

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 3.6.1 (2019-07-05)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2012 R2 x64 (build 9600)
```

```
Matrix products: default
```

```
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:
```



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

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

other attached packages:

```
[1] rTRMui_1.24.0
```

loaded via a namespace (and not attached):

```
[1] SummarizedExperiment_1.16.0 lattice_0.20-38
[3] vctrs_0.2.0             htmltools_0.4.0
[5] stats4_3.6.1            rtracklayer_1.46.0
[7] blob_1.2.0              XML_3.98-1.20
[9] rlang_0.4.1             later_1.0.0
[11] pillar_1.4.2           DBI_1.0.0
[13] BiocParallel_1.20.0     BiocGenerics_0.32.0
[15] bit64_0.9-7            splitstackshape_1.4.8
[17] matrixStats_0.55.0     GenomeInfoDbData_1.2.2
[19] zlibbioc_1.32.0        Biobase_2.46.0
[21] memoise_1.1.0          fastmap_1.0.1
[23] IRanges_2.20.0
```

[25] httpuv_1.5.2	GenomeInfoDb_1.22.0
[27] parallel_3.6.1	AnnotationDbi_1.48.0
[29] MotifDb_1.28.0	Rcpp_1.0.2
[31] xtable_1.8-4	promises_1.1.0
[33] backports_1.1.5	DelayedArray_0.12.0
[35] org.Hs.eg.db_3.10.0	S4Vectors_0.24.0
[37] XVector_0.26.0	rTRM_1.24.0
[39] mime_0.7	bit_1.1-14
[41] Rsamtools_2.2.0	digest_0.6.22
[43] shiny_1.4.0	GenomicRanges_1.38.0
[45] grid_3.6.1	tools_3.6.1
[47] bitops_1.0-6	magrittr_1.5
[49] RCurl_1.95-4.12	tibble_2.1.3
[51] RSQLite_2.1.2	crayon_1.3.4
[53] pkgconfig_2.0.3	zeallot_0.1.0
[55] Matrix_1.2-17	data.table_1.12.6
[57] org.Mm.eg.db_3.10.0	R6_2.4.0
[59] GenomicAlignments_1.22.0	igraph_1.2.4.1
[61] compiler_3.6.1	