Interactive-Shiny-report-of-HTSanalyzeR2

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Package

HTSanalyzeR2 0.99.15

Contents

1   Introduction

In this short tutorial, we will give a detailed illustration for the interactive Shiny report 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 performing gene set analysis by HTSanalyzeR2, we can get a *GSCA* object and use the function *report* to launch the Shiny report.

```
data(d7_gsca)
report(d7_gsca)
```
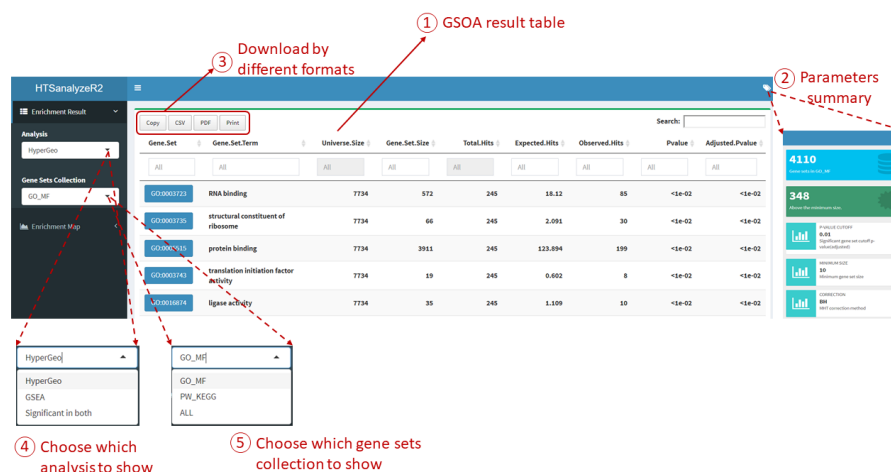
2.1.1   The GSOA result table [Figure1]

Figure 1: The GSOA result table

The above screenshot shows the GSOA result table where users can either get a general summary of the analysis parameters, choose which analysis and which gene set collection to show or download the result by different format.

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.
  - Gravity: Ranging from -50 to 50, users can adjust it step by step. The larger it is, the looser 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 parameters: *Scale*, *Opacity*, *Border Width* and *Border Color*.
- **Edge**: A widge to modify the edges with two parameters: *Edge Scale* and *Edge Color*.
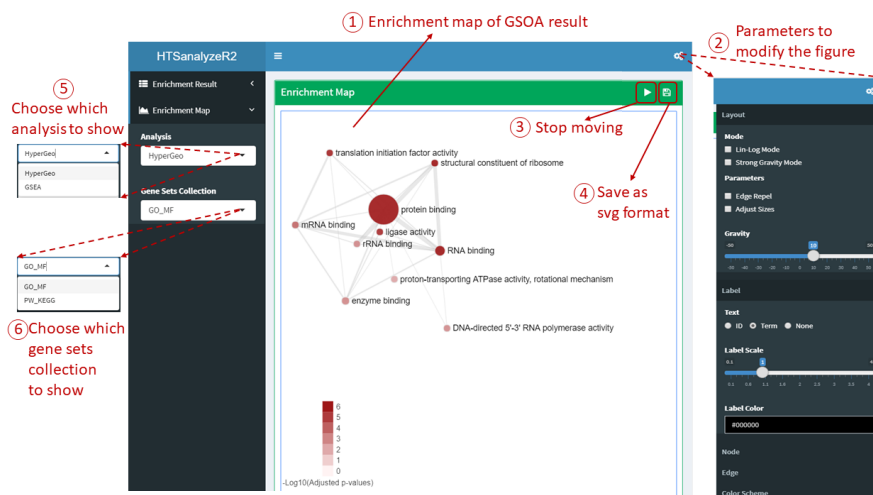- **Color Scheme**: A widge to change the default color.

Figure 2: **The enrichment map of GSOA result**

The above screenshot shows the enrichment map of GSOA result. Users can click the topright button to modify the figure based on their data and preference.

2.2 Visualize single *NWA* object for individual data set

For single data set analysis, after performing enriched subnetwork analysis by HTSanalyzeR2, we can get a *NWA* object and use the function *report* to launch the Shiny report.

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

2.2.1 The identified subnetwork [Figure3]

The below screenshot shows the identified subnetwork where users can either get a general summary of the subnetwork attributes, modify the subnetwork based on their data and preference or download the subnetwork in svg format for further use.
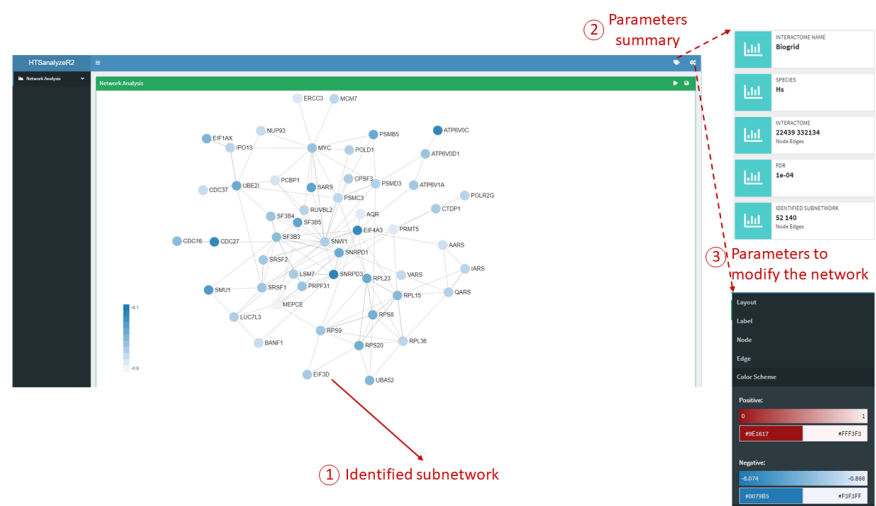
Figure 3: **The identified subnetwork**

2.3 Visualize a list of *GSCA* objects for "Time-course" data

```
data(gscaTS)
## To make the figure more compact, we set a cutoff
## to move any other edges with low Jaccard coefficient.
reportAll(gscaTS, cutoff = 0.03)
```

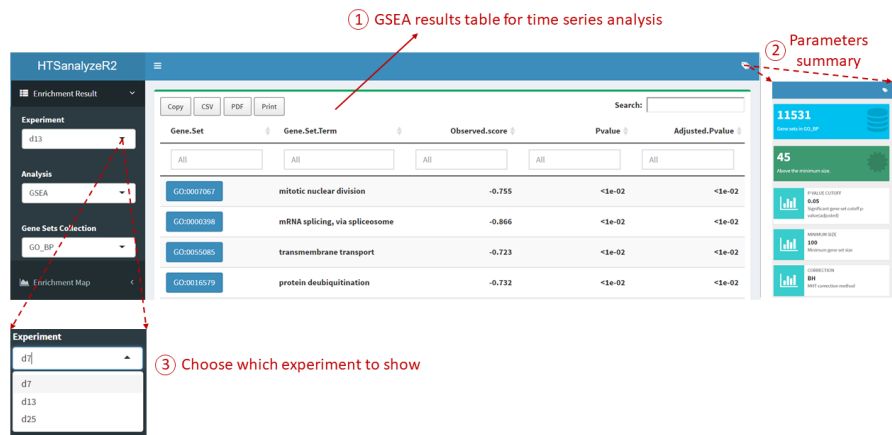### 2.3.1 GSEA results table for "Time-course" data [Figure4]

Figure 4: **GSEA results table for "Time-course" data**

The above screenshot shows the GSOA result tables for Time-course data with three time points where users can either get a general summary of the analysis parameters, choose which analysis, which gene set collection and which experiment result to show or download the result by different format.

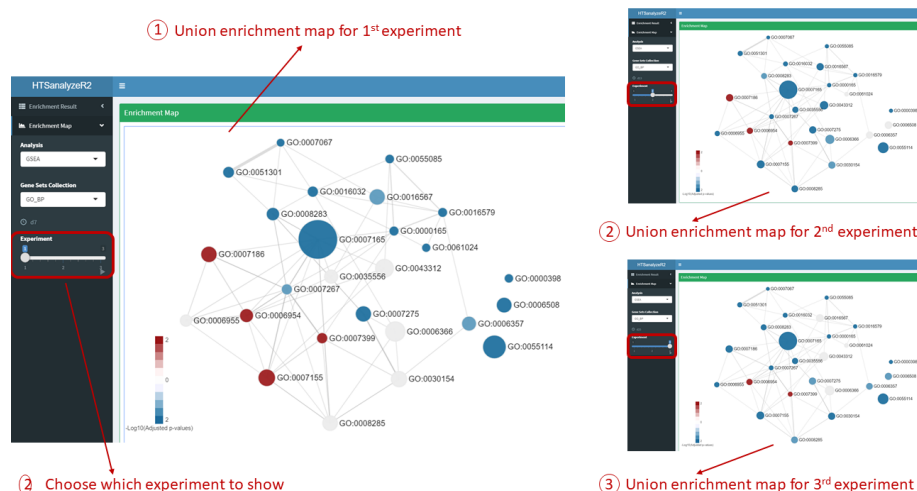### 2.3.2 Union enrichment map for "Time-course" data [Figure5]

Figure 5: **Union enrichment map for "Time-course" data**

The below screenshot shows the union enrichment maps of GSEA result for "Time-course" data with filtered edges by setting a cutoff on the edges. Users can click the topright button to modify the figure based on their data and preference. Here, we can clearly see a gradual change among three union enrichment maps with the same layout.

2.4 Visualize a list of *NWA* objects for "Time-course" data

```
data(nwaTS)
reportAll(nwa = nwaTS)
```

2.4.1 Union subnetwork for "Time-course" data [Figure6]

2.5 Visualize both *GSCA* and *NWA* objects simultaneously

```
reportAll(gsca = gscaTS, nwa = nwaTS)
```

The above screenshot shows the union subnetworks for "Time-course" data. Users can click the topright button to modify the figure based on their data and preference. We can clearly see a gradual change among three union subnetworks with the same layout.
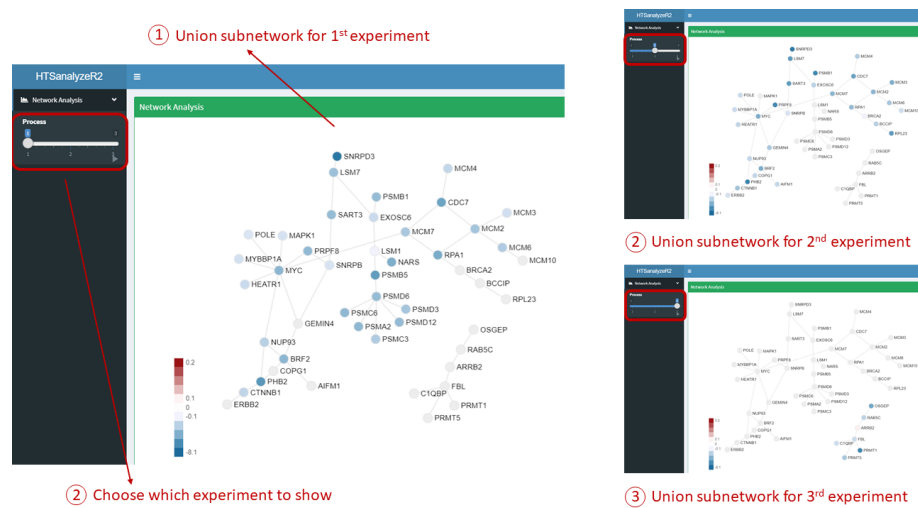
Figure 6: **Union subnetwork for "Time-course" data**

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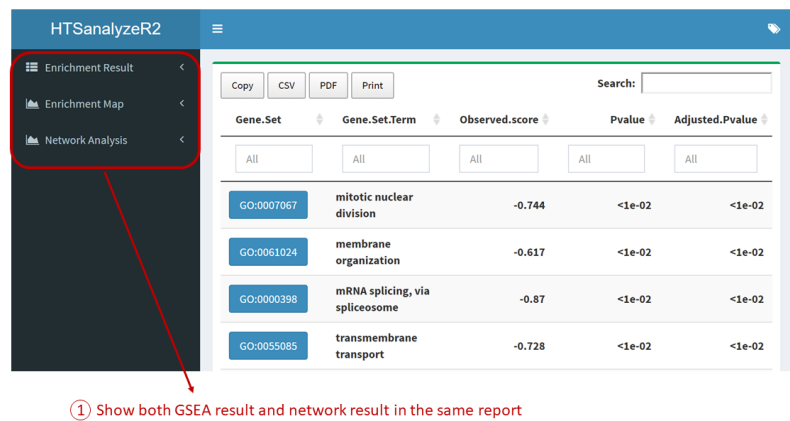

Figure 7: **Visualize both GSEA and network result in the same report**

If you do both gene set analysis and enriched subnetwork analysis, it's also possible to visualize both of them in the same Shiny report as showed here.

3 Session Info

```
## R version 3.5.2 (2018-12-20)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 18.04.1 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
##  [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] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] BiocStyle_2.10.0
##
## loaded via a namespace (and not attached):
##  [1] BiocManager_1.30.4 compiler_3.5.2     bookdown_0.9
##  [4] magrittr_1.5       tools_3.5.2        htmltools_0.3.6
##  [7] yaml_2.2.0         Rcpp_1.0.0         stringi_1.2.4
## [10] rmarkdown_1.11     knitr_1.21         stringr_1.3.1
## [13] xfun_0.4           digest_0.6.18      evaluate_0.12
```