

# 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 r84257)
Platform: x86_64-apple-darwin20 (64-bit)
Running under: macOS Monterey 12.6.4

Matrix products: default
BLAS:      /Library/Frameworks/R.framework/Versions/4.3-x86_64/Resources/lib/libRblas.0.dylib
LAPACK:    /Library/Frameworks/R.framework/Versions/4.3-x86_64/Resources/lib/libRlapack.dylib

locale:
[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

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

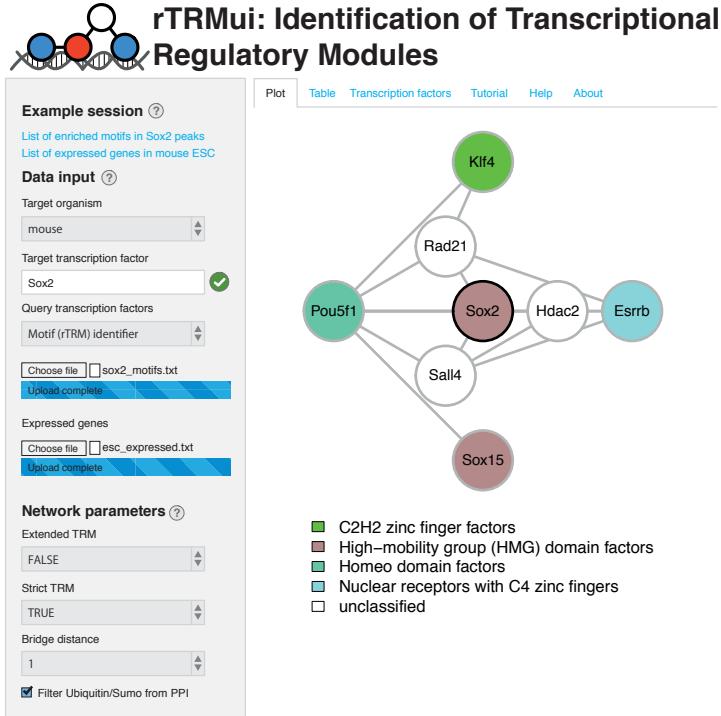


Figure 1: rTRMUI home page showing the TRM identified using the sample datasets from the tutorial.

```

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_1.30.1
[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_1.62.1     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_0.38.1
[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_1.6.11
[27] GenomeInfoDb_1.36.0      htmltools_0.5.5
[29] RCurl_1.98-1.12         yaml_2.3.7
[31] later_1.3.1              crayon_1.5.2
[33] ellipsis_0.3.2          BiocParallel_1.34.1
[35] cachem_1.0.8            DelayedArray_0.26.2
[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] S4Arrays_1.0.4           XML_3.99-0.14
[47] promises_1.2.0.1         bit64_4.0.5
[49] org.Mm.eg.db_3.17.0      XVector_0.40.0
[51] httr_1.4.6               matrixStats_0.63.0
[53] igraph_1.4.2             bit_4.0.5
[55] png_0.1-8                memoise_2.0.1
[57] shiny_1.7.4              GenomicRanges_1.52.0
[59] IRanges_2.34.0           BiocIO_1.10.0
[61] rtracklayer_1.60.0        rlang_1.1.1
[63] Rcpp_1.0.10               xtable_1.8-4
[65] DBI_1.1.3                BiocGenerics_0.46.0
[67] splitstackshape_1.4.8     R6_2.5.1
[69] MatrixGenerics_1.12.0    GenomicAlignments_1.36.0
[71] zlibbioc_1.46.0
```