

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

Diego Diez

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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 3.6.0 (2019-04-26)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 18.04.2 LTS
```

```
Matrix products: default
BLAS: /home/biocbuild/bbs-3.9-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.9-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
```

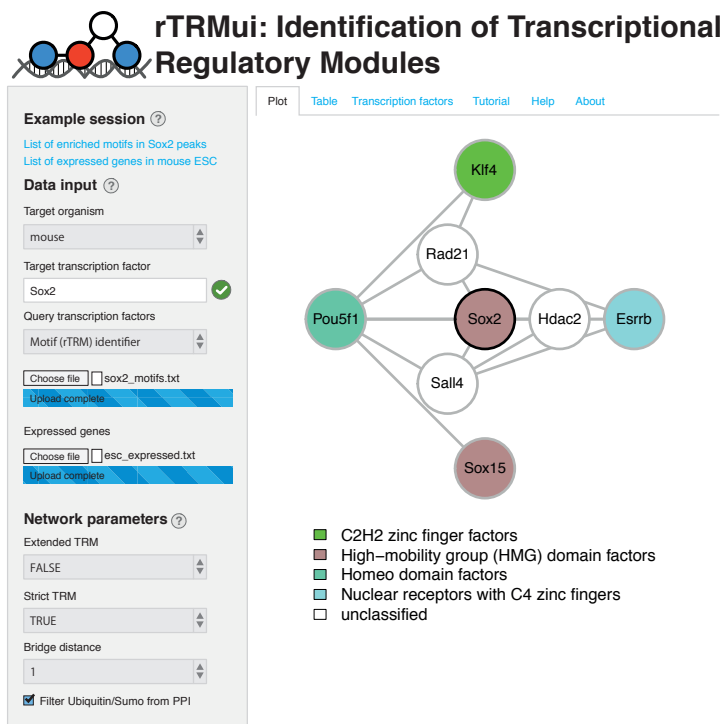


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[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_1.22.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_1.0.1           GenomeInfoDb_1.20.0
[3] compiler_3.6.0      later_0.8.0
[5] MotifDb_1.26.0      XVector_0.24.0
[7] bitops_1.0-6        tools_3.6.0
[9] zlibbioc_1.30.0     digest_0.6.18
[11] bit_1.1-14          lattice_0.20-38
[13] RSQLite_2.1.1       memoise_1.1.0
[15] pkgconfig_2.0.2     Matrix_1.2-17
[17] igraph_1.2.4.1      DelayedArray_0.10.0
```

[19]	shiny_1.3.2	DBI_1.0.0
[21]	parallel_3.6.0	GenomeInfoDbData_1.2.1
[23]	org.Mm.eg.db_3.8.2	rtracklayer_1.44.0
[25]	Biostrings_2.52.0	S4Vectors_0.22.0
[27]	IRanges_2.18.0	grid_3.6.0
[29]	stats4_3.6.0	bit64_0.9-7
[31]	data.table_1.12.2	Biobase_2.44.0
[33]	R6_2.4.0	AnnotationDbi_1.46.0
[35]	BiocParallel_1.18.0	XML_3.98-1.19
[37]	org.Hs.eg.db_3.8.2	blob_1.1.1
[39]	magrittr_1.5	matrixStats_0.54.0
[41]	GenomicAlignments_1.20.0	Rsamtools_2.0.0
[43]	GenomicRanges_1.36.0	promises_1.0.1
[45]	htmltools_0.3.6	BiocGenerics_0.30.0
[47]	SummarizedExperiment_1.14.0	splitstackshape_1.4.8
[49]	mime_0.6	xtable_1.8-4
[51]	httpuv_1.5.1	RCurl_1.95-4.12
[53]	rTRM_1.22.0	