

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

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May 19, 2021

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 4.1.0 beta (2021-05-03 r80259)
```

```
Platform: x86_64-pc-linux-gnu (64-bit)
```

```
Running under: Ubuntu 20.04.2 LTS
```

```
Matrix products: default
```

```
BLAS: /home/biocbuild/bbs-3.14-bioc/R/lib/libRblas.so
```

```
LAPACK: /home/biocbuild/bbs-3.14-bioc/R/lib/libRlapack.so
```

```
locale:
```

[1] LC_CTYPE=en_US.UTF-8	LC_NUMERIC=C
[3] LC_TIME=en_GB	LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8	LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8	LC_NAME=C
[9] LC_ADDRESS=C	LC_TELEPHONE=C



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

```
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

attached base packages:

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

other attached packages:

```
[1] rTRMui_1.31.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_1.0.6          lattice_0.20-44
[3] png_0.1-7           Rsamtools_2.9.0
[5] Biostrings_2.61.0   digest_0.6.27
[7] mime_0.10           org.Mm.eg.db_3.13.0
[9] R6_2.5.0            GenomeInfoDb_1.29.0
[11] stats4_4.1.0        RSQLite_2.2.7
[13] httr_1.4.2          zlibbioc_1.39.0
[15] rlang_0.4.11        data.table_1.14.0
[17] rstudioapi_0.13     blob_1.2.1
```

[19] S4Vectors_0.31.0	Matrix_1.3-3
[21] BiocParallel_1.27.0	igraph_1.2.6
[23] RCurl_1.98-1.3	bit_4.0.4
[25] shiny_1.6.0	DelayedArray_0.19.0
[27] compiler_4.1.0	httpuv_1.6.1
[29] rtracklayer_1.53.0	pkgconfig_2.0.3
[31] BiocGenerics_0.39.0	htmltools_0.5.1.1
[33] KEGGREST_1.33.0	SummarizedExperiment_1.23.0
[35] rTRM_1.31.0	GenomeInfoDbData_1.2.6
[37] IRanges_2.27.0	matrixStats_0.58.0
[39] XML_3.99-0.6	crayon_1.4.1
[41] later_1.2.0	GenomicAlignments_1.29.0
[43] bitops_1.0-7	grid_4.1.0
[45] xtable_1.8-4	lifecycle_1.0.0
[47] DBI_1.1.1	magrittr_2.0.1
[49] cachem_1.0.5	XVector_0.33.0
[51] promises_1.2.0.1	splitstackshape_1.4.8
[53] ellipsis_0.3.2	vctrs_0.3.8
[55] org.Hs.eg.db_3.13.0	rjson_0.2.20
[57] restfulr_0.0.13	tools_4.1.0
[59] bit64_4.0.5	Biobase_2.53.0
[61] MotifDb_1.35.0	MatrixGenerics_1.5.0
[63] parallel_4.1.0	fastmap_1.1.0
[65] yaml_2.2.1	AnnotationDbi_1.55.0
[67] GenomicRanges_1.45.0	memoise_2.0.0
[69] BiocIO_1.3.0	