Package ‘erna’

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Title epigenomic road map adventures

Version 0.8.0

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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License: Artistic-2.0
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
mapmeta create a DataFrame instance providing metadata
stateProfile create a ggplot2 visualization of chromatin
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)
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.

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
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")
```
create a DataFrame instance providing metadata about the Epigenomics Roadmap

Usage

mapmeta()

Details

originates at https://docs.google.com/spreadsheet/ccc?key=0Am6FxqAtrFDwdHUL1UC3ZJLyYwXJEzVZ6METQmQ0Q&usp=sharing#gid=15

Value

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

Examples

mapmeta()

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>ermaset</code></td>
<td>instance of <code>ErmaSet-class</code></td>
</tr>
<tr>
<td><code>symbol</code></td>
<td>gene symbol resolvable in <code>Homo.sapiens</code></td>
</tr>
<tr>
<td><code>upstream</code>, <code>downstream</code></td>
<td>parameters passed to <code>promoters</code> to limit region to view</td>
</tr>
<tr>
<td><code>ctsize</code></td>
<td>font size for cell type labels</td>
</tr>
<tr>
<td><code>shortCellType</code></td>
<td>logical, if FALSE, full cell type labels are used, otherwise ad hoc abbreviations are used for facet labeling</td>
</tr>
<tr>
<td><code>useShiny</code></td>
<td>logical; if TRUE, shiny app is run permitting interactive selection of gene, and scope of view</td>
</tr>
<tr>
<td><code>tsswidth</code></td>
<td>width in base pairs of the base of a black rectangle used to depict location of transcription start site</td>
</tr>
</tbody>
</table>

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")
```

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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