

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 3.5.0 (2018-04-23)
```

```
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/3.5/Resources/lib/libRblas.0.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/3.5/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_1.18.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.16           GenomeInfoDb_1.16.0
[3] compiler_3.5.0         later_0.7.1
[5] MotifDb_1.22.0         XVector_0.20.0
[7] bitops_1.0-6           tools_3.5.0
[9] zlibbioc_1.26.0        digest_0.6.15
[11] bit_1.1-12             lattice_0.20-35
[13] RSQLite_2.1.0          memoise_1.1.0
[15] pkgconfig_2.0.1        Matrix_1.2-14
[17] igraph_1.2.1           DelayedArray_0.6.0
[19] shiny_1.0.5            DBI_0.8
[21] parallel_3.5.0         GenomeInfoDbData_1.1.0
[23] org.Mm.eg.db_3.6.0     rtracklayer_1.40.0
[25] Biostrings_2.48.0      S4Vectors_0.18.0
[27] IRanges_2.14.0         grid_3.5.0
```

[29]	stats4_3.5.0	bit64_0.9-7
[31]	data.table_1.10.4-3	Biobase_2.40.0
[33]	R6_2.2.2	AnnotationDbi_1.42.0
[35]	BiocParallel_1.14.0	XML_3.98-1.11
[37]	org.Hs.eg.db_3.6.0	blob_1.1.1
[39]	magrittr_1.5	matrixStats_0.53.1
[41]	GenomicAlignments_1.16.0	Rsamtools_1.32.0
[43]	GenomicRanges_1.32.0	promises_1.0.1
[45]	htmltools_0.3.6	BiocGenerics_0.26.0
[47]	SummarizedExperiment_1.10.0	splitstackshape_1.4.4
[49]	mime_0.5	xtable_1.8-2
[51]	httpuv_1.4.1	RCurl_1.95-4.10
[53]	rTRM_1.18.0	