

# 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) (2019-11-03 r77362)
Platform: x86_64-apple-darwin15.6.0 (64-bit)
Running under: OS X El Capitan 10.11.6
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.0.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_1.25.0
```

loaded via a namespace (and not attached):

```
[1] SummarizedExperiment_1.17.0 lattice_0.20-38
[3] vctrs_0.2.0 htmltools_0.4.0
[5] stats4_4.0.0 rtracklayer_1.47.0
[7] blob_1.2.0 XML_3.98-1.20
[9] rlang_0.4.1 later_1.0.0
[11] pillar_1.4.2 DBI_1.0.0
[13] BiocParallel_1.21.0 BiocGenerics_0.33.0
[15] bit64_0.9-7 splitstackshape_1.4.8
[17] matrixStats_0.55.0 GenomeInfoDbData_1.2.2
[19] zlibbioc_1.33.0 Biobase_2.47.0
[21] memoise_1.1.0 fastmap_1.0.1
[23] IRanges_2.21.1 GenomeInfoDb_1.23.0
[25] httpuv_1.5.2 AnnotationDbi_1.49.0
[27] parallel_4.0.0
```

[29]	MotifDb_1.29.0	Rcpp_1.0.2
[31]	xtable_1.8-4	promises_1.1.0
[33]	backports_1.1.5	DelayedArray_0.13.0
[35]	org.Hs.eg.db_3.10.0	S4Vectors_0.25.0
[37]	XVector_0.27.0	rTRM_1.25.0
[39]	mime_0.7	bit_1.1-14
[41]	Rsamtools_2.3.2	digest_0.6.22
[43]	shiny_1.4.0	GenomicRanges_1.39.1
[45]	grid_4.0.0	tools_4.0.0
[47]	bitops_1.0-6	magrittr_1.5
[49]	RCurl_1.95-4.12	tibble_2.1.3
[51]	RSQLite_2.1.2	crayon_1.3.4
[53]	pkgconfig_2.0.3	zeallot_0.1.0
[55]	Matrix_1.2-17	data.table_1.12.6
[57]	org.Mm.eg.db_3.10.0	R6_2.4.0
[59]	GenomicAlignments_1.23.0	igraph_1.2.4.1
[61]	compiler_4.0.0	