

Package ‘erma’

October 12, 2016

Title epigenomic road map adventures

Version 0.4.2

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

R topics documented:

erma-package	2
ErmaSet-class	3
genemodel	4
mapmeta	5
stateProfile	5
states_25	6
Index	8

 erma-package

 epigenomic road map adventures

Description

Software and data to support epigenomic road map adventures.

Details

The DESCRIPTION file:

```

Package:      erma
Title:        epigenomic road map adventures
Version:      0.4.2
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
Maintainer:  VJ Carey <stvjc@channing.harvard.edu>
License:     Artistic-2.0
LazyLoad:    yes
BiocViews:   epigenetics, panomics, annotation, chipseq
VignetteBuilder: knitr
  
```

Index of help topics:

ErmaSet-class	Class '"ErmaSet"'
erma-package	epigenomic road map adventures
genemodel	create GRanges instance with model for a gene
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)
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 "characterORNULL" ~~
elementMetadata: Object of class "DataFrame" ~~
metadata: Object of class "list" ~~

Extends

Class "[GenomicFiles-class](#)", directly. Class "[RangedSummarizedExperiment-class](#)", by class "GenomicFiles", distance 2. Class "[SummarizedExperiment-class](#)", by class "GenomicFiles", distance 3. Class "[Vector](#)", by class "GenomicFiles", distance 4. Class "[Annotated](#)", by class "GenomicFiles", distance 5.

Methods

cellTypes signature(x = "ErmaSet"): ...

Note

We would like to have methods for AnnotationHub entities too.

Examples

```
showClass("ErmaSet")
makeErmaSet()
```

genemodel	<i>create GRanges instance with model for a gene</i>
-----------	------------------------------------------------------

Description

create GRanges instance with model for a gene

Usage

```
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

genemodel revised Aug 10 2015. Direct operations on Homo.sapiens, much faster. geneTxRange added Aug 10 2015.

Examples

```
genemodel("IL33")
geneTxRange("IL33")
map2range("17q12")
```

mapmeta	<i>create a DataFrame instance providing metadata about the Epigenomics Roadmap</i>
---------	-------------------------------------------------------------------------------------

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>

Value

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

Examples

```
mapmeta()
```

stateProfile	<i>create a ggplot2 visualization of chromatin states over genomic addresses for a family of cell types managed in an ErmaSet instance</i>
--------------	--------------------------------------------------------------------------------------------------------------------------------------------

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

states_25	<i>metadata on states of 25-state model of chromatin from ChromImpute, and on cell types in the epigenome road map of April 2015</i>
-----------	--------------------------------------------------------------------------------------------------------------------------------------

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) ...
```

Index

- *Topic **classes**
 - ErmaSet-class, [3](#)
- *Topic **datasets**
 - states_25, [6](#)
- *Topic **models**
 - genemodel, [4](#)
 - mapmeta, [5](#)
 - stateProfile, [5](#)
- *Topic **package**
 - erma-package, [2](#)

abbCIColors (erma-package), [2](#)
abbCIstates (erma-package), [2](#)
Annotated, [3](#)

cellTypes (ErmaSet-class), [3](#)
cellTypes, ErmaSet-method
(ErmaSet-class), [3](#)
csProfile (stateProfile), [5](#)

DataFrame, [5](#)

erma (erma-package), [2](#)
erma-package, [2](#)
ErmaSet-class, [3](#)

farhSE (erma-package), [2](#)

genemodel, [4](#)
geneTxRange (genemodel), [4](#)
GRanges, [4](#)

Homo.sapiens, [6](#)

makeErmaSet (ErmaSet-class), [3](#)
map2range (genemodel), [4](#)
mapmeta, [5](#)

promoters, [6](#)

short_celltype (states_25), [6](#)

stateProf (stateProfile), [5](#)
stateProfile, [5](#)
states_25, [6](#)

Vector, [3](#)