, smfilt

**Examples**

```r
dn <- "remethdb-h5se_gr-test_0-0-1_1590090412 29-May-2020 07:28 -"
sm <- get_servermatrix(dn = dn)
```

**Description**

Set up a new virtual environment for search index construction using the basilisk package.

**Usage**

```r
setup_sienv(
  env.name = "dnam_si_hnswlib",
  pkgv = c("python==3.7.1", "hnswlib==0.5.1", "pandas==1.2.2", "numpy==1.20.1",
            "mmh3==3.0.0", "h5py==3.2.1")
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>env.name</code></td>
<td>Name of the new virtual environment (required, &quot;dnam_si-hnswlib&quot;)</td>
</tr>
<tr>
<td><code>pkgv</code></td>
<td>Vector of the dependencies and their versions for the new virtual environment (required, format: &quot;packagename==versionnum&quot;).</td>
</tr>
</tbody>
</table>

**Value**

New basilisk environment object.
**smfilt**

---

**Description**
Filters the data matrix returned from servermatrix().

**Usage**

```r
smfilt(sm, typesdf = NULL)
```

**Arguments**

- `sm` : Data matrix returned from servermatrix().
- `typesdf` : Data.frame containing database file info for dm filters.

**Value**
Filtered data matrix of server file info.

**See Also**
get_rmdl, servermatrix

**Examples**

```r
dm <- matrix(c("remethdb_h5-rg_epic_0-0-2_1589820348.h5","08-Jan-2021","09:46","66751358297"), nrow = 1)
smfilt(dm)
```
Index

ba.background, 2
ba.biotinstaining.grn (ba.background), 2
ba.biotinstaining.red (ba.background), 2
ba.bisulfiteconv1.grn (ba.background), 2
ba.bisulfiteconv1.red (ba.background), 2
ba.bisulfiteconv2 (ba.background), 2
ba.extension.grn (ba.background), 2
ba.extension.red (ba.background), 2
ba.hybridization.hi.vs.med
   (ba.background), 2
ba.hybridization.med.vs.low
   (ba.background), 2
ba.nonpolymorphic.grn (ba.background), 2
ba.nonpolymorphic.red (ba.background), 2
ba.restoration (ba.background), 2
ba.specificity1.grn (ba.background), 2
ba.specificity1.red (ba.background), 2
ba.specificity2 (ba.background), 2
ba.targetremoval1 (ba.background), 2
ba.targetremoval2 (ba.background), 2
bacrl, 7
bathresh, 9
data_mdpost, 9
gds_idat2rg, 10
gds_idatquery, 11
get_crossreactive_cpgs, 15
get_fh, 16
get_qcsignal, 17
get_rmdl, 18
get_servermatrix, 19
getdb, 12
getdb_h5_rg (getdb), 12
getdb_h5_test (getdb), 12
getdb_h5se_gm (getdb), 12
getdb_h5se_gr (getdb), 12
getdb_h5se_rg (getdb), 12
getdb_h5se_test (getdb), 12
getrg, 13
hread, 20
make_si, 21
matchds_1to2, 22
query_si, 23
rgse, 24
servermatrix, 25
setup_sienv, 26
smfilt, 27