

# Package ‘erma’

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**Title** epigenomic road map adventures

**Version** 1.24.1

**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

**PackageStatus** Deprecated

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| erma-package | <i>epigenomic road map adventures</i> |
|--------------|---------------------------------------|

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**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
```

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|               |                        |
|---------------|------------------------|
| 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()
```

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|           |                                                      |
|-----------|------------------------------------------------------|
| genemodel | <i>create GRanges instance with model for a gene</i> |
|-----------|------------------------------------------------------|

---

## 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/spreadsheet/ccc?key=0Am6FxqAtrFDwdHU1UC13ZUxKYy1XVEJPuzV6MEtQOXc&usp=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=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> |
|-----------|--------------------------------------------------------------------------------------------------------------------------------------|

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**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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