

# Package ‘erma’

April 15, 2024

**Title** epigenomic road map adventures

**Version** 1.18.0

**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\_18

**git\_last\_commit** bed2908

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.18

**Date/Publication** 2024-04-15

## 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 | <i>epigenomic road map adventures</i> |
|--------------|---------------------------------------|

---

### 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 | <i>Class "ErmaSet"</i> |
|---------------|------------------------|

---

### Description

Wrap a GenomicFiles instance representing roadmap bed files.

### Usage

```
makeErmaSet()
subsetByRanges( ermaset, range )
```

### Arguments

|         |  |
|---------|--|
| ermaset | an instance of <a href="#">ErmaSet-class</a> |
| range   | an instance of <a href="#">GRanges-class</a> |

## 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/spreadsheets/ccc?key=0Am6FxqAtrFDwdHU1UC13ZUxKYy1XVEJPUzV6MEtQOXc&usp=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

- \* **classes**
  - ErmaSet-class, 2
- \* **datasets**
  - states\_25, 6
- \* **models**
  - genemodel, 3
  - mapmeta, 4
  - stateProfile, 5
- \* **package**
  - erma-package, 2

abbCICols (erma-package), 2

abbCIstates (erma-package), 2

Annotated, 3

cellTypes (ErmaSet-class), 2

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

csProfile (stateProfile), 5

DataFrame, 5

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