

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

Diego Diez

April 11, 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 RC (2014-04-02 r65358)
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 stats      graphics grDevices utils      datasets  methods
[8] base
```

```
other attached packages:
```

```
[1] rTRMui_1.2.0      AnnotationDbi_1.26.0 GenomeInfoDb_1.0.0
[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] BatchJobs_1.2	BBmisc_1.5	BiocParallel_0.6.0
[4] Biostrings_2.32.0	bitops_1.0-6	brew_1.0-6
[7] BSgenome_1.32.0	caTools_1.16	codetools_0.2-8
[10] digest_0.6.4	fail_1.2	foreach_1.4.2
[13] GenomicAlignments_1.0.0	GenomicRanges_1.16.0	httpuv_1.3.0
[16] igraph_0.7.0	IRanges_1.21.45	iterators_1.0.7
[19] MotifDb_1.6.0	org.Hs.eg.db_2.14.0	org.Mm.eg.db_2.14.0
[22] plyr_1.8.1	Rcpp_0.11.1	RCurl_1.95-4.1
[25] RJSONIO_1.0-3	Rsamtools_1.16.0	rtracklayer_1.24.0
[28] rTRM_1.2.0	sendmailR_1.1-2	shiny_0.9.1
[31] stats4_3.1.0	stringr_0.6.2	tools_3.1.0
[34] XML_3.98-1.1	xtable_1.7-3	XVector_0.4.0
[37] zlibbioc_1.10.0		