

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

Diego Diez

October 29, 2024

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 4.4.1 (2024-06-14)
```

```
Platform: x86_64-apple-darwin20
```

```
Running under: macOS Monterey 12.7.6
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.4-x86_64/Resources/lib/libRblas.0.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/4.4-x86_64/Resources/lib/libRlapack.dylib;
```

```
locale:
```

```
[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
time zone: America/New_York
```

```
tzcode source: internal
```



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

attached base packages:

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

other attached packages:

```
[1] rTRMui_1.44.0
```

loaded via a namespace (and not attached):

```
[1] KEGGREST_1.46.0      SummarizedExperiment_1.36.0
[3] rjson_0.2.23         lattice_0.22-6
[5] Biobase_2.66.0       vctrs_0.6.5
[7] tools_4.4.1          bitops_1.0-9
[9] stats4_4.4.1         curl_5.2.3
[11] parallel_4.4.1       AnnotationDbi_1.68.0
[13] RSQLite_2.3.7        MotifDb_1.48.0
[15] blob_1.2.4           pkgconfig_2.0.3
[17] Matrix_1.7-1         data.table_1.16.2
[19] S4Vectors_0.44.0     lifecycle_1.0.4
[21] GenomeInfoDbData_1.2.13 rTRM_1.44.0
```

[23]	compiler_4.4.1	Rsamtools_2.22.0
[25]	Biostrings_2.74.0	codetools_0.2-20
[27]	httpuv_1.6.15	GenomeInfoDb_1.42.0
[29]	htmltools_0.5.8.1	RCurl_1.98-1.16
[31]	yaml_2.3.10	later_1.3.2
[33]	crayon_1.5.3	BiocParallel_1.40.0
[35]	DelayedArray_0.32.0	cachem_1.1.0
[37]	org.Hs.eg.db_3.20.0	abind_1.4-8
[39]	mime_0.12	digest_0.6.37
[41]	restfulr_0.0.15	grid_4.4.1
[43]	fastmap_1.2.0	SparseArray_1.6.0
[45]	cli_3.6.3	magrittr_2.0.3
[47]	S4Arrays_1.6.0	XML_3.99-0.17
[49]	UCSC.utils_1.2.0	promises_1.3.0
[51]	bit64_4.5.2	org.Mm.eg.db_3.20.0
[53]	XVector_0.46.0	httr_1.4.7
[55]	matrixStats_1.4.1	igraph_2.1.1
[57]	bit_4.5.0	png_0.1-8
[59]	memoise_2.0.1	shiny_1.9.1
[61]	GenomicRanges_1.58.0	IRanges_2.40.0
[63]	BiocIO_1.16.0	rtracklayer_1.66.0
[65]	rlang_1.1.4	Rcpp_1.0.13
[67]	xtable_1.8-4	DBI_1.2.3
[69]	BiocGenerics_0.52.0	splitstackshape_1.4.8
[71]	jsonlite_1.8.9	R6_2.5.1
[73]	MatrixGenerics_1.18.0	GenomicAlignments_1.42.0
[75]	zlibbioc_1.52.0	