

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

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October 29, 2019

## 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 3.6.1 (2019-07-05)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 18.04.3 LTS

Matrix products: default
BLAS: /home/biocbuild/bbs-3.10-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.10-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
```

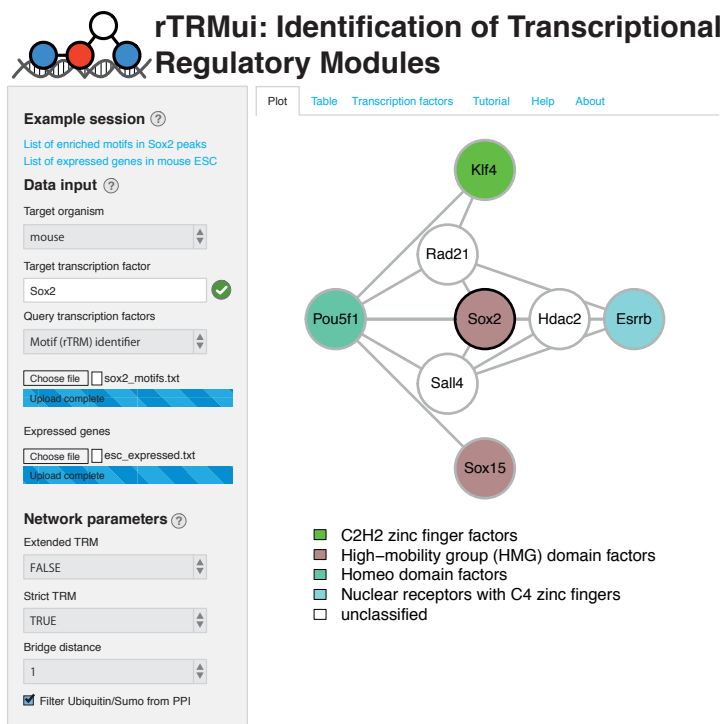


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[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_1.24.0
```

loaded via a namespace (and not attached):

```
[1] SummarizedExperiment_1.16.0 lattice_0.20-38
[3] vctrs_0.2.0          htmltools_0.4.0
[5] stats4_3.6.1         rtracklayer_1.46.0
[7] blob_1.2.0           XML_3.98-1.20
[9] rlang_0.4.1          later_1.0.0
[11] pillar_1.4.2         DBI_1.0.0
[13] BiocParallel_1.20.0  BiocGenerics_0.32.0
[15] bit64_0.9-7          splitstackshape_1.4.8
[17] matrixStats_0.55.0  GenomeInfoDbData_1.2.2
```

[19]	zlibbioc_1.32.0	Biostrings_2.54.0
[21]	memoise_1.1.0	Biobase_2.46.0
[23]	IRanges_2.20.0	fastmap_1.0.1
[25]	httpuv_1.5.2	GenomeInfoDb_1.22.0
[27]	parallel_3.6.1	AnnotationDbi_1.48.0
[29]	MotifDb_1.28.0	Rcpp_1.0.2
[31]	xtable_1.8-4	promises_1.1.0
[33]	backports_1.1.5	DelayedArray_0.12.0
[35]	org.Hs.eg.db_3.10.0	S4Vectors_0.24.0
[37]	XVector_0.26.0	rTRM_1.24.0
[39]	mime_0.7	bit_1.1-14
[41]	Rsamtools_2.2.0	digest_0.6.22
[43]	shiny_1.4.0	GenomicRanges_1.38.0
[45]	grid_3.6.1	tools_3.6.1
[47]	bitops_1.0-6	magrittr_1.5
[49]	RCurl_1.95-4.12	tibble_2.1.3
[51]	RSQLite_2.1.2	crayon_1.3.4
[53]	pkgconfig_2.0.3	zeallot_0.1.0
[55]	Matrix_1.2-17	data.table_1.12.6
[57]	org.Mm.eg.db_3.10.0	R6_2.4.0
[59]	GenomicAlignments_1.22.0	igraph_1.2.4.1
[61]	compiler_3.6.1	