

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 4.5.2 (2025-10-31)
```

```
Platform: x86_64-pc-linux-gnu
```

```
Running under: Ubuntu 24.04.3 LTS
```

```
Matrix products: default
```

```
BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
```

```
LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-p-r0.3.26.so; LAPACK version
```

```
locale:
```

[1] LC_CTYPE=en_US.UTF-8	LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8	LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8	LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8	LC_NAME=C
[9] LC_ADDRESS=C	LC_TELEPHONE=C



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

```
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

```
time zone: Etc/UTC
```

```
tzcode source: system (glibc)
```

```
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_1.51.1      SummarizedExperiment_1.41.0
[3] rjson_0.2.23         xfun_0.55
[5] lattice_0.22-7       Biobase_2.71.0
[7] vctrs_0.6.5          tools_4.5.2
[9] bitops_1.0-9         generics_0.1.4
[11] stats4_4.5.2         curl_7.0.0
```

[13] parallel_4.5.2	AnnotationDbi_1.73.0
[15] RSQLite_2.4.5	MotifDb_1.51.0
[17] blob_1.2.4	pkgconfig_2.0.3
[19] Matrix_1.7-4	data.table_1.18.0
[21] cigarillo_1.1.0	S4Vectors_0.49.0
[23] lifecycle_1.0.5	rTRM_1.49.0
[25] compiler_4.5.2	Rsamtools_2.27.0
[27] Biostrings_2.79.4	Seqinfo_1.1.0
[29] codetools_0.2-20	httpuv_1.6.16
[31] htmltools_0.5.9	sys_3.4.3
[33] buildtools_1.0.0	RCurl_1.98-1.17
[35] yaml_2.3.12	later_1.4.5
[37] crayon_1.5.3	BiocParallel_1.45.0
[39] DelayedArray_0.37.0	cachem_1.1.0
[41] org.Hs.eg.db_3.22.0	abind_1.4-8
[43] mime_0.13	digest_0.6.39
[45] restfulr_0.0.16	maketools_1.3.2
[47] grid_4.5.2	fastmap_1.2.0
[49] SparseArray_1.11.10	cli_3.6.5
[51] magrittr_2.0.4	S4Arrays_1.11.1
[53] XML_3.99-0.20	promises_1.5.0
[55] bit64_4.6.0-1	org.Mm.eg.db_3.22.0
[57] XVector_0.51.0	httr_1.4.7
[59] matrixStats_1.5.0	igraph_2.2.1
[61] bit_4.6.0	otel_0.2.0
[63] png_0.1-8	memoise_2.0.1
[65] shiny_1.12.1	evaluate_1.0.5
[67] knitr_1.51	GenomicRanges_1.63.1
[69] IRanges_2.45.0	BiocIO_1.21.0
[71] rtracklayer_1.71.3	rlang_1.1.7
[73] Rcpp_1.1.0.8.2	xtable_1.8-4
[75] DBI_1.2.3	BiocGenerics_0.57.0
[77] splitstackshape_1.4.8	R6_2.6.1
[79] MatrixGenerics_1.23.0	GenomicAlignments_1.47.0