

# 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 ??). 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 3.3.0 RC (2016-04-26 r70550)
Platform: x86_64-apple-darwin13.4.0 (64-bit)
Running under: OS X 10.9.5 (Mavericks)
```

```
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
```

```
other attached packages:
```

```
[1] rTRMui_1.10.0
```

```
loaded via a namespace (and not attached):
```



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

```
[1] igraph_1.0.1
[3] AnnotationDbi_1.34.0
[5] XVector_0.12.0
[7] GenomicAlignments_1.8.0
[9] BiocGenerics_0.18.0
[11] IRanges_2.6.0
[13] xtable_1.8-2
[15] org.Hs.eg.db_3.3.0
[17] tools_3.3.0
[19] parallel_3.3.0
[21] DBI_0.4
[23] digest_0.6.9
[25] org.Mm.eg.db_3.3.0
[27] S4Vectors_0.10.0
[29] RCurl_1.95-4.8
[31] mime_0.4
[33] Biostrings_2.40.0
[35] XML_3.98-1.4

Rcpp_0.12.4.5
MotifDb_1.14.0
magrittr_1.5
GenomicRanges_1.24.0
zlibbioc_1.18.0
BiocParallel_1.6.0
R6_2.1.2
GenomeInfoDb_1.8.0
SummarizedExperiment_1.2.0
Biobase_2.32.0
htmltools_0.3.5
shiny_0.13.2
rtracklayer_1.32.0
bitops_1.0-6
RSQLite_1.0.0
Rsamtools_1.24.0
stats4_3.3.0
rTRM_1.10.0
```

[37] `httpuv_1.3.3`