

# Package ‘erma’

April 15, 2020

**Title** epigenomic road map adventures

**Version** 1.2.0

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

**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

**git\_url** <https://git.bioconductor.org/packages/erma>

**git\_branch** RELEASE\_3\_10

**git\_last\_commit** eadfd0d

**git\_last\_commit\_date** 2019-10-29

**Date/Publication** 2020-04-14

## R topics documented:

erma-package . . . . .	2
ErmaSet-class . . . . .	2
genemodel . . . . .	3
mapmeta . . . . .	4
stateProfile . . . . .	5
states_25 . . . . .	6
<b>Index</b>	<b>7</b>

---

 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)

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
```

---

 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/spreadsheets/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 <a href="#">ErmaSet-class</a>
symbol	gene symbol resolvable in <a href="#">Homo.sapiens</a>
upstream, downstream	parameters passed to <a href="#">promoters</a> 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	<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) ...
```

# Index

## \*Topic **classes**

ErmaSet-class, 2

## \*Topic **datasets**

states\_25, 6

## \*Topic **models**

genemodel, 3

mapmeta, 4

stateProfile, 5

## \*Topic **package**

erma-package, 2

abbCIColors (erma-package), 2

abbCIstates (erma-package), 2

Annotated, 3

cellTypes (ErmaSet-class), 2

cellTypes, ErmaSet-method  
(ErmaSet-class), 2

csProfile (stateProfile), 5

DataFrame, 4

erma (erma-package), 2

erma-package, 2

ErmaSet-class, 2

farhSE (erma-package), 2

genemodel, 3

geneTxRange (genemodel), 3

GRanges, 4

Homo.sapiens, 5

makeErmaSet (ErmaSet-class), 2

map2range (genemodel), 3

mapmeta, 4

promoters, 5

short\_celltype (states\_25), 6

stateProf (stateProfile), 5

stateProfile, 5

states\_25, 6

subsetByRanges (ErmaSet-class), 2

Vector, 3