

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 3.5.1 Patched (2018-07-12 r74967)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 16.04.5 LTS
```

```
Matrix products: default
BLAS: /home/biocbuild/bbs-3.8-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.8-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
```

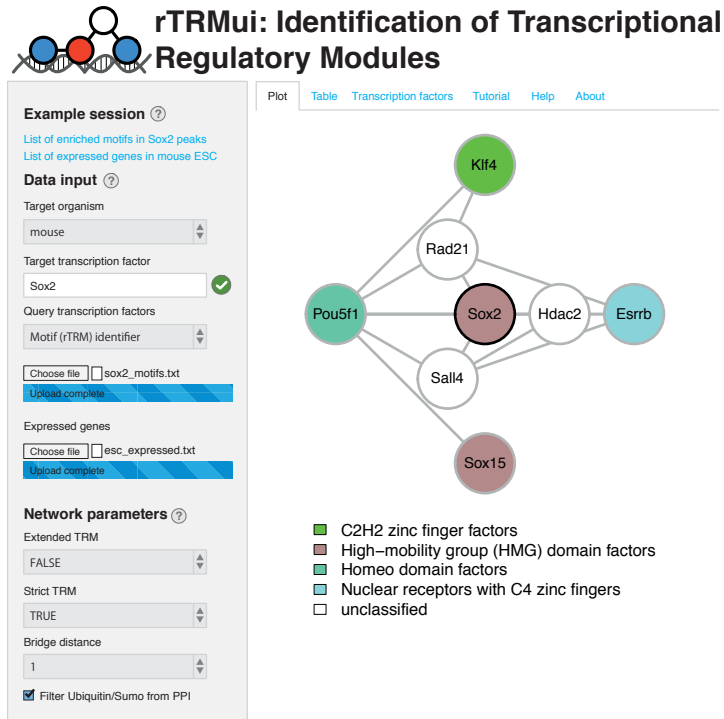


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[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_1.20.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.19           GenomeInfoDb_1.18.0
[3] compiler_3.5.1        later_0.7.5
[5] MotifDb_1.24.0        XVector_0.22.0
[7] bitops_1.0-6          tools_3.5.1
[9] zlibbioc_1.28.0       digest_0.6.18
[11] bit_1.1-14            lattice_0.20-35
[13] RSQLite_2.1.1         memoise_1.1.0
[15] pkgconfig_2.0.2       Matrix_1.2-14
[17] igraph_1.2.2          DelayedArray_0.8.0
```

[19]	shiny_1.1.0	DBI_1.0.0
[21]	parallel_3.5.1	GenomeInfoDbData_1.2.0
[23]	org.Mm.eg.db_3.7.0	rtracklayer_1.42.0
[25]	Biostrings_2.50.0	S4Vectors_0.20.0
[27]	IRanges_2.16.0	grid_3.5.1
[29]	stats4_3.5.1	bit64_0.9-7
[31]	data.table_1.11.8	Biobase_2.42.0
[33]	R6_2.3.0	AnnotationDbi_1.44.0
[35]	BiocParallel_1.16.0	XML_3.98-1.16
[37]	org.Hs.eg.db_3.7.0	blob_1.1.1
[39]	magrittr_1.5	matrixStats_0.54.0
[41]	GenomicAlignments_1.18.0	Rsamtools_1.34.0
[43]	GenomicRanges_1.34.0	promises_1.0.1
[45]	htmltools_0.3.6	BiocGenerics_0.28.0
[47]	SummarizedExperiment_1.12.0	splitstackshape_1.4.6
[49]	mime_0.6	xtable_1.8-3
[51]	httpuv_1.4.5	RCurl_1.95-4.11
[53]	rTRM_1.20.0	