

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 4.1.0 (2021-05-18)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.2 LTS

Matrix products: default
BLAS: /home/biocbuild/bbs-3.13-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.13-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
```

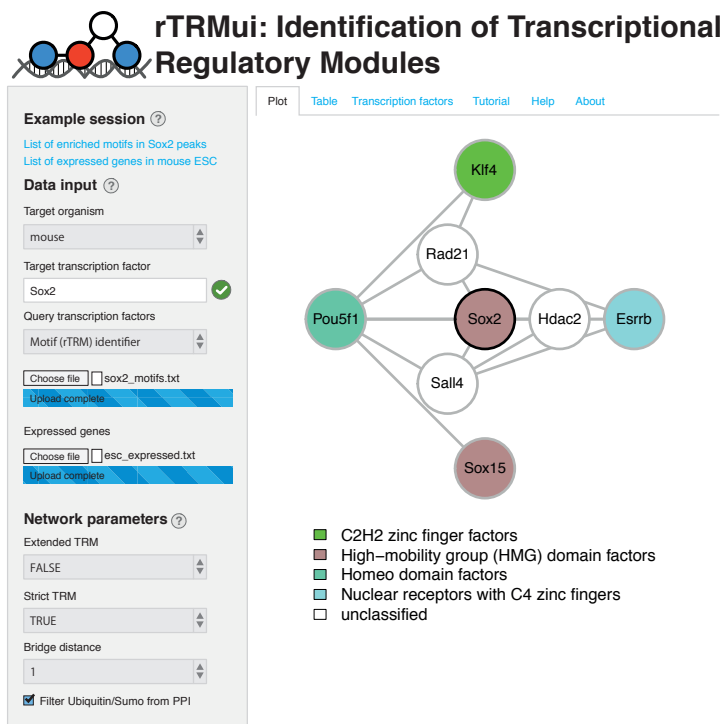


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[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_1.30.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_1.0.6           lattice_0.20-44
[3] png_0.1-7           Rsamtools_2.8.0
[5] Biostrings_2.60.0   digest_0.6.27
[7] mime_0.10           org.Mm.eg.db_3.13.0
[9] R6_2.5.0            GenomeInfoDb_1.28.0
[11] stats4_4.1.0        RSQLite_2.2.7
[13] httr_1.4.2          zlibbioc_1.38.0
[15] rlang_0.4.11        data.table_1.14.0
[17] rstudioapi_0.13     blob_1.2.1
```

[19]	S4Vectors_0.30.0	Matrix_1.3-3
[21]	BiocParallel_1.26.0	igraph_1.2.6
[23]	RCurl_1.98-1.3	bit_4.0.4
[25]	shiny_1.6.0	DelayedArray_0.18.0
[27]	compiler_4.1.0	httpuv_1.6.1
[29]	rtracklayer_1.52.0	pkgconfig_2.0.3
[31]	BiocGenerics_0.38.0	htmltools_0.5.1.1
[33]	KEGGREST_1.32.0	SummarizedExperiment_1.22.0
[35]	rTRM_1.30.0	GenomeInfoDbData_1.2.6
[37]	IRanges_2.26.0	matrixStats_0.58.0
[39]	XML_3.99-0.6	crayon_1.4.1
[41]	later_1.2.0	GenomicAlignments_1.28.0
[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_0.32.0
[51]	promises_1.2.0.1	splitstackshape_1.4.8
[53]	ellipsis_0.3.2	vctr_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_2.52.0
[61]	MotifDb_1.34.0	MatrixGenerics_1.4.0
[63]	parallel_4.1.0	fastmap_1.1.0
[65]	yaml_2.2.1	AnnotationDbi_1.54.0
[67]	GenomicRanges_1.44.0	memoise_2.0.0
[69]	BiocIO_1.2.0	