

Package ‘ELMER.data’

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Title Data for the ELMER package

Version 2.19.1

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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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git_last_commit_date 2021-11-21

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ELMER.data	<i>Data for ELMER package</i>
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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 occurrences within ± 250 bp 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 following command: `browseVignettes("ELMER.data")`

See Also

[EPIC.hg19.manifest](#), [EPIC.hg38.manifest](#), [hm450.hg19.manifest](#), [hm450.hg38.manifest](#), [Probes.motif.hg19.450K](#), [Probes.motif.hg38.450K](#), [Probes.motif.hg38.EPIC](#), [Probes.motif.hg19.EPIC](#), [Human_genes__GRCh37_p13__tss](#), [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
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