

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

Diego Diez

October 26, 2021

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 4.1.1 Patched (2021-08-22 r80813)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Mojave 10.14.6
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.1/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_1.32.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_1.0.7          lattice_0.20-45
[3] png_0.1-7           Rsamtools_2.10.0
[5] Biostrings_2.62.0   digest_0.6.28
[7] mime_0.12           org.Mm.eg.db_3.14.0
[9] R6_2.5.1            GenomeInfoDb_1.30.0
[11] stats4_4.1.1        RSQLite_2.2.8
[13] httr_1.4.2          zlibbioc_1.40.0
[15] rlang_0.4.12        data.table_1.14.2
[17] rstudioapi_0.13     blob_1.2.2
[19] S4Vectors_0.32.0    Matrix_1.3-4
[21] BiocParallel_1.28.0 igraph_1.2.7
[23] RCurl_1.98-1.5      bit_4.0.4
[25] shiny_1.7.1         DelayedArray_0.20.0
[27] compiler_4.1.1      httpuv_1.6.3
```

[29]	rtracklayer_1.54.0	pkgconfig_2.0.3
[31]	BiocGenerics_0.40.0	htmltools_0.5.2
[33]	KEGGREST_1.34.0	SummarizedExperiment_1.24.0
[35]	rTRM_1.32.0	GenomeInfoDbData_1.2.7
[37]	IRanges_2.28.0	matrixStats_0.61.0
[39]	XML_3.99-0.8	crayon_1.4.1
[41]	later_1.3.0	GenomicAlignments_1.30.0
[43]	bitops_1.0-7	grid_4.1.1
[45]	xtable_1.8-4	lifecycle_1.0.1
[47]	DBI_1.1.1	magrittr_2.0.1
[49]	cachem_1.0.6	XVector_0.34.0
[51]	promises_1.2.0.1	splitstackshape_1.4.8
[53]	ellipsis_0.3.2	vctrs_0.3.8
[55]	org.Hs.eg.db_3.14.0	rjson_0.2.20
[57]	restfulr_0.0.13	tools_4.1.1
[59]	bit64_4.0.5	Biobase_2.54.0
[61]	MotifDb_1.36.0	MatrixGenerics_1.6.0
[63]	parallel_4.1.1	fastmap_1.1.0
[65]	yaml_2.2.1	AnnotationDbi_1.56.0
[67]	GenomicRanges_1.46.0	memoise_2.0.0
[69]	BiocIO_1.4.0	