Package ‘erma’

March 5, 2024

Title epigenomic road map adventures
Version 1.18.0
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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
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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_18
git_last_commit bed2908
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-03-05

R topics documented:

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Description

Software and data to support epigenomic road map adventures.

Details

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This package provides infrastructure for working with products of the NIH epigenome roadmap project.

Author(s)

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Examples

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

ErmaSet-class 

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 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 "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

- `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
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")
```

---

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

```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) ...
```
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