

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

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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 4.2.1 (2022-06-23)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.5 LTS

Matrix products: default
BLAS: /home/biocbuild/bbs-3.16-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.16-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
```

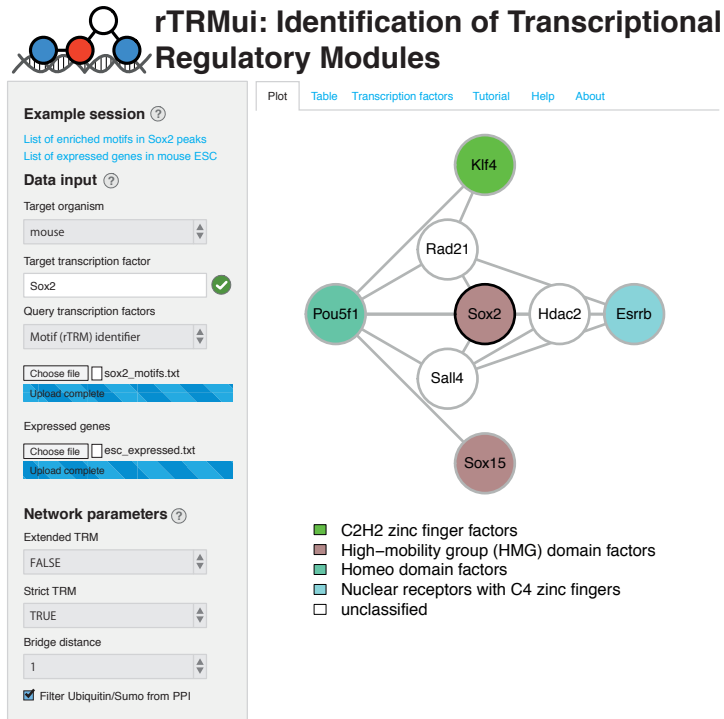


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[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_1.36.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_1.0.9 lattice_0.20-45
[3] png_0.1-7 Rsamtools_2.14.0
[5] Biostrings_2.66.0 digest_0.6.30
[7] mime_0.12 org.Mm.eg.db_3.16.0
[9] R6_2.5.1 GenomeInfoDb_1.34.0
[11] stats4_4.2.1 RSQLite_2.2.18
[13] httr_1.4.4 zlibbioc_1.44.0
[15] rlang_1.0.6 data.table_1.14.4
[17] blob_1.2.3 S4Vectors_0.36.0
```

[19]	Matrix_1.5-1	BiocParallel_1.32.0
[21]	igraph_1.3.5	RCurl_1.98-1.9
[23]	bit_4.0.4	shiny_1.7.3
[25]	DelayedArray_0.24.0	compiler_4.2.1
[27]	httpuv_1.6.6	rtracklayer_1.58.0
[29]	pkgconfig_2.0.3	BiocGenerics_0.44.0
[31]	htmltools_0.5.3	KEGGREST_1.38.0
[33]	SummarizedExperiment_1.28.0	rTRM_1.36.0
[35]	GenomeInfoDbData_1.2.9	IRanges_2.32.0
[37]	codetools_0.2-18	matrixStats_0.62.0
[39]	XML_3.99-0.12	crayon_1.5.2
[41]	later_1.3.0	GenomicAlignments_1.34.0
[43]	bitops_1.0-7	grid_4.2.1
[45]	xtable_1.8-4	lifecycle_1.0.3
[47]	DBI_1.1.3	magrittr_2.0.3
[49]	cli_3.4.1	cachem_1.0.6
[51]	XVector_0.38.0	promises_1.2.0.1
[53]	splitstackshape_1.4.8	ellipsis_0.3.2
[55]	vctrs_0.5.0	org.Hs.eg.db_3.16.0
[57]	rjson_0.2.21	restfulr_0.0.15
[59]	tools_4.2.1	bit64_4.0.5
[61]	Biobase_2.58.0	MotifDb_1.40.0
[63]	MatrixGenerics_1.10.0	parallel_4.2.1
[65]	fastmap_1.1.0	yaml_2.3.6
[67]	AnnotationDbi_1.60.0	GenomicRanges_1.50.0
[69]	memoise_2.0.1	BiocIO_1.8.0