

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 4.5.2 (2025-10-31)
```

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

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

```
Matrix products: default
```

```
BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
```

```
LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-p-r0.3.26.so; LAPACK version
```

```
locale:
```

[1] LC_CTYPE=en_US.UTF-8	LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8	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

[13]	parallel_4.5.2	AnnotationDbi_1.72.0
[15]	RSQLite_2.4.4	MotifDb_1.52.0
[17]	blob_1.2.4	pkgconfig_2.0.3
[19]	Matrix_1.7-4	data.table_1.17.8
[21]	cigarillo_1.0.0	S4Vectors_0.48.0
[23]	lifecycle_1.0.4	rTRM_1.48.0
[25]	compiler_4.5.2	Rsamtools_2.26.0
[27]	Biostrings_2.78.0	Seqinfo_1.0.0
[29]	codetools_0.2-20	httpuv_1.6.16
[31]	htmltools_0.5.8.1	sys_3.4.3
[33]	buildtools_1.0.0	RCurl_1.98-1.17
[35]	yaml_2.3.10	later_1.4.4
[37]	crayon_1.5.3	BiocParallel_1.44.0
[39]	DelayedArray_0.36.0	cachem_1.1.0
[41]	org.Hs.eg.db_3.22.0	abind_1.4-8
[43]	mime_0.13	digest_0.6.37
[45]	restfulr_0.0.16	maketools_1.3.2
[47]	grid_4.5.2	fastmap_1.2.0
[49]	SparseArray_1.10.1	cli_3.6.5
[51]	magrittr_2.0.4	S4Arrays_1.10.0
[53]	XML_3.99-0.20	promises_1.5.0
[55]	bit64_4.6.0-1	org.Mm.eg.db_3.22.0
[57]	XVector_0.50.0	httr_1.4.7
[59]	matrixStats_1.5.0	igraph_2.2.1
[61]	bit_4.6.0	otel_0.2.0
[63]	png_0.1-8	memoise_2.0.1
[65]	shiny_1.11.1	evaluate_1.0.5
[67]	knitr_1.50	GenomicRanges_1.62.0
[69]	IRanges_2.44.0	BiocIO_1.20.0
[71]	rtracklayer_1.70.0	rlang_1.1.6
[73]	Rcpp_1.1.0	xtable_1.8-4
[75]	DBI_1.2.3	BiocGenerics_0.56.0
[77]	splitstackshape_1.4.8	R6_2.6.1
[79]	MatrixGenerics_1.22.0	GenomicAlignments_1.46.0