Package ‘erma’

January 26, 2024

Title epigenomic road map adventures
Version 1.18.0
Author VJ Carey <stvjc@channing.harvard.edu>
Description Software and data to support epigenomic road map adventures.
Suggests rmarkdown, BiocStyle, knitr, GO.db, png, DT, doParallel
Depends R (>= 3.1), methods, Homo.sapiens, GenomicFiles (>= 1.5.2)
Imports rtracklayer (>= 1.38.1), S4Vectors (>= 0.23.18), BiocGenerics, GenomicRanges, SummarizedExperiment, ggplot2, GenomeInfoDb, Biobase, shiny, BiocParallel, IRanges, AnnotationDbi
Maintainer VJ Carey <stvjc@channing.harvard.edu>
License Artistic-2.0
LazyLoad yes
BiocViews Epigenetics, panomics, Annotation, ChIPSeq
VignetteBuilder knitr
git_url https://git.bioconductor.org/packages/erma
git_branch RELEASE_3_18
git_last_commit bed2908
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-01-26

R topics documented:

<table>
<thead>
<tr>
<th>R Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>erma-package</td>
<td>2</td>
</tr>
<tr>
<td>ErmaSet-class</td>
<td>2</td>
</tr>
<tr>
<td>genemodel</td>
<td>3</td>
</tr>
<tr>
<td>mapmeta</td>
<td>4</td>
</tr>
<tr>
<td>stateProfile</td>
<td>5</td>
</tr>
<tr>
<td>states_25</td>
<td>6</td>
</tr>
</tbody>
</table>

Index 7
ErmaSet-class

Description

Software and data to support epigenomic road map adventures.

Details

The DESCRIPTION file: This package was not yet installed at build time.

Index: This package was not yet installed at build time.

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.

Usage

makeErmaSet()
subsetByRanges( ertasat, 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)
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; genemodel will also work with an EnsDb instance
- **keepStandardChromosomes**: if true, will eliminate non-standard chromosomes using the eponymous function from GenomeInfoDb, with pruning.mode = 'coarse'

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

- 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=0Am6FxqAtrFDwdHU1UC13ZuxKYy1XVEJPUzV6MEtQOXc&usp=sharing#gid=15
stateProfile

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, 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**

```r
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**

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

* classes
  ErmaSet-class, 2
* datasets
  states_25, 6
* models
  genemodel, 3
  mapmeta, 4
  stateProfile, 5
* package
  erma-package, 2

abbCIcols (erna-package), 2
abbCIstates (erna-package), 2
Annotated, 3

cellTypes (ErmaSet-class), 2
cellTypes,ErmaSet-method
  (ErmaSet-class), 2
csProfile (stateProfile), 5

DataFrame, 5

erna (erna-package), 2
erna-package, 2
ErmaSet-class, 2

farhSE (erna-package), 2

genemodel, 3
geneTxRange (genemodel), 3
GRanges, 4

Homo.sapiens, 5

makeErmaSet (ErmaSet-class), 2
map2range (genemodel), 3
mapmeta, 4

promoters, 5

short_celltype (states_25), 6

stateProf (stateProfile), 5
stateProfile, 5
states_25, 6
subsetByRanges (ErmaSet-class), 2

Vector, 3