

Package ‘erma’

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Title epigenomic road map adventures

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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, 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

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R topics documented:

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 erma-package

epigenomic road map adventures

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)

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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 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

Class "[GenomicFiles-class](#)", directly. Class "[RangedSummarizedExperiment-class](#)", by class "GenomicFiles", distance 2. Class "[SummarizedExperiment-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

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 | <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/spreadsheet/ccc?key=0Am6FxqAtrFDwdHU1UC13ZUxKYy1XVEJPUzV6MEtQusp=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, 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

```
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

```
data(states_25)  
## maybe str(states_25) ; plot(states_25) ...
```

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