Package ‘encoDnaseI’

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Title data provided by UCSC for Cd4 raw measures of DnaseI hypersensitivity

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Version 0.2.0

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Depends R (>= 2.15.0), methods, Biobase (>= 2.5.5), lattice, GGtools,GGBase

Suggests GGdata

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biocViews ExperimentData

R topics documented:

`hg18track-class` *Class "hg18track" container for hg18 annotation found in genome browser track files; class "chrnum" extends numeric for an indexing application on hg18track objects.*

Description

container for hg18 annotation found in genome browser track files

Objects from the Class

Objects can be created by calls of the form `new("hg18track", assayData, featureData, experimentData, annotation` These are single-sample eSet instances.

Note that `demoTrk19` is a restriction of the `rawCD4` structure to the interval of chromosome 19 that was assayed in the ENCODE project for DnaseI hypersensitivity.

Slots

`assayData`**:** Object of class `"AssayData"` ~~

`phenoData`**:** Object of class `"AnnotatedDataFrame"` ~~

`featureData`**:** Object of class `"AnnotatedDataFrame"` ~~

`experimentData`**:** Object of class `"MIAME"` ~~

`annotation`**:** Object of class `"character"` ~~

`.__classVersion__`**:** Object of class `"Versions"` ~~

Extends

Class `"eSet"`, directly. Class `"VersionedBiobase"`, by class "eSet", distance 2. Class `"Versioned"`, by class "eSet", distance 3.

Methods

[`signature(x = "hg18track")`: select using numeric, logical, or chrnum indices.

chrnum `signature(object = "hg18track")`: extract numeric tokens for chromosome number at which data values are obtained; note that chrnum is also used as name of a class.

dataVals `signature(object = "hg18track")`: actual data values

getTrkXY `signature(object = "hg18track", type = "character")`: obtain a list with components x, y indicating location and data value respectively; location is within chromosome; default type is 'midpoint' of locations given as intervals

getTrkXY `signature(object = "hg18track", type = "missing")`: take default midpoint x values corresponding to data values

rangeLocs `signature(object = "hg18track")`: if measures from only one chromosome are present , this returns low and high values of chromStart and chromEnd respectively, otherwise error.

clipTrk `signature(obj = "hg18track", low="numeric", hi="numeric", attr="ANY")`: create a restriction of the track using an interval specification. by default the `chromStart` featureData component is used for coordinates to clip; if `attr` is non-missing, the featureData component named by `attr` will be used.

initialize `signature(.Object = "hg18track")`: create a new instance

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Examples

```
showClass("hg18track")
data(rawCD4)
rawCD4
rawCD4.chr1 = rawCD4[ chrnum(1), ]
rangeLocs(rawCD4.chr1)
plot(getTrkXY(rawCD4.chr1), ylab="data value", xlab="interval midpt on chr 1" )
c52 = clipTrk(rawCD4[ chrnum(5), ], 1.30e8, 1.33e8 )
plot(getTrkXY(c52))
```

`juxtaPlot` *two-panel plot with track info and snp screen t-values*

Description

two-panel plot with track info and snp screen t-values

Usage

```
juxtaPlot(trk, ssr, locstr)
```

Arguments

`trk`	instance of `hg18track`
`ssr`	instance of GGtools `snpScreenResult`
`locstr`	matrix with 2 rows: rsid (numeric component of dbSNP id) and loc

Details

`xyplot` of lattice package is used.

Value

`xyplot` output; use `print` in Sweave.

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Examples

```
## Not run:
# see vignette
data(sOSR2)
data(c19g)  # track excerpt
juxtaPlot(c19g, sOSR2)

## End(Not run)
```

`rawCd4DnaseI` *A data frame with information on the UCSC browser track related to DNaseI hypersensitivity*

Description

A data frame with information on the UCSC browser track related to DNaseI hypersensitivity; the rawCD4 object is an eSet extension representing the same information; rawHelaDnaseI is like rawCD4 but results on Hela cells.

Usage

```
data(rawCd4DnaseI)
data(rawHelaDnaseI)
data(rawCD4)
```

Details

Obtained from a MySQL representation of the data distributed at the Genome Browser FTP site

Value

a data.frame

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

References

`hgdownload.cse.ucsc.edu` ... it appears that they do not offer the MYD/MYI representations, just the txt.gz and sql files now. So if you obtain the encodeNhgriDnaseHsChipRawCd4.txt and .sql files at goldenPath/currentGenomes/Homo_Sapiens/encode/database, you can reconstruct the underlying data for this data.frame (hg18, Nov 2007).

Examples

```
data(rawCd4DnaseI)
dim(rawCd4DnaseI)
rawCd4DnaseI[1:5,]
library(lattice)
xyplot(dataValue~chromStart|chrom, data=rawCd4DnaseI, subset=chrom %in%
  c("chr1", "chr10", "chr19", "chr20"), scales=list(x=list(relation="free")))
```

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