

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 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

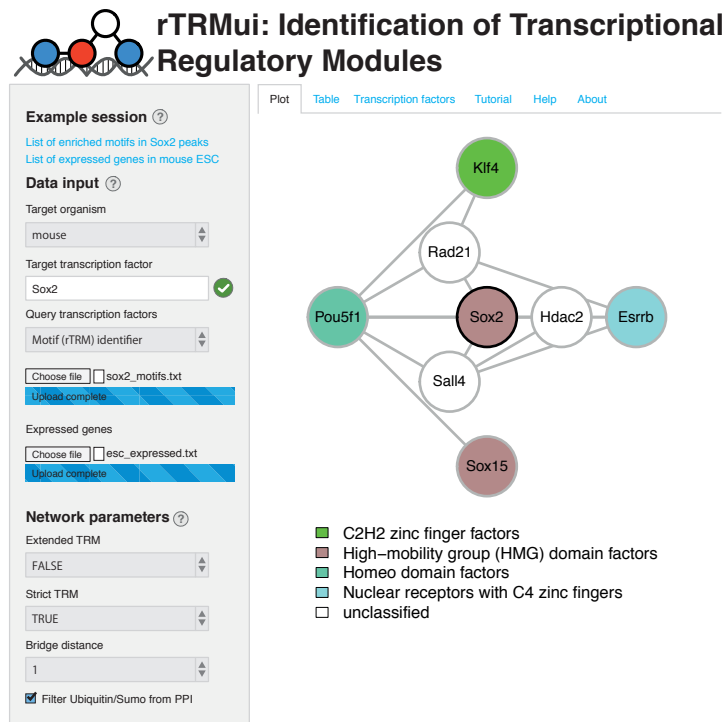


Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

```
[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_1.51.0
```

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

```
[1] KEGGREST_1.53.0      SummarizedExperiment_1.43.0
[3] rjson_0.2.23         xfun_0.57
[5] lattice_0.22-9       Biobase_2.73.1
[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_1.75.0
[15] RSQLite_2.4.6	MotifDb_1.55.0
[17] blob_1.3.0	pkgconfig_2.0.3
[19] BiocBaseUtils_1.15.0	Matrix_1.7-5
[21] data.table_1.18.2.1	cigarillo_1.3.0
[23] S4Vectors_0.51.1	lifecycle_1.0.5
[25] rTRM_1.50.0	compiler_4.6.0
[27] Rsamtools_2.28.0	Biostrings_2.81.1
[29] Seqinfo_1.3.0	codetools_0.2-20
[31] httpuv_1.6.17	htmltools_0.5.9
[33] sys_3.4.3	buildtools_1.0.0
[35] RCurl_1.98-1.18	yaml_2.3.12
[37] later_1.4.8	crayon_1.5.3
[39] BiocParallel_1.47.0	DelayedArray_0.39.1
[41] cachem_1.1.0	org.Hs.eg.db_3.23.1
[43] abind_1.4-8	mime_0.13
[45] digest_0.6.39	restfulr_0.0.16
[47] maketools_1.3.2	grid_4.6.0
[49] fastmap_1.2.0	SparseArray_1.13.0
[51] cli_3.6.6	magrittr_2.0.5
[53] S4Arrays_1.13.0	XML_3.99-0.23
[55] promises_1.5.0	bit64_4.8.0
[57] org.Mm.eg.db_3.23.0	XVector_0.53.0
[59] httr_1.4.8	matrixStats_1.5.0
[61] igraph_2.3.0	bit_4.6.0
[63] otel_0.2.0	png_0.1-9
[65] memoise_2.0.1	shiny_1.13.0
[67] evaluate_1.0.5	knitr_1.51
[69] GenomicRanges_1.65.0	IRanges_2.47.0
[71] BiocIO_1.23.3	rtracklayer_1.73.0
[73] rlang_1.2.0	Rcpp_1.1.1-1.1
[75] xtable_1.8-8	DBI_1.3.0
[77] BiocGenerics_0.59.0	splitstackshape_1.4.8.1
[79] R6_2.6.1	MatrixGenerics_1.25.0
[81] GenomicAlignments_1.49.0	