Package 'erma'

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Title epigenomic road map adventures

Version 1.24.1

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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

Maintainer VJ Carey <stvjc@channing.harvard.edu>

License Artistic-2.0

LazyLoad yes

BiocViews Epigenetics, panomics, Annotation, ChIPSeq

VignetteBuilder knitr

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`erma-package` *epigenomic road map adventures*

Description

Software and data to support epigenomic road map adventures.

Details

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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 *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

```
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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