

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

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October 23, 2013

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 3.0.2 (2013-09-25)
Platform: x86_64-unknown-linux-gnu (64-bit)
```

```
locale:
```

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      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
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

```
attached base packages:
```

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

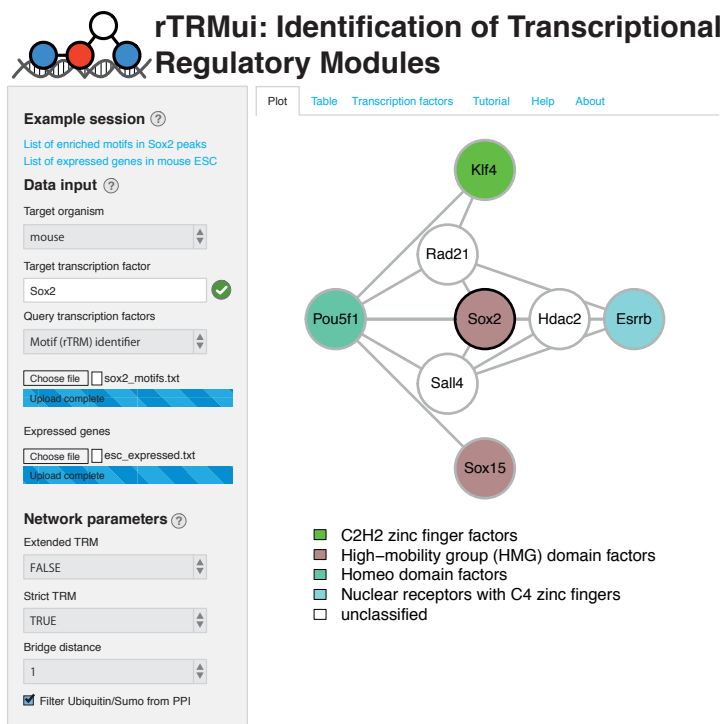


Figure 1: rTRMui home page showing the TRM identified using the sample datasets from the tutorial.

other attached packages:

```
[1] rTRMui_1.0.4          org.Mm.eg.db_2.10.1  org.Hs.eg.db_2.10.1
[4] MotifDb_1.4.0        Biostings_2.30.0    XVector_0.2.0
[7] IRanges_1.20.0       rTRM_1.0.3          annotate_1.40.0
[10] AnnotationDbi_1.24.0 Biobase_2.22.0      BiocGenerics_0.8.0
[13] RSQLite_0.11.4       DBI_0.2-7           igraph_0.6.5-2
[16] shiny_0.7.0
```

loaded via a namespace (and not attached):

```
[1] BSgenome_1.30.0      GenomicRanges_1.14.1 RCurl_1.95-4.1
[4] RJSONIO_1.0-3        Rsamtools_1.14.1    XML_3.98-1.1
[7] bitops_1.0-6         caTools_1.14        digest_0.6.3
[10] httpuv_1.2.0         rtracklayer_1.22.0  stats4_3.0.2
[13] tools_3.0.2          xtable_1.7-1        zlibbioc_1.8.0
```