

# GO\_enrichment

```
library(clusterProfiler) # For functional enrichment analysis
```

```
##
```

```
## clusterProfiler v4.8.1 For help: https://yulab-smu.top/biomedical-knowledge-mining-book/
```

```
##
```

```
## If you use clusterProfiler in published research, please cite:
```

```
## T Wu, E Hu, S Xu, M Chen, P Guo, Z Dai, T Feng, L Zhou, W Tang, L Zhan, X Fu, S Liu, X Bo, and G Yu.
```

```
##
```

```
## Attache Paket: 'clusterProfiler'
```

```
## Das folgende Objekt ist maskiert 'package:stats':
```

```
##
```

```
## filter
```

```
library(org.Hs.eg.db) # Annotation database for human genes
```

```
## Lade nötiges Paket: AnnotationDbi
```

```
## Lade nötiges Paket: stats4
```

```
## Lade nötiges Paket: BiocGenerics
```

```
##
```

```
## Attache Paket: 'BiocGenerics'
```

```
## Die folgenden Objekte sind maskiert von 'package:stats':
```

```
##
```

```
## IQR, mad, sd, var, xtabs
```

```
## Die folgenden Objekte sind maskiert von 'package:base':
```

```
##
```

```
## anyDuplicated, aperm, append, as.data.frame, basename, cbind,  
## colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,  
## get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,  
## match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,  
## Position, rank, rbind, Reduce, rownames, sapply, setdiff, sort,  
## table, tapply, union, unique, unsplit, which.max, which.min
```

```
## Lade nötiges Paket: Biobase
```

```
## Welcome to Bioconductor
##
## Vignettes contain introductory material; view with
## 'browseVignettes()'. To cite Bioconductor, see
## 'citation("Biobase")', and for packages 'citation("pkgname")'.
```

```
## Lade nötiges Paket: IRanges
```

```
## Lade nötiges Paket: S4Vectors
```

```
##
```

```
## Attache Paket: 'S4Vectors'
```

```
## Das folgende Objekt ist maskiert 'package:clusterProfiler':
```

```
##
```

```
## rename
```

```
## Das folgende Objekt ist maskiert 'package:utils':
```

```
##
```

```
## findMatches
```

```
## Die folgenden Objekte sind maskiert von 'package:base':
```

```
##
```

```
## expand.grid, I, unname
```

```
##
```

```
## Attache Paket: 'IRanges'
```

```
## Das folgende Objekt ist maskiert 'package:clusterProfiler':
```

```
##
```

```
## slice
```

```
## Das folgende Objekt ist maskiert 'package:grDevices':
```

```
##
```

```
## windows
```

```
##
```

```
## Attache Paket: 'AnnotationDbi'
```

```
## Das folgende Objekt ist maskiert 'package:clusterProfiler':
```

```
##
```

```
## select
```

```
##
```

```
library(AnnotationDbi) # Annotation utilities
```

```
# Read data from a CSV file named "go.csv" and store it in the "data" variable.
```

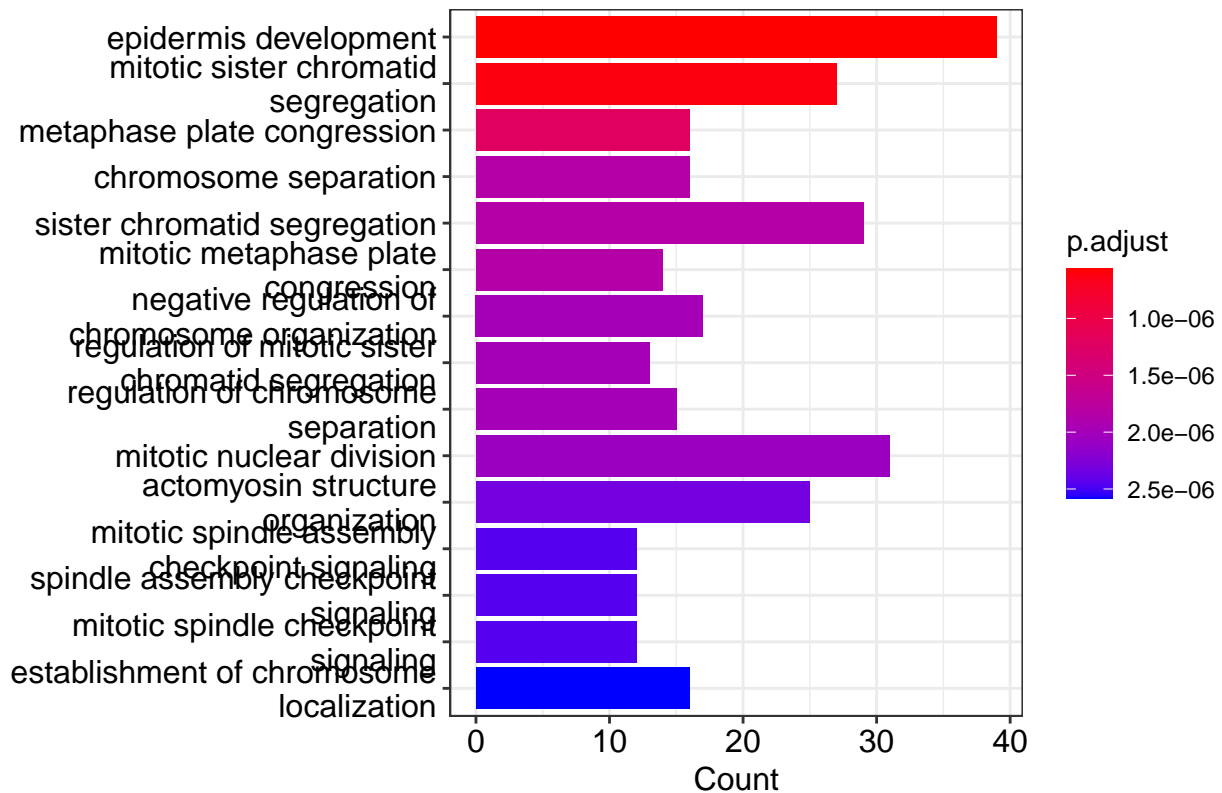
```
data <- read.csv("go.csv", sep = ";", header = TRUE)
```

```
# Extract the ENSEMBL gene IDs from the "data" variable and store them in "genes_to_test".
```

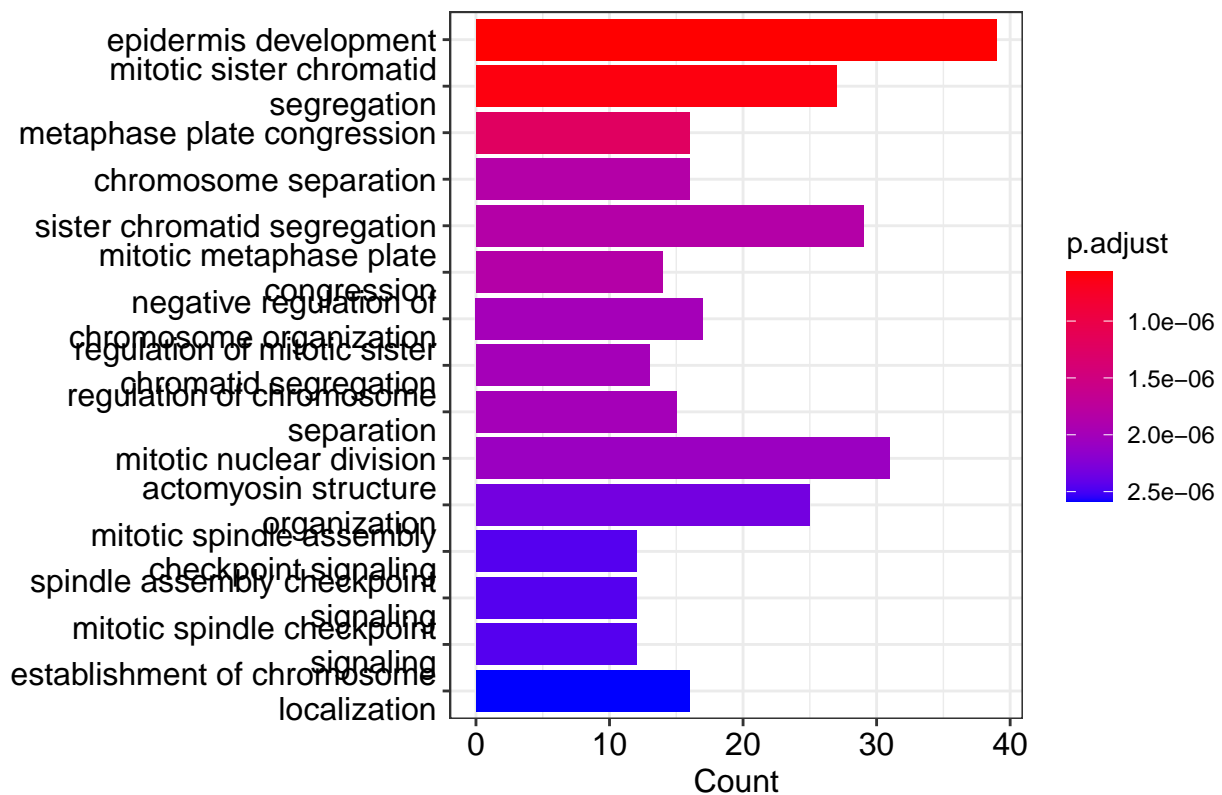
```
genes_to_test <- data$ensembl_gene_id
```

```
# Perform Gene Ontology (GO) enrichment analysis for Biological Process (BP) terms using "enrichGO" fun
GO_results <- enrichGO(gene = genes_to_test, OrgDb = "org.Hs.eg.db", keyType = "ENSEMBL", ont = "BP")
#as.data.frame(GO_results)
```

```
# Create a barplot visualizing the top 15 enriched GO terms for Biological Process.
fit <- plot(barplot(GO_results, showCategory = 15))
```

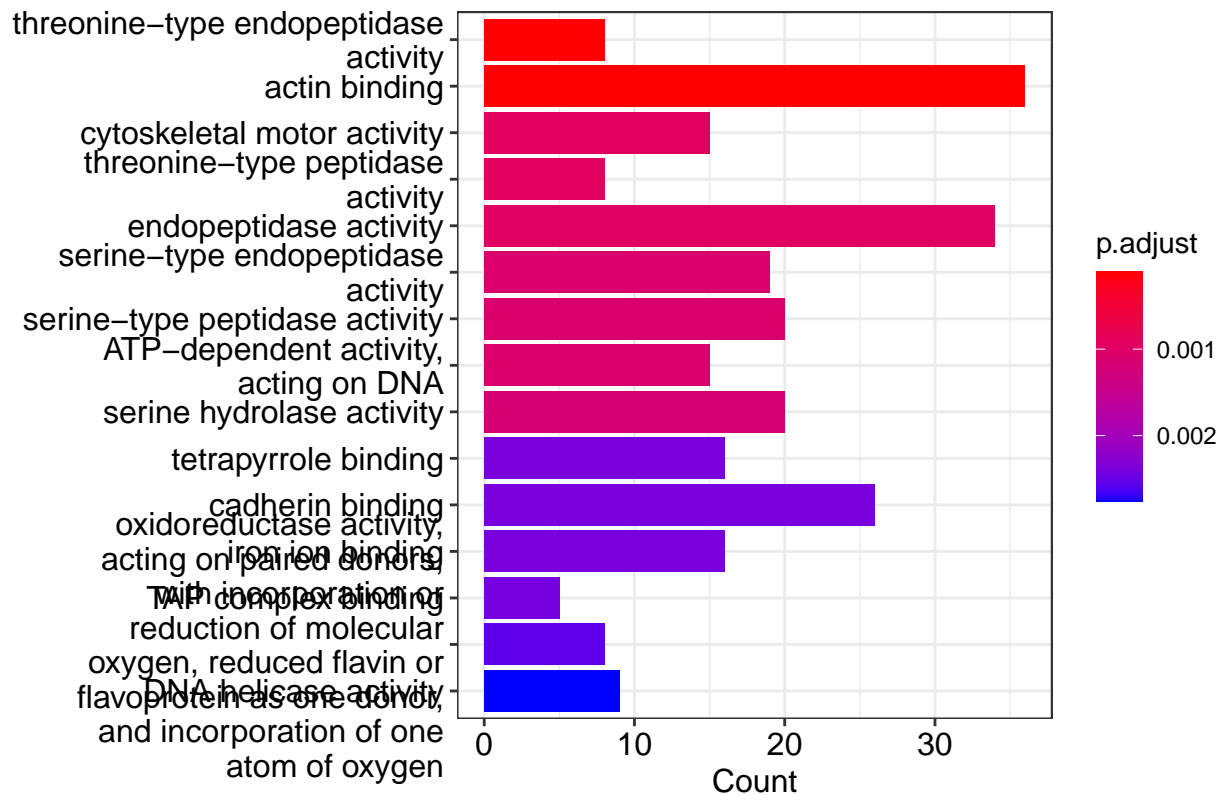


```
fit
```



```
# Perform GO enrichment analysis for Molecular Function (MF) terms using "enrichGO" function.
GO_results2 <- enrichGO(gene = genes_to_test, OrgDb = "org.Hs.eg.db", keyType = "ENSEMBL", ont = "MF")
#as.data.frame(GO_results2)
```

```
# Create a barplot visualizing the top 15 enriched GO terms for Molecular Function.
fit2 <- plot(barplot(GO_results2, showCategory = 15))
```



```
# Perform GO enrichment analysis for Cellular Component (CC) terms using "enrichGO" function.
GO_results3 <- enrichGO(gene = genes_to_test, OrgDb = "org.Hs.eg.db", keyType = "ENSEMBL", ont = "CC")
#as.data.frame(GO_results3)
```

```
# Create a barplot visualizing the top 15 enriched GO terms for Cellular Component.
fit3 <- plot(barplot(GO_results3, showCategory = 15))
```

