

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 4.3.0 RC (2023-04-13 r84269 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2022 x64 (build 20348)
```

```
Matrix products: default
```

```
locale:
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8
```

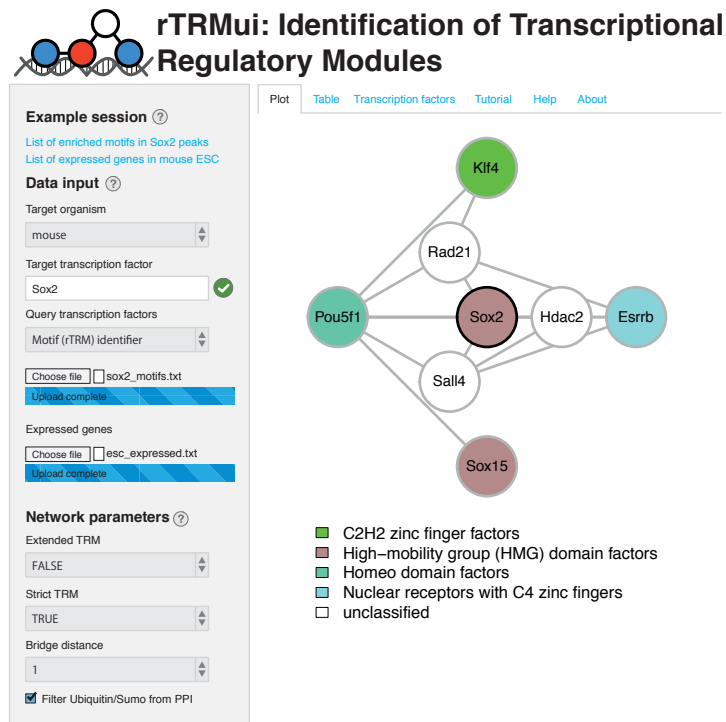


Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

```
time zone: America/New_York
tzcode source: internal
```

```
attached base packages:
```

```
[1] stats      graphics  grDevices  utils      datasets  methods   base
```

```
other attached packages:
```

```
[1] rTRMui_1.38.0
```

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

```
[1] KEGGREST_1.40.0      SummarizedExperiment_1.30.0
[3] rjson_0.2.21         Biobase_2.60.0
[5] lattice_0.21-8       vctrs_0.6.2
[7] tools_4.3.0          bitops_1.0-7
[9] stats4_4.3.0         parallel_4.3.0
[11] AnnotationDbi_1.62.0 RSQlite_2.3.1
[13] MotifDb_1.42.0       blob_1.2.4
[15] pkgconfig_2.0.3      Matrix_1.5-4
```

[17] data.table_1.14.8	S4Vectors_0.38.0
[19] lifecycle_1.0.3	GenomeInfoDbData_1.2.10
[21] rTRM_1.38.0	compiler_4.3.0
[23] Rsamtools_2.16.0	Biostrings_2.68.0
[25] codetools_0.2-19	httpuv_1.6.9
[27] GenomeInfoDb_1.36.0	htmltools_0.5.5
[29] RCurl_1.98-1.12	yaml_2.3.7
[31] later_1.3.0	crayon_1.5.2
[33] ellipsis_0.3.2	BiocParallel_1.34.0
[35] cachem_1.0.7	DelayedArray_0.26.0
[37] org.Hs.eg.db_3.17.0	mime_0.12
[39] digest_0.6.31	restfulr_0.0.15
[41] fastmap_1.1.1	grid_4.3.0
[43] cli_3.6.1	magrittr_2.0.3
[45] XML_3.99-0.14	promises_1.2.0.1
[47] bit64_4.0.5	org.Mm.eg.db_3.17.0
[49] XVector_0.40.0	httr_1.4.5
[51] matrixStats_0.63.0	igraph_1.4.2
[53] bit_4.0.5	png_0.1-8
[55] memoise_2.0.1	shiny_1.7.4
[57] GenomicRanges_1.52.0	IRanges_2.34.0
[59] BiocIO_1.10.0	rtracklayer_1.60.0
[61] rlang_1.1.0	Rcpp_1.0.10
[63] xtable_1.8-4	DBI_1.1.3
[65] BiocGenerics_0.46.0	splitstackshape_1.4.8
[67] R6_2.5.1	MatrixGenerics_1.12.0
[69] GenomicAlignments_1.36.0	zlibbioc_1.46.0