

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 4.0.0 (2020-04-24)
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_1.26.0
```

loaded via a namespace (and not attached):

```
[1] SummarizedExperiment_1.18.0 lattice_0.20-41
[3] vctrs_0.2.4             htmltools_0.4.0
[5] stats4_4.0.0            rtracklayer_1.48.0
[7] blob_1.2.1              XML_3.99-0.3
[9] rlang_0.4.5             later_1.0.0
[11] DBI_1.1.0               BiocParallel_1.22.0
[13] BiocGenerics_0.34.0     bit64_0.9-7
[15] splitstackshape_1.4.8   matrixStats_0.56.0
[17] GenomeInfoDbData_1.2.3  zlibbioc_1.34.0
[19] Biostrings_2.56.0       memoise_1.1.0
[21] Biobase_2.48.0          IRanges_2.22.0
[23] fastmap_1.0.1           httpuv_1.5.2
```

[25]	GenomeInfoDb_1.24.0	parallel_4.0.0
[27]	AnnotationDbi_1.50.0	MotifDb_1.30.0
[29]	Rcpp_1.0.4.6	xtable_1.8-4
[31]	promises_1.1.0	DelayedArray_0.14.0
[33]	org.Hs.eg.db_3.10.0	S4Vectors_0.26.0
[35]	XVector_0.28.0	rTRM_1.26.0
[37]	mime_0.9	bit_1.1-15.2
[39]	Rsamtools_2.4.0	digest_0.6.25
[41]	shiny_1.4.0.2	GenomicRanges_1.40.0
[43]	grid_4.0.0	tools_4.0.0
[45]	bitops_1.0-6	magrittr_1.5
[47]	RCurl_1.98-1.2	RSQLite_2.2.0
[49]	crayon_1.3.4	pkgconfig_2.0.3
[51]	Matrix_1.2-18	data.table_1.12.8
[53]	org.Mm.eg.db_3.10.0	R6_2.4.1
[55]	GenomicAlignments_1.24.0	igraph_1.2.5
[57]	compiler_4.0.0	