

Rembrandt pathway analysis

TF

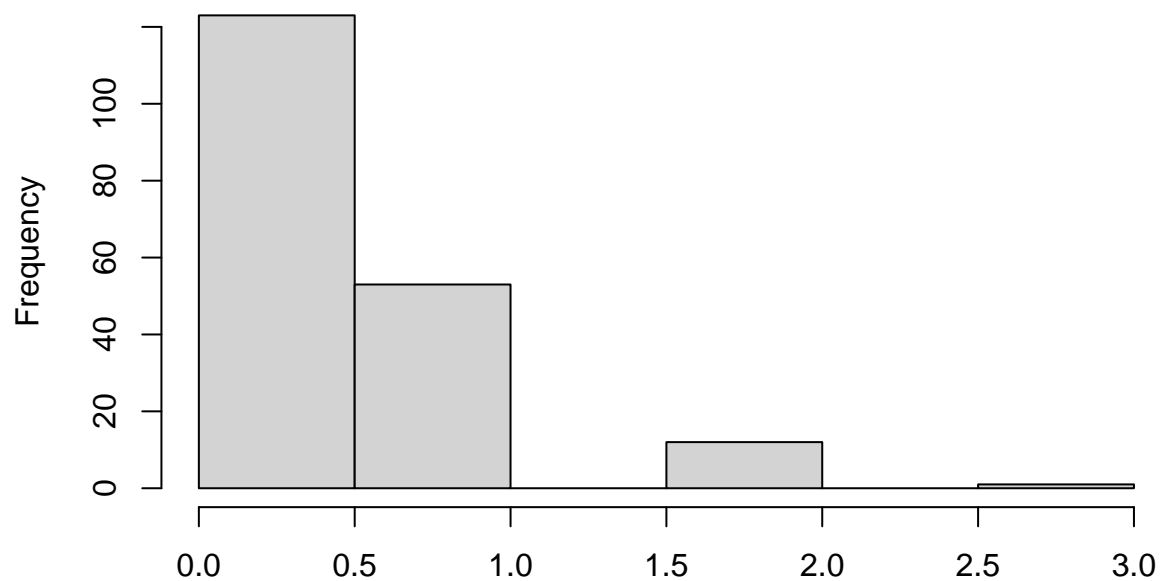
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```
library(dplyr)
library(ggplot2)
library(survival)
```

```
dfRemb <- readRDS(file = "../../data/rembrandt/dfGenesAndClinical.rds")
pathways <- GSA::GSA.read.gmt("../../data/rembrandt/c6.all.v7.1.symbols.gmt")
```

```
lapply(pathways$genesets,
  function(vec_genes){
    dfRemb %>% select(any_of(vec_genes)) %>% ncol()
  }) %>%
  unlist() %>%
  hist(main = "Number of genes by pathway found in Rembrandt data")
```

Number of genes by pathway found in Rembrandt data



```
lapply(pathways$genesets,  
       length) %>%  
  unlist() %>%  
  hist(main = "Number of genes by pathway")
```

