

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

Diego Diez

April 7, 2020

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 4.0.0 alpha (2020-04-05 r78150)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Mojave 10.14.6
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
```

```
locale:
```

```
[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
attached base packages:
```

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

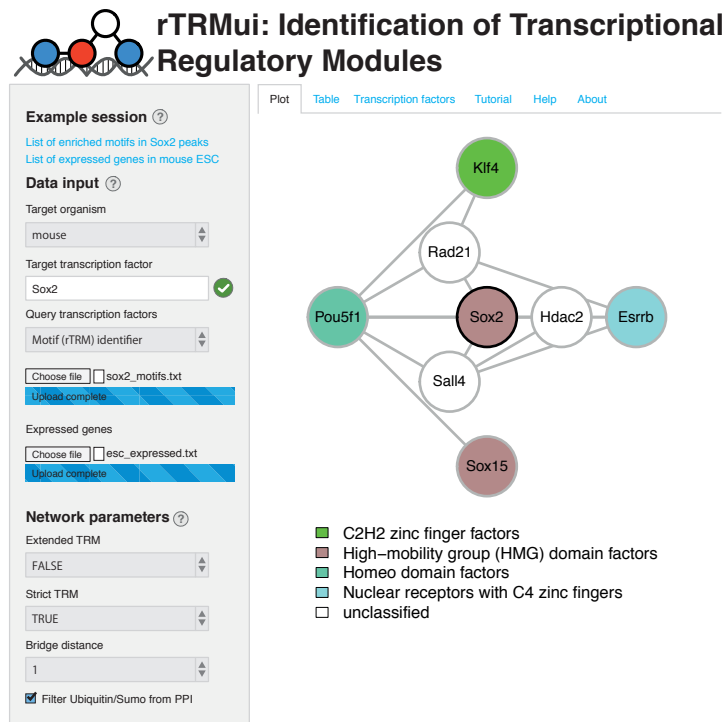


Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

other attached packages:

```
[1] rTRMui_1.25.0
```

loaded via a namespace (and not attached):

```
[1] SummarizedExperiment_1.17.5 lattice_0.20-41
[3] vctrs_0.2.4 htmltools_0.4.0
[5] stats4_4.0.0 rtracklayer_1.47.0
[7] blob_1.2.1 XML_3.99-0.3
[9] rlang_0.4.5 later_1.0.0
[11] DBI_1.1.0 BiocParallel_1.21.2
[13] BiocGenerics_0.33.3 bit64_0.9-7
[15] splitstackshape_1.4.8 matrixStats_0.56.0
[17] GenomeInfoDbData_1.2.2 zlibbioc_1.33.1
[19] Biostrings_2.55.7 memoise_1.1.0
[21] Biobase_2.47.3 IRanges_2.21.8
[23] fastmap_1.0.1 httpuv_1.5.2
[25] GenomeInfoDb_1.23.16 parallel_4.0.0
[27] AnnotationDbi_1.49.1 MotifDb_1.29.9
```

[29] Rcpp_1.0.4.6	xtable_1.8-4
[31] promises_1.1.0	DelayedArray_0.13.10
[33] org.Hs.eg.db_3.10.0	S4Vectors_0.25.15
[35] XVector_0.27.2	rTRM_1.25.0
[37] mime_0.9	bit_1.1-15.2
[39] Rsamtools_2.3.7	digest_0.6.25
[41] shiny_1.4.0.2	GenomicRanges_1.39.3
[43] grid_4.0.0	tools_4.0.0
[45] bitops_1.0-6	magrittr_1.5
[47] RCurl_1.98-1.1	RSQLite_2.2.0
[49] crayon_1.3.4	pkgconfig_2.0.3
[51] Matrix_1.2-18	data.table_1.12.8
[53] org.Mm.eg.db_3.10.0	R6_2.4.1
[55] GenomicAlignments_1.23.2	igraph_1.2.5
[57] compiler_4.0.0	