

# 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 3.1.0 (2014-04-10)
Platform: x86_64-unknown-linux-gnu (64-bit)
```

```
locale:
```

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C             LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

```
attached base packages:
```

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

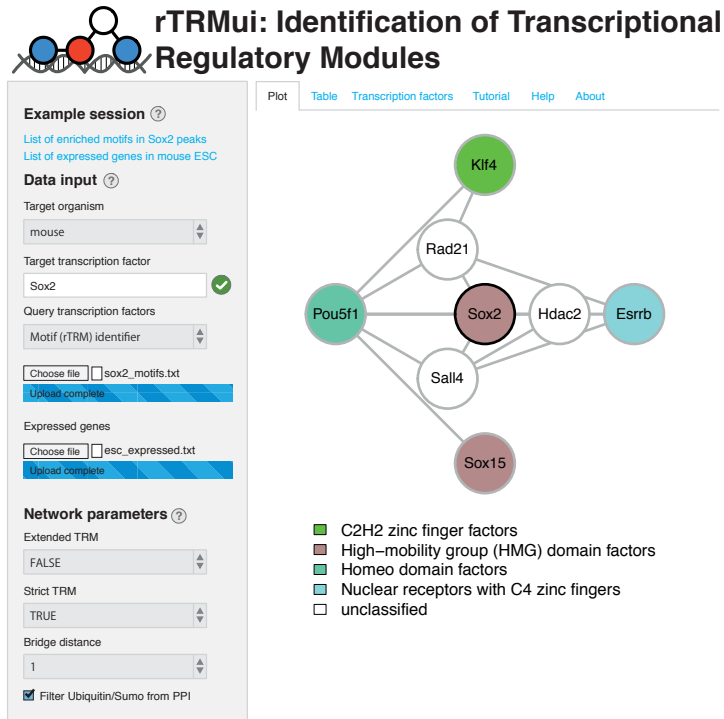


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

other attached packages:

```
[1] rTRMui_1.2.0      AnnotationDbi_1.26.0 GenomeInfoDb_1.0.0
[4] Biobase_2.24.0    BiocGenerics_0.10.0 RSQLite_0.11.4
[7] DBI_0.2-7
```

loaded via a namespace (and not attached):

```
[1] BBmisc_1.5          BSgenome_1.32.0      BatchJobs_1.2
[4] BiocParallel_0.6.0 Biostrings_2.32.0    GenomicAlignments_1.0.0
[7] GenomicRanges_1.16.0 IRanges_1.21.45     MotifDb_1.6.0
[10] RCurl_1.95-4.1     RJSONIO_1.0-3       Rcpp_0.11.1
[13] Rsamtools_1.16.0   XML_3.98-1.1        XVector_0.4.0
[16] bitops_1.0-6       brew_1.0-6           caTools_1.16
[19] codetools_0.2-8    digest_0.6.4         fail_1.2
[22] foreach_1.4.2      httpuv_1.3.0        igraph_0.7.0
[25] iterators_1.0.7    org.Hs.eg.db_2.14.0 org.Mm.eg.db_2.14.0
[28] plyr_1.8.1         rTRM_1.2.0          rtracklayer_1.24.0
[31] sendmailR_1.1-2    shiny_0.9.1         stats4_3.1.0
```

[34] stringr\_0.6.2            tools\_3.1.0            xtable\_1.7-3  
[37] zlibbioc\_1.10.0