rTRMui: a shiny user interface for the identification of transcriptional regulatory modules

Diego Diez

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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 beta (2024-04-14 r86421)
Platform: x86_64-apple-darwin20
Running under: macOS Monterey 12.7.1

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.4-x86_64/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.4-x86_64/Resources/lib/libRlapack.dylib;

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

time zone: America/New_York
tzcode source: internal
```
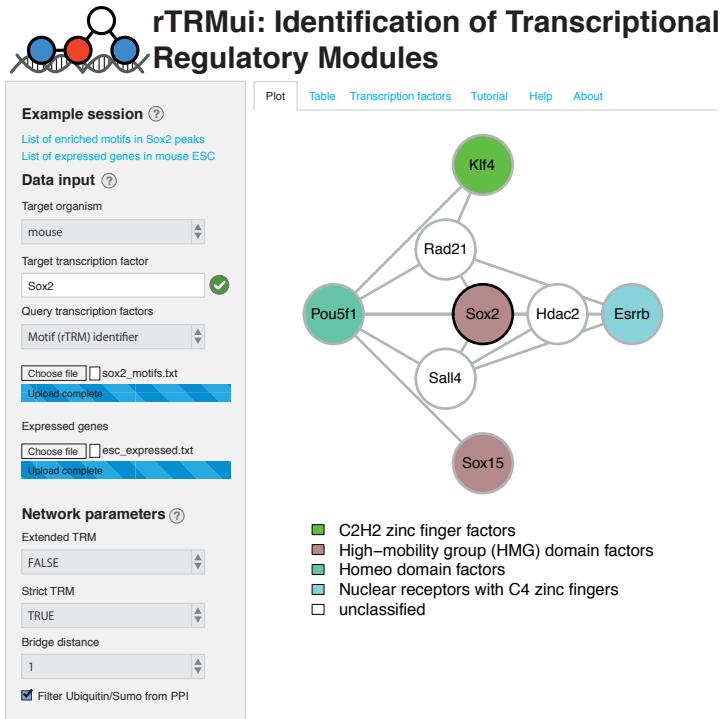
Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

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

other attached packages:
[1] rTRMui_1.42.0

loaded via a namespace (and not attached):
 [1] KEGGREST_1.44.0            SummarizedExperiment_1.34.0
 [3] rjson_0.2.21              lattice_0.22-6
 [5] Biobase_2.64.0            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_1.66.0
[13] RSQLite_2.3.6            MotifDb_1.46.0
[15] blob_1.2.4               pkgconfig_2.0.3
[17] Matrix_1.7-0             data.table_1.15.4
[19] S4Vectors_0.42.0         lifecycle_1.0.4
[21] GenomeInfoDbData_1.2.12   rTRM_1.42.0
```

```
[23] compiler_4.4.0            Rsamtools_2.20.0
[25] Biostrings_2.72.0         codetools_0.2-20
[27] httpuv_1.6.15             GenomeInfoDb_1.40.0
[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_1.38.0
[35] DelayedArray_0.30.0       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_1.4.0
[45] cli_3.6.2                 magrittr_2.0.3
[47] S4Arrays_1.4.0            XML_3.99-0.16.1
[49] UCSC.utils_1.0.0          promises_1.3.0
[51] bit64_4.0.5               org.Mm.eg.db_3.19.1
[53] XVector_0.44.0            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_1.56.0      IRanges_2.38.0
[63] BiocIO_1.14.0             rtracklayer_1.64.0
[65] rlang_1.1.3               Rcpp_1.0.12
[67] xtable_1.8-4              DBI_1.2.2
[69] BiocGenerics_0.50.0       splitstackshape_1.4.8
[71] jsonlite_1.8.8            R6_2.5.1
[73] MatrixGenerics_1.16.0     GenomicAlignments_1.40.0
[75] zlibbioc_1.50.0
```