

# 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 4.5.1 Patched (2025-08-23 r88802)
```

```
Platform: x86_64-pc-linux-gnu
```

```
Running under: Ubuntu 24.04.3 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.22-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          |

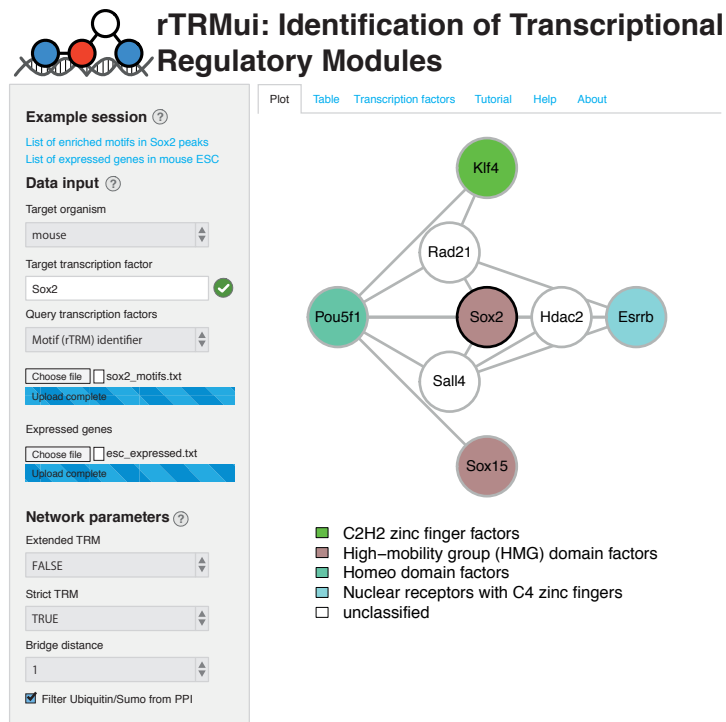


Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

```
[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_1.47.0
```

```
loaded via a namespace (and not attached):
```

```
[1] KEGGREST_1.49.1      SummarizedExperiment_1.39.2
[3] rjson_0.2.23         Biobase_2.69.1
[5] lattice_0.22-7       vctrs_0.6.5
[7] tools_4.5.1          bitops_1.0-9
[9] generics_0.1.4       stats4_4.5.1
[11] curl_7.0.0           parallel_4.5.1
```

|      |                       |                          |
|------|-----------------------|--------------------------|
| [13] | AnnotationDbi_1.71.1  | RSQLite_2.4.3            |
| [15] | MotifDb_1.51.0        | blob_1.2.4               |
| [17] | pkgconfig_2.0.3       | Matrix_1.7-4             |
| [19] | data.table_1.17.8     | S4Vectors_0.47.4         |
| [21] | lifecycle_1.0.4       | rTRM_1.47.0              |
| [23] | compiler_4.5.1        | Rsamtools_2.25.3         |
| [25] | Biostrings_2.77.2     | Seqinfo_0.99.2           |
| [27] | codetools_0.2-20      | httpuv_1.6.16            |
| [29] | htmltools_0.5.8.1     | RCurl_1.98-1.17          |
| [31] | yaml_2.3.10           | later_1.4.4              |
| [33] | crayon_1.5.3          | BiocParallel_1.43.4      |
| [35] | DelayedArray_0.35.3   | cachem_1.1.0             |
| [37] | org.Hs.eg.db_3.21.0   | abind_1.4-8              |
| [39] | mime_0.13             | digest_0.6.37            |
| [41] | restfulr_0.0.16       | fastmap_1.2.0            |
| [43] | grid_4.5.1            | SparseArray_1.9.1        |
| [45] | cli_3.6.5             | magrittr_2.0.4           |
| [47] | S4Arrays_1.9.1        | XML_3.99-0.19            |
| [49] | promises_1.3.3        | bit64_4.6.0-1            |
| [51] | org.Mm.eg.db_3.21.0   | XVector_0.49.1           |
| [53] | httr_1.4.7            | matrixStats_1.5.0        |
| [55] | igraph_2.1.4          | bit_4.6.0                |
| [57] | png_0.1-8             | memoise_2.0.1            |
| [59] | shiny_1.11.1          | GenomicRanges_1.61.5     |
| [61] | IRanges_2.43.5        | BiocIO_1.19.0            |
| [63] | rtracklayer_1.69.1    | rlang_1.1.6              |
| [65] | Rcpp_1.1.0            | xtable_1.8-4             |
| [67] | DBI_1.2.3             | BiocGenerics_0.55.1      |
| [69] | splitstackshape_1.4.8 | R6_2.6.1                 |
| [71] | MatrixGenerics_1.21.0 | GenomicAlignments_1.45.4 |