Package ‘erma’

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Title epigenomic road map adventures

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Description Software and data to support
epigenomic road map adventures.

Suggests rmarkdown, BiocStyle, knitr, GO.db, png, DT, doParallel

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Maintainer VJ Carey <stvjc@channing.harvard.edu>

License Artistic-2.0

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erma-package *epigenomic road map adventures*

Description

Software and data to support epigenomic road map adventures.

Details

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This package provides infrastructure for working with products of the NIH epigenome roadmap project.

Author(s)

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Examples

```
data(farhSE)
farhSE
ee = makeErmaSet()
stateProfile(ee[,1:4], symbol="A2M")
data(abbCIcols)
abbCIcols
```

ErmaSet-class *Class* "ErmaSet"

Description

Wrap a GenomicFiles instance representing roadmap bed files.

Usage

```
makeErmaSet()
subsetByRanges( ermaset, range )
```

Arguments

ermaset	an instance of ErmaSet-class
range	an instance of GRanges-class

Objects from the Class

Objects can be created by calls of the form `new("ErmaSet", ...)`. Simple extension of GenomicFiles.

Slots

`files`: Object of class `"ANY"` ~~

`rowRanges`: Object of class `"GenomicRangesORGRangesList"` ~~

`colData`: Object of class `"DataFrame"` ~~

`assays`: Object of class `"Assays"` ~~

`NAMES`: Object of class `"character_OR_NULL"` ~~

`elementMetadata`: Object of class `"DataFrame"` ~~

`metadata`: Object of class `"list"` ~~

Extends

Class "GenomicFiles-class", directly. Class "RangedSummarizedExperiment-class", by class "GenomicFiles", distance 2. Class "SummarizedExperiment-class", by class "GenomicFiles", distance 3. Class "Vector", by class "GenomicFiles", distance 4. Class "Annotated", by class "GenomicFiles", distance 5.

Methods

cellTypes `signature(x = "ErmaSet")`: ...

Note

We would like to have methods for AnnotationHub entities too.

Examples

```
showClass("ErmaSet")
makeErmaSet()
```

---

genemodel *create GRanges instance with model for a gene*

Description

create GRanges instance with model for a gene

Usage

```
genemodel(key, keytype, annoResource = Homo.sapiens,
   keepStandardChromosomes=TRUE)
geneTxRange(sym, annoResource = Homo.sapiens)
map2range(maptag="17q12", annoResource = Homo.sapiens)
```

Arguments

`sym`	symbol used as key into `annoResource` with keytype SYMBOL
`key`	string used as key into `annoResource` with keytype `keytype`
`maptag`	string used as key into `annoResource` with keytype MAP
`keytype`	string used as keytype for `select` with `annoResource`
`annoResource`	OrganismDb instance; genemodel will also work with an EnsDb instance
`keepStandardChromosomes`	if true, will eliminate non-standard chromosomes using the eponymous function from GenomeInfoDb, with pruning.mode = 'coarse'

Details

map2range will obtain all TXSTART and TXEND for genes identified through select with key maptag and return a single range with min TXSTART and max TXEND

Value

a `GRanges` instance

Note

genemodel revised Aug 10 2015. Direct operations on Homo.sapiens, much faster. geneTxRange added Aug 10 2015.

Examples

```
genemodel("IL33")
geneTxRange("IL33")
map2range("17q12")
```

---

mapmeta — *create a DataFrame instance providing metadata about the Epigenomics Roadmap*

Description

create a DataFrame instance providing metadata about the Epigenomics Roadmap

Usage

```
mapmeta()
```

Details

originates at https://docs.google.com/spreadsheet/ccc?key=0Am6FxqAtrFDwdHU1UC13ZUxKYy1XVEJPUzV6MEtQOXc&usp=sharing#gid=15

Value

a DataFrame instance that is wrapped to limit sprawl over columns when shown.

Examples

```
mapmeta()
```

---

stateProfile — *create a ggplot2 visualization of chromatin states over genomic addresses for a family of cell types managed in an ErmaSet instance*

Description

Create a ggplot2 visualization of chromatin states over genomic addresses for a family of cell types managed in an ErmaSet instance.

Usage

```
stateProfile(ermaset, symbol = "IL33", upstream = 2000,
   downstream = 200, ctsize = 10,
   shortCellType = TRUE, tsswidth=3 )
stateProf(ermaset, shortCellType=TRUE, ctsize=10, iniSym="IL7R")
csProfile(ermaset, symbol, upstream = 2000, downstream = 200,
                 useShiny = FALSE, ctsize = 10, shortCellType = TRUE,
                 tsswidth = 3)
```

Arguments

ermaset	instance of ErmaSet-class
symbol	gene symbol resolvable in Homo.sapiens
upstream, downstream	parameters passed to promoters to limit region to view
ctsize	font size for cell type labels
iniSym	a character(1) gene symbol
shortCellType	logical, if FALSE, full cell type labels are used, otherwise ad hoc abbreviations are used for facet labeling
useShiny	logical; if TRUE, shiny app is run permitting interactive selection of gene, and scope of view
tsswidth	width in base pairs of the base of a black rectangle used to depict location of transcription start site

Value

if useShiny is FALSE, an instance of c("gg", "ggplot") is returned

Examples

```
ermaset = makeErmaSet()
# set useShiny=TRUE for interactive display
csProfile(ermaset[,1:5], "CD28")
```

`states_25` *metadata on states of 25-state model of chromatin from ChromImpute, and on cell types in the epigenome road map of April 2015*

Description

metadata on states of 25-state model of chromatin from ChromImpute

Usage

```
data("states_25")
```

Format

A data frame with 25 observations on the following 5 variables.

`STATENO.` a numeric vector

`MNEMONIC` a character vector

`DESCRIPTION` a character vector

`COLOR.NAME` a character vector, partly non-compliant with R colors

`COLOR.CODE` a character vector, RGB numerics, comma-delimited

`rgb` a character vector, RGB scores in R atomic format

Details

Some modifications needed to remove registered trademark symbol mistakenly present in 'regulatory' and non-ascii elements of prime notations

Source

retrieved from http://egg2.wustl.edu/roadmap/web_portal/imputed.html#chr_imp 28 April 2015

Examples

```
data(states_25)
## maybe str(states_25) ; plot(states_25) ...
```

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