

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

Diego Diez

April 26, 2022

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 4.2.0 RC (2022-04-19 r82224)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Mojave 10.14.6
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.2/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_1.34.0

loaded via a namespace (and not attached):

```
[1] Rcpp_1.0.8.3          lattice_0.20-45
[3] png_0.1-7             Rsamtools_2.12.0
[5] Biostrings_2.64.0     digest_0.6.29
[7] mime_0.12             org.Mm.eg.db_3.15.0
[9] R6_2.5.1              GenomeInfoDb_1.32.0
[11] stats4_4.2.0          RSQLite_2.2.12
[13] httr_1.4.2            zlibbioc_1.42.0
[15] rlang_1.0.2           data.table_1.14.2
[17] blob_1.2.3            S4Vectors_0.34.0
[19] Matrix_1.4-1          BiocParallel_1.30.0
[21] igraph_1.3.1          RCurl_1.98-1.6
[23] bit_4.0.4             shiny_1.7.1
[25] DelayedArray_0.22.0   compiler_4.2.0
[27] httpuv_1.6.5          rtracklayer_1.56.0
```

[29] pkgconfig_2.0.3	BiocGenerics_0.42.0
[31] htmltools_0.5.2	SummarizedExperiment_1.26.0
[33] KEGGREST_1.36.0	rTRM_1.34.0
[35] GenomeInfoDbData_1.2.8	IRanges_2.30.0
[37] matrixStats_0.62.0	XML_3.99-0.9
[39] crayon_1.5.1	later_1.3.0
[41] GenomicAlignments_1.32.0	bitops_1.0-7
[43] grid_4.2.0	xtable_1.8-4
[45] lifecycle_1.0.1	DBI_1.1.2
[47] magrittr_2.0.3	cli_3.3.0
[49] cachem_1.0.6	XVector_0.36.0
[51] promises_1.2.0.1	splitstackshape_1.4.8
[53] ellipsis_0.3.2	vctrs_0.4.1
[55] org.Hs.eg.db_3.15.0	rjson_0.2.21
[57] restfulr_0.0.13	tools_4.2.0
[59] bit64_4.0.5	Biobase_2.56.0
[61] MotifDb_1.38.0	MatrixGenerics_1.8.0
[63] parallel_4.2.0	fastmap_1.1.0
[65] yaml_2.3.5	AnnotationDbi_1.58.0
[67] GenomicRanges_1.48.0	memoise_2.0.1
[69] BiocIO_1.6.0	