

# 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 4.3.0 RC (2023-04-13 r84269)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 22.04.2 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.17-bioc/R/lib/libRblas.so
```

```
LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.10.0
```

```
locale:
```

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_GB             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
```

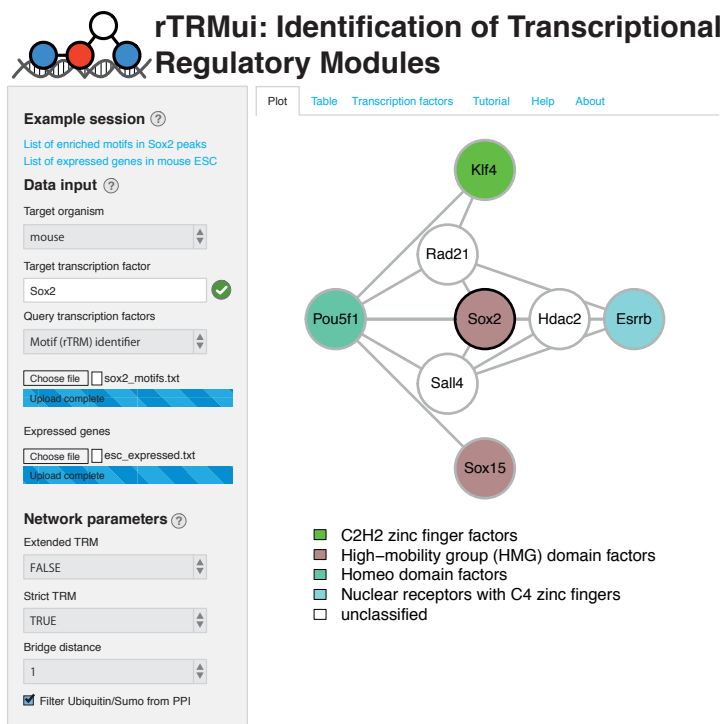


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

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

```
time zone: America/New_York
tzcode source: system (glibc)
```

```
attached base packages:
```

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

```
other attached packages:
```

```
[1] rTRMui_1.38.0
```

```
loaded via a namespace (and not attached):
```

```
[1] KEGGREST_1.40.0           SummarizedExperiment_1.30.0
[3] rjson_0.2.21             Biobase_2.60.0
[5] lattice_0.21-8          vctrs_0.6.2
[7] tools_4.3.0              bitops_1.0-7
[9] stats4_4.3.0             parallel_4.3.0
[11] AnnotationDbi_1.62.0     RSQLite_2.3.1
```

[13]	MotifDb_1.42.0	blob_1.2.4
[15]	pkgconfig_2.0.3	Matrix_1.5-4
[17]	data.table_1.14.8	S4Vectors_0.38.0
[19]	lifecycle_1.0.3	GenomeInfoDbData_1.2.10
[21]	rTRM_1.38.0	compiler_4.3.0
[23]	Rsamtools_2.16.0	Biostrings_2.68.0
[25]	codetools_0.2-19	httpuv_1.6.9
[27]	GenomeInfoDb_1.36.0	htmltools_0.5.5
[29]	RCurl_1.98-1.12	yaml_2.3.7
[31]	later_1.3.0	crayon_1.5.2
[33]	ellipsis_0.3.2	BiocParallel_1.34.0
[35]	cachem_1.0.7	DelayedArray_0.26.0
[37]	org.Hs.eg.db_3.17.0	mime_0.12
[39]	digest_0.6.31	restfulr_0.0.15
[41]	fastmap_1.1.1	grid_4.3.0
[43]	cli_3.6.1	magrittr_2.0.3
[45]	XML_3.99-0.14	promises_1.2.0.1
[47]	bit64_4.0.5	org.Mm.eg.db_3.17.0
[49]	XVector_0.40.0	httr_1.4.5
[51]	matrixStats_0.63.0	igraph_1.4.2
[53]	bit_4.0.5	png_0.1-8
[55]	memoise_2.0.1	shiny_1.7.4
[57]	GenomicRanges_1.52.0	IRanges_2.34.0
[59]	BiocIO_1.10.0	rtracklayer_1.60.0
[61]	rlang_1.1.0	Rcpp_1.0.10
[63]	xtable_1.8-4	DBI_1.1.3
[65]	BiocGenerics_0.46.0	splitstackshape_1.4.8
[67]	R6_2.5.1	MatrixGenerics_1.12.0
[69]	GenomicAlignments_1.36.0	zlibbioc_1.46.0