Package ‘erna’

March 29, 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/ernam
git_branch RELEASE_3_18
git_last_commit bed2908
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-03-29

R topics documented:

erna-package .................................................. 2
ErmaSet-class ................................................ 2
genemodel .................................................... 3
mapmeta ....................................................... 4
stateProfile .................................................. 5
states_25 ..................................................... 6

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 <stvj@channing.harvard.edu>
Maintainer: VJ Carey <stvj@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( ermaset, 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 Genomic-Files.

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()

---

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,
    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

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  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
**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**

```r
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

`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

```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 (erma-package), 2
abbCIsates (erma-package), 2
Annotated, 3
cellTypes (ErmaSet-class), 2
cellTypes,ErmaSet-method
  (ErmaSet-class), 2
csProfile (stateProfile), 5

DataFrame, 5
erma (erma-package), 2
erma-package, 2
ErmaSet-class, 2

farhSE (erma-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