

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 Under development (unstable) (2023-10-22 r85388)
```

```
Platform: x86_64-pc-linux-gnu
```

```
Running under: Ubuntu 22.04.3 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.19-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

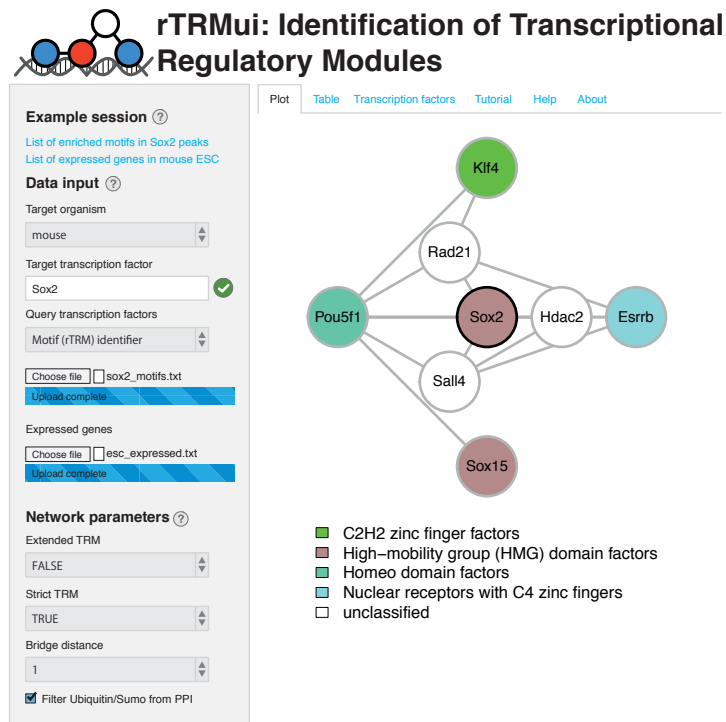


Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

```
[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_1.41.0    S4Vectors_0.41.0
```

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

```
[1] KEGGREST_1.43.0      SummarizedExperiment_1.33.0
[3] rjson_0.2.21         Biobase_2.63.0
[5] lattice_0.22-5       vctrs_0.6.4
[7] tools_4.4.0          bitops_1.0-7
[9] stats4_4.4.0         parallel_4.4.0
[11] AnnotationDbi_1.65.0 RSQlite_2.3.1
```

[13]	MotifDb_1.45.0	blob_1.2.4
[15]	pkgconfig_2.0.3	Matrix_1.6-1.1
[17]	data.table_1.14.8	lifecycle_1.0.3
[19]	GenomeInfoDbData_1.2.11	rTRM_1.41.0
[21]	compiler_4.4.0	Rsamtools_2.19.0
[23]	Biostrings_2.71.1	codetools_0.2-19
[25]	httpuv_1.6.12	GenomeInfoDb_1.39.0
[27]	htmltools_0.5.6.1	RCurl_1.98-1.12
[29]	yaml_2.3.7	later_1.3.1
[31]	crayon_1.5.2	ellipsis_0.3.2
[33]	BiocParallel_1.37.0	cachem_1.0.8
[35]	DelayedArray_0.29.0	org.Hs.eg.db_3.18.0
[37]	abind_1.4-5	mime_0.12
[39]	digest_0.6.33	restfulr_0.0.15
[41]	fastmap_1.1.1	grid_4.4.0
[43]	cli_3.6.1	SparseArray_1.3.0
[45]	magrittr_2.0.3	S4Arrays_1.3.0
[47]	XML_3.99-0.14	promises_1.2.1
[49]	bit64_4.0.5	org.Mm.eg.db_3.18.0
[51]	XVector_0.43.0	httr_1.4.7
[53]	matrixStats_1.0.0	igraph_1.5.1
[55]	bit_4.0.5	png_0.1-8
[57]	memoise_2.0.1	shiny_1.7.5.1
[59]	GenomicRanges_1.55.0	IRanges_2.37.0
[61]	BiocIO_1.13.0	rtracklayer_1.63.0
[63]	rlang_1.1.1	Rcpp_1.0.11
[65]	xtable_1.8-4	DBI_1.1.3
[67]	BiocGenerics_0.49.0	splitstackshape_1.4.8
[69]	R6_2.5.1	MatrixGenerics_1.15.0
[71]	GenomicAlignments_1.39.0	zlibbioc_1.49.0