

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 3.2.2 (2015-08-14)
Platform: x86_64-apple-darwin13.4.0 (64-bit)
Running under: OS X 10.9.5 (Mavericks)
```

```
locale:
```

```
[1] C/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_1.8.0  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_0.12.1	futile.logger_1.4.1
[3] GenomeInfoDb_1.6.0	XVector_0.10.0
[5] MotifDb_1.12.0	bitops_1.0-6
[7] futile.options_1.0.0	tools_3.2.2
[9] zlibbioc_1.16.0	digest_0.6.8
[11] igraph_1.0.1	shiny_0.12.2
[13] parallel_3.2.2	rtracklayer_1.30.0
[15] org.Mm.eg.db_3.2.3	Biostings_2.38.0
[17] S4Vectors_0.8.0	IRanges_2.4.0
[19] stats4_3.2.2	Biobase_2.30.0
[21] R6_2.1.1	AnnotationDbi_1.32.0
[23] XML_3.98-1.3	BiocParallel_1.4.0
[25] lambda.r_1.1.7	org.Hs.eg.db_3.2.3
[27] magrittr_1.5	Rsamtools_1.22.0
[29] htmltools_0.2.6	BiocGenerics_0.16.0
[31] GenomicRanges_1.22.0	GenomicAlignments_1.6.0
[33] SummarizedExperiment_1.0.0	mime_0.4
[35] xtable_1.7-4	httpuv_1.3.3

[37] RCurl_1.95-4.7

rTRM_1.8.0