

# Package ‘erma’

April 11, 2018

**Title** epigenomic road map adventures

**Version** 0.10.1

**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, GenomicFiles (>= 1.5.2)

**Imports** rtracklayer, S4Vectors, BiocGenerics, GenomicRanges,  
SummarizedExperiment, ggplot2, Biobase, shiny, foreach,  
AnnotationDbi

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

**License** Artistic-2.0

**LazyLoad** yes

**BiocViews** epigenetics, panomics, annotation, chipseq

**VignetteBuilder** knitr

**NeedsCompilation** no

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 erma-package

 epigenomic road map adventures
 

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## Description

Software and data to support epigenomic road map adventures.

## Details

The DESCRIPTION file:

```

Package:      erma
Title:        epigenomic road map adventures
Version:      0.10.1
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, GenomicFiles (>= 1.5.2)
Imports:      rtracklayer, S4Vectors, BiocGenerics, GenomicRanges, SummarizedExperiment, ggplot2, Biobase, shif
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)

VJ Carey <stvjc@channing.harvard.edu>

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

## Examples

```
data(farhSE)
```

```

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

```

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ErmaSet-class	Class "ErmaSet"
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## 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" ~~
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)
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

genemodel revised Aug 10 2015. Direct operations on Homo.sapiens, much faster. geneTxRange added Aug 10 2015.

### Examples

```
genemodel("IL33")
geneTxRange("IL33")
map2range("17q12")
```

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mapmeta	<i>create a DataFrame instance providing metadata about the Epigenomics Roadmap</i>
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---

### Description

create a DataFrame instance providing metadata about the Epigenomics Roadmap

### Usage

```
mapmeta()
```

### Details

originates at <https://docs.google.com/spreadsheets/ccc?key=0Am6FxqAtrFDwdHU1UC13ZUxKYy1XVEJPUzV6MEtQ0usp=sharing#gid=15>

### Value

a [DataFrame](#) instance that is wrapped to limit sprawl over columns when shown.

### Examples

```
mapmeta()
```

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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=FALSE, ctsize=10, iniSym="IL7R")
csProfile(ermaset, symbol, upstream = 2000, downstream = 200,
          useShiny = FALSE, ctsize = 10, shortCellType = TRUE,
          tsswidth = 3)
subsetByRanges(ermaset, range)
```

**Arguments**

ermaset	instance of <a href="#">ErmaSet-class</a>
symbol	gene symbol resolvable in <a href="#">Homo.sapiens</a>
iniSym	initial symbol for display, when using shiny app in stateProf
upstream, downstream	parameters passed to <a href="#">promoters</a> to limit region to view
ctsize	font size for cell type labels
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
range	instance of <a href="#">GRanges</a>

**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	<i>metadata on states of 25-state model of chromatin from ChromImpute, and on cell types in the epigenome road map of April 2015</i>
-----------	--

---

**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](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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