

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

Diego Diez

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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 3.3.0 RC (2016-04-25 r70549)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2008 R2 x64 (build 7601) Service Pack 1
```

```
locale:
```

```
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.1252
[3] LC_MONETARY=English_United States.1252
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.1252
```

```
attached base packages:
```

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



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

other attached packages:

```
[1] rTRMui_1.10.0
```

loaded via a namespace (and not attached):

```
[1] igraph_1.0.1           Rcpp_0.12.4.5
[3] AnnotationDbi_1.34.0   MotifDb_1.14.0
[5] XVector_0.12.0         magrittr_1.5
[7] GenomicAlignments_1.8.0 GenomicRanges_1.24.0
[9] BiocGenerics_0.18.0    zlibbioc_1.18.0
[11] IRanges_2.6.0          BiocParallel_1.6.0
[13] xtable_1.8-2           R6_2.1.2
[15] org.Hs.eg.db_3.3.0     GenomeInfoDb_1.8.0
[17] tools_3.3.0            SummarizedExperiment_1.2.0
[19] parallel_3.3.0         Biobase_2.32.0
[21] DBI_0.4                htmltools_0.3.5
[23] digest_0.6.9           shiny_0.13.2
[25] org.Mm.eg.db_3.3.0     rtracklayer_1.32.0
[27] S4Vectors_0.10.0       bitops_1.0-6
```

[29]	RCurl_1.95-4.8	RSQLite_1.0.0
[31]	mime_0.4	Rsamtools_1.24.0
[33]	Biostrings_2.40.0	stats4_3.3.0
[35]	XML_3.98-1.4	rTRM_1.10.0
[37]	httpuv_1.3.3	