Package ‘dominatRData’

January 22, 2026

Type Package

Title Datasets for R Package dominatR

Version 0.99.1

Description dominatRData is a data package useful for showcasing dominatR examples. dominatR is an R package for quantifying and visualizing feature dominance in datasets. dominatR makes use of entropy-based triangular projections and compositional comparison metrics.

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Encoding UTF-8

biocViews ExperimentData, ChIPSeqData, Tissue, PackageTypeData

LazyData false

URL https://github.com/VanBortleLab/dominatRData

BugReports https://github.com/VanBortleLab/dominatRData/issues

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Depends R (>= 4.5.0)

Suggests knitr, rmarkdown

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/dominatRData

git_branch devel

git_last_commit eca9c4c

git_last_commit_date 2025-10-22

Repository Bioconductor 3.23

Date/Publication 2026-01-22

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`atac_tissue_counts` *ATAC-Seq rawcounts for POL3 Genes Dataframe*

Description

A list of tissues and the corresponding counts for RNA POL3 genes for each of them.

Usage

```
data('atac_tissue_counts')
```

Format

A dataframe with 9817 rows and 26 variables:

core_type Category for genes based on their expression across tissues

Chr Chromosome where the RNA of interest is located

Start Gene start coordinate

End Gene end coordinate

Gene Gene name

Index Unique RNA Sequence identifier - Can be retrieved from RNA Central

Type Type of RNA POL3 Transcript

Tissue Remaining columns contain the name of different assessed tissues

Source

Created by The VanBortle lab at UIUC to serve as an example

References

Simon Lizarazo et al., 2025 bioRxiv Preprint

`atac_tissue_score` *ATAC-Seq Score for POL3 Genes Dataframe*

Description

A list of tissues and the corresponding counts for RNA POL3 genes for each of them. Values represent a binary call on significance for accessibility. If the value is 1 the gene is accessible in the respective tissue.

Usage

```
data('atac_tissue_score')
```

Format

A dataframe with 9817 rows and 23 variables:

core_type Category for genes based on their expression across tissues

Chr Chromosome where the RNA of interest is located

Start Gene start coordinate

End Gene end coordinate

Gene Gene name

Index Unique RNA Sequence identifier - Can be retrieved from RNA Central

Type Type of RNA POL3 Transcript

Tissue Remaining columns contain the name of different assessed tissues

Source

Created by The VanBortle lab at UIUC to serve as an example

References

Simon Lizarazo et al., 2025 bioRxiv Preprint

`rnapol_counts` *RNA Polymerase raw counts dataframe*

Description

A subset of data obtained from CHIP-Seq Data for RNA Polymerase I, II and III

Usage

`data('rnapol_counts')`

Format

A dataframe with 1061 rows and 7 variables:

Chr Chromosome where the gene is located

Start Gene start coordinate

Stop Gene stop coordinate

RNA_Type Type of transcript

pol1 Raw counts for RNA Polymerase I Chip-Seq

pol2 Raw counts for RNA Polymerase II Chip-Seq

pol3 Raw counts for RNA Polymerase III Chip-Seq

Source

Created by The VanBortle lab at UIUC to serve as an example

References

Rajendra K C et al., 2024 Molecular Cell

`rnapol_score` *RNA Polymerase score dataframe*

Description

A subset of data obtained from CHIP-Seq Data for RNA Polymerase I, II and III. Values are represented as the -log10(p-value)

Usage

`data('rnapol_score')`

Format

A dataframe with 1061 rows and 7 variables:

Chr	Chromosome where the gene is located
Start	Gene start coordinate
Stop	Gene stop coordinate
RNA_Type	Type of transcript
pol1	Score for RNA Polymerase I Chip-Seq
pol2	Score for RNA Polymerase II Chip-Seq
pol3	Score for RNA Polymerase III Chip-Seq

Source

Created by The VanBortle lab at UIUC to serve as an example

References

Rajendra K C et al., 2024 Molecular Cell

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