

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

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May 2, 2014

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 3.1.0 (2014-04-10)
```

```
Platform: x86_64-apple-darwin13.1.0 (64-bit)
```

```
locale:
```

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

```
attached base packages:
```

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

```
other attached packages:
```

```
[1] rTRMui_1.2.0      AnnotationDbi_1.26.0 GenomeInfoDb_1.0.2
[4] Biobase_2.24.0    BiocGenerics_0.10.0 RSQLite_0.11.4
[7] DBI_0.2-7
```

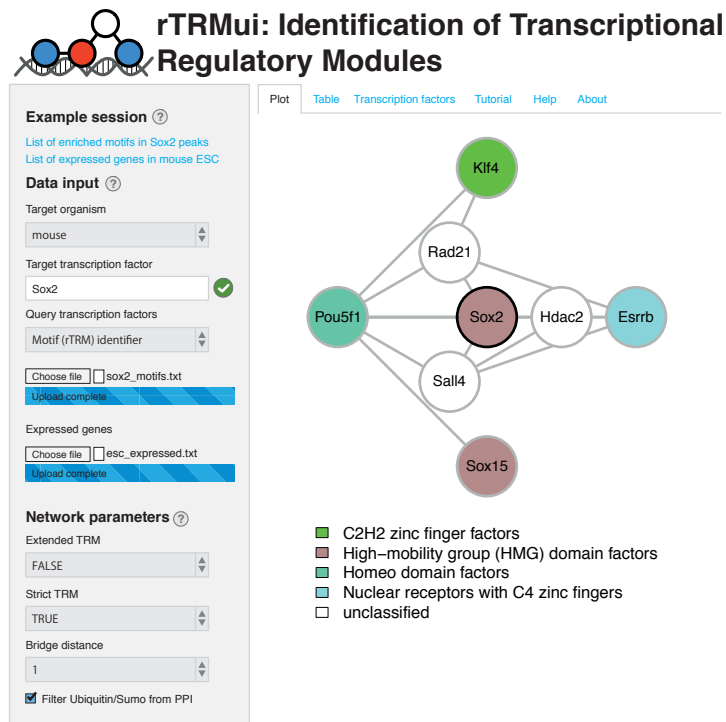


Figure 1: rTRMui home page showing the TRM indentified using the sample datasets from the tutorial.

loaded via a namespace (and not attached):

[1] BBmisc_1.6	BSgenome_1.32.0	BatchJobs_1.2
[4] BiocParallel_0.6.0	Biostrings_2.32.0	GenomicAlignments_1.0.1
[7] GenomicRanges_1.16.3	IRanges_1.22.5	MotifDb_1.6.0
[10] RCurl_1.95-4.1	RJSONIO_1.2-0.2	Rcpp_0.11.1
[13] Rsamtools_1.16.0	XML_3.98-1.1	XVector_0.4.0
[16] bitops_1.0-6	brew_1.0-6	caTools_1.17
[19] codetools_0.2-8	digest_0.6.4	fail_1.2
[22] foreach_1.4.2	httpuv_1.3.0	igraph_0.7.1
[25] iterators_1.0.7	org.Hs.eg.db_2.14.0	org.Mm.eg.db_2.14.0
[28] plyr_1.8.1	rTRM_1.2.0	rtracklayer_1.24.0
[31] sendmailR_1.1-2	shiny_0.9.1	stats4_3.1.0
[34] stringr_0.6.2	tools_3.1.0	xtable_1.7-3
[37] zlibbioc_1.10.0		