

# Gene Enrichment Report

Ehsan Zangene

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## Contents

|  |   |
|--|---|
| 1. Load Required Libraries . . . . .   | 1 |
| 2. Input Gene Lists . . . . .          | 1 |
| 3. Enrichment Analysis . . . . .       | 2 |
| 4. Export Results (Optional) . . . . . | 5 |

## 1. Load Required Libraries

```
library(readxl)
library(clusterProfiler)
library(org.Hs.eg.db)
library(org.Ce.eg.db)
library(enrichplot)
library(ReactomePA)
library(ggplot2)
library(dplyr)
```

## 2. Input Gene Lists

### 2.1 Human Orthologs

```
file_path_human <- "./30-05-25/List of human orthologs_RNAi screen.xlsx"
human_df <- read_excel(file_path_human)
symbol_col <- grep("symbol", names(human_df), ignore.case = TRUE, value = TRUE)
human_df <- human_df %>% rename(GeneSymbolColumn = all_of(symbol_col))
human_symbols <- human_df$GeneSymbolColumn
human_map <- bitr(human_symbols, fromType="SYMBOL", toType="ENTREZID", OrgDb=org.Hs.eg.db)
human_entrez <- unique(human_map$ENTREZID)
```

### 2.2 Worm Genes

```

file_path_worm <- "./06-2024/List of verified genes.xlsx"
worm_df <- read_excel(file_path_worm)
wb_col <- grep("WormBase Gene", colnames(worm_df), ignore.case = TRUE, value = TRUE)
worm_df <- worm_df %>% rename(GeneID = all_of(wb_col))
worm_map <- bitr(worm_df$GeneID, fromType = "WORMBASE", toType = "ENTREZID", OrgDb = org.Ce.eg.db)
worm_entrez <- unique(worm_map$ENTREZID)

```

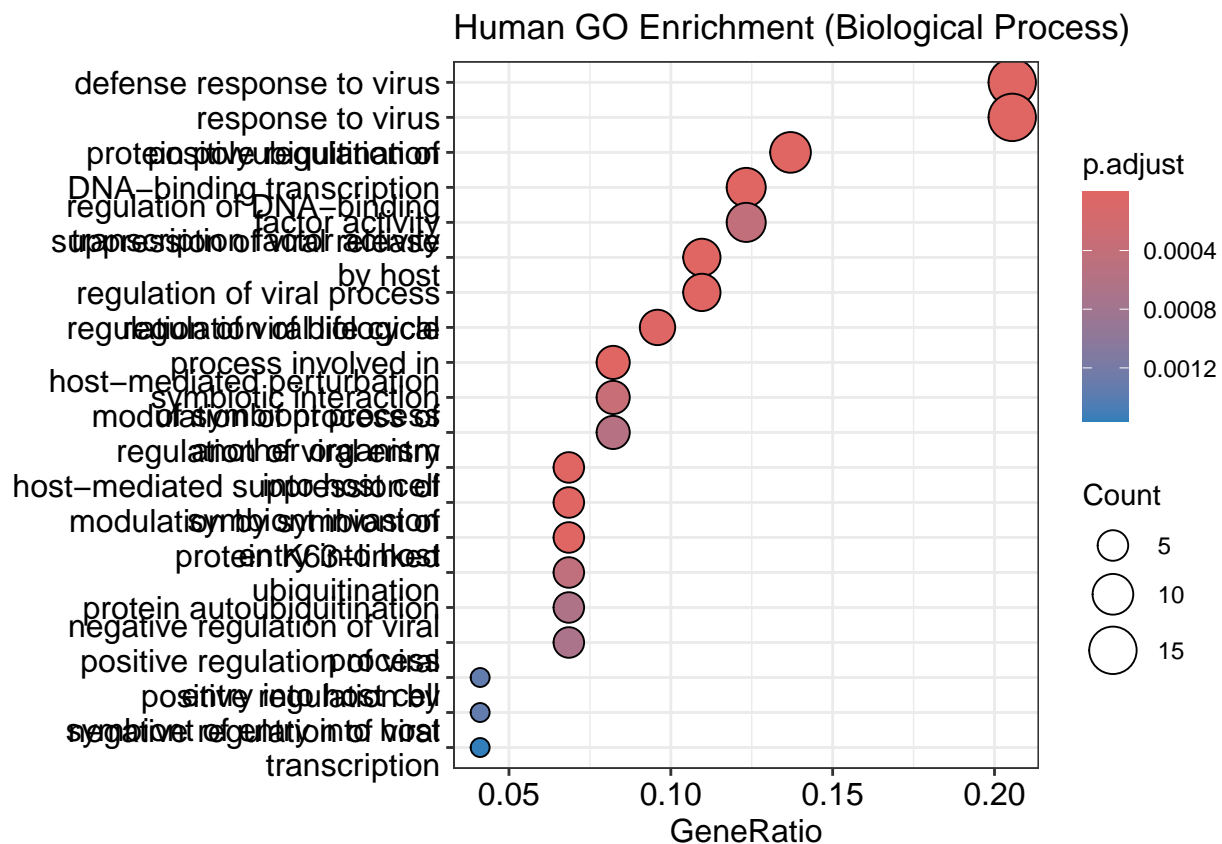
### 3. Enrichment Analysis

#### 3.1 Human GO: Biological Process

```

ego_bp <- enrichGO(gene = human_entrez, OrgDb = org.Hs.eg.db, keyType = "ENTREZID",
  ont = "BP", pAdjustMethod = "BH", pvalueCutoff = 0.05,
  qvalueCutoff = 0.2, readable = TRUE)
dotplot(ego_bp, showCategory = 20) + ggtitle("Human GO Enrichment (Biological Process)")

```



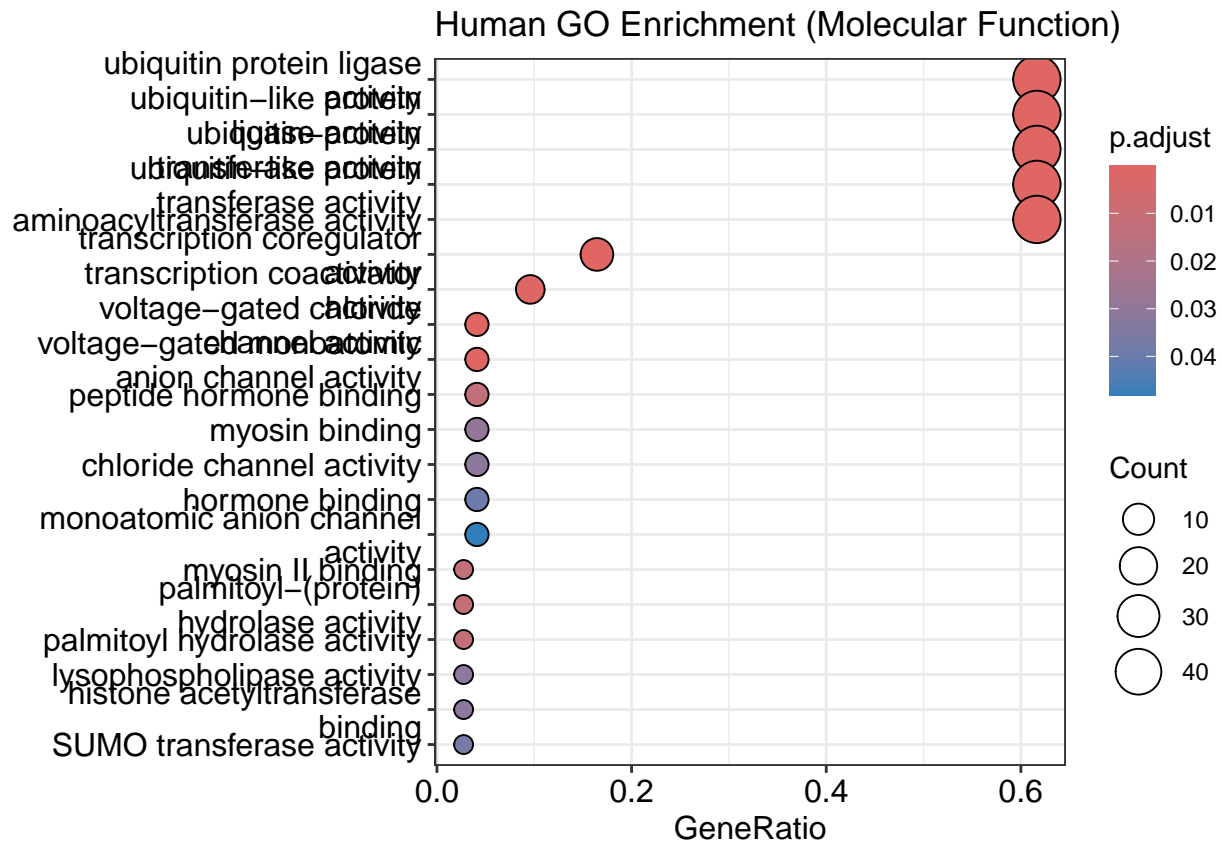
#### 3.2 Human GO: Molecular Function

```

ego_mf <- enrichGO(gene = human_entrez, OrgDb = org.Hs.eg.db, keyType = "ENTREZID",
  ont = "MF", pAdjustMethod = "BH", pvalueCutoff = 0.05,

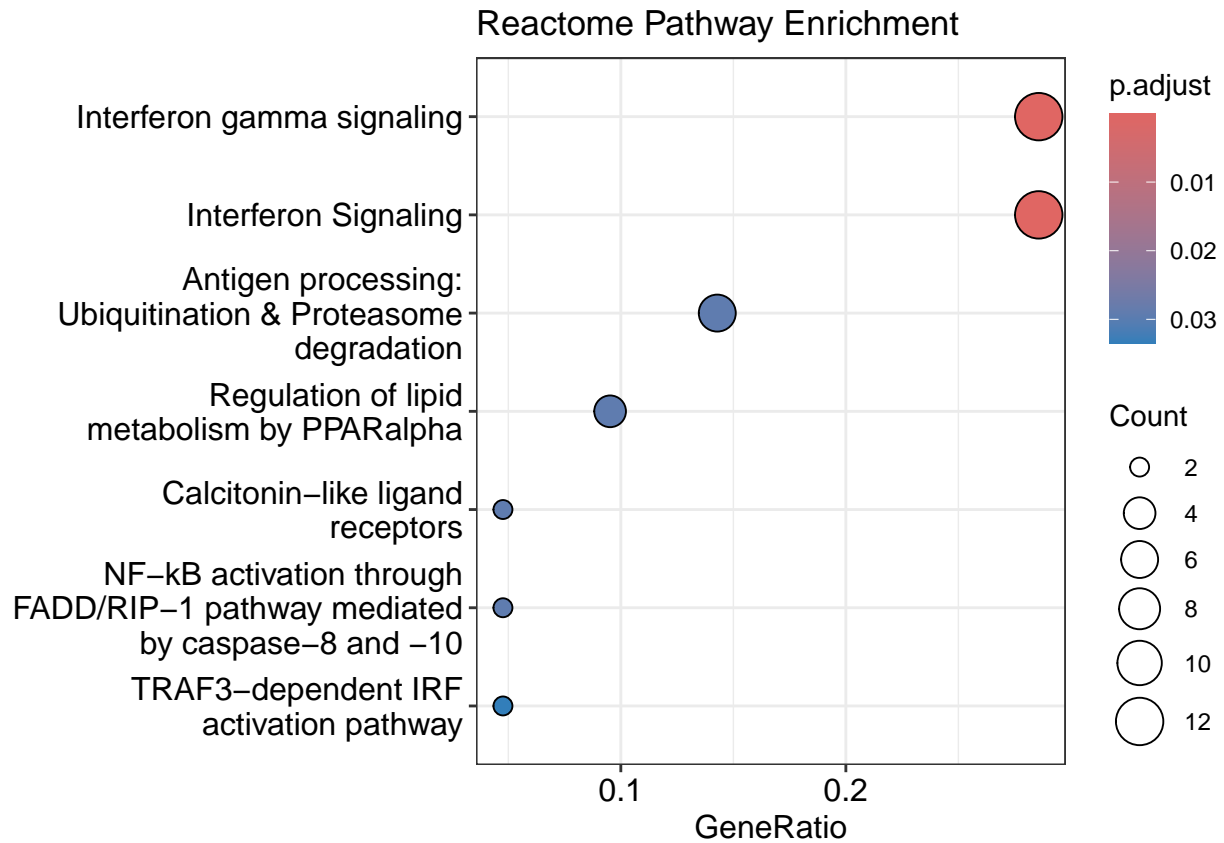
```

```
qvalueCutoff = 0.2, readable = TRUE)
dotplot(ego_mf, showCategory = 20) + ggtitle("Human GO Enrichment (Molecular Function)")
```



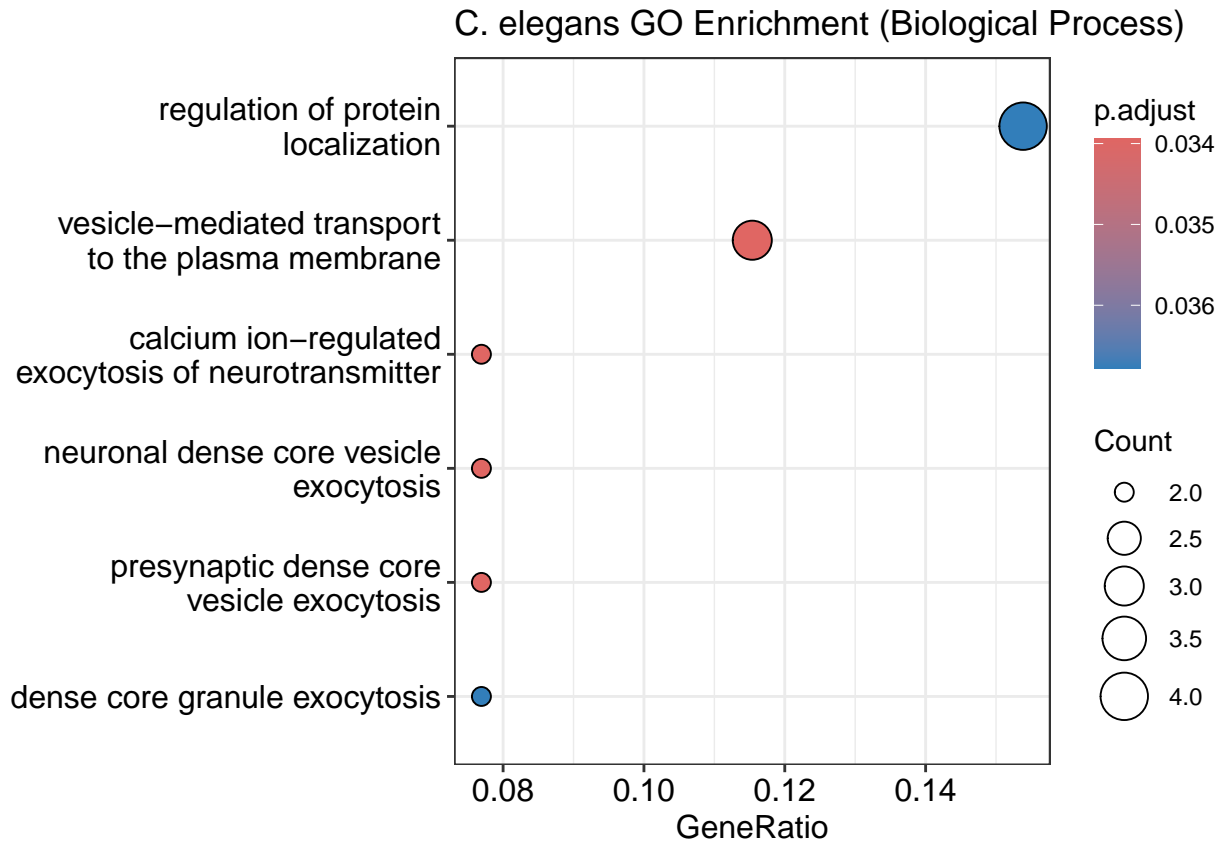
### 3.3 Human Reactome Pathways

```
ereactome <- enrichPathway(gene = human_entrez, organism = "human",
pvalueCutoff = 0.05, readable = TRUE)
dotplot(ereactome, showCategory = 20) + ggtitle("Reactome Pathway Enrichment")
```



### 3.4 C. elegans GO: Biological Process

```
ego_ce_bp <- enrichGO(gene = worm_entrez, OrgDb = org.Ce.eg.db, keyType = "ENTREZID",
  ont = "BP", pAdjustMethod = "BH", pvalueCutoff = 0.05,
  qvalueCutoff = 0.2, readable = TRUE)
dotplot(ego_ce_bp, showCategory = 20) + ggtitle("C. elegans GO Enrichment (Biological Process)")
```



#### 4. Export Results (Optional)

```
write.csv(as.data.frame(ego_bp), "Human_GO_BP.csv", row.names = FALSE)
write.csv(as.data.frame(ego_mf), "Human_GO_MF.csv", row.names = FALSE)
write.csv(as.data.frame(ereactome), "Human_Reactome.csv", row.names = FALSE)
write.csv(as.data.frame(ego_ce_bp), "Worm_GO_BP.csv", row.names = FALSE)
```