

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 Under development (unstable) (2025-11-04 r88984)
Platform: aarch64-apple-darwin20
Running under: macOS Ventura 13.7.8
```

```
Matrix products: default
```

```
BLAS: /System/Library/Frameworks/Accelerate.framework/Versions/A/Frameworks/vecLib.framework/Versions/A/Libraries/libBLAS.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.6-arm64/Resources/lib/libRlapack.dylib;
```

```
locale:
```

```
[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
time zone: America/New_York
```

```
tzcode source: internal
```



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

attached base packages:

```
[1] stats      graphics  grDevices  utils      datasets  methods   base
```

other attached packages:

```
[1] rTRMui_1.49.0
```

loaded via a namespace (and not attached):

```
[1] KEGGREST_1.51.0      SummarizedExperiment_1.41.0
[3] rjson_0.2.23         Biobase_2.71.0
[5] lattice_0.22-7       vctrs_0.6.5
[7] tools_4.6.0          bitops_1.0-9
[9] generics_0.1.4       stats4_4.6.0
[11] curl_7.0.0           parallel_4.6.0
[13] AnnotationDbi_1.73.0 RSQLite_2.4.4
[15] MotifDb_1.53.0       blob_1.2.4
[17] pkgconfig_2.0.3      Matrix_1.7-4
[19] data.table_1.17.8    cigarillo_1.1.0
[21] S4Vectors_0.49.0     lifecycle_1.0.4
```

[23] rTRM_1.49.0	compiler_4.6.0
[25] Rsamtools_2.27.0	Biostrings_2.79.2
[27] Seqinfo_1.1.0	codetools_0.2-20
[29] httpuv_1.6.16	htmltools_0.5.8.1
[31] RCurl_1.98-1.17	yaml_2.3.10
[33] later_1.4.4	crayon_1.5.3
[35] BiocParallel_1.45.0	DelayedArray_0.37.0
[37] cachem_1.1.0	org.Hs.eg.db_3.22.0
[39] abind_1.4-8	mime_0.13
[41] digest_0.6.38	restfulr_0.0.16
[43] fastmap_1.2.0	grid_4.6.0
[45] SparseArray_1.11.1	cli_3.6.5
[47] magrittr_2.0.4	S4Arrays_1.11.0
[49] XML_3.99-0.20	promises_1.5.0
[51] bit64_4.6.0-1	org.Mm.eg.db_3.22.0
[53] XVector_0.51.0	httr_1.4.7
[55] matrixStats_1.5.0	igraph_2.2.1
[57] bit_4.6.0	otel_0.2.0
[59] png_0.1-8	memoise_2.0.1
[61] shiny_1.11.1	GenomicRanges_1.63.0
[63] IRanges_2.45.0	BiocIO_1.21.0
[65] rtracklayer_1.71.0	rlang_1.1.6
[67] Rcpp_1.1.0	xtable_1.8-4
[69] DBI_1.2.3	BiocGenerics_0.57.0
[71] splitstackshape_1.4.8	R6_2.6.1
[73] MatrixGenerics_1.23.0	GenomicAlignments_1.47.0