

# 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 3.4.0 (2017-04-21)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 16.04.2 LTS
```

```
Matrix products: default
BLAS: /home/biocbuild/bbs-3.5-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.5-bioc/R/lib/libRlapack.so
```

```
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
```

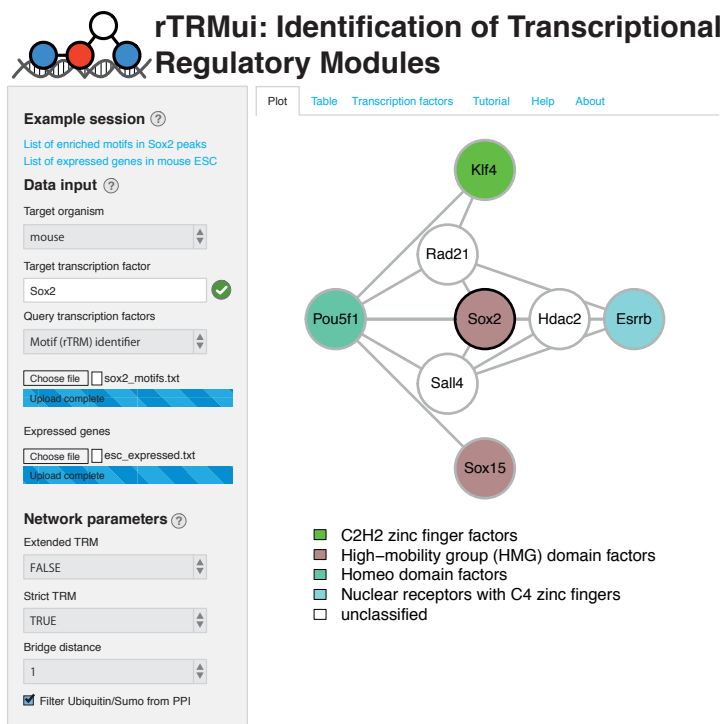


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

attached base packages:

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

other attached packages:

```
[1] rTRMui_1.14.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.10      compiler_3.4.0
[3] GenomeInfoDb_1.12.0 MotifDb_1.18.0
[5] XVector_0.16.0    bitops_1.0-6
[7] tools_3.4.0       zlibbioc_1.22.0
[9] digest_0.6.12     lattice_0.20-35
[11] RSQLite_1.1-2     memoise_1.1.0
[13] Matrix_1.2-9      igraph_1.0.1
[15] DelayedArray_0.2.0 shiny_1.0.2
[17] DBI_0.6-1         parallel_3.4.0
```

[19]	GenomeInfoDbData_0.99.0	org.Mm.eg.db_3.4.1
[21]	rtracklayer_1.36.0	Biostrings_2.44.0
[23]	S4Vectors_0.14.0	IRanges_2.10.0
[25]	grid_3.4.0	stats4_3.4.0
[27]	Biobase_2.36.0	R6_2.2.0
[29]	AnnotationDbi_1.38.0	XML_3.98-1.6
[31]	BiocParallel_1.10.0	org.Hs.eg.db_3.4.1
[33]	magrittr_1.5	matrixStats_0.52.2
[35]	Rsamtools_1.28.0	htmltools_0.3.5
[37]	BiocGenerics_0.22.0	GenomicRanges_1.28.0
[39]	GenomicAlignments_1.12.0	SummarizedExperiment_1.6.0
[41]	mime_0.5	xtable_1.8-2
[43]	httpuv_1.3.3	RCurl_1.95-4.8
[45]	rTRM_1.14.0	