Package ‘erna’

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Title epigenomic road map adventures
Version 0.6.0
Author VJ Carey <stvjc@channing.harvard.edu>
Description Software and data to support
epigenomic road map adventures.
Suggests rmarkdown, BiocStyle, knitr, GO.db, BiocParallel, png, DT,
doParallel
Depends R (>= 3.1), methods, Homo.sapiens
Imports GenomicFiles (>= 1.5.2), rtracklayer, S4Vectors, BiocGenerics,
GenomicRanges, SummarizedExperiment, ggplot2, Biobase, shiny,
foreach, AnnotationDbi
Maintainer VJ Carey <stvjc@channing.harvard.edu>
License Artistic-2.0
LazyLoad yes
BioCViews epigenetics, panomics, annotation, chipseq
VignetteBuilder knitr
NeedsCompilation no

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Description

Software and data to support epigenomic road map adventures.

Details

The DESCRIPTION file:

Package: erma
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BiocViews: epigenetics, panomics, annotation, chipseq
VignetteBuilder: knitr

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ErmaSet-class Class ’”ErmaSet”’
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mapmeta create a DataFrame instance providing metadata about the Epigenomics Roadmap
stateProfile create a ggplot2 visualization of chromatin states over genomic addresses for a family of cell types managed in an ErmaSet instance
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

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)
**ErmaSet-class**

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

---

**Class** "ErmaSet"

---

**Description**

Wrap a GenomicFiles instance representing roadmap bed files.

**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 "characterORNULL" ~
- `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()
```
create GRanges instance with model for a gene

Usage

```r
genemodel(key, keytype, annoResource = Homo.sapiens)
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

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
mapmeta()

Details
originates at https://docs.google.com/spreadsheet/ccc?key=0Am6FxqAtrFDwdHU1UC13ZUy1XVEJPUzV6MEtQOi8&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, csize=10)
csProfile(ermaset, symbol, upstream = 2000, downstream = 200, useShiny = FALSE, csize = 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
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

Examples

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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