Package ‘erma’

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


**Methods**

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

**Note**

We would like to have methods for AnnotationHub entities too.

**Examples**

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

---

**Description**

create GRanges instance with model for a gene

**Usage**

```r
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


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=0Am6FxqAtrFDwdHU1UC13ZUxKYy1XEJPUzV6MEtQOxc&usp=sharing#gid=15
stateProfile

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

```r
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

```r
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

```r
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](http://egg2.wustl.edu/roadmap/web_portal/imputed.html#chr_imp) 28 April 2015

Examples

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