FDb.InfiniumMethylation.hg18

November 11, 2026

`getNearest` *Annotate a group of probes supplied as a GenomicRanges object*

Description

This function encapsulates the common task of finding what gene/tx/tss is closest to a list of probes, as might be the case after a model fit.

Author(s)

Tim Triche, Jr.

Examples

```
## not run
##
## hm450 <- get450k()
## probenames <- c("cg16392865", "cg00395291", "cg09310185", "cg21749424")
## probes <- hm450[probenames]
##
## getNearestTSS(probes)
## getNearestTranscript(probes)
##
## Notice that cg16392865 sits within PTCRA, but the nearest TSS is CNPY3.
##
```

`getPlatform` *Retrieve annotations for HumanMethylation27 or HumanMethylation450 chips*

Description

FDb.InfiniumMethylation.hg19 is an omnibus package that merges all of the existing Illumina Infinium DNA methylation probe annotations into one FDb. However, most users will be analyzing one of the two chips at any given time. The utility functions getPlatform(platform), get450k(), and get27k() retrieve a compact GenomicRanges form of the annotations for the requested platform.

Author(s)

Tim Triche, Jr.

Examples

```
hm450.hg18 <- getPlatform(platform='HM450', genome='hg18')
show(hm450.hg18)

hm27.hg18 <- get27k(genome='hg18')
genome(hm27.hg18)
```

`hg18.islands` *CpG islands found by Wu, Irizarry, and Feinberg via hidden Markov model*

Description

This GRanges object was constructed from the data provided at http://rafalab.jhsph.edu/CGI/model-based-cpg-islands-hg18.txt

Additional species and software to run the model can be found at http://rafalab.jhsph.edu/CGI/index.html

Author(s)

Tim Triche, Jr. (with data from Wu, Irizarry, and Feinberg)

Examples

```
data(hg18.islands)
split(hg18.islands, seqnames(hg18.islands))
```

miscData *miscellaneous data used in the construction of this FeatureDb package*

Description

In the subdirectory inst/build/, there are several scripts that rebuild this FeatureDb from scratch. A handful of intermediate results from dbSNP and comparison of existing datasets are required to patch small gaps in the Illumina manifests. These datasets supply those intermediate results.

Author(s)

Tim Triche, Jr.

Examples

```
data(hm450.rsProbes)
data(hm27.SNP.colors)
```

FDb.InfiniumMethylation.hg18 *Annotation package for Illumina Infinium DNA methylation probes*

Description

This package loads one or more FeatureDb objects. Such FeatureDb objects are an R interface to prefabricated databases contained by this package. In the case of the Infinium methylation FDb, it is FDb.InfiniumMethylation.hg18 (for the moment; hg18 may come later, or alternatively users can use liftOver() from rtracklayer to do it).

Author(s)

Tim Triche, Jr.

See Also

features makeFeatureDbFromUCSC import.bed getPlatform get450k get27k

Examples

```
## load the library
library(FDb.InfiniumMethylation.hg18)

## list the contents that are loaded into memory
ls('package:FDb.InfiniumMethylation.hg18')
```

```
## show the db object that is loaded by calling it's name
FDb.InfiniumMethylation.hg18

## extract features for use in constructing SummarizedExperiments
## or comparing chip features against other data (e.g. ChIP-seq)
InfiniumMethylation <- features(FDb.InfiniumMethylation.hg18)

## it's much more convenient to address ranges by their probe ID:
names(InfiniumMethylation) <- values(InfiniumMethylation)$name

## we'd prefer if R would stop us from comparing across assemblies:
met <- metadata(FDb.InfiniumMethylation.hg18) ## need to fetch genome
genome(InfiniumMethylation) <- met[which(met[,'name']=='Genome'),'value']

## last but not least, sort the probes in genomic order
InfiniumMethylation <- sort(InfiniumMethylation)
show(InfiniumMethylation)

## Example: probes that overlap Irizarry's HMM CpG islands
data(hg18.islands)
CGI.probes <- subsetByOverlaps(InfiniumMethylation, hg18.islands)
head(CGI.probes)
tail(CGI.probes)

## Same as above, but now for "shores"
hg18.shores <- c(flank(hg18.islands, 2000, start=TRUE),
                 flank(hg18.islands, 2000, start=FALSE))
shore.probes <- subsetByOverlaps(InfiniumMethylation, hg18.shores)
head(shore.probes)
tail(shore.probes)

## The same logic works for overlapping probes with other data.
## For example, we can easily do this for old 27k data as well:
hm27 <- get27k()
hm27.shores <- subsetByOverlaps(hm27, hg18.shores)

## The same approach works to overlap (e.g.) ChIP-seq peaks or DNAseI footprints
## Much more data is available via GenomicFeatures and rtracklayer:
help(makeFeatureDbFromUCSC)
```

`seqinfo.hg18` *Sequence names, lengths, and circularity for hg18*

Description

These avoid having to load a BSgenome package just to assign seqinfo(GR).

Author(s)

Tim Triche, Jr.

Examples

```
## FDb.InfiniumMethylation.hg18
hm450.hg18 <- get450k(genome='hg18')
```

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