

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 4.2.0 RC (2022-04-21 r82226)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.4 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
```

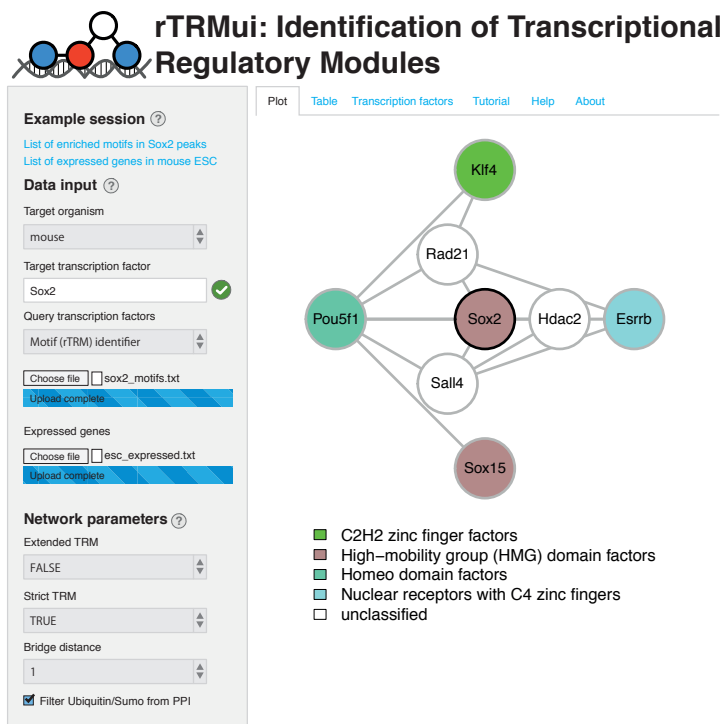


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

```
[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_1.35.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_1.0.8.3 lattice_0.20-45
[3] png_0.1-7 Rsamtools_2.13.0
[5] Biostrings_2.65.0 digest_0.6.29
[7] mime_0.12 org.Mm.eg.db_3.15.0
[9] R6_2.5.1 GenomeInfoDb_1.33.0
[11] stats4_4.2.0 RSQLite_2.2.12
[13] httr_1.4.2 zlibbioc_1.43.0
[15] rlang_1.0.2 data.table_1.14.2
[17] blob_1.2.3 S4Vectors_0.35.0
```

[19] Matrix_1.4-1	BiocParallel_1.31.0
[21] igraph_1.3.1	RCurl_1.98-1.6
[23] bit_4.0.4	shiny_1.7.1
[25] DelayedArray_0.23.0	compiler_4.2.0
[27] httpuv_1.6.5	rtracklayer_1.57.0
[29] pkgconfig_2.0.3	BiocGenerics_0.43.0
[31] htmltools_0.5.2	SummarizedExperiment_1.27.0
[33] KEGGREST_1.37.0	rTRM_1.35.0
[35] GenomeInfoDbData_1.2.8	IRanges_2.31.0
[37] matrixStats_0.62.0	XML_3.99-0.9
[39] crayon_1.5.1	later_1.3.0
[41] GenomicAlignments_1.33.0	bitops_1.0-7
[43] grid_4.2.0	xtable_1.8-4
[45] lifecycle_1.0.1	DBI_1.1.2
[47] magrittr_2.0.3	cli_3.3.0
[49] cachem_1.0.6	XVector_0.37.0
[51] promises_1.2.0.1	splitstackshape_1.4.8
[53] ellipsis_0.3.2	vctr_0.4.1
[55] org.Hs.eg.db_3.15.0	rjson_0.2.21
[57] restfulr_0.0.13	tools_4.2.0
[59] bit64_4.0.5	Biobase_2.57.0
[61] MotifDb_1.39.0	MatrixGenerics_1.9.0
[63] parallel_4.2.0	fastmap_1.1.0
[65] yaml_2.3.5	AnnotationDbi_1.59.0
[67] GenomicRanges_1.49.0	memoise_2.0.1
[69] BiocIO_1.7.0	