

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

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April 16, 2015

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 3.2.0 RC (2015-04-08 r68161)
Platform: x86_64-apple-darwin10.8.0 (64-bit)
Running under: OS X 10.6.8 (Snow Leopard)
```

```
locale:
```

```
[1] en_US.UTF-8/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_1.6.0  RSQLite_1.0.0 DBI_0.3.1
```

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

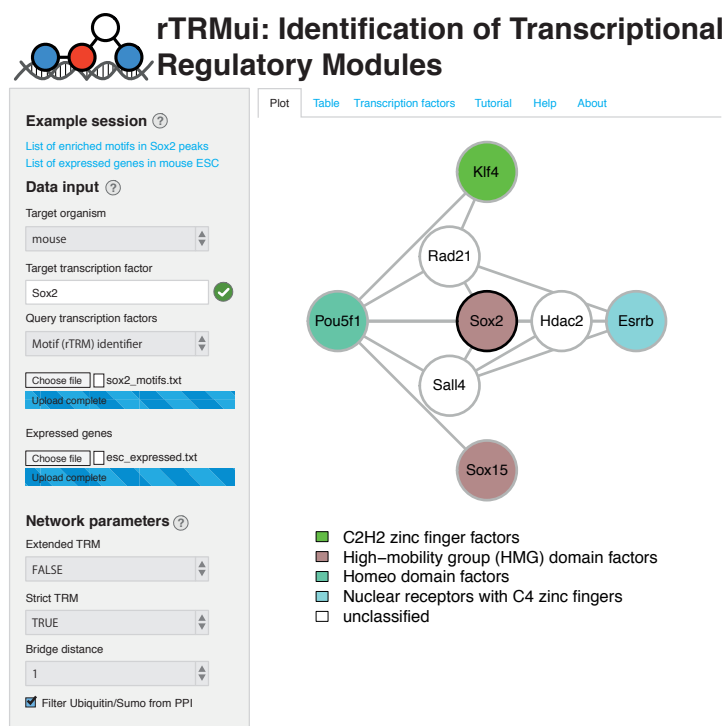


Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

[1] Rcpp_0.11.5	futile.logger_1.4	GenomeInfoDb_1.4.0
[4] MotifDb_1.10.0	XVector_0.8.0	bitops_1.0-6
[7] futile.options_1.0.0	tools_3.2.0	zlibbioc_1.14.0
[10] digest_0.6.8	igraph_0.7.1	shiny_0.11.1
[13] parallel_3.2.0	org.Mm.eg.db_3.1.2	rtracklayer_1.28.0
[16] Biostrings_2.36.0	S4Vectors_0.6.0	IRanges_2.2.0
[19] stats4_3.2.0	Biobase_2.28.0	R6_2.0.1
[22] AnnotationDbi_1.30.0	XML_3.98-1.1	BiocParallel_1.2.0
[25] RJSONIO_1.3-0	org.Hs.eg.db_3.1.2	lambda.r_1.1.7
[28] Rsamtools_1.20.0	htmltools_0.2.6	BiocGenerics_0.14.0
[31] GenomicRanges_1.20.0	GenomicAlignments_1.4.0	mime_0.3
[34] xtable_1.7-4	httpuv_1.3.2	RCurl_1.95-4.5
[37] rTRM_1.6.0		