Package ‘erma’

May 27, 2024

Title  epigenomic road map adventures
Version  1.20.0
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_19
git_last_commit  acb7b03
git_last_commit_date  2024-04-30
Repository  Bioconductor 3.19
Date/Publication  2024-05-27

Contents

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

Index  7
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
```r
data(farhSE)
farhSE
ee = makeErmaSet()
stateProfile(ee[,1:4], symbol="A2M")
data(abbCIcols)
abbCIcols```

Description
Wrap a GenomicFiles instance representing roadmap bed files.

Usage
```r
makeErmaSet()
subsetByRanges( ermaset, range )
```

Arguments
- `ermaset` an instance of `ErmaSet-class`
- `range` an instance of `GRanges-class`
**genemodel**

**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()
```

---

**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


Examples

```r
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

```r
mapmeta()
```

Details

- originates at https://docs.google.com/spreadsheet/ccc?key=0Am6FxqAtrFDwdHU1UC13ZUxKYy1XVEJPUzV6MEtQOxctN&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")
```

---

**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**

```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 (erma-package), 2
abbCIstates (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