

# 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 4.5.0 RC (2025-04-04 r88126)
Platform: x86_64-apple-darwin20
Running under: macOS Monterey 12.7.6
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.5-x86_64/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.5-x86_64/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_1.46.0
```

loaded via a namespace (and not attached):

```
[1] KEGGREST_1.48.0      SummarizedExperiment_1.38.0
[3] rjson_0.2.23         lattice_0.22-7
[5] Biobase_2.68.0       vctrs_0.6.5
[7] tools_4.5.0          bitops_1.0-9
[9] generics_0.1.3       stats4_4.5.0
[11] curl_6.2.2           parallel_4.5.0
[13] AnnotationDbi_1.70.0 RSQLite_2.3.9
[15] MotifDb_1.50.0       blob_1.2.4
[17] pkgconfig_2.0.3      Matrix_1.7-3
[19] data.table_1.17.0    S4Vectors_0.46.0
[21] lifecycle_1.0.4      GenomeInfoDbData_1.2.14
```

[23]	rTRM_1.46.0	compiler_4.5.0
[25]	Rsamtools_2.24.0	Biostings_2.76.0
[27]	codetools_0.2-20	httpuv_1.6.15
[29]	GenomeInfoDb_1.44.0	htmltools_0.5.8.1
[31]	RCurl_1.98-1.17	yaml_2.3.10
[33]	later_1.4.2	crayon_1.5.3
[35]	BiocParallel_1.42.0	DelayedArray_0.34.0
[37]	cachem_1.1.0	org.Hs.eg.db_3.21.0
[39]	abind_1.4-8	mime_0.13
[41]	digest_0.6.37	restfulr_0.0.15
[43]	grid_4.5.0	fastmap_1.2.0
[45]	SparseArray_1.8.0	cli_3.6.4
[47]	magrittr_2.0.3	S4Arrays_1.8.0
[49]	XML_3.99-0.18	UCSC.utils_1.4.0
[51]	promises_1.3.2	bit64_4.6.0-1
[53]	org.Mm.eg.db_3.21.0	XVector_0.48.0
[55]	httr_1.4.7	matrixStats_1.5.0
[57]	igraph_2.1.4	bit_4.6.0
[59]	png_0.1-8	memoise_2.0.1
[61]	shiny_1.10.0	GenomicRanges_1.60.0
[63]	IRanges_2.42.0	BiocIO_1.18.0
[65]	rtracklayer_1.68.0	rlang_1.1.6
[67]	Rcpp_1.0.14	xtable_1.8-4
[69]	DBI_1.2.3	BiocGenerics_0.54.0
[71]	splitstackshape_1.4.8	jsonlite_2.0.0
[73]	R6_2.6.1	MatrixGenerics_1.20.0
[75]	GenomicAlignments_1.44.0	