

Package ‘erma’

April 23, 2016

Title epigenomic road map adventures

Version 0.2.0

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, ggplot2, Biobase, shiny, foreach

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
Title:        epigenomic road map adventures
Version:      0.2.0
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, ggplot2, Biobase, shiny,
Maintainer:   VJ Carey <stvjc@channing.harvard.edu>
License:      Artistic-2.0
LazyLoad:    yes
BiocViews:    epigenetics, panomics, annotation, chipseq
VignetteBuilder: knitr
  
```

Index of help topics:

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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 "[SummarizedExperiment0-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/spreadsheets/ccc?key=0Am6FqxqAtrFDwdHU1UC13ZUxKYy1XVEJPUzV6MEtQOXc&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) ...
```

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