

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

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June 4, 2025

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 4.5.0 (2025-04-11 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows Server 2022 x64 (build 20348)
```

```
Matrix products: default
  LAPACK version 3.12.1
```

```
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_1.47.0
```

```
loaded via a namespace (and not attached):
[1] KEGGREST_1.49.0      SummarizedExperiment_1.39.0
[3] rjson_0.2.23         lattice_0.22-7
[5] Biobase_2.69.0       vctrs_0.6.5
[7] tools_4.5.0          bitops_1.0-9
[9] generics_0.1.4       stats4_4.5.0
[11] curl_6.2.3           parallel_4.5.0
[13] AnnotationDbi_1.71.0 RSQLite_2.4.0
[15] MotifDb_1.51.0       blob_1.2.4
```

[17] pkgconfig_2.0.3	Matrix_1.7-3
[19] data.table_1.17.4	S4Vectors_0.47.0
[21] lifecycle_1.0.4	rTRM_1.47.0
[23] compiler_4.5.0	Rsamtools_2.25.0
[25] Biostrings_2.77.1	codetools_0.2-20
[27] httpuv_1.6.16	GenomeInfoDb_1.45.4
[29] htmltools_0.5.8.1	RCurl_1.98-1.17
[31] yaml_2.3.10	later_1.4.2
[33] crayon_1.5.3	BiocParallel_1.43.3
[35] DelayedArray_0.35.1	cachem_1.1.0
[37] org.Hs.eg.db_3.21.0	abind_1.4-8
[39] mime_0.13	digest_0.6.37
[41] restfulr_0.0.15	grid_4.5.0
[43] fastmap_1.2.0	SparseArray_1.9.0
[45] cli_3.6.5	magrittr_2.0.3
[47] S4Arrays_1.9.1	XML_3.99-0.18
[49] UCSC.utils_1.5.0	promises_1.3.3
[51] bit64_4.6.0-1	org.Mm.eg.db_3.21.0
[53] XVector_0.49.0	httr_1.4.7
[55] matrixStats_1.5.0	igraph_2.1.4
[57] bit_4.6.0	png_0.1-8
[59] memoise_2.0.1	shiny_1.10.0
[61] GenomicRanges_1.61.0	IRanges_2.43.0
[63] BiocIO_1.19.0	rtracklayer_1.69.0
[65] rlang_1.1.6	Rcpp_1.0.14
[67] xtable_1.8-4	DBI_1.2.3
[69] BiocGenerics_0.55.0	splitstackshape_1.4.8
[71] jsonlite_2.0.0	R6_2.6.1
[73] MatrixGenerics_1.21.0	GenomicAlignments_1.45.0