

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 3.0.2 (2013-09-25)
Platform: i386-w64-mingw32/i386 (32-bit)
```

```
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] parallel stats      graphics  grDevices utils      datasets  methods
[8] base
```



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

other attached packages:

```
[1] rTRMui_1.0.4      org.Mm.eg.db_2.10.1  org.Hs.eg.db_2.10.1
[4] MotifDb_1.4.0     Biostrings_2.30.0    XVector_0.2.0
[7] IRanges_1.20.0    rTRM_1.0.3           annotate_1.40.0
[10] AnnotationDbi_1.24.0 Biobase_2.22.0       BiocGenerics_0.8.0
[13] RSQLite_0.11.4    DBI_0.2-7            igraph_0.6.5-2
[16] shiny_0.7.0
```

loaded via a namespace (and not attached):

```
[1] BSgenome_1.30.0    GenomicRanges_1.14.1 RCurl_1.95-4.1
[4] RJSONIO_1.0-3      Rsamtools_1.14.1    XML_3.98-1.1
[7] bitops_1.0-6       caTools_1.14        digest_0.6.3
[10] httpuv_1.2.0       rtracklayer_1.22.0  stats4_3.0.2
[13] tools_3.0.2        xtable_1.7-1        zlibbioc_1.8.0
```