IlluminaHumanMethylationEPICv2anno.20a1.hg38

November 11, 2026

`IlluminaHumanMethylationEPICv2anno.20a1.hg38`
Annotation data for the 'IlluminaHumanMethylationEPIC' micro array.

Description

This package is based on the file https://support.illumina.com/content/dam/illumina-support/documents/downloads/productfiles/methylationepic/MethylationEPIC%20v2%20Files.zip from https://support.illumina.com/array/array_kits/infinium-methylationepic-beadchip-kit/downloads.html.

Additional SNP annotation is generated by the authors (described in `SNPs.CommonSingle`).

A script for creating the data object in this package is contained in `scripts/createAnno.R`.

Format

An object of class `IlluminaMethylationAnnotation` for `IlluminaHumanMethylationEPIv2Canno.20a1.hg38`. All others are of class `DataFrame`

Details

The following changes/ modifications / addition has been made to the source material.

For the annotation related to UCSC islands, a value of `""` has been changed to `"OpenSea"`.

The creation of this object based on the Illumina annotation and additional SNP information (see `SNPs.CommonSingle`) is contained in the `createAnno.R` script in the `scripts` directory.

Contents of the columns are the responsibility of Illumina; see their documentation for details.

Source

See description.

Examples

```
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Locations
Manifest
data(SNPs.Illumina)  # data object too large, need to be loaded manually by data()
Islands.UCSC
data(Other)  # data object too large, need to be loaded manually by data()
```

SNPs.CommonSingle *SNP annotation from various versions of dbSNP as represented on UCSC Common SNP table.*

Description

SNP annotation from various versions of dbSNP as represented on UCSC Common SNP table. Overlap is based on genomic mappings from the annotation package.

Format

An object of class `DataFrame`. Rownames are CpG identifiers. There are 6 columns `Probe_rs`, `Probe_maf`, `CpG_rs`, `CpG_maf`, `SBE_rs`, and `SBE_maf`. 'Probe' indicates a SNP in the probe, 'CpG' a SNP in the CpG site and 'SBE' in the single base extension site. The `_rs` gives the SNP RS identifier and the `_maf` gives the minor allele frequency.

Details

In addition to the SNP information provided by Illumina, we have added independent information on the overlap of the EPIC (v2.0) array with various versions of dbSNP. The overlap is based on the mappings of the array to the hg38 genome provided by Illumina. As dbSNP we have used the 'Common' table from UCSC (ie. 'snp151Common'). This track contains variants from dbSNP which have a minor allele frequency (MAF) of greater than 1 percent (specifically, this requires dbSNP to actually contain MAF information). Furthermore, we only kept variants marked as 'single' (ie. standard single nucleotide changes, but not insertions or deletions). Scripts for retrieving the UCSC dbSNP table and doing the overlap are contained in the `scripts` directory. The variants are described in 6 different columns. `Probe_rs` tells us the RS number (SNP ID number) for a SNP overlapping the probe, and `Probe_maf` is the minor allelle frequency for the SNP (in case multiple SNPs overlap, only one is recorded). Similarly, `CpG_rs` describe SNPs overlapping the CpG site and `SBE_rs` the single base extension of the measured methylation loci.

Source

UCSC Common SNP Table.

Examples

```
SNPs.141CommonSingle
SNPs.142CommonSingle
SNPs.144CommonSingle
SNPs.146CommonSingle
SNPs.147CommonSingle
SNPs.150CommonSingle
SNPs.151CommonSingle
```

`aggregate_to_probes` *Aggregate to the probe-level*

Description

Aggregate to the probe-level

Usage

```
aggregate_to_probes(x)
```

Arguments

`x`	A data frame or a matrix.

Details

If `x` is a data frame, it should be one of the following objects: Islands.UCSC, Locations, Other, SNPs.Illumina, SNPs.141CommonSingle, SNPs.142CommonSingle, SNPs.144CommonSingle, SNPs.146CommonSingle, SNPs.147CommonSingle, SNPs.150CommonSingle, SNPs.151CommonSingle.

If `x` is a matrix, it should come from the analysis with the **minfi** package. If multiple rows correspond to the same probe, the average value of rows is simply used.

Examples

```
# There is no example
NULL
```

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