

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 3.3.1 (2016-06-21)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2012 R2 x64 (build 9600)
```

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

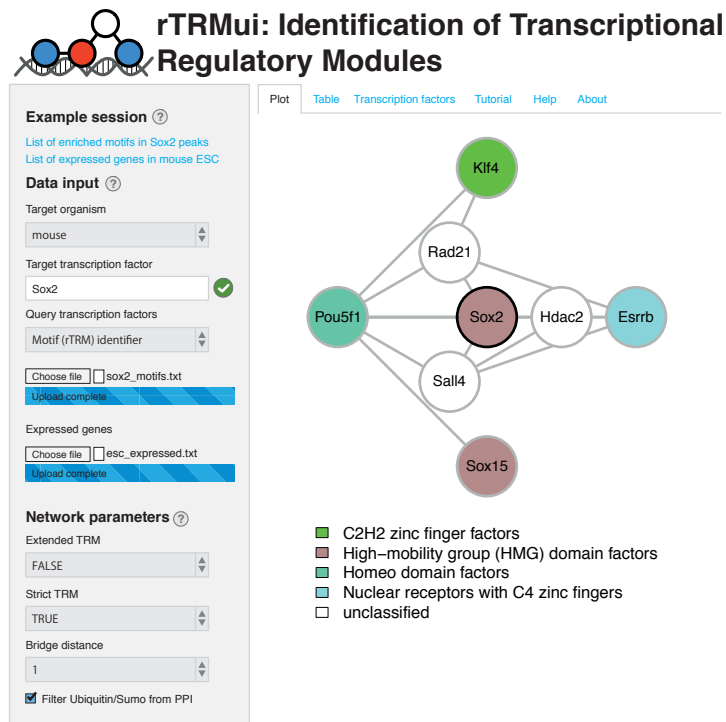


Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

other attached packages:

```
[1] rTRMui_1.12.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.7           GenomeInfoDb_1.10.0
[3] XVector_0.14.0        MotifDb_1.16.0
[5] bitops_1.0-6          tools_3.3.1
[7] zlibbioc_1.20.0       digest_0.6.10
[9] RSQLite_1.0.0         lattice_0.20-34
[11] Matrix_1.2-7.1        igraph_1.0.1
[13] shiny_0.14.1          DBI_0.5-1
[15] parallel_3.3.1        rtracklayer_1.34.0
[17] org.Mm.eg.db_3.4.0    Biostrings_2.42.0
[19] S4Vectors_0.12.0     IRanges_2.8.0
[21] stats4_3.3.1          grid_3.3.1
[23] Biobase_2.34.0        R6_2.2.0
[25] AnnotationDbi_1.36.0  XML_3.98-1.4
[27] BiocParallel_1.8.0    org.Hs.eg.db_3.4.0
```

[29]	magrittr_1.5	Rsamtools_1.26.0
[31]	htmltools_0.3.5	BiocGenerics_0.20.0
[33]	GenomicRanges_1.26.0	GenomicAlignments_1.10.0
[35]	SummarizedExperiment_1.4.0	mime_0.5
[37]	xtable_1.8-2	httpuv_1.3.3
[39]	RCurl_1.95-4.8	rTRM_1.12.0