IlluminaHumanMethylation27kanno.ilmn12.hg19

November 11, 2026

`IlluminaHumanMethylation27kanno.ilmn12.hg19`
Annotation data for the 'IlluminaHumanMethylation27k' micro array.

Description

This package is based on the file 'HumanMethylation27_v-1-2.csv' from the zip archive from www.illumina.com.

Additional SNP annotation is generated by the authors (described below).

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

Format

An object of class `IlluminaMethylationAnnotation` for `IlluminaHumanMethylation27kanno.ilmn12.hg19`. All others are of class `DataFrame`

Details

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

The creation of this object based on the Illumina annotation and additional SNP information (see below) 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

```
data(IlluminaHumanMethylation27kanno.ilmn12.hg19)
data(Locations)
data(Other)
data(Manifest)
```

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 450k with various versions of dbSNP. The overlap is based on the mappings of the array to the hg19 genome provided by Illumina. As dbSNP we have used the 'Common' table from UCSC (ie. 'snp137Common'). 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

```
data(SNPs.147CommonSingle)
data(SNPs.146CommonSingle)
data(SNPs.144CommonSingle)
data(SNPs.142CommonSingle)
data(SNPs.141CommonSingle)
data(SNPs.138CommonSingle)
data(SNPs.137CommonSingle)
data(SNPs.135CommonSingle)
data(SNPs.132CommonSingle)
```

Index

∗ **datasets**
IlluminaHumanMethylation27kanno.ilmn12.hg19, 1
SNPs.CommonSingle, 2

IlluminaHumanMethylation27kanno.ilmn12.hg19, 1

Locations
*(*IlluminaHumanMethylation27kanno.ilmn12.hg19*)*, 1

Manifest
*(*IlluminaHumanMethylation27kanno.ilmn12.hg19*)*, 1

Other
*(*IlluminaHumanMethylation27kanno.ilmn12.hg19*)*, 1

SNPs.132CommonSingle
*(*SNPs.CommonSingle*)*, 2
SNPs.135CommonSingle
*(*SNPs.CommonSingle*)*, 2
SNPs.137CommonSingle
*(*SNPs.CommonSingle*)*, 2
SNPs.138CommonSingle
*(*SNPs.CommonSingle*)*, 2
SNPs.141CommonSingle
*(*SNPs.CommonSingle*)*, 2
SNPs.142CommonSingle
*(*SNPs.CommonSingle*)*, 2
SNPs.144CommonSingle
*(*SNPs.CommonSingle*)*, 2
SNPs.146CommonSingle
*(*SNPs.CommonSingle*)*, 2
SNPs.147CommonSingle
*(*SNPs.CommonSingle*)*, 2
SNPs.CommonSingle, 2