

# 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 3.4.2 (2017-09-28)
```

```
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/3.4/Resources/lib/libRblas.0.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/3.4/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_1.16.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.13           GenomeInfoDb_1.14.0
[3] compiler_3.4.2         MotifDb_1.20.0
[5] XVector_0.18.0         bitops_1.0-6
[7] tools_3.4.2            zlibbioc_1.24.0
[9] digest_0.6.12          bit_1.1-12
[11] lattice_0.20-35        RSQLite_2.0
[13] memoise_1.1.0          tibble_1.3.4
[15] pkgconfig_2.0.1        rlang_0.1.2
[17] Matrix_1.2-11          igraph_1.1.2
[19] DelayedArray_0.4.0     shiny_1.0.5
[21] DBI_0.7                parallel_3.4.2
[23] GenomeInfoDbData_0.99.1 org.Mm.eg.db_3.4.2
[25] rtracklayer_1.38.0     Biostrings_2.46.0
[27] S4Vectors_0.16.0      IRanges_2.12.0
```

[29]	grid_3.4.2	stats4_3.4.2
[31]	bit64_0.9-7	data.table_1.10.4-3
[33]	Biobase_2.38.0	R6_2.2.2
[35]	AnnotationDbi_1.40.0	BiocParallel_1.12.0
[37]	XML_3.98-1.9	org.Hs.eg.db_3.4.2
[39]	blob_1.1.0	magrittr_1.5
[41]	matrixStats_0.52.2	GenomicAlignments_1.14.0
[43]	Rsamtools_1.30.0	GenomicRanges_1.30.0
[45]	htmltools_0.3.6	BiocGenerics_0.24.0
[47]	SummarizedExperiment_1.8.0	splitstackshape_1.4.2
[49]	mime_0.5	xtable_1.8-2
[51]	httpuv_1.3.5	RCurl_1.95-4.8
[53]	rTRM_1.16.0	