

# 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 4.4.0 alpha (2024-03-27 r86216)
Platform: aarch64-apple-darwin20
Running under: macOS Ventura 13.6.5
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib;
```

```
locale:
```

```
[1] en_US.UTF-8/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_1.42.0
```

loaded via a namespace (and not attached):

```
[1] KEGGREST_1.44.0      SummarizedExperiment_1.34.0
[3] rjson_0.2.21         lattice_0.22-6
[5] Biobase_2.64.0       vctrs_0.6.5
[7] tools_4.4.0          bitops_1.0-7
[9] stats4_4.4.0         curl_5.2.1
[11] parallel_4.4.0       AnnotationDbi_1.66.0
[13] RSQLite_2.3.5        MotifDb_1.46.0
[15] blob_1.2.4           pkgconfig_2.0.3
[17] Matrix_1.7-0         data.table_1.15.4
[19] S4Vectors_0.42.0     lifecycle_1.0.4
[21] GenomeInfoDbData_1.2.12 rTRM_1.42.0
```

[23]	compiler_4.4.0	Rsamtools_2.20.0
[25]	Biostrings_2.72.0	codetools_0.2-19
[27]	httpuv_1.6.15	GenomeInfoDb_1.40.0
[29]	htmltools_0.5.8	RCurl_1.98-1.14
[31]	yaml_2.3.8	later_1.3.2
[33]	crayon_1.5.2	BiocParallel_1.38.0
[35]	DelayedArray_0.30.0	cachem_1.0.8
[37]	org.Hs.eg.db_3.19.0	abind_1.4-5
[39]	mime_0.12	digest_0.6.35
[41]	restfulr_0.0.15	grid_4.4.0
[43]	fastmap_1.1.1	SparseArray_1.4.0
[45]	cli_3.6.2	magrittr_2.0.3
[47]	S4Arrays_1.4.0	XML_3.99-0.16.1
[49]	UCSC.utils_1.0.0	promises_1.2.1
[51]	bit64_4.0.5	org.Mm.eg.db_3.19.0
[53]	XVector_0.44.0	httr_1.4.7
[55]	matrixStats_1.2.0	igraph_2.0.3
[57]	bit_4.0.5	png_0.1-8
[59]	memoise_2.0.1	shiny_1.8.1
[61]	GenomicRanges_1.56.0	IRanges_2.38.0
[63]	BiocIO_1.14.0	rtracklayer_1.64.0
[65]	rlang_1.1.3	Rcpp_1.0.12
[67]	xtable_1.8-4	DBI_1.2.2
[69]	BiocGenerics_0.50.0	splitstackshape_1.4.8
[71]	jsonlite_1.8.8	R6_2.5.1
[73]	MatrixGenerics_1.16.0	GenomicAlignments_1.40.0
[75]	zlibbioc_1.50.0	