Package ‘erma’

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Author  VJ Carey <stvjc@channing.harvard.edu>
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              epigenomic road map adventures.
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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

The DESCRIPTION file: This package was not yet installed at build time.

Index: This package was not yet installed at build time.

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

Author(s)

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

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
genemodel

Objects from the Class

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

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 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


Examples

```r
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

```r
mapmeta()
```

Details

originates at [https://docs.google.com/spreadsheet/ccc?key=0Am6FxqAtrFDwdHU1UC13ZUxKYy1XVEJPUzV6MEtQOXc&usp=sharing#gid=15](https://docs.google.com/spreadsheet/ccc?key=0Am6FxqAtrFDwdHU1UC13ZUxKYy1XVEJPUzV6MEtQOXc&usp=sharing#gid=15)
**stateProfile**

**Value**

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

**Examples**

```r
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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