GSEA output

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Loading Package

```
suppressMessages(library(ggplot2))
suppressMessages(library("forcats"))
```

Modify dataframe format

```
modify_GSEA_data <- function(GSEA_results){
  GSEA_results<- GSEA_results[order(GSEA_results$NES, decreasing = T),]
  GSEA_results <- GSEA_results[1:20,]

  # define the column has a factor so that the order of Ontology is maintain in the plot.
  GSEA_results$NAME <- factor(GSEA_results$NAME, levels = GSEA_results$NAME)
  GSEA_results$NAME <- fct_rev(GSEA_results$NAME)

  GSEA_results
}
```
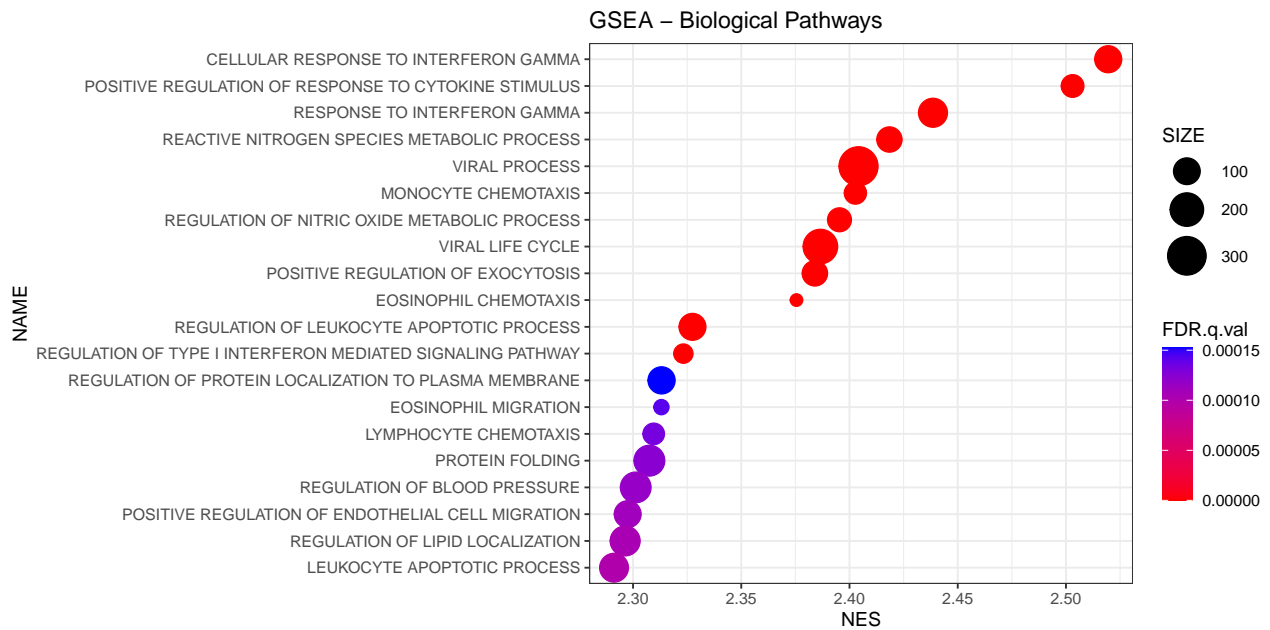
Creating Dotplot for BP results

```
dir <- "GSEA_Output/"
GSEA_BP_res <-
read.table(paste0(dir,"my_analysis.Gsea.1675247466167_BP/gsea_report_for_2_1675247466167.tsv"),
header = T, sep = "\t")

GSEA_BP_res <- modify_GSEA_data(GSEA_BP_res)

GSEA_BP_res$NAME <- substring(GSEA_BP_res$NAME, 6)
GSEA_BP_res$NAME <- gsub("_", " ", GSEA_BP_res$NAME)

GSEA_BP_res$NAME <- fct_rev(factor(GSEA_BP_res$NAME, levels = GSEA_BP_res$NAME))

ggplot(GSEA_BP_res, aes(x = NES,y =NAME, size = SIZE, color = FDR.q.val)) + geom_point()
+ ggtitle("GSEA - Biological Pathways") + scale_color_gradient(low = "red", high =
"blue") + theme_bw()+ scale_size(range = c(3,10))
```

GSEA – Biological Pathways

```
#ggsave("plot_result/GSEA_results_BP_céci2.pdf", width = 12, height = 8)
```

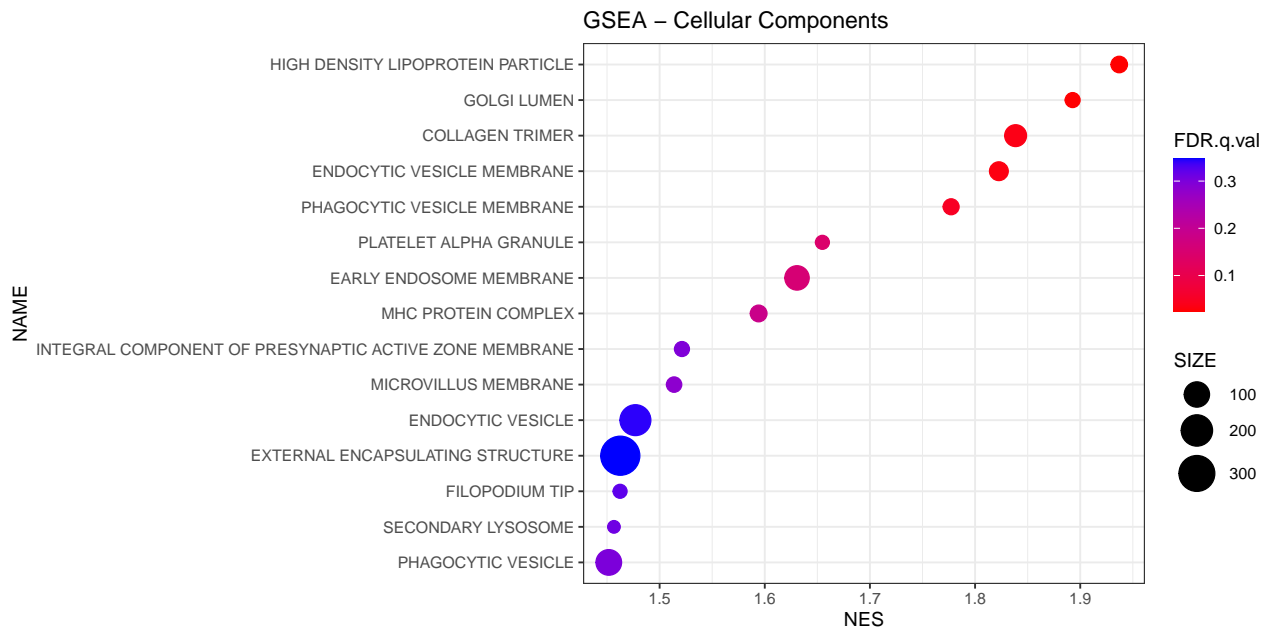# Creating Dotplot for CC results

```
GSEA_CC_res <-
read.table(paste0(dir,"my_analysis.Gsea.1675339652585_CC/gsea_report_for_2_1675339652585.tsv"),
header = T, sep = "\t")

GSEA_CC_res <- modify_GSEA_data(GSEA_CC_res)

GSEA_CC_res <- GSEA_CC_res[1:15,]

GSEA_CC_res$NAME <- substring(GSEA_CC_res$NAME, 6)
GSEA_CC_res$NAME <- gsub("_", " ", GSEA_CC_res$NAME)
GSEA_CC_res$NAME <- fct_rev(factor(GSEA_CC_res$NAME, levels = GSEA_CC_res$NAME))

ggplot(GSEA_CC_res, aes(x = NES,y =NAME, size = SIZE, color = FDR.q.val)) + geom_point()
+ ggtitle("GSEA - Cellular Components") + scale_color_gradient(low = "red", high =
"blue") + theme_bw() + scale_size(range = c(3,10))
```

GSEA – Cellular Components

```
#ggsave("plot_result/GSEA_results_CC_céci2.pdf", width = 12, height = 8)
```

# Creating Dotplot for BP results

```
GSEA_MF_res <-
read.table(paste0(dir,"my_analysis.Gsea.1675341806364_MF/gsea_report_for_2_1675341806364.tsv"),
header = T, sep = "\t")

GSEA_MF_res <- modify_GSEA_data(GSEA_MF_res)

GSEA_MF_res$NAME <- substring(GSEA_MF_res$NAME, 6)
GSEA_MF_res$NAME <- gsub("_", " ", GSEA_MF_res$NAME)

GSEA_MF_res$NAME <- fct_rev(factor(GSEA_MF_res$NAME, levels = GSEA_MF_res$NAME))

ggplot(GSEA_MF_res, aes(x = NES,y =NAME, size = SIZE, color = FDR.q.val)) + geom_point()
+ ggtitle("GSEA - Molecular Function") + scale_color_gradient(low = "red", high = "blue")
+ theme_bw()+ scale_size(range = c(3,10))
```

GSEA – Molecular Function
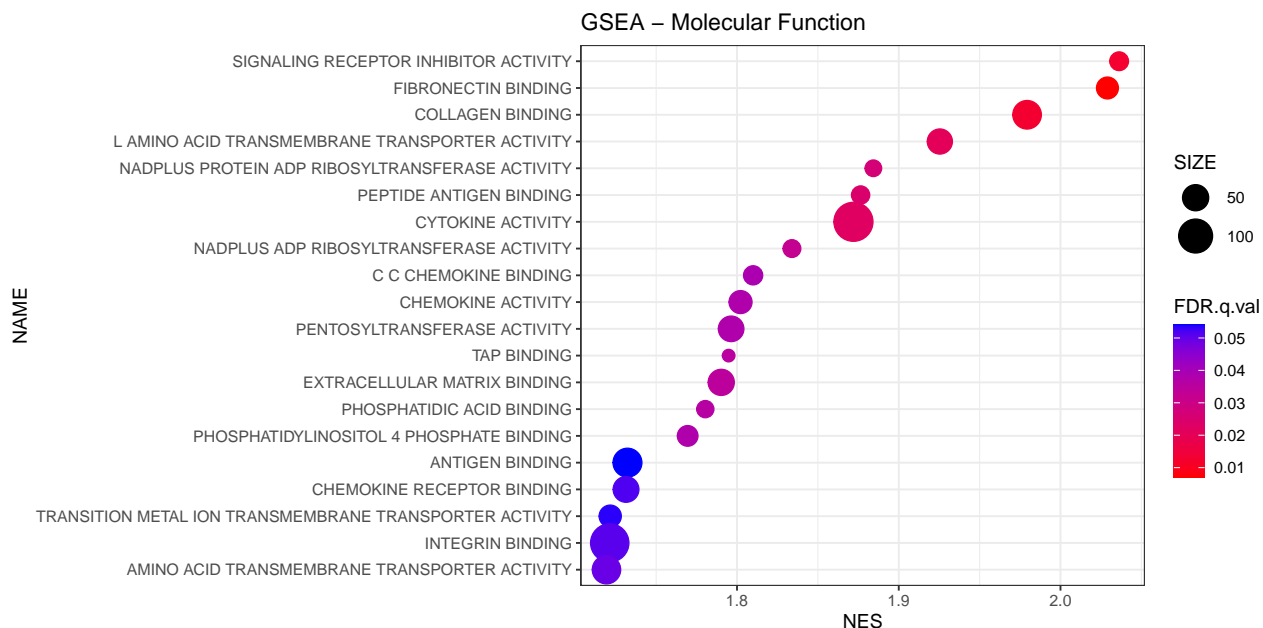

```
#ggsave("plot_result/GSEA_results_MF_céci2.pdf", width = 12, height = 8)
```

```
sessionInfo()
```

```
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.6 LTS
##
## Matrix products: default
## BLAS:   /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/liblapack.so.3
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=fr_BE.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=fr_BE.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=fr_BE.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=fr_BE.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] forcats_0.5.2 ggplot2_3.4.0
##
## loaded via a namespace (and not attached):
##  [1] pillar_1.8.1      compiler_4.0.3    highr_0.10        tools_4.0.3
##  [5] digest_0.6.31     evaluate_0.20     lifecycle_1.0.3  tibble_3.1.8
##  [9] gtable_0.3.1      pkgconfig_2.0.3   rlang_1.0.6      cli_3.6.0
## [13] DBI_1.1.3         rstudioapi_0.14   yaml_2.3.7       xfun_0.37
## [17] fastmap_1.1.1     withr_2.5.0       dplyr_1.0.10     knitr_1.42
## [21] generics_0.1.3    vctrs_0.5.2       grid_4.0.3       tidyselect_1.2.0
## [25] glue_1.6.2        R6_2.5.1          fansi_1.0.4      rmarkdown_2.19
```

```
## [29] farver_2.1.1     magrittr_2.0.3   scales_1.2.1     htmltools_0.5.4
## [33] assertthat_0.2.1 colorspace_2.1-0 labeling_0.4.2   utf8_1.2.3
## [37] munsell_0.5.0
```