

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

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October 28, 2020

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 4.0.3 (2020-10-10)
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_1.28.0
```

loaded via a namespace (and not attached):

```
[1] SummarizedExperiment_1.20.0 lattice_0.20-41
[3] vctrs_0.3.4             htmltools_0.5.0
[5] stats4_4.0.3            rtracklayer_1.50.0
[7] blob_1.2.1              XML_3.99-0.5
[9] rlang_0.4.8             later_1.1.0.1
[11] DBI_1.1.0               BiocParallel_1.24.0
[13] BiocGenerics_0.36.0     bit64_4.0.5
[15] splitstackshape_1.4.8   matrixStats_0.57.0
[17] GenomeInfoDbData_1.2.4  zlibbioc_1.36.0
[19] MatrixGenerics_1.2.0    Biostings_2.58.0
[21] memoise_1.1.0           Biobase_2.50.0
[23] IRanges_2.24.0          fastmap_1.0.1
```

[25]	httpuv_1.5.4	GenomeInfoDb_1.26.0
[27]	parallel_4.0.3	AnnotationDbi_1.52.0
[29]	MotifDb_1.32.0	Rcpp_1.0.5
[31]	xtable_1.8-4	promises_1.1.1
[33]	DelayedArray_0.16.0	org.Hs.eg.db_3.12.0
[35]	S4Vectors_0.28.0	XVector_0.30.0
[37]	rTRM_1.28.0	mime_0.9
[39]	bit_4.0.4	Rsamtools_2.6.0
[41]	digest_0.6.27	shiny_1.5.0
[43]	GenomicRanges_1.42.0	grid_4.0.3
[45]	tools_4.0.3	bitops_1.0-6
[47]	magrittr_1.5	RCurl_1.98-1.2
[49]	RSQLite_2.2.1	crayon_1.3.4
[51]	pkgconfig_2.0.3	Matrix_1.2-18
[53]	data.table_1.13.2	org.Mm.eg.db_3.12.0
[55]	R6_2.4.1	GenomicAlignments_1.26.0
[57]	igraph_1.2.6	compiler_4.0.3