

rTRMUi: a shiny user interface for the identification of transcriptional regulatory modules

Diego Diez

May 1, 2024

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 4.4.0 RC (2024-04-16 r86468 ucrt)
Platform: x86_64-w64-mingw32/x64
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
```

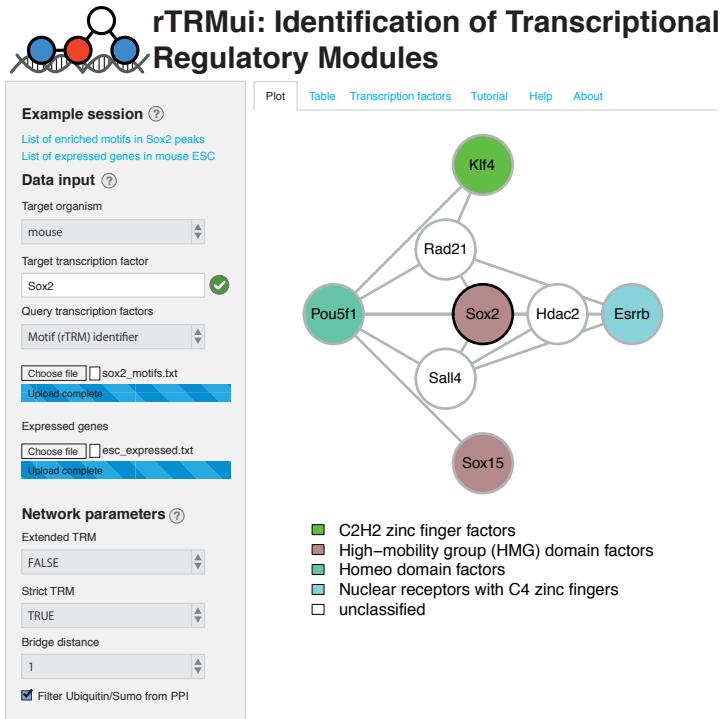


Figure 1: rTRMUI home page showing the TRM identified using the sample datasets from the tutorial.

```

time zone: America/New_York
tzcode source: internal

attached base packages:
[1] stats      graphics   grDevices utils      datasets   methods    base

other attached packages:
[1] rTRMUI_1.43.0

loaded via a namespace (and not attached):
[1] KEGGREST_1.45.0           SummarizedExperiment_1.35.0
[3] rjson_0.2.21              lattice_0.22-6
[5] Biobase_2.65.0            vctrs_0.6.5
[7] tools_4.4.0                bitops_1.0-7
[9] stats4_4.4.0              curl_5.2.1
[11] parallel_4.4.0            AnnotationDbi_1.67.0
[13] RSQLite_2.3.6              MotifDb_1.47.0
[15] blob_1.2.4                pkgconfig_2.0.3

```

```

[17] Matrix_1.7-0           data.table_1.15.4
[19] S4Vectors_0.43.0       lifecycle_1.0.4
[21] GenomeInfoDbData_1.2.12 rTRM_1.43.0
[23] compiler_4.4.0         Rsamtools_2.21.0
[25] Biostrings_2.73.0      codetools_0.2-20
[27] httpuv_1.6.15          GenomeInfoDb_1.41.0
[29] htmltools_0.5.8.1      RCurl_1.98-1.14
[31] yaml_2.3.8             later_1.3.2
[33] crayon_1.5.2           BiocParallel_1.39.0
[35] DelayedArray_0.31.0     cachem_1.0.8
[37] org.Hs.eg.db_3.19.1     abind_1.4-5
[39] mime_0.12               digest_0.6.35
[41] restfulr_0.0.15         grid_4.4.0
[43] fastmap_1.1.1          SparseArray_1.5.0
[45] cli_3.6.2               magrittr_2.0.3
[47] S4Arrays_1.5.0          XML_3.99-0.16.1
[49] UCSC.utils_1.1.0        promises_1.3.0
[51] bit64_4.0.5              org.Mm.eg.db_3.19.1
[53] XVector_0.45.0          httr_1.4.7
[55] matrixStats_1.3.0        igraph_2.0.3
[57] bit_4.0.5                png_0.1-8
[59] memoise_2.0.1            shiny_1.8.1.1
[61] GenomicRanges_1.57.0      IRanges_2.39.0
[63] BiocIO_1.15.0            rtracklayer_1.65.0
[65] rlang_1.1.3               Rcpp_1.0.12
[67] xtable_1.8-4              DBI_1.2.2
[69] BiocGenerics_0.51.0       splitstackshape_1.4.8
[71] jsonlite_1.8.8            R6_2.5.1
[73] MatrixGenerics_1.17.0     GenomicAlignments_1.41.0
[75] zlibbioc_1.51.0

```