

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) (2024-10-26 r87273 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows Server 2022 x64 (build 20348)
```

```
Matrix products: default
```

```
locale:
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8
```



Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

```
time zone: America/New_York
```

```
tzcode source: internal
```

```
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_5.2.3           parallel_4.5.0
[13] AnnotationDbi_1.69.0  RSQLite_2.3.7
[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_0.45.0
[21] lifecycle_1.0.4	GenomeInfoDbData_1.2.13
[23] rTRM_1.45.0	compiler_4.5.0
[25] Rsamtools_2.23.0	Biostings_2.75.0
[27] codetools_0.2-20	httpuv_1.6.15
[29] GenomeInfoDb_1.43.0	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_0.33.1
[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_1.7.0	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_1.59.0
[63] IRanges_2.41.0	BiocIO_1.17.0
[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_0.53.1
[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