

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 4.1.1 (2021-08-10)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.3 LTS

Matrix products: default
BLAS: /home/biocbuild/bbs-3.14-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.14-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
```

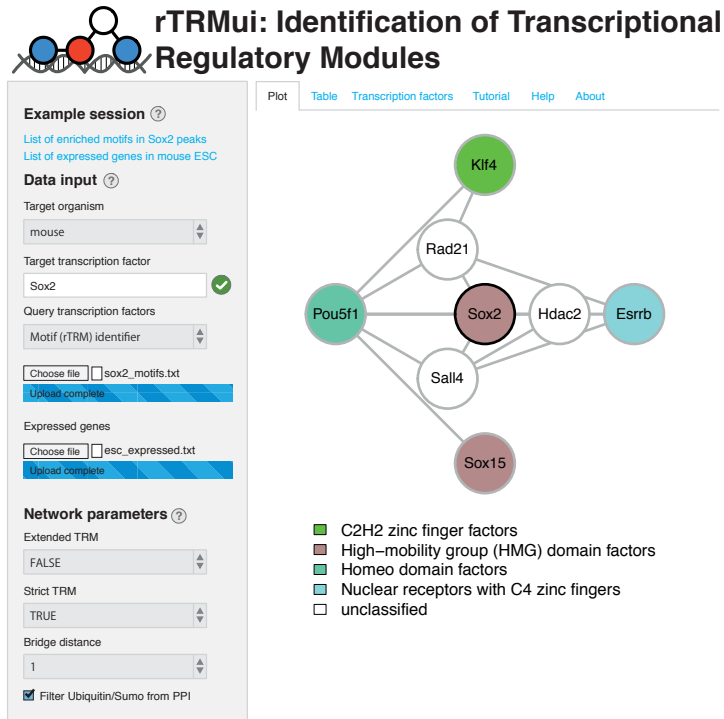


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[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_1.32.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_1.0.7           lattice_0.20-45
[3] png_0.1-7           Rsamtools_2.10.0
[5] Biostrings_2.62.0   digest_0.6.28
[7] mime_0.12           org.Mm.eg.db_3.14.0
[9] R6_2.5.1            GenomeInfoDb_1.30.0
[11] stats4_4.1.1        RSQLite_2.2.8
[13] httr_1.4.2          zlibbioc_1.40.0
[15] rlang_0.4.12        data.table_1.14.2
[17] rstudioapi_0.13     blob_1.2.2
```

| | | |
|------|----------------------|-----------------------------|
| [19] | S4Vectors_0.32.0 | Matrix_1.3-4 |
| [21] | BiocParallel_1.28.0 | igraph_1.2.7 |
| [23] | RCurl_1.98-1.5 | bit_4.0.4 |
| [25] | shiny_1.7.1 | DelayedArray_0.20.0 |
| [27] | compiler_4.1.1 | httpuv_1.6.3 |
| [29] | rtracklayer_1.54.0 | pkgconfig_2.0.3 |
| [31] | BiocGenerics_0.40.0 | htmltools_0.5.2 |
| [33] | KEGGREST_1.34.0 | SummarizedExperiment_1.24.0 |
| [35] | rTRM_1.32.0 | GenomeInfoDbData_1.2.7 |
| [37] | IRanges_2.28.0 | matrixStats_0.61.0 |
| [39] | XML_3.99-0.8 | crayon_1.4.1 |
| [41] | later_1.3.0 | GenomicAlignments_1.30.0 |
| [43] | bitops_1.0-7 | grid_4.1.1 |
| [45] | xtable_1.8-4 | lifecycle_1.0.1 |
| [47] | DBI_1.1.1 | magrittr_2.0.1 |
| [49] | cachem_1.0.6 | XVector_0.34.0 |
| [51] | promises_1.2.0.1 | splitstackshape_1.4.8 |
| [53] | ellipsis_0.3.2 | vctr_0.3.8 |
| [55] | org.Hs.eg.db_3.14.0 | rjson_0.2.20 |
| [57] | restfulr_0.0.13 | tools_4.1.1 |
| [59] | bit64_4.0.5 | Biobase_2.54.0 |
| [61] | MotifDb_1.36.0 | MatrixGenerics_1.6.0 |
| [63] | parallel_4.1.1 | fastmap_1.1.0 |
| [65] | yaml_2.2.1 | AnnotationDbi_1.56.0 |
| [67] | GenomicRanges_1.46.0 | memoise_2.0.0 |
| [69] | BiocIO_1.4.0 | |