ermab-package

epigenomic road map adventures

Description

Software and data to support epigenomic road map adventures.

Details

The DESCRIPTION file:

Package: erma
Title: epigenomic road map adventures
Version: 0.6.0
Author: VJ Carey <stvjc@channing.harvard.edu>
Description: Software and data to support epigenomic road map adventures.
Suggests: rmarkdown, BiocStyle, knitr, GO.db, BiocParallel, png, DT, doParallel
Depends: R (>= 3.1), methods, Homo.sapiens
Imports: GenomicFiles (>= 1.5.2), rtracklayer, S4Vectors, BiocGenerics, GenomicRanges, SummarizedExperiment
Maintainer: VJ Carey <stvjc@channing.harvard.edu>
License: Artistic-2.0
LazyLoad: yes
BiocViews: epigenetics, panomics, annotation, chipseq
VignetteBuilder: knitr

Index of help topics:

ErmaSet-class Class "ErmaSet"
erma-package epigenomic road map adventures
genemodel create GRanges instance with model for a gene
mapmeta create a DataFrame instance providing metadata about the Epigenomics Roadmap
stateProfile create a ggplot2 visualization of chromatin states over genomic addresses for a family of cell types managed in an ErmaSet instance
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

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

Author(s)

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

Examples

data(farhSE)
ErmaSet-class

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.

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"
asstays: Object of class "Assays"
NAMES: Object of class "characterORNULL"
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)
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

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=0Am6F8xatrFDwdHU1UC13ZUxXYy1XVEJPUzV6METQO
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, ctsiz e = 10, 
shortCellType = TRUE, tsswidth=3 )
stateProf(ermaset, shortCellType=TRUE, ctsize=10)
csProfile(ermaset, symbol, upstream = 2000, downstream = 200, 
useShiny = FALSE, ctsize = 10, shortCellType = TRUE, 
tsswidth = 3)
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ermaset</td>
<td>instance of <code>ErmaSet-class</code></td>
</tr>
<tr>
<td>symbol</td>
<td>gene symbol resolvable in <code>Homo.sapiens</code></td>
</tr>
<tr>
<td>upstream, downstream</td>
<td>parameters passed to <code>promoters</code> to limit region to view</td>
</tr>
<tr>
<td>ctsize</td>
<td>font size for cell type labels</td>
</tr>
<tr>
<td>shortCellType</td>
<td>logical, if FALSE, full cell type labels are used, otherwise ad hoc abbreviations are used for facet labeling</td>
</tr>
<tr>
<td>useShiny</td>
<td>logical; if TRUE, shiny app is run permitting interactive selection of gene, and scope of view</td>
</tr>
<tr>
<td>tsswidth</td>
<td>width in base pairs of the base of a black rectangle used to depict location of transcription start site</td>
</tr>
</tbody>
</table>

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
states_25

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) ...
Index

*Topic **classes**
  ErmaSet-class, 3

*Topic **datasets**
  states_25, 6

*Topic **models**
  genemodel, 4
  mapmeta, 5
  stateProfile, 5

*Topic **package**
  erma-package, 2

  abbCIcols (ermab-package), 2
  abbCIstates (ermab-package), 2
  Annotated, 3

  cellTypes (ErmaSet-class), 3
  cellTypes, ErmaSet-method (ErmaSet-class), 3
  csProfile (stateProfile), 5

  DataFrame, 5
  erma (ermab-package), 2
  erma-package, 2
  ErmaSet-class, 3

  farhSE (ermab-package), 2

  genemodel, 4
  geneTxRange (genemodel), 4
  GRanges, 4

  Homo.sapiens, 6

  makeErmaSet (ErmaSet-class), 3
  map2range (genemodel), 4
  mapmeta, 5

  promoters, 6

  short_celltype (states_25), 6
  stateProf (stateProfile), 5
  stateProfile, 5
  states_25, 6

  Vector, 3