

# 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 4.5.0 beta (2025-04-02 r88102)
```

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

```
Running under: Ubuntu 24.04.2 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.22-bioc/R/lib/libRblas.so
```

```
LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.12.0 LAPACK version 3.12.0
```

```
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
```

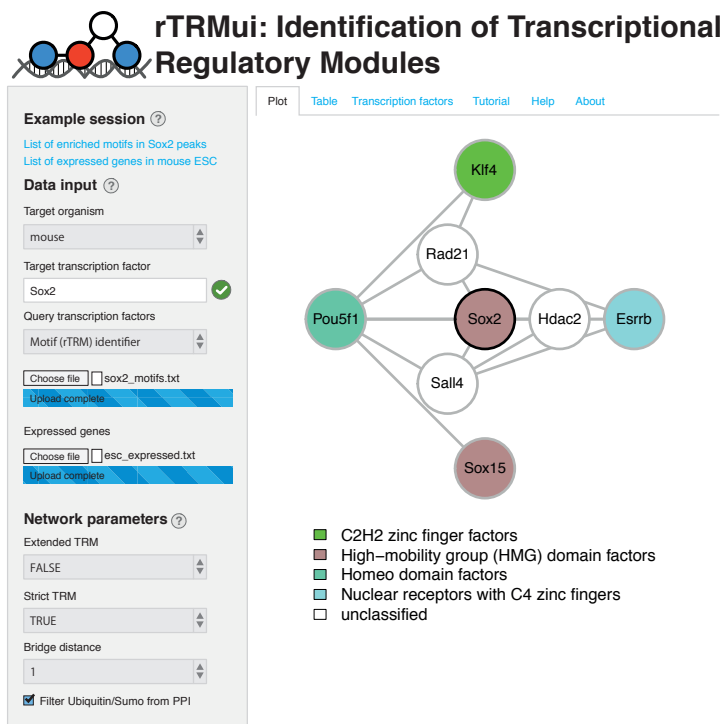


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[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_1.47.0
```

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

```
[1] KEGGREST_1.49.0      SummarizedExperiment_1.39.0
[3] rjson_0.2.23        lattice_0.22-7
[5] Biobase_2.69.0      vctrs_0.6.5
[7] tools_4.5.0         bitops_1.0-9
[9] generics_0.1.3     stats4_4.5.0
[11] curl_6.2.2          parallel_4.5.0
```

[13]	AnnotationDbi_1.71.0	RSQLite_2.3.9
[15]	MotifDb_1.51.0	blob_1.2.4
[17]	pkgconfig_2.0.3	Matrix_1.7-3
[19]	data.table_1.17.0	S4Vectors_0.47.0
[21]	lifecycle_1.0.4	GenomeInfoDbData_1.2.14
[23]	rTRM_1.47.0	compiler_4.5.0
[25]	Rsamtools_2.25.0	Biostrings_2.77.0
[27]	codetools_0.2-20	httpuv_1.6.15
[29]	GenomeInfoDb_1.45.0	htmltools_0.5.8.1
[31]	RCurl_1.98-1.17	yaml_2.3.10
[33]	later_1.4.2	crayon_1.5.3
[35]	BiocParallel_1.43.0	DelayedArray_0.35.0
[37]	cachem_1.1.0	org.Hs.eg.db_3.21.0
[39]	abind_1.4-8	mime_0.13
[41]	digest_0.6.37	restfulr_0.0.15
[43]	grid_4.5.0	fastmap_1.2.0
[45]	SparseArray_1.9.0	cli_3.6.4
[47]	magrittr_2.0.3	S4Arrays_1.9.0
[49]	XML_3.99-0.18	UCSC.utils_1.5.0
[51]	promises_1.3.2	bit64_4.6.0-1
[53]	org.Mm.eg.db_3.21.0	XVector_0.49.0
[55]	httr_1.4.7	matrixStats_1.5.0
[57]	igraph_2.1.4	bit_4.6.0
[59]	png_0.1-8	memoise_2.0.1
[61]	shiny_1.10.0	GenomicRanges_1.61.0
[63]	IRanges_2.43.0	BiocIO_1.19.0
[65]	rtracklayer_1.69.0	rlang_1.1.6
[67]	Rcpp_1.0.14	xtable_1.8-4
[69]	DBI_1.2.3	BiocGenerics_0.55.0
[71]	splitstackshape_1.4.8	jsonlite_2.0.0
[73]	R6_2.6.1	MatrixGenerics_1.21.0
[75]	GenomicAlignments_1.45.0	