

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 3.4.0 (2017-04-21)
```

```
Platform: x86_64-apple-darwin15.6.0 (64-bit)
```

```
Running under: OS X El Capitan 10.11.6
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRblas.0.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRlapack.dylib
```

```
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
```



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

other attached packages:

```
[1] rTRMui_1.14.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.10          compiler_3.4.0
[3] GenomeInfoDb_1.12.0   MotifDb_1.18.0
[5] XVector_0.16.0         bitops_1.0-6
[7] tools_3.4.0           zlibbioc_1.22.0
[9] digest_0.6.12         lattice_0.20-35
[11] RSQLite_1.1-2         memoise_1.1.0
[13] Matrix_1.2-9          igraph_1.0.1
[15] DelayedArray_0.2.0    shiny_1.0.2
[17] DBI_0.6-1             parallel_3.4.0
[19] GenomeInfoDbData_0.99.0 org.Mm.eg.db_3.4.1
[21] rtracklayer_1.36.0    Biostrings_2.44.0
[23] S4Vectors_0.14.0      IRanges_2.10.0
[25] grid_3.4.0            stats4_3.4.0
[27] Biobase_2.36.0        R6_2.2.0
```

[29]	AnnotationDbi_1.38.0	XML_3.98-1.6
[31]	BiocParallel_1.10.0	org.Hs.eg.db_3.4.1
[33]	magrittr_1.5	matrixStats_0.52.2
[35]	Rsamtools_1.28.0	htmltools_0.3.5
[37]	BiocGenerics_0.22.0	GenomicRanges_1.28.0
[39]	GenomicAlignments_1.12.0	SummarizedExperiment_1.6.0
[41]	mime_0.5	xtable_1.8-2
[43]	httpuv_1.3.3	RCurl_1.95-4.8
[45]	rTRM_1.14.0	