```r
# Load required libraries
library(readxl)    # For reading data from Excel files
library(multiMiR)  # For querying validated miRNA-mRNA interactions
library(writexl)   # For writing data to Excel files


# Read data from an Excel file named "miRNAmRNA.xlsx" and store it in the "new_list" variable
new_list <- read_excel("C:/Users/Emre/Desktop/miRNAmRNA.xlsx")
mirnames <- new_list$miRNA


# Get validated miRNA-mRNA interactions using the "multiMiR" package.
# In this case, the interactions are queried for human (hsa) miRNAs (mirnames) from the "validated" tab
# The results will be summarized and stored in the "multimir_results" variable.
multimir_results <- get_multimir(org     = 'hsa',
                                 mirna   = mirnames,
                                 table   = 'validated',
                                 summary = TRUE)


## Searching mirecords ...
## Searching mirtarbase ...
## Searching tarbase ...

# Display the first few rows of the "multimir_results" data to get an overview of the miRNA-mRNA intera
head(multimir_results@data)


##     database mature_mirna_acc mature_mirna_id target_symbol target_entrez
## 1 mirecords     MIMAT0000073  hsa-miR-19a-3p           PTEN          5728
## 2 mirecords     MIMAT0000073  hsa-miR-19a-3p           PTEN          5728
## 3 mirecords     MIMAT0000073  hsa-miR-19a-3p           PTEN          5728
## 4 mirecords     MIMAT0000073  hsa-miR-19a-3p           PTEN          5728
## 5 mirecords     MIMAT0000073  hsa-miR-19a-3p           PTEN          5728
## 6 mirecords     MIMAT0000073  hsa-miR-19a-3p           PTEN          5728
##     target_ensembl experiment support_type pubmed_id      type
## 1 ENSG00000171862                           14697198 validated
## 2 ENSG00000171862                           14697198 validated
## 3 ENSG00000171862                           14697198 validated
## 4 ENSG00000171862                           14697198 validated
## 5 ENSG00000171862                           14697198 validated
## 6 ENSG00000171862                           14697198 validated


targets <- multimir_results@data

#excel_file <- "C:/Users/Emre/Desktop/Bioinformatik/Bioinformatik 2.Semester Master/Data Science in the
#write_xlsx(targets, path = excel_file)


df <- read_excel("C:/Users/Emre/Desktop/multimir_results.xlsx")

#Read data from the "mRNAs.xlsx" file into the "mrna" variable.
mrna <- read_excel("C:/Users/Emre/Desktop/mRNAs.xlsx")
```

```r
# Extract the mrna names from the table
mrna_genes <-  mrna$mRNA


# Filter the "df" data based on whether the "target_symbol" column contains gene names present in the "
filtered_df <- df[df$target_symbol %in% mrna_genes | duplicated(df$target_symbol) %in% mrna_genes, ]

# Print the filtered data.
print(filtered_df)
```

```
## # A tibble: 277 x 10
##    database    mature_mirna_acc mature_mirna_id target_symbol target_entrez
##    <chr>       <chr>            <chr>           <chr>         <chr>
##  1 mirecords  MIMAT0000681     hsa-miR-29c-3p  COL1A1        1277
##  2 mirecords  MIMAT0000681     hsa-miR-29c-3p  COL1A1        1277
##  3 mirecords  MIMAT0000681     hsa-miR-29c-3p  COL1A1        1277
##  4 mirecords  MIMAT0000681     hsa-miR-29c-3p  COL1A1        1277
##  5 mirecords  MIMAT0000681     hsa-miR-29c-3p  COL1A1        1277
##  6 mirecords  MIMAT0000681     hsa-miR-29c-3p  COL1A1        1277
##  7 mirtarbase MIMAT0000257     hsa-miR-181b-5p ALDH9A1       223
##  8 mirtarbase MIMAT0000257     hsa-miR-181b-5p ID4           3400
##  9 mirtarbase MIMAT0000257     hsa-miR-181b-5p TMF1          7110
## 10 mirtarbase MIMAT0000076     hsa-miR-21-5p   COL5A2        1290
## # i 267 more rows
## # i 5 more variables: target_ensembl <chr>, experiment <chr>,
## #   support_type <chr>, pubmed_id <chr>, type <chr>
```