

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 Under development (unstable) (2024-11-20 r87352)
```

```
Platform: aarch64-apple-darwin20
```

```
Running under: macOS Ventura 13.7.1
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.5-arm64/Resources/lib/libRblas.0.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/4.5-arm64/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_1.45.0
```

loaded via a namespace (and not attached):

```
[1] KEGGREST_1.47.0      SummarizedExperiment_1.37.0
[3] rjson_0.2.23         lattice_0.22-6
[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_6.0.1           parallel_4.5.0
[13] AnnotationDbi_1.69.0 RSQLite_2.3.8
[15] MotifDb_1.49.0       blob_1.2.4
[17] pkgconfig_2.0.3      Matrix_1.7-1
[19] data.table_1.16.2    S4Vectors_0.45.2
[21] lifecycle_1.0.4      GenomeInfoDbData_1.2.13
```

[23]	rTRM_1.45.0	compiler_4.5.0
[25]	Rsamtools_2.23.0	Biostrings_2.75.1
[27]	codetools_0.2-20	httpuv_1.6.15
[29]	GenomeInfoDb_1.43.1	htmltools_0.5.8.1
[31]	RCurl_1.98-1.16	yaml_2.3.10
[33]	later_1.3.2	crayon_1.5.3
[35]	BiocParallel_1.41.0	DelayedArray_0.33.2
[37]	cachem_1.1.0	org.Hs.eg.db_3.20.0
[39]	abind_1.4-8	mime_0.12
[41]	digest_0.6.37	restfulr_0.0.15
[43]	grid_4.5.0	fastmap_1.2.0
[45]	SparseArray_1.7.2	cli_3.6.3
[47]	magrittr_2.0.3	S4Arrays_1.7.1
[49]	XML_3.99-0.17	UCSC.utils_1.3.0
[51]	promises_1.3.0	bit64_4.5.2
[53]	org.Mm.eg.db_3.20.0	XVector_0.47.0
[55]	httr_1.4.7	matrixStats_1.4.1
[57]	igraph_2.1.1	bit_4.5.0
[59]	png_0.1-8	memoise_2.0.1
[61]	shiny_1.9.1	GenomicRanges_1.59.1
[63]	IRanges_2.41.1	BiocIO_1.17.1
[65]	rtracklayer_1.67.0	rlang_1.1.4
[67]	Rcpp_1.0.13-1	xtable_1.8-4
[69]	DBI_1.2.3	BiocGenerics_0.53.3
[71]	splitstackshape_1.4.8	jsonlite_1.8.9
[73]	R6_2.5.1	MatrixGenerics_1.19.0
[75]	GenomicAlignments_1.43.0	zlibbioc_1.53.0