Package 'aries'

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Title Accessible Resource for Integrated Epigenomic Studies (ARIES)

Description Functions for loading the ARIES DNA methylation profiles

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Depends gdsfmt

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URL https://github.com/MRCIEU/aries

LazyData yes

biocViews DNAMethylation, Microarray

RoxygenNote 7.0.2

R topics documented:

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aries.feature.sets *aries.feature.sets*

Description

List of Illumina BeadChip formats available in ARIES

Usage

```
aries.feature.sets(path)
```

Arguments

path   Base directory of ARIES.

Value

Vector listing available format identifiers.

---

aries.info   *aries.info*

Description

Provide comprehensive sample and probe information for all of ARIES

Usage

```
aries.info(path)
```

Arguments

path   Base directory of ARIES.

Value

A list containing ARIES information for each Illumina BeadChip format, run aries.feature.sets()
to get a list of valid identifiers. Each of these is in turn a list of items describing the samples with
methylation profiles in that format:

- samples - Data frame providing sample information, one sample per row.

- probe.names - Illumina probe identifiers.

- control.matrix - Matrix providing control probe values (rows=samples, columns=control probes).

- cell.counts - List of cell count estimates for various references. Each is a matrix (rows=samples,
  columns=cell types).

Examples

```
## Not run:
aries <- aries.info(aries.dir)
## See CD4+ T cell estimate for the third sample
## with an Illumina EPIC profile.
aries$epic$cell.counts[["blood-gse35069"]][3,"CD4T"]

## End(Not run)
```

`aries.methylation`   *aries.methylation*

Description

Load DNA methylation profiles for a specified ARIES subset

Usage

```
aries.methylation(selection, start = 1, count = -1)
```

Arguments

selection	Output of aries.select().
start	Index of the first CpG in the profile (Default: 1). Indexing is with respect to selection$probe.names.
count	Number of CpG sites to load (Default: -1). A value of -1 indicates all available.

Value

A matrix filled with methylation estimates from 0 to 1 (rows=CpG sites, columns=samples).

Examples

```
## Not run:
## Load the first 1000 CpG sites for all blood samples collected around age 15
aries <- aries.select(aries.dir, featureset="common", time.point="15up")
aries$meth <- aries.methylation(aries, start=1, count=1000)

## End(Not run)
```

`aries.samples`   *aries.samples*

Description

Obtain sample information for all of ARIES.

Usage

```
aries.samples(path)
```

Arguments

path	Base directory of ARIES.

Value

Data frame listing all samples.

---

aries.select   *aries.select*

Description

Provide comprehensive sample and probe information for a subset of ARIES

Usage

```
aries.select(
  path,
  featureset,
  time.point = NULL,
  sample.names = NULL,
  replicates = F
)
```

Arguments

path	Base directory of ARIES.
featureset	Illumina BeadChip format. #' Run aries.feature.sets() to get a list of valid identifiers. If all selected profiles are from the Illumina 450K (or EPIC) array, then the default is "450" (or "epic"). If there is a mix, then "common" is the default.
time.point	Optional. Restrict to profiles for samples collected at specific time points (Default: NULL). Run aries.time.points() to get a list.
sample.names	Optional. Restrict to profiles for a set of samples (Default: NULL). Run aries.samples()$Samp to get a list of sample identifiers.
replicates	Include replicate methylation profiles (Default: FALSE). Ignored if is.null(sample.names)==

Value

A list containing ARIES information for the ARIES subset:

- samples - Data frame providing sample information, one sample per row.
- probe.names - Illumina probe identifiers.
- control.matrix - Matrix providing control probe values (rows=samples, columns=control probes).
- cell.counts - List of cell count estimates for various references. Each is a matrix (rows=samples, columns=cell types).

Examples

```
## Not run:
## Define subsets of ARIES restricted to samples collected around age 15
## with Illumina 450K and EPIC BeadChip profiles.
aries.15.450 <- aries.select(aries.dir, featureset="450", time.point="15up")
aries.15.epic <- aries.select(aries.dir, featureset="epic", time.point="15up")

## End(Not run)
```

---

aries.time.points *aries.time.points*

Description

List of ARIES time-point identifiers

Usage

```
aries.time.points(path)
```

Arguments

path   Base directory of ARIES.

Value

A vector of valid time-point identifiers.

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