

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 4.4.0 RC (2024-04-16 r86468)
```

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

```
Running under: Ubuntu 22.04.4 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.20-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
```

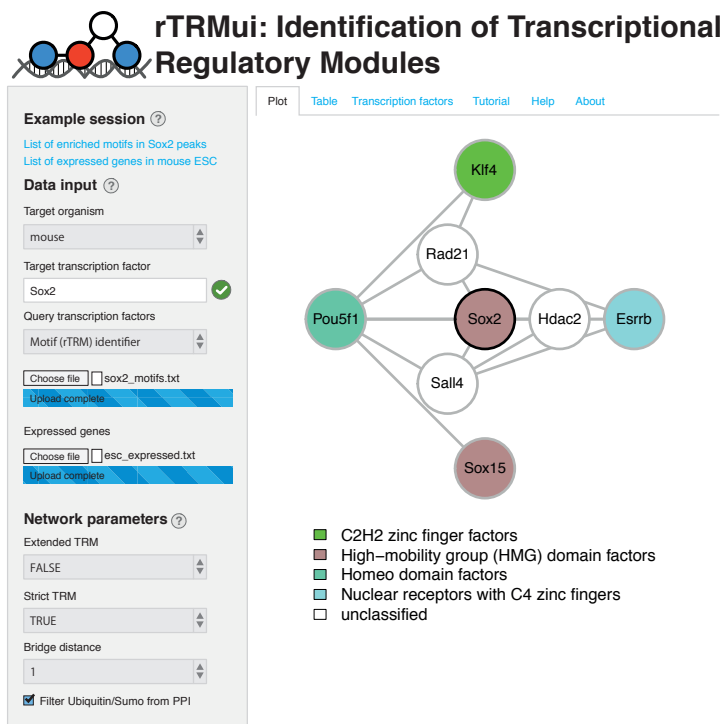


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[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_1.43.0
```

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

```
[1] KEGGEST_1.45.0           SummarizedExperiment_1.35.0
[3] rjson_0.2.21             lattice_0.22-6
[5] Biobase_2.65.0           vctrs_0.6.5
[7] tools_4.4.0              bitops_1.0-7
[9] stats4_4.4.0             curl_5.2.1
[11] parallel_4.4.0          AnnotationDbi_1.67.0
```

[13]	RSQLite_2.3.6	MotifDb_1.47.0
[15]	blob_1.2.4	pkgconfig_2.0.3
[17]	Matrix_1.7-0	data.table_1.15.4
[19]	S4Vectors_0.43.0	lifecycle_1.0.4
[21]	GenomeInfoDbData_1.2.12	rTRM_1.43.0
[23]	compiler_4.4.0	Rsamtools_2.21.0
[25]	Biostrings_2.73.0	codetools_0.2-20
[27]	httpuv_1.6.15	GenomeInfoDb_1.41.0
[29]	htmltools_0.5.8.1	RCurl_1.98-1.14
[31]	yaml_2.3.8	later_1.3.2
[33]	crayon_1.5.2	BiocParallel_1.39.0
[35]	DelayedArray_0.31.0	cachem_1.0.8
[37]	org.Hs.eg.db_3.19.1	abind_1.4-5
[39]	mime_0.12	digest_0.6.35
[41]	restfulr_0.0.15	grid_4.4.0
[43]	fastmap_1.1.1	SparseArray_1.5.0
[45]	cli_3.6.2	magrittr_2.0.3
[47]	S4Arrays_1.5.0	XML_3.99-0.16.1
[49]	UCSC.utils_1.1.0	promises_1.3.0
[51]	bit64_4.0.5	org.Mm.eg.db_3.19.1
[53]	XVector_0.45.0	httr_1.4.7
[55]	matrixStats_1.3.0	igraph_2.0.3
[57]	bit_4.0.5	png_0.1-8
[59]	memoise_2.0.1	shiny_1.8.1.1
[61]	GenomicRanges_1.57.0	IRanges_2.39.0
[63]	BiocIO_1.15.0	rtracklayer_1.65.0
[65]	rlang_1.1.3	Rcpp_1.0.12
[67]	xtable_1.8-4	DBI_1.2.2
[69]	BiocGenerics_0.51.0	splitstackshape_1.4.8
[71]	jsonlite_1.8.8	R6_2.5.1
[73]	MatrixGenerics_1.17.0	GenomicAlignments_1.41.0
[75]	zlibbioc_1.51.0	