

rTRMui: a shiny user interface for the identification of transcriptional regulatory modules

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1 Introduction

To install rTRMui you need to have installed rTRM and shiny. To use rTRMui load the library and then just run `runTRM()` from the R prompt:

```
> library(rTRMui)
> runTRM()
```

This will open a web browser and show the rTRMui home page (Figure 1). Instructions on how to use rTRMui are available in the *Help* tab from the rTRMui server. Example datasets can be downloaded from the home page and used with the *Tutorial*.

2 System information

```
> sessionInfo()
```

```
R version 4.4.1 (2024-06-14 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows Server 2022 x64 (build 20348)
```

```
Matrix products: default
```

```
locale:
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8
```



Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

time zone: America/New_York

tzcode source: internal

attached base packages:

[1] stats graphics grDevices utils datasets methods base

other attached packages:

[1] rTRMui_1.43.0

loaded via a namespace (and not attached):

[1] KEGGREST_1.45.1 SummarizedExperiment_1.35.4
 [3] rjson_0.2.23 lattice_0.22-6
 [5] Biobase_2.65.1 vctrs_0.6.5
 [7] tools_4.4.1 bitops_1.0-9
 [9] stats4_4.4.1 curl_5.2.3
 [11] parallel_4.4.1 AnnotationDbi_1.67.0
 [13] RSQLite_2.3.7 MotifDb_1.47.0
 [15] blob_1.2.4 pkgconfig_2.0.3

[17] Matrix_1.7-1	data.table_1.16.2
[19] S4Vectors_0.43.2	lifecycle_1.0.4
[21] GenomeInfoDbData_1.2.13	rTRM_1.43.0
[23] compiler_4.4.1	Rsamtools_2.21.2
[25] Biostrings_2.73.2	codetools_0.2-20
[27] httpuv_1.6.15	GenomeInfoDb_1.41.2
[29] htmltools_0.5.8.1	RCurl_1.98-1.16
[31] yaml_2.3.10	later_1.3.2
[33] crayon_1.5.3	BiocParallel_1.39.0
[35] DelayedArray_0.31.14	cachem_1.1.0
[37] org.Hs.eg.db_3.20.0	abind_1.4-8
[39] mime_0.12	digest_0.6.37
[41] restfulr_0.0.15	grid_4.4.1
[43] fastmap_1.2.0	SparseArray_1.5.45
[45] cli_3.6.3	magrittr_2.0.3
[47] S4Arrays_1.5.11	XML_3.99-0.17
[49] UCSC.utils_1.1.0	promises_1.3.0
[51] bit64_4.5.2	org.Mm.eg.db_3.20.0
[53] XVector_0.45.0	httr_1.4.7
[55] matrixStats_1.4.1	igraph_2.1.1
[57] bit_4.5.0	png_0.1-8
[59] memoise_2.0.1	shiny_1.9.1
[61] GenomicRanges_1.57.2	IRanges_2.39.2
[63] BiocIO_1.15.2	rtracklayer_1.65.0
[65] rlang_1.1.4	Rcpp_1.0.13
[67] xtable_1.8-4	DBI_1.2.3
[69] BiocGenerics_0.51.3	splitstackshape_1.4.8
[71] jsonlite_1.8.9	R6_2.5.1
[73] MatrixGenerics_1.17.0	GenomicAlignments_1.41.0
[75] zlibbioc_1.51.2	