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 4.2.0 RC (2022-04-19 r82224)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.4 LTS

Matrix products: default
BLAS:   /home/biocbuild/bbs-3.15-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.15-bioc/R/lib/libRlapack.so

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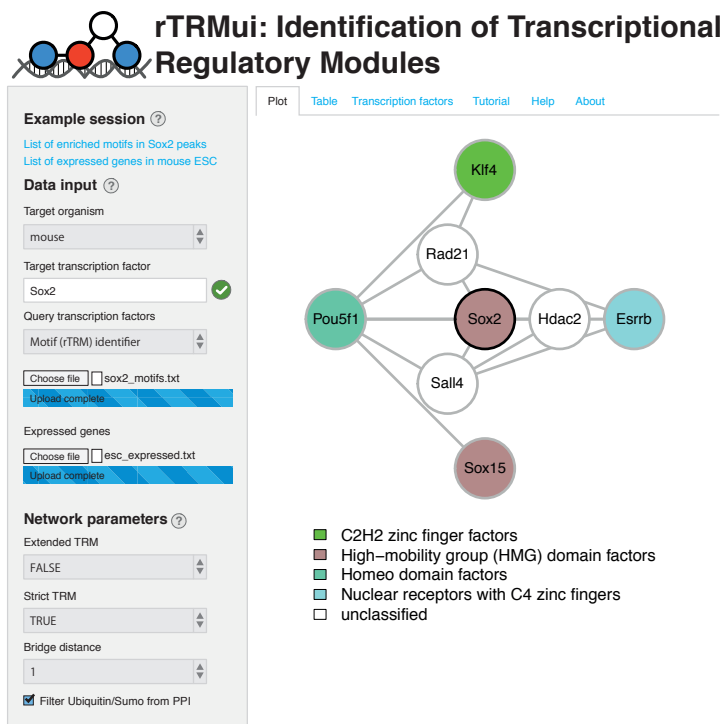
Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

```
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

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

other attached packages:
[1] rTRMui_1.34.0

loaded via a namespace (and not attached):
 [1] Rcpp_1.0.8.3              lattice_0.20-45
 [3] png_0.1-7                 Rsamtools_2.12.0
 [5] Biostrings_2.64.0         digest_0.6.29
 [7] mime_0.12                 org.Mm.eg.db_3.15.0
 [9] R6_2.5.1                  GenomeInfoDb_1.32.0
[11] stats4_4.2.0             RSQLite_2.2.12
[13] httr_1.4.2               zlibbioc_1.42.0
[15] rlang_1.0.2              data.table_1.14.2
[17] blob_1.2.3               S4Vectors_0.34.0
```

```
[19] Matrix_1.4-1                    BiocParallel_1.30.0
[21] igraph_1.3.1                    RCurl_1.98-1.6
[23] bit_4.0.4                       shiny_1.7.1
[25] DelayedArray_0.22.0             compiler_4.2.0
[27] httpuv_1.6.5                    rtracklayer_1.56.0
[29] pkgconfig_2.0.3                 BiocGenerics_0.42.0
[31] htmltools_0.5.2                 SummarizedExperiment_1.26.0
[33] KEGGREST_1.36.0                 rTRM_1.34.0
[35] GenomeInfoDbData_1.2.8          IRanges_2.30.0
[37] matrixStats_0.62.0             XML_3.99-0.9
[39] crayon_1.5.1                    later_1.3.0
[41] GenomicAlignments_1.32.0        bitops_1.0-7
[43] grid_4.2.0                      xtable_1.8-4
[45] lifecycle_1.0.1                 DBI_1.1.2
[47] magrittr_2.0.3                  cli_3.3.0
[49] cachem_1.0.6                    XVector_0.36.0
[51] promises_1.2.0.1               splitstackshape_1.4.8
[53] ellipsis_0.3.2                  vctrs_0.4.1
[55] org.Hs.eg.db_3.15.0             rjson_0.2.21
[57] restfulr_0.0.13                 tools_4.2.0
[59] bit64_4.0.5                     Biobase_2.56.0
[61] MotifDb_1.38.0                  MatrixGenerics_1.8.0
[63] parallel_4.2.0                  fastmap_1.1.0
[65] yaml_2.3.5                      AnnotationDbi_1.58.0
[67] GenomicRanges_1.48.0            memoise_2.0.1
[69] BiocIO_1.6.0
```