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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erma-package

epigenomic road map adventures

Description

Software and data to support epigenomic road map adventures.

Details

The DESCRIPTION file:

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

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erma-package epigenomic road map adventures
genemodel create GRanges instance with model for a gene
gmapmeta 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)

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

Examples

data(farhSE)
ErmaSet-class

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

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

showClass("ErmaSet")
makeErmaSet()
**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

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=0Am6FxqAtrFDwdHU1UC13ZUxKYYy1XVEJPUzV6METQ0YXsseyJzYXh0fGZpc29yYXRpb25z
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, ctsize=10)
csProfile(ermaset, symbol, upstream = 2000, downstream = 200, 
useShiny = FALSE, ctsize = 10, shortCellType = TRUE, 
tsswidth = 3)
Arguments

ermaset instance of \texttt{ErmaSet-class}
symbol gene symbol resolvable in \texttt{Homo.sapiens}
upstream, downstream parameters passed to \texttt{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 \texttt{useShiny} is FALSE, an instance of \texttt{c("gg", "ggplot")} is returned

Examples

\begin{verbatim}
ermaset = makeErmaSet()
# set useShiny=TRUE for interactive display
csProfile(ermaset[,1:5], "CD28")
\end{verbatim}

\begin{verbatim}
states_25
\end{verbatim}

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

\begin{verbatim}
data("states_25")
\end{verbatim}

Format

A data frame with 25 observations on the following 5 variables.

\begin{verbatim}
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
\end{verbatim}

Details

Some modifications needed to remove registered trademark symbol mistakenly present in 'regulatory' and non-ascii elements of prime notations
states_25

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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