Package 'ELMER.data'

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Title Data for the ELMER package

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Description Supporting data for the ELMER package. It includes
Union.TSS, Union.enhancer, Probe.motif, human.TF and
motif.relavent.TFs.

License GPL-3

LazyData true

Depends R (>= 3.2.0)

Imports GenomicRanges

Suggests BiocStyle, knitr

biocViews AssayDomainData

VignetteBuilder knitr

NeedsCompilation no

R topics documented:

Combined.TSS   *Human TSS regions consist of TSS from hg19 UCSC gene and GEN-
                             CODE V15*

Description

This data set contains all TSS from hg19 UCSC gene annotation and hg19 GENCODE V15. This
is used for identification of distal elements.

1

Usage

```
data("Combined.TSS")
```

Format

A GRanges object contains coordinates of combined TSS.

Value

A GRanges object contains coordinates of combined TSS.

Source

GENCODE : `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_15/gencode.v15.annotation.gtf.gz`

References

Yao L, Shen H, Laird PW, Farnham PJ,Berman BP: Inferring Regulatory Element Landscapes and Transcription Factor Networks from Cancer Methylomes. in revision of Genome Biology

Examples

```
data("Combined.TSS")
Combined.TSS
```

---

human.TF *All human transcription factors*

Description

A data frame contains symbols and gene ids for 1982 human trancription factors. This data is used for get.TFs function in **ELMER**.

Usage

```
data("human.TF")
```

Format

A data frame contains symbols and gene ids for 1982 human transcription factors

Value

A data frame contains symbols and gene ids for 1982 human transcription factors

Source

Ravasi T, Suzuki H, Cannistraci CV, Katayama S, Bajic VB, Tan K, Akalin A, Schmeier S, Kanamori-Katayama M, Bertin N, et al: An atlas of combinatorial transcriptional regulation in mouse and man. Cell 2010, 140:744-752.

References

1. Ravasi T, Suzuki H, Cannistraci CV, Katayama S, Bajic VB, Tan K, Akalin A, Schmeier S, Kanamori-Katayama M, Bertin N, et al: An atlas of combinatorial transcriptional regulation in mouse and man. Cell 2010, 140:744-752.

2. Yao L, Shen H, Laird PW, Farnham PJ,Berman BP: Inferring Regulatory Element Landscapes and Transcription Factor Networks from Cancer Methylomes. in revision of Genome Biology

Examples

```
data("human.TF")
dim(human.TF)
head(human.TF)
```

---

motif.relavent.TFs *TFs may recognize the same motif.*

Description

The transcription factor from the same family may recognize the similar motif. We collect the TFs that recognize a similar motif for each motif.

Usage

```
data("motif.relavent.TFs")
```

Format

A list with names (motif) and contents (TF which recognize a similar motif) for each list.

Value

A list with names (motif) and contents (TF which recognize a similar motif) for each list.

References

Yao L, Shen H, Laird PW, Farnham PJ,Berman BP: Inferring Regulatory Element Landscapes and Transcription Factor Networks from Cancer Methylomes. in revision of Genome Biology

Examples

```
data("motif.relavent.TFs")
str(motif.relavent.TFs)
```

Probes.motif   *Motif occurences within -/+100bp of probe sites on HM450K array.*

Description

FIMO was used with a p-value < 0.0001 to scan a +/- 100bp region around each probe using Factor-book motif position weight matrices (PWMs) and Jasper core human motif PWMs generated from the R package MotifDb.This data set is used in get.enriched.motif function in **ELMER**

Usage

```
data("Probes.motif")
```

Format

A matrix with 485512 row and 91 column. Each row is each probe regions and each column is motif from Factorbook and Jasper. The value 1 indicates the occurrence of a motif in a particular probe and 0 means no occurrence.

Value

A matrix with 485512 row and 91 column. Each row is each probe regions and each column is motif from Factorbook and Jasper. The value 1 indicates the occurrence of a motif in a particular probe and 0 means no occurrence.

References

1. Wang J, Zhuang J, Iyer S, Lin XY, Greven MC, Kim BH, Moore J, Pierce BG, Dong X, Virgil D, et al: Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. Nucleic Acids Res 2013, 41:D171-176. 2. Grant CE, Bailey TL, Noble WS: FIMO: scanning for occurrences of a given motif. Bioinformatics 2011, 27:1017-1018. 3. Wang J, Zhuang J, Iyer S, Lin X, Whitfield TW, Greven MC, Pierce BG, Dong X, Kundaje A, Cheng Y, et al: Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. Genome Res 2012, 22:1798-1812. 4. Shannon P: MotifDb: An annotated collection of Protein-DNA binding sequence motifs. Bioconductor 2014, R package version 1.8.0. 5. Yao L, Shen H, Laird PW, Farnham PJ,Berman BP: Inferring Regulatory Element Landscapes and Transcription Factor Networks from Cancer Methylomes. in revision of Genome Biology

Examples

```
data("Probes.motif")
dim(Probes.motif)
str(Probes.motif)
```

| Union.enhancer | *A comprehensive list of genomic strong enhancers* |

Description

Human comprehensive genomic enhancer set came from a combination of enhancers from the Roadmap Epigenomics Mapping Consortium (REMC) and the Encyclopedia of DNA Elements (ENCODE) Project, in which enhancers were identified using ChromHMM for 98 tissues or cell lines. We used the union of genomic elements labeled as EnhG1, EnhG2, EnhA1 or EnhA2 (representing intergenic and intragenic active enhancers) in any of the 98 cell types, resulting in a total of 389,967 non-overlapping enhancer regions. FANTOM5 enhancers (43,011) identified by eRNAs for 400 distinct cell types were added to this list.

Usage

```
data("Union.enhancer")
```

Format

A GRanges object contains coordinates of this human comprehensive genomic enhancer set.

Value

A GRanges object contains coordinates of this human comprehensive genomic enhancer set.

Source

REMC ChromHMM : http://egg2.wustl.edu/roadmap/data/byFileType/chromhmmSegmentations/ChmmModels/core_K27ac/jointModel/final FANTOM5 eRNA : http://enhancer.binf.ku.dk/Welcome.html

References

1. RoadmapEpigenomicsConsortium: Integrative analysis of 111 reference human epigenomes. Nature 2015, 19:317-330. 2. Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B, Milosavljevic A, Meissner A, Kellis M, Marra MA, Beaudet AL, Ecker JR, et al: The NIH Roadmap Epigenomics Mapping Consortium. Nat Biotechnol 2010, 28:1045-1048. 3. ENCODE_Project_Consortium: An integrated encyclopedia of DNA elements in the human genome. Nature 2012, 489:57-74. 4. Andersson R, Gebhard C, Miguel-Escalada I, Hoof I, Bornholdt J, Boyd M, Chen Y, Zhao X, Schmidl C, Suzuki T, et al: An atlas of active enhancers across human cell types and tissues. Nature 2014, 507:455-461. 5. Yao L, Shen H, Laird PW, Farnham PJ,Berman BP: Inferring Regulatory Element Landscapes and Transcription Factor Networks from Cancer Methylomes. in revision of Genome Biology

Examples

```
data("Union.enhancer")
Union.enhancer
```

Index