

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

Diego Diez

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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 (2026-05-01 r89994)
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_1.51.0
```

loaded via a namespace (and not attached):

```
[1] KEGGREST_1.53.0           SummarizedExperiment_1.43.0
[3] rjson_0.2.23              lattice_0.22-9
[5] Biobase_2.73.1            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_1.75.0      RSQLite_3.52.0
[15] MotifDb_1.55.0            blob_1.3.0
[17] pkgconfig_2.0.3           BiocBaseUtils_1.15.1
[19] Matrix_1.7-5              data.table_1.18.4
[21] cigarillo_1.3.0           S4Vectors_0.51.2
```

[23] lifecycle_1.0.5	rTRM_1.51.0
[25] compiler_4.6.0	Rsamtools_2.29.0
[27] Biostrings_2.81.1	Seqinfo_1.3.0
[29] codetools_0.2-20	httpuv_1.6.17
[31] htmltools_0.5.9	RCurl_1.98-1.18
[33] yaml_2.3.12	later_1.4.8
[35] crayon_1.5.3	BiocParallel_1.47.0
[37] DelayedArray_0.39.2	cachem_1.1.0
[39] org.Hs.eg.db_3.23.1	abind_1.4-8
[41] mime_0.13	digest_0.6.39
[43] restfulr_0.0.16	fastmap_1.2.0
[45] grid_4.6.0	SparseArray_1.13.2
[47] cli_3.6.6	magrittr_2.0.5
[49] S4Arrays_1.13.0	XML_3.99-0.23
[51] promises_1.5.0	bit64_4.8.0
[53] org.Mm.eg.db_3.23.0	XVector_0.53.0
[55] httr_1.4.8	matrixStats_1.5.0
[57] igraph_2.3.1	bit_4.6.0
[59] otel_0.2.0	png_0.1-9
[61] memoise_2.0.1	shiny_1.13.0
[63] GenomicRanges_1.65.0	IRanges_2.47.1
[65] BiocIO_1.23.3	rtracklayer_1.73.0
[67] rlang_1.2.0	Rcpp_1.1.1-1.1
[69] xtable_1.8-8	DBI_1.3.0
[71] BiocGenerics_0.59.2	splitstackshape_1.4.8.1
[73] R6_2.6.1	MatrixGenerics_1.25.0
[75] GenomicAlignments_1.49.0	