

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

Diego Diez

October 13, 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 3.1.1 Patched (2014-09-25 r66681)
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 stats4 stats graphics grDevices utils datasets
[8] methods base
```

```
other attached packages:
```

```
[1] rTRMui_1.4.0 AnnotationDbi_1.28.0 GenomeInfoDb_1.2.0
[4] IRanges_2.0.0 S4Vectors_0.4.0 Biobase_2.26.0
[7] BiocGenerics_0.12.0 RSQLite_0.11.4 DBI_0.3.1
```



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_1.7	BatchJobs_1.4	BiocParallel_1.0.0
[4] Biostrings_2.34.0	GenomicAlignments_1.2.0	GenomicRanges_1.18.0
[7] MotifDb_1.8.0	R6_2.0	RCurl_1.95-4.3
[10] RJSONIO_1.3-0	Rcpp_0.11.3	Rsamtools_1.18.0
[13] XML_3.98-1.1	XVector_0.6.0	base64enc_0.1-2
[16] bitops_1.0-6	brew_1.0-6	checkmate_1.4
[19] codetools_0.2-9	digest_0.6.4	fail_1.2
[22] foreach_1.4.2	htmltools_0.2.6	httpuv_1.3.0
[25] igraph_0.7.1	iterators_1.0.7	mime_0.2
[28] org.Hs.eg.db_3.0.0	org.Mm.eg.db_3.0.0	rTRM_1.4.0
[31] rtracklayer_1.26.0	sendmailR_1.2-1	shiny_0.10.2.1
[34] stringr_0.6.2	tools_3.1.1	xtable_1.7-4
[37] zlibbioc_1.12.0		