

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 ??). 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-apple-darwin13.4.0 (64-bit)
Running under: OS X 10.9.5 (Mavericks)
```

```
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
```

```
other attached packages:
```

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

```
loaded via a namespace (and not attached):
```

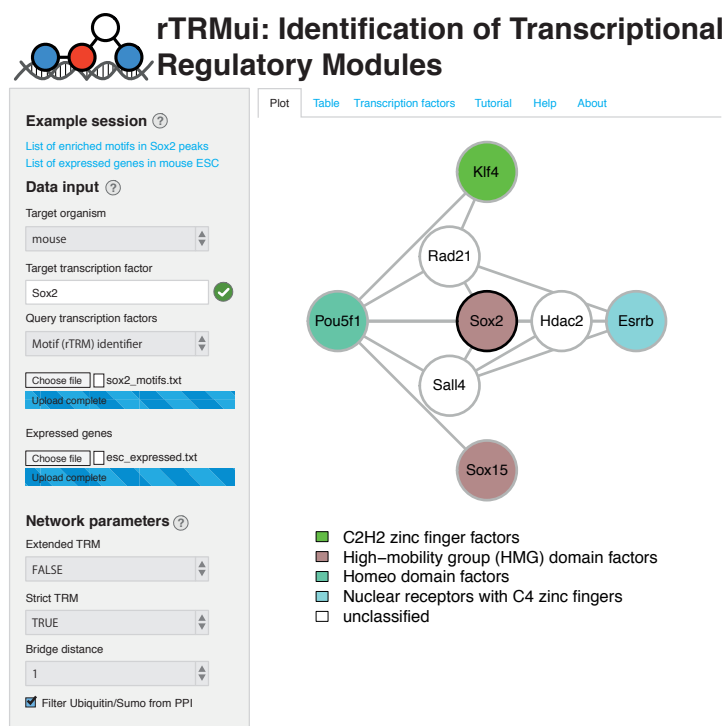


Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

[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	Biostings_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