

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

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October 13, 2014

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 3.1.1 Patched (2014-09-25 r66681)
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 stats4 stats graphics grDevices utils datasets
[8] methods base
```

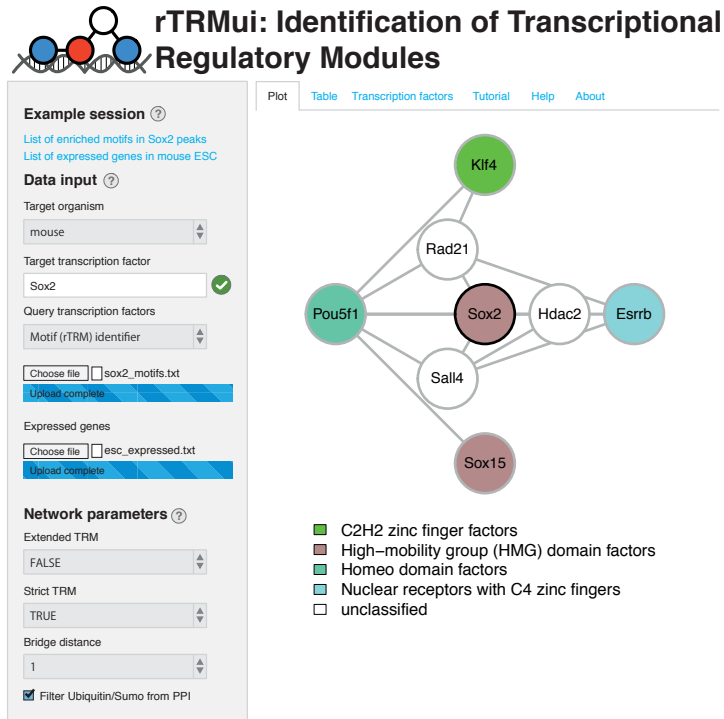


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

other attached packages:

```
[1] rTRMui_1.4.0      AnnotationDbi_1.28.0 GenomeInfoDb_1.2.0
[4] IRanges_2.0.0     S4Vectors_0.4.0    Biobase_2.26.0
[7] BiocGenerics_0.12.0 RSQLite_0.11.4     DBI_0.3.1
```

loaded via a namespace (and not attached):

```
[1] BBmisc_1.7          BatchJobs_1.4       BiocParallel_1.0.0
[4] Biostrings_2.34.0   GenomicAlignments_1.2.0 GenomicRanges_1.18.0
[7] MotifDb_1.8.0      R6_2.0              RCurl_1.95-4.3
[10] RJSONIO_1.3-0      Rcpp_0.11.3         Rsamtools_1.18.0
[13] XML_3.98-1.1       XVector_0.6.0       base64enc_0.1-2
[16] bitops_1.0-6       brew_1.0-6          checkmate_1.4
[19] codetools_0.2-9    digest_0.6.4        fail_1.2
[22] foreach_1.4.2      htmltools_0.2.6     httpuv_1.3.0
[25] igraph_0.7.1       iterators_1.0.7     mime_0.2
[28] org.Hs.eg.db_3.0.0 org.Mm.eg.db_3.0.0  rTRM_1.4.0
[31] rtracklayer_1.26.0 sendmailR_1.2-1     shiny_0.10.2.1
```

[34] stringr_0.6.2 tools_3.1.1 xtable_1.7-4
[37] zlibbioc_1.12.0