Package ‘erma’

November 20, 2016

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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Description

Software and data to support epigenomic road map adventures.

Details

The DESCRIPTION file:

Package:  erma
Title:    epigenomic road map adventures
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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_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)
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()
```
genemodel

create GRanges instance with model for a gene

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

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=0Am6FxqAtrFDwdHU1UC13ZUxKYYy1XEJPUzV6MEtQOFk&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 `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

```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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