Interactive-Shiny-report-of-HTSanalyzeR2

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Package

HTSanalyzeR2 0.99.14

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1 Introduction

In this short tutorial, we give a detailed illustration for the shiny report part of **HTSanalyzeR2** to visualize the results and modify figures in different aspects.

2 Interactive Shiny report visualization

2.1 Visualize single GSCA object for individual data set

For single data set analysis, after analyzed by HTSanalyzeR2, we can get a *GSCA* object and use the function *report* to launch the shiny report.

```
data(d7_gsca)
report(d7_gsca)
```

2.1.1 The hypergeometric test result table [Figure 1]

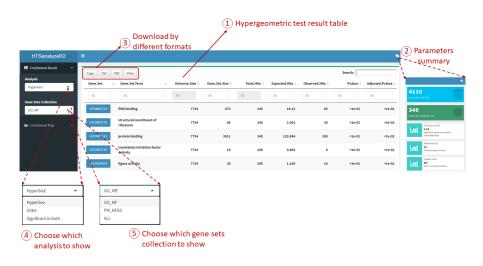


Figure 1: The hypergeometric test result table

2.1.2 Parameters for modifying the figure [Figure2]

There are five main parts for users to modify their figure by interactive operations including: **Layout**, **Label**, **Node**, **Edge** and **Color Scheme**. Following is a detailed explanation for each part.

- Layout: A widge to control the whole pattern
 - Mode: There are two layout modes inside this Shiny report, users can choose any of them to get better visualization based on their data.
 - Parameters: Two more parameters *Egde Repel* and *Adjust Sizes* could be used to make the figure looser.

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- Gravity: Ranging from -50 to 50, users can adjust it step by step. The larger it is, the more even the pattern would be.
- **Label**: A widge to modify the label of nodes with three easy-to-understand parameters: *Text, Label Scale* and *Label color*.
- **Node**: A widge to modify the nodes with four easy-to-understand parameters: *Scale*, *Opacity*, *Border Width* and *Border Color*.
- **Edge**: A widge to modify the edges with two easy-to-understand parameters: *Edge Scale* and *Edge Color*.
- Color Scheme: A widge to change the default color.

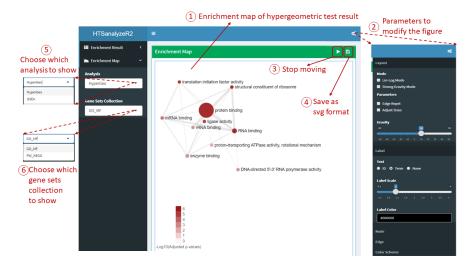


Figure 2: The enrichment map of hypergeometric test result

2.2 Visualize single *NWA* object for individual data set

```
data(d7_nwa)
report(d7_nwa)
```

2.2.1 The identified subnetwork [Figure3]

2.3 Visualize a list of *GSCA* objects for time series/comparative analysis

```
data(gscaTS)
## To make the figure more compact, we set a cutoff
## to move any other edges with low Jaccard coefficient.
reportAll(gscaTS, cutoff = 0.035)
```

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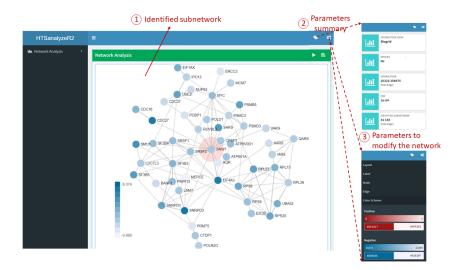


Figure 3: The identified subnetwork

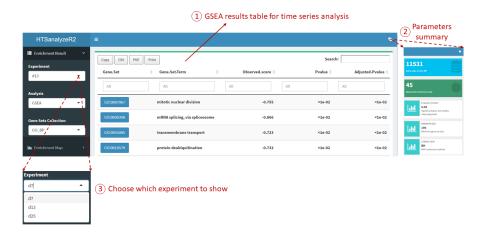


Figure 4: GSEA results table for time series/comparative analysis

- 2.3.1 GSEA results table for time series/comparative analysis [Figure4]
- 2.3.2 Union enrichment map for time series/comparative analysis [Figure5]
- 2.4 Visualize a list of *NWA* objects for time series/comparative analysis

```
data(nwaTS)
reportAll(nwaTS)
```

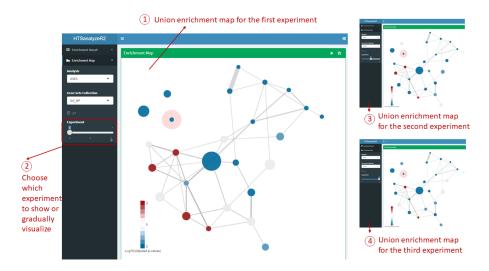


Figure 5: Union enrichment map for time series/comparative analysis

2.4.1 Union subnetwork for time series/comparative analysis [Figure6]

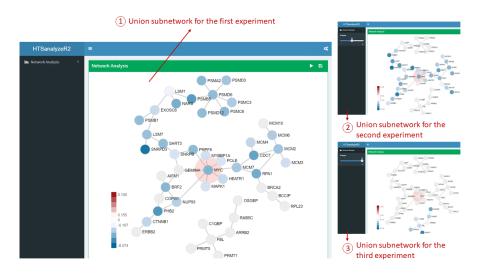


Figure 6: Union subnetwork for time series/comparative analysis

2.5 Visualize both GSCA and NWA objects simultaneously

reportAll(gsca = gscaTS, nwa = nwaTS)

2.5.1 Visualize both GSEA and netwrok result in the same report [Figure7]

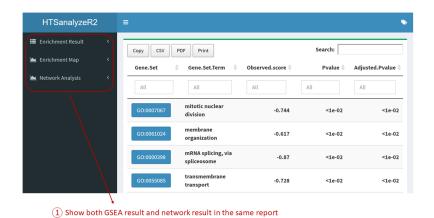


Figure 7: Visualize both GSEA and netwrok result in the same report

3 Session Info

```
## R version 3.5.0 (2018-04-23)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 18.04 LTS
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/openblas/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/libopenblasp-r0.2.20.so
## locale:
## [1] LC_CTYPE=en_US.UTF-8
                                  LC_NUMERIC=C
## [3] LC_TIME=en_US.UTF-8
                                  LC_COLLATE=en_US.UTF-8
## [5] LC_MONETARY=en_US.UTF-8
                                  LC_MESSAGES=en_US.UTF-8
                                  LC_NAME=C
## [7] LC_PAPER=en_US.UTF-8
## [9] LC_ADDRESS=C
                                  LC_TELEPHONE=C
## [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] BiocStyle_2.8.2
## loaded via a namespace (and not attached):
## [1] compiler_3.5.0 backports_1.1.2 bookdown_0.7
                                                       magrittr_1.5
## [5] rprojroot_1.3-2 tools_3.5.0
                                      htmltools_0.3.6 yaml_2.1.19
## [9] Rcpp_0.12.17
                       stringi_1.2.3 rmarkdown_1.10 knitr_1.20
## [13] xfun_0.2
                       stringr_1.3.1 digest_0.6.15 evaluate_0.10.1
```