

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 4.6.0 (2026-04-24)
Platform: x86_64-pc-linux-gnu
Running under: Ubuntu 24.04.4 LTS
```

```
Matrix products: default
```

```
BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
```

```
LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-p-r0.3.26.so; LAPACK version
```

```
locale:
```

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

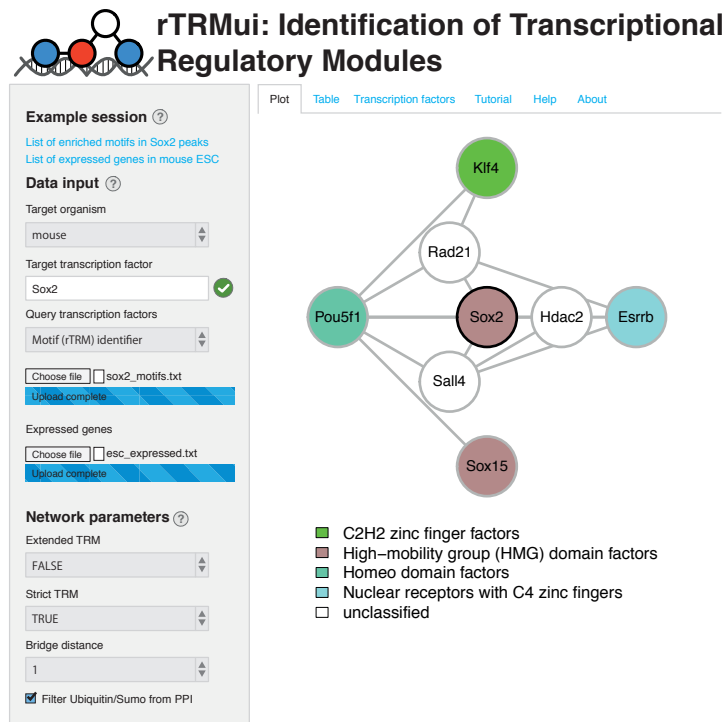


Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

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

```
time zone: Etc/UTC
```

```
tzcode source: system (glibc)
```

```
attached base packages:
```

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

```
other attached packages:
```

```
[1] rTRMui_1.50.0
```

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

```
[1] KEGGREST_1.52.0      SummarizedExperiment_1.42.0
[3] rjson_0.2.23         xfun_0.57
[5] lattice_0.22-9       Biobase_2.72.0
[7] vctrs_0.7.3          tools_4.6.0
[9] bitops_1.0-9         generics_0.1.4
[11] stats4_4.6.0         curl_7.1.0
```

[13]	parallel_4.6.0	AnnotationDbi_1.74.0
[15]	RSQLite_2.4.6	MotifDb_1.54.0
[17]	blob_1.3.0	pkgconfig_2.0.3
[19]	Matrix_1.7-5	data.table_1.18.2.1
[21]	cigarillo_1.2.0	S4Vectors_0.50.0
[23]	lifecycle_1.0.5	rTRM_1.48.0
[25]	compiler_4.6.0	Rsamtools_2.28.0
[27]	Biostrings_2.80.0	Seqinfo_1.2.0
[29]	codetools_0.2-20	httpuv_1.6.17
[31]	htmltools_0.5.9	sys_3.4.3
[33]	buildtools_1.0.0	RCurl_1.98-1.18
[35]	yaml_2.3.12	later_1.4.8
[37]	crayon_1.5.3	BiocParallel_1.46.0
[39]	DelayedArray_0.38.1	cachem_1.1.0
[41]	org.Hs.eg.db_3.22.0	abind_1.4-8
[43]	mime_0.13	digest_0.6.39
[45]	restfulr_0.0.16	maketools_1.3.2
[47]	grid_4.6.0	fastmap_1.2.0
[49]	SparseArray_1.12.0	cli_3.6.6
[51]	magrittr_2.0.5	S4Arrays_1.12.0
[53]	XML_3.99-0.23	promises_1.5.0
[55]	bit64_4.8.0	org.Mm.eg.db_3.22.0
[57]	XVector_0.52.0	httr_1.4.8
[59]	matrixStats_1.5.0	igraph_2.3.0
[61]	bit_4.6.0	otel_0.2.0
[63]	png_0.1-9	memoise_2.0.1
[65]	shiny_1.13.0	evaluate_1.0.5
[67]	knitr_1.51	GenomicRanges_1.64.0
[69]	IRanges_2.46.0	BiocIO_1.22.0
[71]	rtracklayer_1.72.0	rlang_1.2.0
[73]	Rcpp_1.1.1-1.1	xtable_1.8-8
[75]	DBI_1.3.0	BiocGenerics_0.58.0
[77]	splitstackshape_1.4.8.1	R6_2.6.1
[79]	MatrixGenerics_1.24.0	GenomicAlignments_1.48.0