Package: slideimp.extra (via r-universe)

June 3, 2026

Type Package

Title slideimp Package Helpers

Version 0.6.8

Description Contains helper functions for the slideimp package. These functions handle the pathing, download the Illumina Methylation manifests, clean them, and store the cleaned objects locally.

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Depends R (>= 4.1.0)

Imports checkmate, data.table, fs, fst, rlang, slideimp (>= 1.0.0.9000), stats, utils, withr

Suggests testthat (>= 3.0.0)

Remotes hhp94/slideimp

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RemoteRef HEAD

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Contents

`clear_cache` *Clear Cached Manifests*

Description

Removes cleaned manifest files from the slideimp data directory.

Usage

```
clear_cache(chip = NULL, verbose = TRUE, ask = TRUE)
```

Arguments

`chip`	Character string specifying which chip's cache to clear, or `NULL` to clear all cached manifests. Default is `NULL`.
`verbose`	Logical. Print messages. Default is `TRUE`.
`ask`	Ask for permission to download or delete the cache. Default is `TRUE`.

Value

Invisibly returns a character vector of deleted paths.

Examples

```
## Not run:
clear_cache("EPICv2")
clear_cache()

## End(Not run)
```

`dedup_matrix` *De-duplicate Matrix*

Description

The `EPICv2` and `MSA` chips can return duplicated CpG names. This function de-duplicate the beta matrix.

Usage

```
dedup_matrix(obj, chip, method = c("mean", "median"), verbose = TRUE)
```

Arguments

`obj`	A numeric matrix with unique column and row names.
`chip`	Either "MSA", "EPICv2", or a data.frame with `IlmnID` and `Name` columns.
`method`	Aggregation method for duplicates: "mean" or "median".
`verbose`	Logical; if TRUE, print informative messages.

Value

A de-duplicated matrix.

`get_manifest` *Retrieve Cleaned Illumina Methylation Manifest*

Description

Retrieves the cleaned manifest for the specified Illumina methylation array chip. If not already cleaned, it downloads the raw manifest, applies the appropriate cleaning function, and stores the result as an .fst file.

Usage

```
get_manifest(
  chip = NULL,
  rawdir = NULL,
  force = FALSE,
  clean_up = FALSE,
  ask = TRUE,
  verbose = TRUE
)
```

Arguments

`chip`	The name of the Illumina methylation chip. If `NULL`, then all available options are returned
`rawdir`	Directory where raw manifest files are downloaded and stored. Defaults to NULL (a temporary directory).
`force`	Forces re-download and re-cleaning of the manifest. Default to `FALSE`.
`clean_up`	deletes the raw manifest file after cleaning. Useful if `rawdir` is not a temporary folder. Default to `FALSE`.
`ask`	Ask for permission to download or delete the cache. Default is `TRUE`.
`verbose`	prints messages. Default is `TRUE`.

Value

The path to the cleaned manifest file as a character string, or `invisible(NULL)` if the chip is invalid.

Examples

```
## Not run:
get_manifest("450K")

## End(Not run)
```

`get_slideimp_path` *Get Path for slideimp Data*

Description

Retrieves the path to the slideimp data directory.

Usage

```
get_slideimp_path(create = FALSE)
```

Arguments

`create`	Logical. If `TRUE`, creates the directory if it doesn't exist and checks writability. Default is `FALSE`.

Details

The path is determined by:

1. Environment variable `SLIDEIMP` (if set)
2. Base R default via `tools::R_user_dir("slideimp", "data")`

To override permanently, add to your `~/.Renviron` (i.e., `file.edit("~/.Renviron")`):

```
SLIDEIMP="/your/custom/path"
```

To override temporarily, use `set_slideimp_path()`.

Value

A character string with the normalized path.

Examples

```
get_slideimp_path()
```

`ilmn_manifest` *Load Illumina Methylation Manifest Data*

Description

Loads the cleaned manifest data for a specified Illumina methylation array chip, returning a unique data.frame with feature identifiers and their corresponding chromosomal groups.

Usage

```
ilmn_manifest(
  chip = NULL,
  deduped = FALSE,
  rawdir = NULL,
  force = FALSE,
  clean_up = FALSE,
  ask = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

`chip`	The name of the Illumina methylation chip. If `NULL`, then all available options are returned
`deduped`	Use deduplicated probe names for EPICv2 and MSA chips (`TRUE`) or IlmnID (`FALSE`). Default is `FALSE`.
`rawdir`	Directory where raw manifest files are downloaded and stored. Defaults to NULL (a temporary directory).
`force`	Forces re-download and re-cleaning of the manifest. Default to `FALSE`.
`clean_up`	deletes the raw manifest file after cleaning. Useful if `rawdir` is not a temporary folder. Default to `FALSE`.
`ask`	Ask for permission to download or delete the cache. Default is `TRUE`.
`verbose`	prints messages. Default is `TRUE`.
`...`	Additional arguments passed to `fst::read_fst()` for reading the cleaned file.

Value

A `data.frame()` with columns "feature" (probe identifiers) and "group" (chromosomal locations), or `invisible(NULL)` if the chip is invalid.

Examples

```
ilmn_manifest()

## Not run:
ilmn_manifest("EPICv2")

## End(Not run)
```

`set_slideimp_path` *Set Path for slideimp Data*

Description

Sets the slideimp data directory path for the current R session.

Usage

```
set_slideimp_path(path)
```

Arguments

`path`	Character string specifying the directory path, or `NULL` to reset to default.

Value

Invisibly returns `NULL`.

Examples

```
# default path
get_slideimp_path()

# set path for this session
set_slideimp_path("test")
get_slideimp_path()

# reset to default
set_slideimp_path(NULL)
get_slideimp_path()
```

`slideimp_arrays` *Supported Illumina DNA methylation microarray platforms*

Description

A character vector of Illumina Infinium BeadChip microarrays supported by the `slideimp` package. These are the microarrays used for genome-wide DNA methylation profiling.

Usage

```
slideimp_arrays
```

Format

`slideimp_arrays`**:**

A character vector with 6 elements:

EPICv2 Infinium MethylationEPIC v2.0 BeadChip

MSA Infinium Methylation Screening Array (MSA-48)

EPICv2_deduped EPICv2 with duplicated CpG probes collapsed

MSA_deduped MSA with duplicated CpG probes collapsed

EPICv1 Infinium MethylationEPIC v1.0 BeadChip

450K Infinium HumanMethylation450 BeadChip

Details

The vector includes both the original microarrays and their "deduped" variants. For `EPICv2_deduped` and `MSA_deduped`, duplicated CpG probes (which appear multiple times in the official Illumina manifest for the same CpG site) have been collapsed into a single representative entry. This is a standard preprocessing step when working with EPICv2 and MSA data.

Manifest files and versions used to build/support these microarrays:

- **450K** (v1-2): `https://webdata.illumina.com/downloads/productfiles/humanmethylation450/humanmethylation450_15017482_v1-2.csv`
- **EPICv1** (v1-0-b5): `https://webdata.illumina.com/downloads/productfiles/methylationEPIC/infinium-methylationepic-v-1-0-b5-manifest-file-csv.zip`
- **EPICv2** (v2-0_A2): `https://support.illumina.com/content/dam/illumina-support/documents/downloads/productfiles/methylationepic/InfiniumMethylationEPICv2.0ProductFiles(ZIPFormat).zip`
- **MSA** (v1-0_20102838_A1): `https://support.illumina.com/content/dam/illumina-support/documents/downloads/productfiles/infiniummethylationscreening/MSA-48v1-0_20102838_A1.csv`

The _deduped microarrays are derived from the above manifests (no separate public download).

Source

Illumina official manifest files (see @details for exact links and versions used).

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