

# 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 3.2.0 RC (2015-04-08 r68161)
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_1.6.0  RSQLite_1.0.0 DBI_0.3.1
```

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

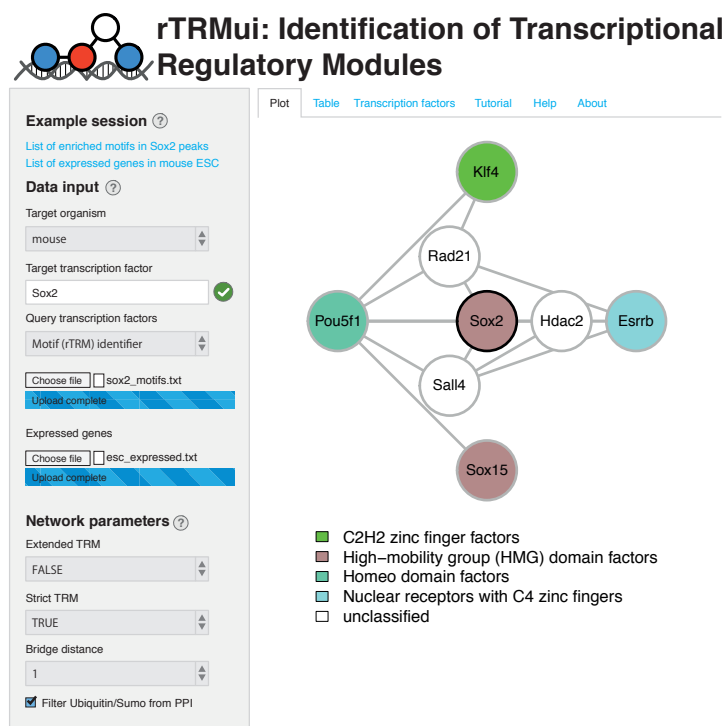


Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

|                           |                         |                     |
|---------------------------|-------------------------|---------------------|
| [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           |                         |                     |