

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 3.4.0 (2017-04-21)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2012 R2 x64 (build 9600)

Matrix products: default

locale:
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.1252
[3] LC_MONETARY=English_United States.1252
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.1252

attached base packages:
```

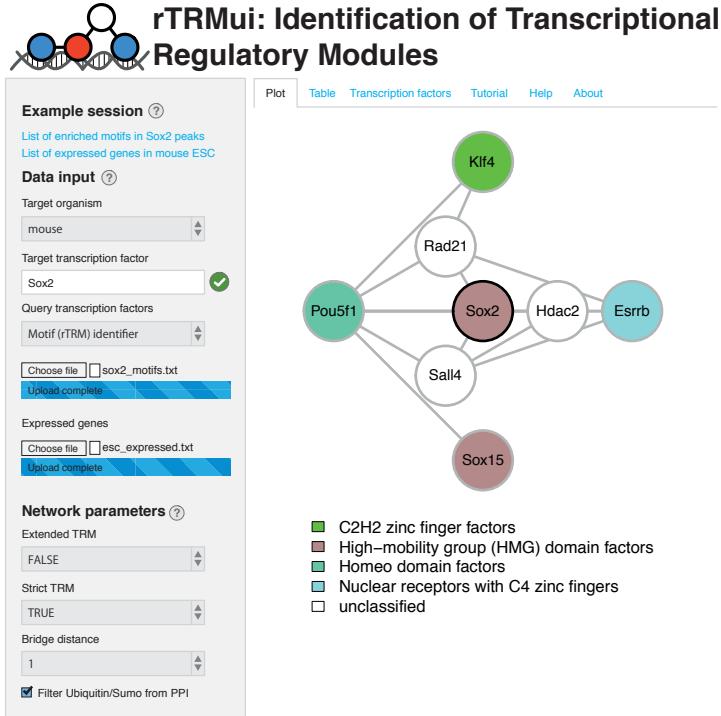


Figure 1: rTRMUI home page showing the TRM identified using the sample datasets from the tutorial.

```
[1] stats      graphics   grDevices utils      datasets   methods    base
other attached packages:
[1] rTRMUI_1.14.0

loaded via a namespace (and not attached):
[1] Rcpp_0.12.10           compiler_3.4.0
[3] GenomeInfoDb_1.12.0    MotifDb_1.18.0
[5] XVector_0.16.0         bitops_1.0-6
[7] tools_3.4.0            zlibbioc_1.22.0
[9] digest_0.6.12          lattice_0.20-35
[11] RSQLite_1.1-2          memoise_1.1.0
[13] Matrix_1.2-9           igraph_1.0.1
[15] DelayedArray_0.2.0     shiny_1.0.2
[17] DBI_0.6-1              parallel_3.4.0
[19] GenomeInfoDbData_0.99.0 org.Mm.eg.db_3.4.1
[21] rtracklayer_1.36.0     Biostrings_2.44.0
[23] S4Vectors_0.14.0       IRanges_2.10.0
```

```
[25] grid_3.4.0                  stats4_3.4.0
[27] Biobase_2.36.0               R6_2.2.0
[29] AnnotationDbi_1.38.0        XML_3.98-1.6
[31] BiocParallel_1.10.0          org.Hs.eg.db_3.4.1
[33] magrittr_1.5                 matrixStats_0.52.2
[35] Rsamtools_1.28.0             htmltools_0.3.5
[37] BiocGenerics_0.22.0          GenomicRanges_1.28.0
[39] GenomicAlignments_1.12.0     SummarizedExperiment_1.6.0
[41] mime_0.5                     xtable_1.8-2
[43] httpuv_1.3.3                RCurl_1.95-4.8
[45] rTRM_1.14.0
```