

# 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 beta (2025-04-02 r88102)
```

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

```
Running under: Ubuntu 24.04.2 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_1.45.0
```

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

```
[1] KEGGREST_1.47.1      SummarizedExperiment_1.37.0
[3] rjson_0.2.23         lattice_0.22-7
[5] Biobase_2.67.0       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_1.69.1	RSQLite_2.3.9
[15] MotifDb_1.49.3	blob_1.2.4
[17] pkgconfig_2.0.3	Matrix_1.7-3
[19] data.table_1.17.0	S4Vectors_0.45.4
[21] lifecycle_1.0.4	GenomeInfoDbData_1.2.14
[23] rTRM_1.45.0	compiler_4.5.0
[25] Rsamtools_2.23.1	Biostrings_2.75.4
[27] codetools_0.2-20	httpuv_1.6.15
[29] GenomeInfoDb_1.43.4	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_1.41.5	DelayedArray_0.33.6
[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_1.7.7	cli_3.6.4
[47] magrittr_2.0.3	S4Arrays_1.7.3
[49] XML_3.99-0.18	UCSC.utils_1.3.1
[51] promises_1.3.2	bit64_4.6.0-1
[53] org.Mm.eg.db_3.21.0	XVector_0.47.2
[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_1.59.1
[63] IRanges_2.41.3	BiocIO_1.17.2
[65] rtracklayer_1.67.1	rlang_1.1.6
[67] Rcpp_1.0.14	xtable_1.8-4
[69] DBI_1.2.3	BiocGenerics_0.53.6
[71] splitstackshape_1.4.8	jsonlite_2.0.0
[73] R6_2.6.1	MatrixGenerics_1.19.1
[75] GenomicAlignments_1.43.0	