

# rTRMui: a shiny user interface for the identification of transcriptional regulatory modules

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April 16, 2015

## 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 3.2.0 RC (2015-04-08 r68161)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2008 R2 x64 (build 7601) Service Pack 1
```

```
locale:
```

```
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.1252
[3] LC_MONETARY=English_United States.1252
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.1252
```

```
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_1.6.0  RSQLite_1.0.0 DBI_0.3.1
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.11.5          futile.logger_1.4    GenomeInfoDb_1.4.0
[4] MotifDb_1.10.0       XVector_0.8.0       bitops_1.0-6
[7] futile.options_1.0.0 tools_3.2.0         zlibbioc_1.14.0
[10] digest_0.6.8         igraph_0.7.1        shiny_0.11.1
[13] parallel_3.2.0       org.Mm.eg.db_3.1.2  rtracklayer_1.28.0
[16] Biostrings_2.36.0    S4Vectors_0.6.0     IRanges_2.2.0
[19] stats4_3.2.0         Biobase_2.28.0      R6_2.0.1
[22] AnnotationDbi_1.30.0 XML_3.98-1.1        BiocParallel_1.2.0
[25] RJSONIO_1.3-0        org.Hs.eg.db_3.1.2  lambda.r_1.1.7
[28] Rsamtools_1.20.0     htmltools_0.2.6     BiocGenerics_0.14.0
[31] GenomicRanges_1.20.0 GenomicAlignments_1.4.0 mime_0.3
[34] xtable_1.7-4         httpuv_1.3.2        RCurl_1.95-4.5
[37] rTRM_1.6.0
```