

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 4.2.0 RC (2022-04-19 r82224 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 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
```

```
attached base packages:
```



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

```
[1] stats      graphics  grDevices  utils      datasets  methods   base
```

other attached packages:

```
[1] rTRMui_1.34.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_1.0.8.3      lattice_0.20-45
[3] png_0.1-7         Rsamtools_2.12.0
[5] Biostrings_2.64.0 digest_0.6.29
[7] mime_0.12         org.Mm.eg.db_3.15.0
[9] R6_2.5.1          GenomeInfoDb_1.32.0
[11] stats4_4.2.0      RSQLite_2.2.12
[13] httr_1.4.2        zlibbioc_1.42.0
[15] rlang_1.0.2       data.table_1.14.2
[17] blob_1.2.3        S4Vectors_0.34.0
[19] Matrix_1.4-1      BiocParallel_1.30.0
[21] igraph_1.3.1      RCurl_1.98-1.6
[23] bit_4.0.4         shiny_1.7.1
```

[25]	DelayedArray_0.22.0	compiler_4.2.0
[27]	httpuv_1.6.5	rtracklayer_1.56.0
[29]	pkgconfig_2.0.3	BiocGenerics_0.42.0
[31]	htmltools_0.5.2	SummarizedExperiment_1.26.0
[33]	KEGGREST_1.36.0	rTRM_1.34.0
[35]	GenomeInfoDbData_1.2.8	IRanges_2.30.0
[37]	matrixStats_0.62.0	XML_3.99-0.9
[39]	crayon_1.5.1	later_1.3.0
[41]	GenomicAlignments_1.32.0	bitops_1.0-7
[43]	grid_4.2.0	xtable_1.8-4
[45]	lifecycle_1.0.1	DBI_1.1.2
[47]	magrittr_2.0.3	cli_3.3.0
[49]	cachem_1.0.6	XVector_0.36.0
[51]	promises_1.2.0.1	splitstackshape_1.4.8
[53]	ellipsis_0.3.2	vctrs_0.4.1
[55]	org.Hs.eg.db_3.15.0	rjson_0.2.21
[57]	restfulr_0.0.13	tools_4.2.0
[59]	bit64_4.0.5	Biobase_2.56.0
[61]	MotifDb_1.38.0	MatrixGenerics_1.8.0
[63]	parallel_4.2.0	fastmap_1.1.0
[65]	yaml_2.3.5	AnnotationDbi_1.58.0
[67]	GenomicRanges_1.48.0	memoise_2.0.1
[69]	BiocIO_1.6.0	