

# 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 (2015-04-16)
Platform: x86_64-unknown-linux-gnu (64-bit)
Running under: Ubuntu 14.04.2 LTS

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] stats      graphics   grDevices utils      datasets  methods   base
```

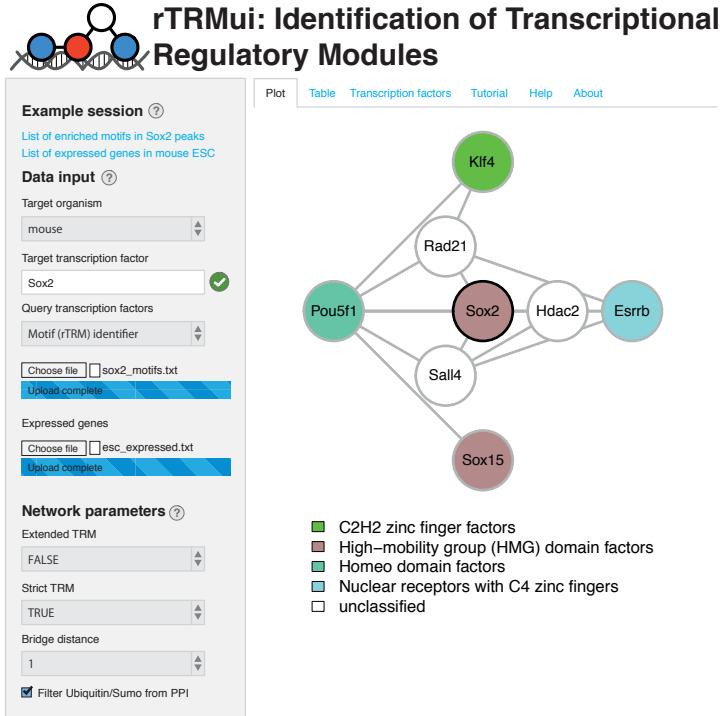


Figure 1: rTRMUI home page showing the TRM identified using the sample datasets from the tutorial.

other attached packages:

```
[1] rTRMUI_1.6.0  RSQLite_1.0.0 DBI_0.3.1
```

loaded via a namespace (and not attached):

[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		