

# 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 3.4.2 (2017-09-28)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 16.04.3 LTS
```

```
Matrix products: default
BLAS: /home/biocbuild/bbs-3.6-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.6-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
```

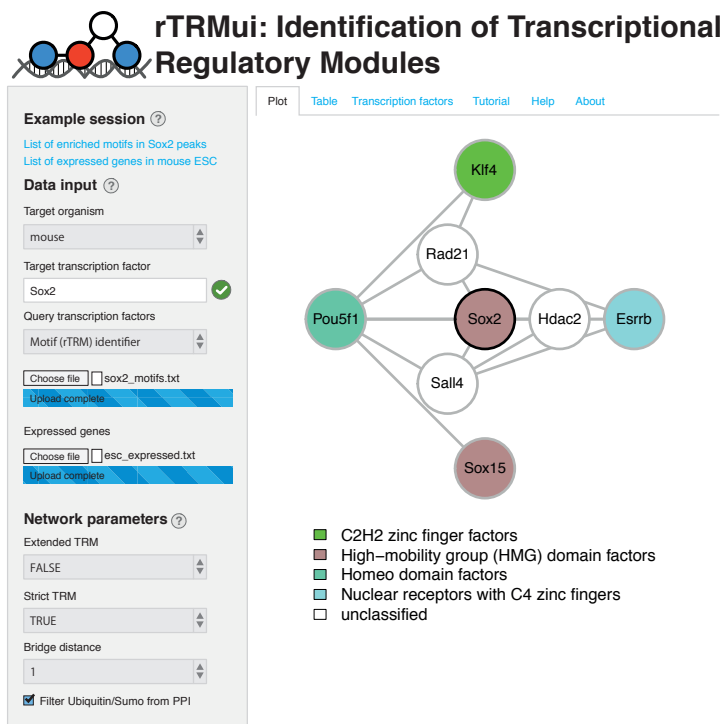


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[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_1.16.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.13      GenomeInfoDb_1.14.0
[3] compiler_3.4.2    MotifDb_1.20.0
[5] XVector_0.18.0    bitops_1.0-6
[7] tools_3.4.2       zlibbioc_1.24.0
[9] digest_0.6.12     bit_1.1-12
[11] lattice_0.20-35   RSQLite_2.0
[13] memoise_1.1.0     tibble_1.3.4
[15] pkgconfig_2.0.1   rlang_0.1.2
[17] Matrix_1.2-11     igraph_1.1.2
```

[19]	DelayedArray_0.4.0	shiny_1.0.5
[21]	DBI_0.7	parallel_3.4.2
[23]	GenomeInfoDbData_0.99.1	org.Mm.eg.db_3.4.2
[25]	rtracklayer_1.38.0	Biostrings_2.46.0
[27]	S4Vectors_0.16.0	IRanges_2.12.0
[29]	grid_3.4.2	stats4_3.4.2
[31]	bit64_0.9-7	data.table_1.10.4-3
[33]	Biobase_2.38.0	R6_2.2.2
[35]	AnnotationDbi_1.40.0	BiocParallel_1.12.0
[37]	XML_3.98-1.9	org.Hs.eg.db_3.4.2
[39]	blob_1.1.0	magrittr_1.5
[41]	matrixStats_0.52.2	GenomicAlignments_1.14.0
[43]	Rsamtools_1.30.0	GenomicRanges_1.30.0
[45]	htmltools_0.3.6	BiocGenerics_0.24.0
[47]	SummarizedExperiment_1.8.0	splitstackshape_1.4.2
[49]	mime_0.5	xtable_1.8-2
[51]	httpuv_1.3.5	RCurl_1.95-4.8
[53]	rTRM_1.16.0	