

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 RC (2026-04-17 r89917)
```

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

```
Running under: Ubuntu 24.04.4 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.23-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_1.50.0
```

```
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