

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 4.5.1 Patched (2025-08-23 r88802)
```

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

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

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.22-bioc/R/lib/libRblas.so
```

```
LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.12.0 LAPACK version 3.12.0
```

```
locale:
```

[1] LC_CTYPE=en_US.UTF-8	LC_NUMERIC=C
[3] LC_TIME=en_GB	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: America/New_York
tzcode source: system (glibc)
```

```
attached base packages:
```

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

```
other attached packages:
```

```
[1] rTRMui_1.48.0
```

```
loaded via a namespace (and not attached):
```

```
[1] KEGGREST_1.50.0      SummarizedExperiment_1.40.0
[3] rjson_0.2.23         Biobase_2.70.0
[5] lattice_0.22-7       vctrs_0.6.5
[7] tools_4.5.1          bitops_1.0-9
[9] generics_0.1.4       stats4_4.5.1
[11] curl_7.0.0           parallel_4.5.1
```

[13] AnnotationDbi_1.72.0	RSQLite_2.4.3
[15] MotifDb_1.52.0	blob_1.2.4
[17] pkgconfig_2.0.3	Matrix_1.7-4
[19] data.table_1.17.8	cigarillo_1.0.0
[21] S4Vectors_0.48.0	lifecycle_1.0.4
[23] rTRM_1.48.0	compiler_4.5.1
[25] Rsamtools_2.26.0	Biostrings_2.78.0
[27] Seqinfo_1.0.0	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_1.44.0	DelayedArray_0.36.0
[37] cachem_1.1.0	org.Hs.eg.db_3.22.0
[39] abind_1.4-8	mime_0.13
[41] digest_0.6.37	restfulr_0.0.16
[43] fastmap_1.2.0	grid_4.5.1
[45] SparseArray_1.10.0	cli_3.6.5
[47] magrittr_2.0.4	S4Arrays_1.10.0
[49] XML_3.99-0.19	promises_1.4.0
[51] bit64_4.6.0-1	org.Mm.eg.db_3.22.0
[53] XVector_0.50.0	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_1.62.0
[63] IRanges_2.44.0	BiocIO_1.20.0
[65] rtracklayer_1.70.0	rlang_1.1.6
[67] Rcpp_1.1.0	xtable_1.8-4
[69] DBI_1.2.3	BiocGenerics_0.56.0
[71] splitstackshape_1.4.8	R6_2.6.1
[73] MatrixGenerics_1.22.0	GenomicAlignments_1.46.0