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*.

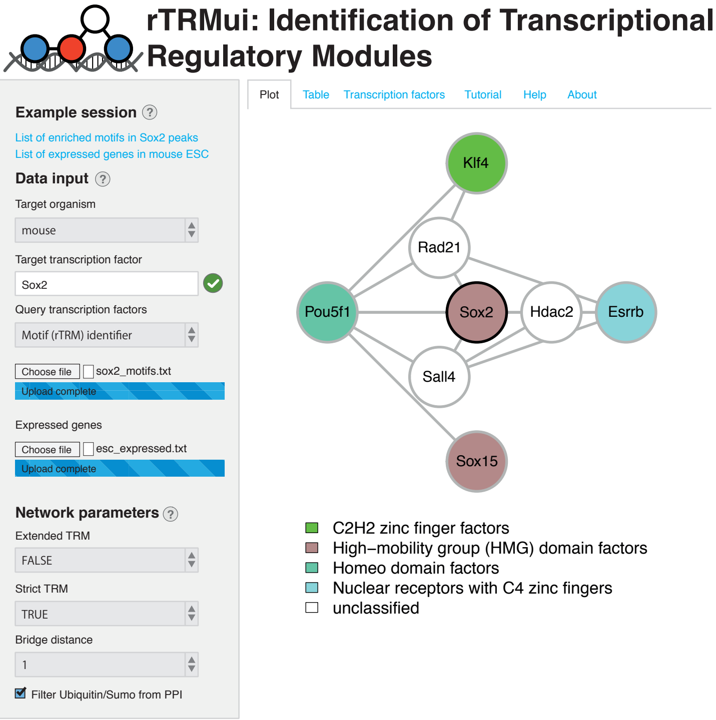
2 System information

```
> sessionInfo()
```

```
R version 4.5.0 RC (2025-04-04 r88126)
Platform: x86_64-pc-linux-gnu
Running under: Ubuntu 24.04.2 LTS

Matrix products: default
BLAS:   /home/biocbuild/bbs-3.21-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
```



rTRMui: Identification of Transcriptional Regulatory Modules

Example session

List of enriched motifs in Sox2 peaks

List of expressed genes in mouse ESC

Data input

Target organism: mouse

Target transcription factor: Sox2

Query transcription factors: Motif (rTRM) identifier

sox2_motifs.txt — Upload complete

Expressed genes: esc_expressed.txt — Upload complete

Network parameters

Extended TRM: FALSE

Strict TRM: TRUE

Bridge distance: 1

☑ Filter Ubiquitin/Sumo from PPI

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_1.46.0

loaded via a namespace (and not attached):
 [1] KEGGREST_1.48.0             SummarizedExperiment_1.38.0
 [3] rjson_0.2.23                lattice_0.22-7
 [5] Biobase_2.68.0              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_1.70.0        RSQLite_2.3.9
[15] MotifDb_1.50.0              blob_1.2.4
[17] pkgconfig_2.0.3             Matrix_1.7-3
[19] data.table_1.17.0           S4Vectors_0.46.0
[21] lifecycle_1.0.4             GenomeInfoDbData_1.2.14
[23] rTRM_1.46.0                 compiler_4.5.0
[25] Rsamtools_2.24.0            Biostrings_2.76.0
[27] codetools_0.2-20            httpuv_1.6.15
[29] GenomeInfoDb_1.44.0         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_1.42.0         DelayedArray_0.34.0
[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_1.8.0           cli_3.6.4
[47] magrittr_2.0.3              S4Arrays_1.8.0
[49] XML_3.99-0.18               UCSC.utils_1.4.0
[51] promises_1.3.2              bit64_4.6.0-1
[53] org.Mm.eg.db_3.21.0         XVector_0.48.0
[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_1.60.0
[63] IRanges_2.42.0              BiocIO_1.18.0
[65] rtracklayer_1.68.0          rlang_1.1.6
[67] Rcpp_1.0.14                 xtable_1.8-4
[69] DBI_1.2.3                   BiocGenerics_0.54.0
[71] splitstackshape_1.4.8       jsonlite_2.0.0
[73] R6_2.6.1                    MatrixGenerics_1.20.0
[75] GenomicAlignments_1.44.0
```