

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 4.0.3 (2020-10-10)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Mojave 10.14.6
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
```

```
locale:
```

```
[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
attached base packages:
```

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



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

other attached packages:

```
[1] rTRMui_1.28.0
```

loaded via a namespace (and not attached):

```
[1] SummarizedExperiment_1.20.0 lattice_0.20-41
[3] vctrs_0.3.4                  htmltools_0.5.0
[5] stats4_4.0.3                rtracklayer_1.50.0
[7] blob_1.2.1                  XML_3.99-0.5
[9] rlang_0.4.8                  later_1.1.0.1
[11] DBI_1.1.0                   BiocParallel_1.24.0
[13] BiocGenerics_0.36.0         bit64_4.0.5
[15] splitstackshape_1.4.8       matrixStats_0.57.0
[17] GenomeInfoDbData_1.2.4     zlibbioc_1.36.0
[19] MatrixGenerics_1.2.0       Biostrings_2.58.0
[21] memoise_1.1.0              Biobase_2.50.0
[23] IRanges_2.24.0             fastmap_1.0.1
[25] httpuv_1.5.4               GenomeInfoDb_1.26.0
[27] parallel_4.0.3             AnnotationDbi_1.52.0
```

[29]	MotifDb_1.32.0	Rcpp_1.0.5
[31]	xtable_1.8-4	promises_1.1.1
[33]	DelayedArray_0.16.0	org.Hs.eg.db_3.12.0
[35]	S4Vectors_0.28.0	XVector_0.30.0
[37]	rTRM_1.28.0	mime_0.9
[39]	bit_4.0.4	Rsamtools_2.6.0
[41]	digest_0.6.27	shiny_1.5.0
[43]	GenomicRanges_1.42.0	grid_4.0.3
[45]	tools_4.0.3	bitops_1.0-6
[47]	magrittr_1.5	RCurl_1.98-1.2
[49]	RSQLite_2.2.1	crayon_1.3.4
[51]	pkgconfig_2.0.3	Matrix_1.2-18
[53]	data.table_1.13.2	org.Mm.eg.db_3.12.0
[55]	R6_2.4.1	GenomicAlignments_1.26.0
[57]	igraph_1.2.6	compiler_4.0.3