

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 4.6.0 Patched (2026-04-24 r89963)
Platform: aarch64-apple-darwin23
Running under: macOS Tahoe 26.3.1
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.6/Resources/lib/libRblas.0.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/4.6/Resources/lib/libRlapack.dylib; LAPACK
```

```
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_1.50.0
```

loaded via a namespace (and not attached):

```
[1] KEGGREST_1.52.0      SummarizedExperiment_1.42.0
[3] rjson_0.2.23         Biobase_2.72.0
[5] lattice_0.22-9       vctrs_0.7.3
[7] tools_4.6.0          bitops_1.0-9
[9] generics_0.1.4       stats4_4.6.0
[11] curl_7.1.0           parallel_4.6.0
[13] AnnotationDbi_1.74.0 RSQLite_2.4.6
[15] MotifDb_1.54.0       blob_1.3.0
[17] pkgconfig_2.0.3      Matrix_1.7-5
[19] data.table_1.18.2.1  cigarillo_1.2.0
[21] S4Vectors_0.50.0     lifecycle_1.0.5
```

[23]	rTRM_1.50.0	compiler_4.6.0
[25]	Rsamtools_2.28.0	Biostrings_2.80.0
[27]	Seqinfo_1.2.0	codetools_0.2-20
[29]	httpuv_1.6.17	htmltools_0.5.9
[31]	RCurl_1.98-1.18	yaml_2.3.12
[33]	later_1.4.8	crayon_1.5.3
[35]	BiocParallel_1.46.0	DelayedArray_0.38.0
[37]	cachem_1.1.0	org.Hs.eg.db_3.23.1
[39]	abind_1.4-8	mime_0.13
[41]	digest_0.6.39	restfulr_0.0.16
[43]	fastmap_1.2.0	grid_4.6.0
[45]	SparseArray_1.12.0	cli_3.6.6
[47]	magrittr_2.0.5	S4Arrays_1.12.0
[49]	XML_3.99-0.23	promises_1.5.0
[51]	bit64_4.8.0	org.Mm.eg.db_3.23.0
[53]	XVector_0.52.0	httr_1.4.8
[55]	matrixStats_1.5.0	igraph_2.3.0
[57]	bit_4.6.0	otel_0.2.0
[59]	png_0.1-9	memoise_2.0.1
[61]	shiny_1.13.0	GenomicRanges_1.64.0
[63]	IRanges_2.46.0	BiocIO_1.22.0
[65]	rtracklayer_1.72.0	rlang_1.2.0
[67]	Rcpp_1.1.1-1.1	xtable_1.8-8
[69]	DBI_1.3.0	BiocGenerics_0.58.0
[71]	splitstackshape_1.4.8.1	R6_2.6.1
[73]	MatrixGenerics_1.24.0	GenomicAlignments_1.48.0