

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 3.1.1 Patched (2014-09-25 r66681)
Platform: x86_64-apple-darwin10.8.0 (64-bit)
```

```
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] 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] base64enc_0.1-2	BatchJobs_1.4	BBmisc_1.7
[4] BiocParallel_1.0.0	Biostrings_2.34.0	bitops_1.0-6
[7] brew_1.0-6	checkmate_1.4	codetools_0.2-9
[10] digest_0.6.4	fail_1.2	foreach_1.4.2
[13] GenomicAlignments_1.2.0	GenomicRanges_1.18.0	htmltools_0.2.6
[16] httpuv_1.3.0	igraph_0.7.1	iterators_1.0.7
[19] mime_0.2	MotifDb_1.8.0	org.Hs.eg.db_3.0.0
[22] org.Mm.eg.db_3.0.0	R6_2.0	Rcpp_0.11.3
[25] RCurl_1.95-4.3	RJSONIO_1.3-0	Rsamtools_1.18.0
[28] rtracklayer_1.26.0	rTRM_1.4.0	sendmailR_1.2-1
[31] shiny_0.10.2.1	stringr_0.6.2	tools_3.1.1
[34] XML_3.98-1.1	xtable_1.7-4	XVector_0.6.0
[37] zlibbioc_1.12.0		