Package ‘erma’

December 21, 2016

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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erma-package epigenomic road map adventures
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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)
**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()
```
genemodel

create GRanges instance with model for a gene

Description

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

**Description**

create a DataFrame instance providing metadata about the Epigenomics Roadmap

**Usage**

mapmeta()

**Details**

originates at https://docs.google.com/spreadsheet/ccc?key=0Am6FxqAtrFDwdHUIUC13ZUxKYy1XVEJPuZv6METQO
usp=sharing#gid=15

**Value**

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

**Examples**

mapmeta()

---

stateProfile

**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)
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
csize 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
csProfile(ermaset[,1:5], "CD28")

Description

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

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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