Package ‘erna’

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Title  epigenomic road map adventures
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    Biobase, shiny, BiocParallel, IRanges, AnnotationDbi
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ErmaSet-class

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.

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

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

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

Description

create GRanges instance with model for a gene

Usage

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

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sym</td>
<td>symbol used as key into annoResource with keytype SYMBOL</td>
</tr>
<tr>
<td>key</td>
<td>string used as key into annoResource with keytype keytype</td>
</tr>
<tr>
<td>maptag</td>
<td>string used as key into annoResource with keytype MAP</td>
</tr>
<tr>
<td>keytype</td>
<td>string used as keytype for select with annoResource</td>
</tr>
<tr>
<td>annoResource</td>
<td>OrganismDb instance; genemodel will also work with an EnsDb instance</td>
</tr>
<tr>
<td>keepStandardChromosomes</td>
<td>if true, will eliminate non-standard chromosomes using the eponymous function from GenomeInfoDb, with pruning.mode = 'coarse'</td>
</tr>
</tbody>
</table>

### 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")
```

---

### Description

create a DataFrame instance providing metadata about the Epigenomics Roadmap

### Usage

mapmeta()

### Details

originates at [https://docs.google.com/spreadsheet/ccc?key=0Am6FxqAtrFDwdHUlUC13ZUxKYy1XVEJPUzV6M5e5QXc&usp=sharing#gid=15](https://docs.google.com/spreadsheet/ccc?key=0Am6FxqAtrFDwdHUlUC13ZUxKYy1XVEJPUzV6M5e5QXc&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

```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**

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**

data(states_25)

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