

# 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 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 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

attached base packages:
```

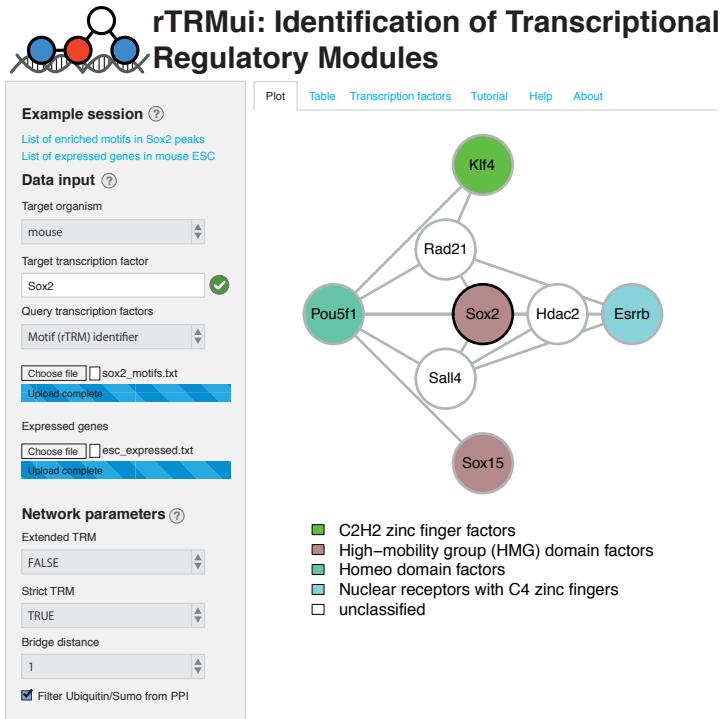


Figure 1: rTRMUI home page showing the TRM identified using the sample datasets from the tutorial.

```
[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
```