

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 4.4.1 (2024-06-14)
Platform: x86_64-pc-linux-gnu
Running under: Ubuntu 24.04.1 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=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
```

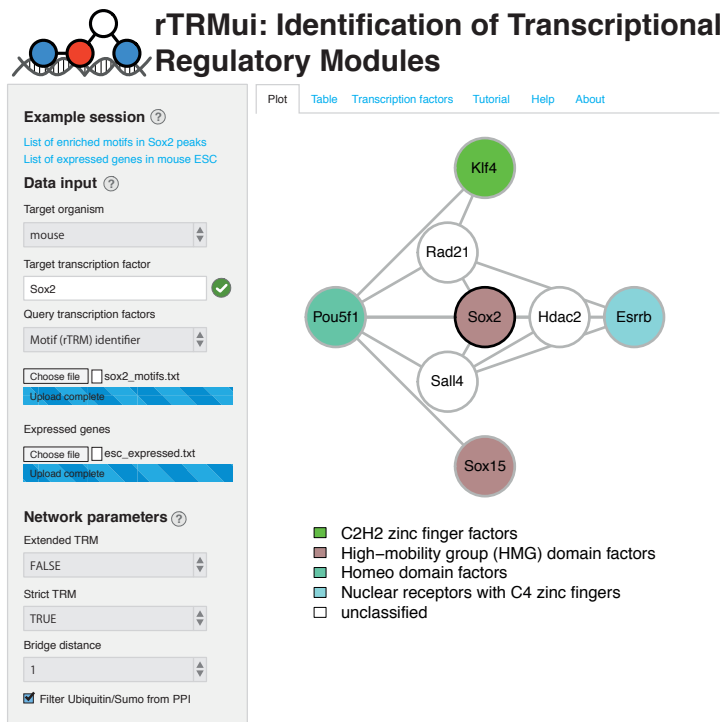


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

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

```
time zone: Etc/UTC
tzcode source: system (glibc)
```

```
attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base
```

```
other attached packages:
[1] rTRMui_1.43.0
```

```
loaded via a namespace (and not attached):
[1] KEGGREST_1.45.1      SummarizedExperiment_1.35.2
[3] rjson_0.2.23        xfun_0.47
[5] lattice_0.22-6      Biobase_2.65.1
[7] vctrs_0.6.5         tools_4.4.1
[9] bitops_1.0-8        stats4_4.4.1
[11] curl_5.2.3          parallel_4.4.1
```

[13]	AnnotationDbi_1.67.0	RSQLite_2.3.7
[15]	MotifDb_1.47.0	blob_1.2.4
[17]	pkgconfig_2.0.3	Matrix_1.7-0
[19]	data.table_1.16.0	S4Vectors_0.43.2
[21]	lifecycle_1.0.4	GenomeInfoDbData_1.2.13
[23]	rTRM_1.43.0	compiler_4.4.1
[25]	Rsamtools_2.21.2	Biostrings_2.73.2
[27]	codetools_0.2-20	httpuv_1.6.15
[29]	GenomeInfoDb_1.41.1	htmltools_0.5.8.1
[31]	sys_3.4.2	buildtools_1.0.0
[33]	RCurl_1.98-1.16	yaml_2.3.10
[35]	later_1.3.2	crayon_1.5.3
[37]	BiocParallel_1.39.0	DelayedArray_0.31.12
[39]	cachem_1.1.0	org.Hs.eg.db_3.20.0
[41]	abind_1.4-8	mime_0.12
[43]	digest_0.6.37	restfulr_0.0.15
[45]	maketools_1.3.0	grid_4.4.1
[47]	fastmap_1.2.0	SparseArray_1.5.41
[49]	cli_3.6.3	magrittr_2.0.3
[51]	S4Arrays_1.5.10	XML_3.99-0.17
[53]	UCSC.utils_1.1.0	promises_1.3.0
[55]	bit64_4.5.2	org.Mm.eg.db_3.20.0
[57]	XVector_0.45.0	httr_1.4.7
[59]	matrixStats_1.4.1	igraph_2.0.3
[61]	bit_4.5.0	png_0.1-8
[63]	memoise_2.0.1	shiny_1.9.1
[65]	knitr_1.48	GenomicRanges_1.57.1
[67]	IRanges_2.39.2	BiocIO_1.15.2
[69]	rtracklayer_1.65.0	rlang_1.1.4
[71]	Rcpp_1.0.13	xtable_1.8-4
[73]	DBI_1.2.3	BiocGenerics_0.51.2
[75]	splitstackshape_1.4.8	jsonlite_1.8.9
[77]	R6_2.5.1	MatrixGenerics_1.17.0
[79]	GenomicAlignments_1.41.0	zlibbioc_1.51.1