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*.

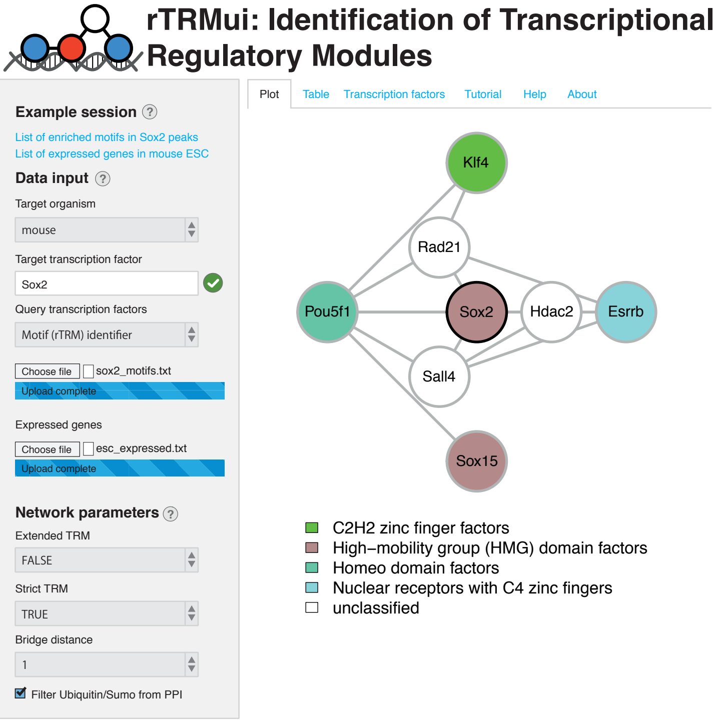
2 System information

```
> 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:   /home/biocbuild/bbs-3.20-bioc/R/lib/libRblas.so
LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.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
```



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
Expressed genes: esc_expressed.txt

Network parameters

Extended TRM: FALSE
Strict TRM: TRUE
Bridge distance: 1
☑ Filter Ubiquitin/Sumo from PPI

🟩 C2H2 zinc finger factors
🟫 High−mobility group (HMG) domain factors
🟩 Homeo domain factors
🟦 Nuclear receptors with C4 zinc fingers
☐ unclassified

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_1.44.0

loaded via a namespace (and not attached):
 [1] KEGGREST_1.46.0             SummarizedExperiment_1.36.0
 [3] rjson_0.2.23                lattice_0.22-6
 [5] Biobase_2.66.0              vctrs_0.6.5
 [7] tools_4.4.1                 bitops_1.0-9
 [9] stats4_4.4.1                curl_5.2.3
[11] parallel_4.4.1              AnnotationDbi_1.68.0
```

```
[13] RSQLite_2.3.7             MotifDb_1.48.0
[15] blob_1.2.4                pkgconfig_2.0.3
[17] Matrix_1.7-1              data.table_1.16.2
[19] S4Vectors_0.44.0          lifecycle_1.0.4
[21] GenomeInfoDbData_1.2.13   rTRM_1.44.0
[23] compiler_4.4.1            Rsamtools_2.22.0
[25] Biostrings_2.74.0         codetools_0.2-20
[27] httpuv_1.6.15             GenomeInfoDb_1.42.0
[29] htmltools_0.5.8.1         RCurl_1.98-1.16
[31] yaml_2.3.10               later_1.3.2
[33] crayon_1.5.3              BiocParallel_1.40.0
[35] DelayedArray_0.32.0       cachem_1.1.0
[37] org.Hs.eg.db_3.20.0       abind_1.4-8
[39] mime_0.12                 digest_0.6.37
[41] restfulr_0.0.15           grid_4.4.1
[43] fastmap_1.2.0             SparseArray_1.6.0
[45] cli_3.6.3                 magrittr_2.0.3
[47] S4Arrays_1.6.0            XML_3.99-0.17
[49] UCSC.utils_1.2.0          promises_1.3.0
[51] bit64_4.5.2               org.Mm.eg.db_3.20.0
[53] XVector_0.46.0            httr_1.4.7
[55] matrixStats_1.4.1         igraph_2.1.1
[57] bit_4.5.0                 png_0.1-8
[59] memoise_2.0.1             shiny_1.9.1
[61] GenomicRanges_1.58.0      IRanges_2.40.0
[63] BiocIO_1.16.0             rtracklayer_1.66.0
[65] rlang_1.1.4               Rcpp_1.0.13
[67] xtable_1.8-4              DBI_1.2.3
[69] BiocGenerics_0.52.0       splitstackshape_1.4.8
[71] jsonlite_1.8.9            R6_2.5.1
[73] MatrixGenerics_1.18.0     GenomicAlignments_1.42.0
[75] zlibbioc_1.52.0
```