

# 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 4.3.0 RC (2023-04-13 r84257)
Platform: x86_64-apple-darwin20 (64-bit)
Running under: macOS Monterey 12.6.4
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.3-x86_64/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.3-x86_64/Resources/lib/libRlapack.dylib;
```

```
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_1.38.0
```

loaded via a namespace (and not attached):

```
[1] KEGGREST_1.40.0      SummarizedExperiment_1.30.1
[3] rjson_0.2.21         Biobase_2.60.0
[5] lattice_0.21-8       vctrs_0.6.2
[7] tools_4.3.0          bitops_1.0-7
[9] stats4_4.3.0         parallel_4.3.0
[11] AnnotationDbi_1.62.1 RSQLite_2.3.1
[13] MotifDb_1.42.0       blob_1.2.4
[15] pkgconfig_2.0.3      Matrix_1.5-4
[17] data.table_1.14.8    S4Vectors_0.38.1
[19] lifecycle_1.0.3      GenomeInfoDbData_1.2.10
[21] rTRM_1.38.0          compiler_4.3.0
```

[23]	Rsamtools_2.16.0	Biostrings_2.68.0
[25]	codetools_0.2-19	httpuv_1.6.11
[27]	GenomeInfoDb_1.36.0	htmltools_0.5.5
[29]	RCurl_1.98-1.12	yaml_2.3.7
[31]	later_1.3.1	crayon_1.5.2
[33]	ellipsis_0.3.2	BiocParallel_1.34.1
[35]	cachem_1.0.8	DelayedArray_0.26.2
[37]	org.Hs.eg.db_3.17.0	mime_0.12
[39]	digest_0.6.31	restfulr_0.0.15
[41]	fastmap_1.1.1	grid_4.3.0
[43]	cli_3.6.1	magrittr_2.0.3
[45]	S4Arrays_1.0.4	XML_3.99-0.14
[47]	promises_1.2.0.1	bit64_4.0.5
[49]	org.Mm.eg.db_3.17.0	XVector_0.40.0
[51]	httr_1.4.6	matrixStats_0.63.0
[53]	igraph_1.4.2	bit_4.0.5
[55]	png_0.1-8	memoise_2.0.1
[57]	shiny_1.7.4	GenomicRanges_1.52.0
[59]	IRanges_2.34.0	BiocIO_1.10.0
[61]	rtracklayer_1.60.0	rlang_1.1.1
[63]	Rcpp_1.0.10	xtable_1.8-4
[65]	DBI_1.1.3	BiocGenerics_0.46.0
[67]	splitstackshape_1.4.8	R6_2.5.1
[69]	MatrixGenerics_1.12.0	GenomicAlignments_1.36.0
[71]	zlibbioc_1.46.0	