Package ‘ELMER.data’

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Title Data for the ELMER package

Version 2.37.0

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Description Supporting data for the ELMER package.
It includes:
- elmer.data.example.promoter: mae.promoter
- elmer.data.example: data
- EPIC.hg38.manifest
- EPIC.hg19.manifest
- hm450.hg38.manifest
- hm450.hg19.manifest
- hocomoco.table
- human.TF
- LUSC_meth_refined: Meth
- LUSC_RNA_refined: GeneExp
- Probes.motif.hg19.450K
- Probes.motif.hg19.EPIC
- Probes.motif.hg38.450K
- Probes.motif.hg38.EPIC
- TF.family
- TF.subfamily
- Human_genes__GRCh37_p13
- Human_genes__GRCh38_p12
- Human_genes__GRCh37_p13__tss
- Human_genes__GRCh38_p12__tss

License GPL-3

LazyData false

Depends R (>= 3.5.0)

Imports GenomicRanges

Suggests BiocStyle, knitr, dplyr, devtools, DT, rmarkdown

biocViews AssayDomainData, TechnologyData, OrganismData

VignetteBuilder knitr

RoxygenNote 6.1.1

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Contents

`data` *A MultiAssayExperiment containing DNA methylation data: 101 probes from platform 450K Gene Expression data: 1026 genes for 234 samples from TCGA-LUSC. This data is used in the examples of ELMER package*

Description

A MultiAssayExperiment containing DNA methylation data: 101 probes from platform 450K Gene Expression data: 1026 genes for 234 samples from TCGA-LUSC. This data is used in the examples of ELMER package

Usage

```
data
```

Format

A MultiAssayExperiment for 234 Samples (8 normal samples, 226 Primary solid tumor)

Examples

```
## Not run:
data("elmer.data.example")

## End(Not run)
```

`ELMER.data` *Data for ELMER package*

Description

ELMER is package using DNA methylation to identify enhancers, and correlates enhancer state with expression of nearby genes to identify one or more transcriptional targets. Transcription factor (TF) binding site analysis of enhancers is coupled with expression analysis of all TFs to infer upstream regulators. ELMER.data provide the necessary data for ELMER analysis:

- Probes.motif: motif occurences within -/+250bp of probe sites on HM450K/EPIC array aligned against hg19/hg38.
- DNA methylation platform manifest: from http://zwdzwd.github.io/InfiniumAnnotation
- TF.family TFs family from TFClass
- TF.subfamily TFs subfamily from TFClass

For more information how to create these objects please read the vignette of this package with the follwing command: `browseVignettes("ELMER.data")`

See Also

`EPIC.hg19.manifest`, `EPIC.hg38.manifest`, `hm450.hg19.manifest`, `hm450.hg38.manifest`, `Probes.motif.hg19.` `Probes.motif.hg38.450K`, `Probes.motif.hg38.EPIC`, `Probes.motif.hg19.EPIC`, `Human_genes__GRCh37_p13__ts` `Human_genes__GRCh37_p13`, `Human_genes__GRCh38_p12`, `Human_genes__GRCh38_p12__tss`, `TF.subfamily`, `TF.family`, and `hocomoco.table`

Examples

```
# Please see the datasets
```

`EPIC.hg19.manifest` *A GRanges containing hg19 annotation with suggested overall masking for EPIC platform*

Description

A GRanges containing hg19 annotation with suggested overall masking for EPIC platform

Usage

```
EPIC.hg19.manifest
```

Format

A GRanges with 866895 elements

Examples

```
## Not run:
data("EPIC.hg19.manifest")

## End(Not run)
```

`EPIC.hg38.manifest` *A GRanges containing hg38 annotation with suggested overall masking for EPIC platform*

Description

A GRanges containing hg38 annotation with suggested overall masking for EPIC platform

Usage

```
EPIC.hg38.manifest
```

Format

A GRanges with 866895 elements

Examples

```
## Not run:
data("EPIC.hg38.manifest")

## End(Not run)
```

`GeneExp` *A matrix containing gene expression data from TCGA Gene Expression data: 3842 genes This data is used in the examples of ELMER package*

Description

A matrix containing gene expression data from TCGA Gene Expression data: 3842 genes This data is used in the examples of ELMER package

Usage

```
GeneExp
```

Format

A gene expression matrix for 234 Samples and 3842 genes

`hm450.hg19.manifest` *A GRanges containing hg19 annotation with suggested overall masking for hm450 platform*

Description

A GRanges containing hg19 annotation with suggested overall masking for hm450 platform

Usage

```
hm450.hg19.manifest
```

Format

A GRanges with 485577 elements

Examples

```
## Not run:
 data("hm450.hg19.manifest")

## End(Not run)
```

`hm450.hg38.manifest` *A GRanges containing hg38 annotation with suggested overall masking for hm450 platform*

Description

A GRanges containing hg38 annotation with suggested overall masking for hm450 platform

Usage

```
hm450.hg38.manifest
```

Format

A GRanges with 485577 elements

Examples

```
## Not run:
data("hm450.hg38.manifest")

## End(Not run)
```

`hocomoco.table` *Table parsed from hocomoco v11*

Description

Table parsed from hocomoco v11

Usage

```
hocomoco.table
```

Format

A dataframe with 771 rows (motifs) and 20 columns

`human.TF` *Table parsed from Lambert, Samuel A., et al. "The human transcription factors." Cell 172.4 (2018): 650-665.*

Description

Table parsed from Lambert, Samuel A., et al. "The human transcription factors." Cell 172.4 (2018): 650-665.

Usage

```
human.TF
```

Format

A dataframe with 1639 rows (motifs) and 27 columns

`Human_genes__GRCh37_p13`
A matrix containing ENSEMBL hg19 gene metadata accessed using biomart This data is used if ensembl cannot be reached

---

Description

A matrix containing ENSEMBL hg19 gene metadata accessed using biomart This data is used if ensembl cannot be reached

Usage

```
Human_genes__GRCh37_p13
```

Format

A matrix with metadata for 60482 genes

`Human_genes__GRCh37_p13__tss`
A matrix containing ENSEMBL hg19 transcripts metadata accessed using biomart This data is used if ensembl cannot be reached

---

Description

A matrix containing ENSEMBL hg19 transcripts metadata accessed using biomart This data is used if ensembl cannot be reached

Usage

```
Human_genes__GRCh37_p13__tss
```

Format

A matrix with metadata for 196317 transcripts

`Human_genes__GRCh38_p12`

A matrix containing ENSEMBL hg38 gene metadata accessed using biomart This data is used if ensembl cannot be reached

---

Description

A matrix containing ENSEMBL hg38 gene metadata accessed using biomart This data is used if ensembl cannot be reached

Usage

```
Human_genes__GRCh38_p12
```

Format

A matrix with metadata for 58639 genes

`Human_genes__GRCh38_p12__tss`

A matrix containing ENSEMBL hg38 transcripts metadata accessed using biomart This data is used if ensembl cannot be reached

---

Description

A matrix containing ENSEMBL hg38 transcripts metadata accessed using biomart This data is used if ensembl cannot be reached

Usage

```
Human_genes__GRCh38_p12__tss
```

Format

A matrix with metadata for 208423 transcripts

`mae.promoter` *A MultiAssayExperiment containing DNA methylation data: 16 promoter probes from platform 450K Gene Expression data: 3808 genes for 234 samples from TCGA-LUSC. This data is used in the examples of ELMER package*

Description

A MultiAssayExperiment containing DNA methylation data: 16 promoter probes from platform 450K Gene Expression data: 3808 genes for 234 samples from TCGA-LUSC. This data is used in the examples of ELMER package

Usage

```
mae.promoter
```

Format

A MultiAssayExperiment for 234 Samples (8 normal samples, 226 Primary solid tumor)

Examples

```
## Not run:
data("elmer.data.example.promoter")

## End(Not run)
```

`Meth` *A matrix containing DNA methylation beta-values from TCGA DNA methylation data: 1728 probes This data is used in the examples of ELMER package*

Description

A matrix containing DNA methylation beta-values from TCGA DNA methylation data: 1728 probes This data is used in the examples of ELMER package

Usage

```
Meth
```

Format

A MultiAssayExperiment for 268 Samples and 1728 probes

`Probes.motif.hg19.450K` *A matrix with 1 if the probe (row) has a motif (column)*

Description

It was generated using HOMER with a p-value < 1e-4 to scan a +/- 250bp region around each probe using HOmo sapiens COmprehensive MOdel COllection [http://hocomoco.autosome.ru/](HOCOMOCO) v10 position weight matrices (PWMs). HOCOMOCO offers 640 PMWs each has a quality rating from A to D where A represents motifs with the highest confidence, and D motifs only weakly describe the pattern with a limited applications for quantitative analyses. By default only quality A and B will be used for the Motif enrichment analysis, but the minimun quality score can be selected by the user. (Addtional information [http://hocomoco.autosome.ru/help](Source) [http://nar.oxfordjournals.org/content/44/D
information)). The DNA methylation information was retrieved from: http://zwdzwd.github.io/InfiniumAnnotation For more information check the vignette.

Usage

```
Probes.motif.hg19.450K
```

Format

A matrix with 466007 rows and 640 columns

Examples

```
## Not run:
data("Probes.motif.hg19.450K")

## End(Not run)
```

`Probes.motif.hg19.EPIC` *A matrix with 1 if the probe (row) has a motif (column)*

Description

It was generated using HOMER with a p-value < 1e-4 to scan a +/- 250bp region around each probe using HOmo sapiens COmprehensive MOdel COllection [http://hocomoco.autosome.ru/](HOCOMOCO) v10 position weight matrices (PWMs). HOCOMOCO offers 640 PMWs each has a quality rating from A to D where A represents motifs with the highest confidence, and D motifs only weakly describe the pattern with a limited applications for quantitative analyses. By default only quality A and B will be used for the Motif enrichment analysis, but the minimun quality score can be seleected by the user. (Addtional information [http://hocomoco.autosome.ru/help](Source) [http://nar.oxfordjournals.org/content/44/D
information)). The DNA methylation information was retrieved from: http://zwdzwd.github.io/InfiniumAnnotation For more information check the vignette.

Usage

```
Probes.motif.hg19.EPIC
```

Format

A matrix with 838881 rows and 640 columns

Examples

```
## Not run:
 data("Probes.motif.hg19.EPIC")

## End(Not run)
```

`Probes.motif.hg38.450K`

A matrix with 1 if the probe (row) has a motif (column)

Description

It was generated using HOMER with a p-value < 1e-4 to scan a +/- 250bp region around each probe using HOmo sapiens COmprehensive MOdel COllection [http://hocomoco.autosome.ru/](HOCOMOCO) v10 position weight matrices (PWMs). HOCOMOCO offers 640 PMWs each has a quality rating from A to D where A represents motifs with the highest confidence, and D motifs only weakly describe the pattern with a limited applications for quantitative analyses. By default only quality A and B will be used for the Motif enrichment analysis, but the minimun quality score can be selected by the user. (Addtional information [http://hocomoco.autosome.ru/help](Source) [http://nar.oxfordjournals.org/content/44/D information)). The DNA methylation information was retrieved from: http://zwdzwd.github.io/InfiniumAnnotation For more information check the vignette.

Usage

```
Probes.motif.hg38.450K
```

Format

A matrix with 466007 rows and 640 columns

Examples

```
## Not run:
data("Probes.motif.hg38.450K")

## End(Not run)
```

`Probes.motif.hg38.EPIC` *A matrix with 1 if the probe (row) has a motif (column)*

Description

It was generated using HOMER with a p-value < 1e-4 to scan a +/- 250bp region around each probe using HOmo sapiens COmprehensive MOdel COllection [http://hocomoco.autosome.ru/](HOCOMOCO) v10 position weight matrices (PWMs). HOCOMOCO offers 640 PMWs each has a quality rating from A to D where A represents motifs with the highest confidence, and D motifs only weakly describe the pattern with a limited applications for quantitative analyses. By default only quality A and B will be used for the Motif enrichment analysis, but the minimun quality score can be seleected by the user. (Addtional information [http://hocomoco.autosome.ru/help](Source) [http://nar.oxfordjournals.org/content/44/D information)). The DNA methylation information was retrieved from: http://zwdzwd.github.io/InfiniumAnnotation For more information check the vignette.

Usage

```
Probes.motif.hg38.EPIC
```

Format

A matrix with 838881 rows and 640 columns

Examples

```
## Not run:
  data("Probes.motif.hg38.EPIC")

## End(Not run)
```

`TF.family` *A list of 641 motifs with TF families (with similar bidings) from TFClass Created with the following function from ELMER pacakge TF.family <- createMotifRelevantTfs()*

Description

A list of 641 motifs with TF families (with similar bidings) from TFClass Created with the following function from ELMER pacakge TF.family <- createMotifRelevantTfs()

Usage

```
TF.family
```

Format

A list of 641 motifs with TF families (with similar bidings)

`TF.subfamily` *A list of 641 motifs with TF subfamilies (with similar bidings) from TFClass Created with the following function from ELMER pacakge TF.family <- createMotifRelevantTfs("subfamily")*

Description

A list of 641 motifs with TF subfamilies (with similar bidings) from TFClass Created with the following function from ELMER pacakge TF.family <- createMotifRelevantTfs("subfamily")

Usage

```
TF.subfamily
```

Format

A list of 641 motifs with TF subfamilies (with similar bidings)

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