Healthcare Analytics Individual Assignment

R Code

Part 0 - Data Import

Importing Libraries

```
library(haven)
library(ggplot2)
```

Extraction of Dataset and Storing it

```
# Define the directory where your files are stored
data_dir <- "/Users/harsh/Downloads/ICPSR_21600"

# Initialize a list to store the datasets
data_list <- list()

# Loop through DS0001 to DS0042
for (i in 1:42) {

  # Format the dataset number with leading zeros (e.g., DS0001)
  ds_num <- sprintf("DS%04d", i)

  # Build the correct file name (note the difference in pattern)
  if (i < 10) {
    file_name <- paste0("21600-000", i, "-Data.dta")
  } else {
    file_name <- paste0("21600-00", i, "-Data.dta")
  }

  # Build the full file path
  file_path <- file.path(data_dir, ds_num, file_name)

  # Print progress (optional)
  cat("Reading:", file_path, "\n")

  # Check if the file exists to avoid crashing
  if (file.exists(file_path)) {
    data_list[[ds_num]] <- read_dta(file_path)
  } else {
    cat("File not found:", file_path, "\n")
  }
}
```

```
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0001/21600-0001-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0002/21600-0002-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0003/21600-0003-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0004/21600-0004-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0005/21600-0005-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0006/21600-0006-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0007/21600-0007-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0008/21600-0008-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0009/21600-0009-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0010/21600-0010-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0011/21600-0011-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0012/21600-0012-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0013/21600-0013-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0014/21600-0014-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0015/21600-0015-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0016/21600-0016-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0017/21600-0017-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0018/21600-0018-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0019/21600-0019-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0020/21600-0020-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0021/21600-0021-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0022/21600-0022-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0023/21600-0023-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0024/21600-0024-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0025/21600-0025-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0026/21600-0026-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0027/21600-0027-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0028/21600-0028-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0029/21600-0029-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0030/21600-0030-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0031/21600-0031-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0032/21600-0032-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0033/21600-0033-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0034/21600-0034-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0035/21600-0035-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0036/21600-0036-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0037/21600-0037-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0038/21600-0038-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0039/21600-0039-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0040/21600-0040-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0041/21600-0041-Data.dta
## Reading: /Users/harsh/Downloads/ICPSR_21600/DS0042/21600-0042-Data.dta
```

```
# Check the loaded datasets
names(data_list)
```

```
##  [1] "DS0001" "DS0002" "DS0003" "DS0004" "DS0005" "DS0006" "DS0007" "DS0008"
##  [9] "DS0009" "DS0010" "DS0011" "DS0012" "DS0013" "DS0014" "DS0015" "DS0016"
## [17] "DS0017" "DS0018" "DS0019" "DS0020" "DS0021" "DS0022" "DS0023" "DS0024"
## [25] "DS0025" "DS0026" "DS0027" "DS0028" "DS0029" "DS0030" "DS0031" "DS0032"
## [33] "DS0033" "DS0034" "DS0035" "DS0036" "DS0037" "DS0038" "DS0039" "DS0040"
## [41] "DS0041" "DS0042"
```

List of Target Variables

```
vars <- c(
  "AID", "H3ID15",  # ID + target
  "H3DA15", "H3FS12", "H3FS11", "H3SP6", "H3WP46", "H3WP53", "H3WP57",  # Friends & F
amily
  "H3DA28", "H3EC7", "H3EC3", "H3DA36", "H3EC26", "H3EC38",             # Socioeconom
ic
  "BIO_SEX3", "H3OD4A"                                                 # Demographics
)
```

Saving the Subset of Dataset

```
wave3_data <- read_dta("/Users/harsh/Downloads/ICPSR_21600/DS0008/21600-0008-Data.dt
a")

data_subset <- wave3_data[ , vars]

str(data_subset)
```

```
## tibble [4,882 × 17] (S3: tbl_df/tbl/data.frame)
##  $ AID     : chr [1:4882] "57100270" "57101310" "57103869" "57104676" ...
##   ..- attr(*, "label")= chr "RESPONDENT IDENTIFIER"
##   ..- attr(*, "format.stata")= chr "%9s"
##  $ H3ID15  : dbl+lbl [1:4882] 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0,...
##    ..@ label       : chr "S11Q15 EVER BEEN DX WITH DEPRESSION-W3"
##    ..@ format.stata: chr "%18.0f"
##    ..@ labels      : Named num [1:4] 0 1 8 9
##    .. ..- attr(*, "names")= chr [1:4] "(0) No" "(1) Yes" "(8) Don't know" "(9) Not
applicable"
##  $ H3DA15  : dbl+lbl [1:4882] 0, 7, 6, 0, 7, 3, 1, 7, 0, 2, 4, 4, 6, 0, 2, 5, 2,
0,...
##    ..@ label       : chr "S33Q15 HANG OUT WITH FRIENDS - W3"
##    ..@ format.stata: chr "%19.0f"
##    ..@ labels      : Named num [1:10] 0 1 2 3 4 5 6 7 96 98
##    .. ..- attr(*, "names")= chr [1:10] "(0) Not at all" "(1) 1 time" "(2) 2 times"
"(3) 3 times" ...
##  $ H3FS12  : dbl+lbl [1:4882] 5, 5, 5, 1, 1, 7, 5, 5, 5, 2, 7, 5, 5, 5, 5, 5, 2,
5,...
##    ..@ label       : chr "S6Q12 FRIEND OR FAMILY INFLUENCE MORE-W3"
##    ..@ format.stata: chr "%41.0f"
##    ..@ labels      : Named num [1:6] 1 2 5 7 8 9
##    .. ..- attr(*, "names")= chr [1:6] "(1) Your friends have influenced you more"
"(2) Your family has influenced you more" "(5) Question not asked of this respondent"
"(7) Legitimate skip" ...
##  $ H3FS11  : dbl+lbl [1:4882] 95, 95, 95,  5,  3, 97, 95, 95, 95,  0, 97, 95, 95,
9...
##    ..@ label       : chr "S6Q11 STILL FRIENDS W/HS FRIENDS-W3"
##    ..@ format.stata: chr "%42.0f"
##    ..@ labels      : Named num [1:9] 0 1 2 3 4 5 95 97 98
##    .. ..- attr(*, "names")= chr [1:9] "(0) None" "(1) One" "(2) A few" "(3) Some"
...
##  $ H3SP6   : dbl+lbl [1:4882] 1, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 1, 3, 0, 0,
2,...
##    ..@ label       : chr "S12Q1 PAST 7 DAYS SHAKE OFF BLUES-W3"
##    ..@ format.stata: chr "%36.0f"
##    ..@ labels      : Named num [1:7] 0 1 2 3 6 8 9
##    .. ..- attr(*, "names")= chr [1:7] "(0) Never/rarely" "(1) Sometimes" "(2) A lo
t of the time" "(3) Most of the time/all of the time" ...
##  $ H3WP46  : dbl+lbl [1:4882] 97, 97, 97, 97, 97, 97, 97, 97, 97, 97, 97, 97, 97,
...
##    ..@ label       : chr "S3Q46 CLOSE TO BIO MOM-W3"
##    ..@ format.stata: chr "%20.0f"
##    ..@ labels      : Named num [1:6] 1 2 3 4 5 97
##    .. ..- attr(*, "names")= chr [1:6] "(1) Extremely close" "(2) Quite close" "(3)
Somewhat close" "(4) Not very close" ...
##  $ H3WP53  : dbl+lbl [1:4882]  1, 97,  1, 97,  2, 97, 97, 97, 97,  5, 97, 97, 97,
...
##    ..@ label       : chr "S3Q53 CLOSE TO BIO DAD-W3"
##    ..@ format.stata: chr "%20.0f"
##    ..@ labels      : Named num [1:7] 1 2 3 4 5 97 99
##    .. ..- attr(*, "names")= chr [1:7] "(1) Extremely close" "(2) Quite close" "(3)
Somewhat close" "(4) Not very close" ...
##  $ H3WP57  : dbl+lbl [1:4882] 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 0, 7, 7, 7,
```

```
7,...
##    ..@ label       : chr "S3Q57 BIO DAD/BIO MOM LIVE TOGETHER-W3"
##    ..@ format.stata: chr "%19.0f"
##    ..@ labels      : Named num [1:5] 0 1 7 8 9
##    .. ..- attr(*, "names")= chr [1:5] "(0) No" "(1) Yes" "(7) Legitimate skip" "
(8) Don't know" ...
##  $ H3DA28  : dbl+lbl [1:4882] 0, 1, 0, 1, 1, 0, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1,
0,...
##    ..@ label       : chr "S33Q28 CURRENTLY HAVE JOB-W3"
##    ..@ format.stata: chr "%21.0f"
##    ..@ labels      : Named num [1:5] 0 1 6 8 9
##    .. ..- attr(*, "names")= chr [1:5] "(0) No (skip to Q.36)" "(1) Yes" "(6) Refus
ed" "(8) Don't know" ...
##  $ H3EC7   : dbl+lbl [1:4882] 97, 97, 97, 97, 97,  8, 97, 97, 97, 97, 97, 97, 97,
9...
##    ..@ label       : chr "S15Q7 BEST GUESS HOUSEHOLD INC B TAX-W3"
##    ..@ format.stata: chr "%21.0f"
##    ..@ labels      : Named num [1:12] 1 2 3 4 5 6 7 8 96 97 ...
##    .. ..- attr(*, "names")= chr [1:12] "(1) Less than $10,000" "(2) $10,000-$14,99
9" "(3) $15,000-$19,999" "(4) $20,000-$29,000" ...
##  $ H3EC3   : dbl+lbl [1:4882] 97, 97, 97, 97, 97,  1, 97, 97, 97, 97, 98, 97, 97,
9...
##    ..@ label       : chr "S15Q3 BEST GUESS INCOME BEFORE TAX-W3"
##    ..@ format.stata: chr "%21.0f"
##    ..@ labels      : Named num [1:12] 1 2 3 4 5 6 7 8 96 97 ...
##    .. ..- attr(*, "names")= chr [1:12] "(1) Less than $10,000" "(2) $10,000-$14,99
9" "(3) $15,000-$19,999" "(4) $20,000-$29,000" ...
##  $ H3DA36  : dbl+lbl [1:4882] 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 0,
0,...
##    ..@ label       : chr "S33Q36 ENROLLED SCHOOL/VOC TRAIN-W3"
##    ..@ format.stata: chr "%21.0f"
##    ..@ labels      : Named num [1:5] 0 1 6 8 9
##    .. ..- attr(*, "names")= chr [1:5] "(0) No (skip to Q.43)" "(1) Yes" "(6) Refus
ed" "(8) Don't know" ...
##  $ H3EC26  : dbl+lbl [1:4882] 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0,
0,...
##    ..@ label       : chr "S15Q26 CURRENTLY GETTING AFDC-W3"
##    ..@ format.stata: chr "%19.0f"
##    ..@ labels      : Named num [1:6] 0 1 6 7 8 9
##    .. ..- attr(*, "names")= chr [1:6] "(0) No" "(1) Yes" "(6) Refused" "(7) Legiti
mate skip" ...
##  $ H3EC38  : dbl+lbl [1:4882] 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
0,...
##    ..@ label       : chr "S15Q38 RECEIVED OTH PUB ASSISTANCE-W3"
##    ..@ format.stata: chr "%41.0f"
##    ..@ labels      : Named num [1:7] 0 1 5 6 7 8 9
##    .. ..- attr(*, "names")= chr [1:7] "(0) No (skip to Q.53)" "(1) Yes" "(5) Quest
ion not asked of this respondent" "(6) Refused" ...
##  $ BIO_SEX3: dbl+lbl [1:4882] 2, 2, 1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 1, 1, 2, 2, 2,
2,...
##    ..@ label       : chr "BIOLOGICAL SEX-W3"
##    ..@ format.stata: chr "%10.0f"
##    ..@ labels      : Named num [1:2] 1 2
##    .. ..- attr(*, "names")= chr [1:2] "(1) Male" "(2) Female"
##  $ H3OD4A  : dbl+lbl [1:4882] 0, 0, 0, 0, 1, 1, 0, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1,
1,...
```

```
##    ..@ label       : chr "S1Q4A RACE-WHITE-W3"
##    ..@ format.stata: chr "%18.0f"
##    ..@ labels      : Named num [1:5] 0 1 6 8 9
##    .. ..- attr(*, "names")= chr [1:5] "(0) Not marked" "(1) Marked" "(6) Refused"
"(8) Don't know" ...
##  - attr(*, "label")= chr "National Longitudinal Study of Adolescent to Adult Healt
h (Add Health), 1994-200"
```

```
summary(data_subset)
```

```
##      AID                H3ID15           H3DA15         H3FS12
##  Length:4882        Min.   :0.0000   Min.   : 0.0   Min.   :1.000
##  Class :character   1st Qu.:0.0000   1st Qu.: 3.0   1st Qu.:5.000
##  Mode  :character   Median :0.0000   Median : 5.0   Median :5.000
##                     Mean   :0.1247   Mean   : 4.8   Mean   :4.404
##                     3rd Qu.:0.0000   3rd Qu.: 7.0   3rd Qu.:5.000
##                     Max.   :9.0000   Max.   :98.0   Max.   :9.000
##
##      H3FS11          H3SP6            H3WP46          H3WP53
##  Min.   : 0.00   Min.   :0.0000   Min.   : 1.00   Min.   : 1.00
##  1st Qu.:95.00   1st Qu.:0.0000   1st Qu.:97.00   1st Qu.:97.00
##  Median :95.00   Median :0.0000   Median :97.00   Median :97.00
##  Mean   :74.88   Mean   :0.3343   Mean   :89.43   Mean   :75.92
##  3rd Qu.:95.00   3rd Qu.:0.0000   3rd Qu.:97.00   3rd Qu.:97.00
##  Max.   :98.00   Max.   :9.0000   Max.   :97.00   Max.   :99.00
##
##      H3WP57          H3DA28           H3EC7           H3EC3
##  Min.   :0.000   Min.   :0.0000   Min.   : 1.00   Min.   : 1.00
##  1st Qu.:7.000   1st Qu.:0.0000   1st Qu.:97.00   1st Qu.:97.00
##  Median :7.000   Median :1.0000   Median :97.00   Median :97.00
##  Mean   :6.736   Mean   :0.7524   Mean   :87.05   Mean   :82.46
##  3rd Qu.:7.000   3rd Qu.:1.0000   3rd Qu.:97.00   3rd Qu.:97.00
##  Max.   :9.000   Max.   :9.0000   Max.   :98.00   Max.   :99.00
##                                   NA's   :5       NA's   :5
##      H3DA36           H3EC26           H3EC38          BIO_SEX3
##  Min.   :0.0000   Min.   :0.0000   Min.   :0.0000   Min.   :1.000
##  1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:1.000
##  Median :0.0000   Median :0.0000   Median :0.0000   Median :2.000
##  Mean   :0.3863   Mean   :0.0609   Mean   :0.1833   Mean   :1.539
##  3rd Qu.:1.0000   3rd Qu.:0.0000   3rd Qu.:0.0000   3rd Qu.:2.000
##  Max.   :9.0000   Max.   :8.0000   Max.   :9.0000   Max.   :2.000
##                   NA's   :5        NA's   :5
##      H3OD4A
##  Min.   :0.0000
##  1st Qu.:0.0000
##  Median :1.0000
##  Mean   :0.7552
##  3rd Qu.:1.0000
##  Max.   :9.0000
##
```

```
colSums(is.na(data_subset))
```

```
##      AID   H3ID15   H3DA15   H3FS12   H3FS11    H3SP6   H3WP46   H3WP53
##        0        0        0        0        0        0        0        0
##   H3WP57   H3DA28    H3EC7    H3EC3   H3DA36   H3EC26   H3EC38 BIO_SEX3
##        0        0        5        5        0        5        5        0
##   H3OD4A
##        0
```

```
cleaned_data <- na.omit(data_subset)

write.csv(cleaned_data, "cleaned_addhealth_data.csv", row.names = FALSE)
```

Dataset Preview

```
head(cleaned_data)
```

```
## # A tibble: 6 × 17
##   AID      H3ID15     H3DA15  H3FS12  H3FS11   H3SP6   H3WP46   H3WP53   H3WP57
##   <chr>    <dbl+lbl>  <dbl+l> <dbl+l> <dbl+lb> <dbl+l> <dbl+lb> <dbl+lb> <dbl+l>
## 1 57100270 0 [(0) No] 0 [(0)… 5 [(5)… 95 [(95… 1 [(1)… 97 [(97…  1 [(1)… 7 [(7)…
## 2 57101310 0 [(0) No] 7 [(7)… 5 [(5)… 95 [(95… 1 [(1)… 97 [(97… 97 [(97… 7 [(7)…
## 3 57103869 0 [(0) No] 6 [(6)… 5 [(5)… 95 [(95… 0 [(0)… 97 [(97…  1 [(1)… 7 [(7)…
## 4 57104676 0 [(0) No] 0 [(0)… 1 [(1)…  5 [(5)… 0 [(0)… 97 [(97… 97 [(97… 7 [(7)…
## 5 57109625 0 [(0) No] 7 [(7)… 1 [(1)…  3 [(3)… 1 [(1)… 97 [(97…  2 [(2)… 7 [(7)…
## 6 57111071 0 [(0) No] 3 [(3)… 7 [(7)… 97 [(97… 0 [(0)… 97 [(97… 97 [(97… 7 [(7)…
## # ℹ 8 more variables: H3DA28 <dbl+lbl>, H3EC7 <dbl+lbl>, H3EC3 <dbl+lbl>,
## #   H3DA36 <dbl+lbl>, H3EC26 <dbl+lbl>, H3EC38 <dbl+lbl>, BIO_SEX3 <dbl+lbl>,
## #   H3OD4A <dbl+lbl>
```

Part 1 - Dataset Preparation

Re-labelling

A) Target Variable

```
# Recode H3ID15 — Have you ever been diagnosed with depression?
# 0 = No, 1 = Yes, all others = NA

cleaned_data$H3ID15_recode <- ifelse(cleaned_data$H3ID15 %in% c(0, 1),
                                     cleaned_data$H3ID15,
                                     NA)

# Convert to labeled factor
cleaned_data$H3ID15_recode <- factor(cleaned_data$H3ID15_recode,
                                     levels = c(0, 1),
                                     labels = c("No Depression", "Diagnosed Depressio
n"))
```

B) Independent Variable

B1) Friends & Family

```
#1
# Recode H3DA15 — Number of times hung out with friends (0–7)
# Set 96/98 to NA

cleaned_data$H3DA15_recode <- ifelse(cleaned_data$H3DA15 %in% 0:7,
                                     cleaned_data$H3DA15,
                                     NA)



#2
# Recode H3FS12 — Who influenced you more: friends or family?
# 1 = Friends, 2 = Family, 5 = Not Asked, 7/8/9 = NA

cleaned_data$H3FS12_recode <- ifelse(cleaned_data$H3FS12 %in% c(1, 2, 5),
                                     cleaned_data$H3FS12,
                                     NA)
# Convert to labeled factor
cleaned_data$H3FS12_recode <- factor(cleaned_data$H3FS12_recode,
                                     levels = c(1, 2, 5),
                                     labels = c("Friends more influential",
                                                "Family more influential",
                                                "Not Asked"))

#3
# Recode H3FS11 — How many high school friends are you still friends with?
# Valid: 0–5 (scale), 95 = "Not Asked", rest = NA

cleaned_data$H3FS11_recode <- ifelse(cleaned_data$H3FS11 %in% c(0:5, 95),
                                     cleaned_data$H3FS11,
                                     NA)

# Convert to factor with "Not Asked" as a separate category
cleaned_data$H3FS11_recode <- factor(cleaned_data$H3FS11_recode,
                                     levels = c(0, 1, 2, 3, 4, 5, 95),
                                     labels = c("None", "One", "A few", "Some", "Mos
t", "All", "Not Asked"),
                                     ordered = FALSE)  # or TRUE if you treat it as o
rdinal


#4
# Recode H3SP6 — How often could you not shake off the blues (past 7 days)?
# Keep 0–3, set 6/8/9 to NA

cleaned_data$H3SP6_recode <- ifelse(cleaned_data$H3SP6 %in% 0:3,
                                    cleaned_data$H3SP6,
                                    NA)

# Convert to ordered factor
cleaned_data$H3SP6_recode <- factor(cleaned_data$H3SP6_recode,
                                    levels = 0:3,
                                    labels = c("Never or rarely",
                                               "Sometimes",
                                               "A lot of the time",
                                               "Most/all of the time"),
```

```
                                    ordered = TRUE)



#5
# Recode H3WP46 — Closeness to biological mother, with skip retained
# Valid: 1–5, 97 = Not applicable

cleaned_data$H3WP46_recode <- ifelse(cleaned_data$H3WP46 %in% c(1:5, 97),
                                     cleaned_data$H3WP46,
                                     NA)

# Convert to labeled factor (including "Skipped/Not Applicable")
cleaned_data$H3WP46_recode <- factor(cleaned_data$H3WP46_recode,
                                     levels = c(1:5, 97),
                                     labels = c("Extremely close",
                                                "Quite close",
                                                "Somewhat close",
                                                "Not very close",
                                                "Not close at all",
                                                "Not applicable / skipped"),
                                     ordered = FALSE)


#6
# Recode H3WP53 — Closeness to biological father
# Valid: 1–5, 97 = "Not applicable/skipped", others = NA

cleaned_data$H3WP53_recode <- ifelse(cleaned_data$H3WP53 %in% c(1:5, 97),
                                     cleaned_data$H3WP53,
                                     NA)

# Convert to labeled factor
cleaned_data$H3WP53_recode <- factor(cleaned_data$H3WP53_recode,
                                     levels = c(1:5, 97),
                                     labels = c("Extremely close",
                                                "Quite close",
                                                "Somewhat close",
                                                "Not very close",
                                                "Not close at all",
                                                "Not applicable / skipped"),
                                     ordered = FALSE)


#7
# Recode H3WP57 — Do your biological parents live together?
# 0 = No, 1 = Yes, 7 = Not applicable/skipped, others = NA

cleaned_data$H3WP57_recode <- ifelse(cleaned_data$H3WP57 %in% c(0, 1, 7),
                                     cleaned_data$H3WP57,
                                     NA)

# Convert to labeled factor
cleaned_data$H3WP57_recode <- factor(cleaned_data$H3WP57_recode,
                                     levels = c(0, 1, 7),
                                     labels = c("No",
```

```
                                                    "Yes",
                                                    "Not applicable / skipped"))
```

B2) Socioeconomic Factors

```r
#1
# Recode H3DA28 — Do you currently have a job?
# 0 = No, 1 = Yes, others = NA

cleaned_data$H3DA28_recode <- ifelse(cleaned_data$H3DA28 %in% c(0, 1),
                                     cleaned_data$H3DA28,
                                     NA)

# Convert to labeled factor
cleaned_data$H3DA28_recode <- factor(cleaned_data$H3DA28_recode,
                                     levels = c(0, 1),
                                     labels = c("No", "Yes"))



#2
# Recode H3EC7 — Estimated total household income
# 1–8 = valid, 97 = "Skipped", others = NA

cleaned_data$H3EC7_recode <- ifelse(cleaned_data$H3EC7 %in% c(1:8, 97),
                                    cleaned_data$H3EC7,
                                    NA)

# Convert to ordered factor
cleaned_data$H3EC7_recode <- factor(cleaned_data$H3EC7_recode,
                                    levels = c(1:8, 97),
                                    labels = c("Less than $10,000",
                                               "$10,000–14,999",
                                               "$15,000–19,999",
                                               "$20,000–29,999",
                                               "$30,000–39,999",
                                               "$40,000–49,999",
                                               "$50,000–74,999",
                                               "$75,000 or more",
                                               "Not applicable / skipped"),
                                    ordered = TRUE)



#3
# Recode H3EC3 — Estimated total personal income
# 1–8 = valid, 97 = "Skipped", others = NA

cleaned_data$H3EC3_recode <- ifelse(cleaned_data$H3EC3 %in% c(1:8, 97),
                                    cleaned_data$H3EC3,
                                    NA)

# Convert to ordered factor
cleaned_data$H3EC3_recode <- factor(cleaned_data$H3EC3_recode,
                                    levels = c(1:8, 97),
                                    labels = c("Less than $10,000",
                                               "$10,000–14,999",
                                               "$15,000–19,999",
                                               "$20,000–29,999",
                                               "$30,000–39,999",
```

```
                                          "$40,000–49,999",
                                          "$50,000–74,999",
                                          "$75,000 or more",
                                          "Not applicable / skipped"),
                                 ordered = TRUE)


#4
# Recode H3DA36 — Enrolled in school/job training/vocational education
# 0 = No, 1 = Yes, others = NA

cleaned_data$H3DA36_recode <- ifelse(cleaned_data$H3DA36 %in% c(0, 1),
                                     cleaned_data$H3DA36,
                                     NA)

# Convert to labeled factor
cleaned_data$H3DA36_recode <- factor(cleaned_data$H3DA36_recode,
                                     levels = c(0, 1),
                                     labels = c("No", "Yes"))


#5
# Recode H3EC26 — Currently receiving AFDC/public assistance/welfare?
# 0 = No, 1 = Yes, others = NA

cleaned_data$H3EC26_recode <- ifelse(cleaned_data$H3EC26 %in% c(0, 1),
                                     cleaned_data$H3EC26,
                                     NA)

# Convert to labeled factor
cleaned_data$H3EC26_recode <- factor(cleaned_data$H3EC26_recode,
                                     levels = c(0, 1),
                                     labels = c("No", "Yes"))


#6
# Recode H3EC38 — Ever received public assistance (excluding food stamps)?
# 0 = No, 1 = Yes, 5 = Not Asked, others = NA

cleaned_data$H3EC38_recode <- ifelse(cleaned_data$H3EC38 %in% c(0, 1, 5),
                                     cleaned_data$H3EC38,
                                     NA)

# Convert to labeled factor
cleaned_data$H3EC38_recode <- factor(cleaned_data$H3EC38_recode,
                                     levels = c(0, 1, 5),
                                     labels = c("No", "Yes", "Not Asked"))
```

B3) Demographics

```r
#1
# Recode BIO_SEX3 – Respondent's gender
# 1 = Male, 2 = Female

cleaned_data$BIO_SEX3_recode <- factor(cleaned_data$BIO_SEX3,
                                       levels = c(1, 2),
                                       labels = c("Male", "Female"))


#2
# Recode H3OD4A – Race: White
# 0 = Not White, 1 = White, others = NA

cleaned_data$H3OD4A_recode <- ifelse(cleaned_data$H3OD4A %in% c(0, 1),
                                     cleaned_data$H3OD4A,
                                     NA)

# Convert to labeled factor
cleaned_data$H3OD4A_recode <- factor(cleaned_data$H3OD4A_recode,
                                     levels = c(0, 1),
                                     labels = c("Not White", "White"))
```

Saving the Recoded Varibles as a separate dataset

```
# Create a new data frame with only recoded variables and AID for reference
recoded_data <- cleaned_data[, c(
  "AID",

  # Target
  "H3ID15_recode",

  # Friends & Family
  "H3DA15_recode",
  "H3FS12_recode",
  "H3FS11_recode",
  "H3SP6_recode",
  "H3WP46_recode",
  "H3WP53_recode",
  "H3WP57_recode",

  # SES
  "H3DA28_recode",
  "H3EC7_recode",
  "H3EC3_recode",
  "H3DA36_recode",
  "H3EC26_recode",
  "H3EC38_recode",

  # Demographics
  "BIO_SEX3_recode",
  "H3OD4A_recode"
)]

# Create a complete-case dataset (drop rows with any NA)
complete_data <- na.omit(recoded_data)

# Save to CSV
write.csv(complete_data, "complete_addhealth_data.csv", row.names = FALSE)
```

Finding NA in each Variable

```
# Count NA values in each variable of your recoded dataset
colSums(is.na(complete_data))
```

```
##             AID   H3ID15_recode   H3DA15_recode   H3FS12_recode   H3FS11_recode
##               0               0               0               0               0
##    H3SP6_recode   H3WP46_recode   H3WP53_recode   H3WP57_recode   H3DA28_recode
##               0               0               0               0               0
##    H3EC7_recode    H3EC3_recode   H3DA36_recode   H3EC26_recode   H3EC38_recode
##               0               0               0               0               0
## BIO_SEX3_recode   H3OD4A_recode
##               0               0
```

Part 2 - Visualisation

```
# Load libraries
library(tidyverse)
```

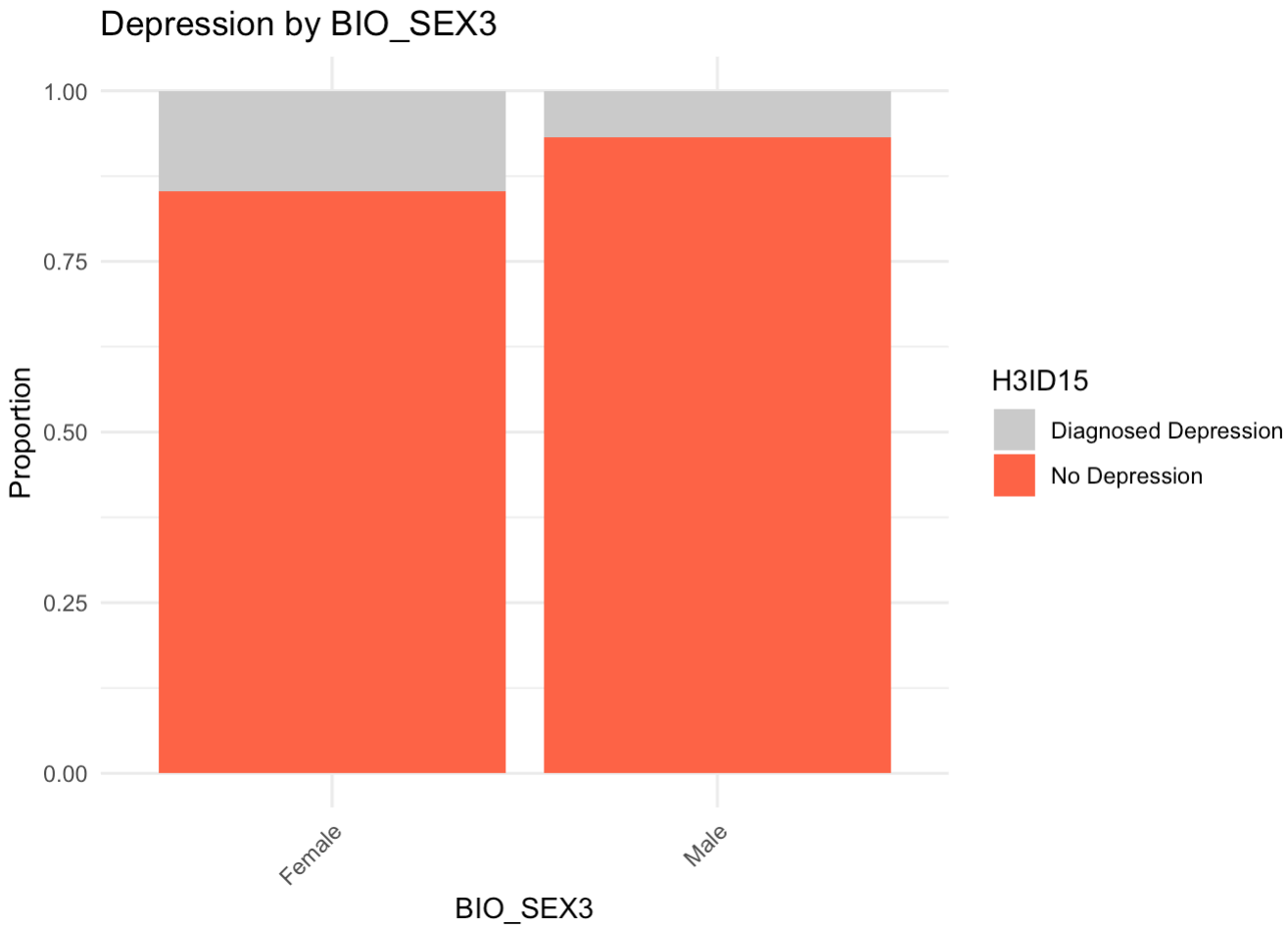
```
## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
## ✔ dplyr     1.1.4     ✔ readr     2.1.5
## ✔ forcats   1.0.0     ✔ stringr   1.5.1
## ✔ lubridate 1.9.4     ✔ tibble    3.2.1
## ✔ purrr     1.0.4     ✔ tidyr     1.3.1
## ── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()    masks stats::lag()
## ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflic
ts to become errors
```

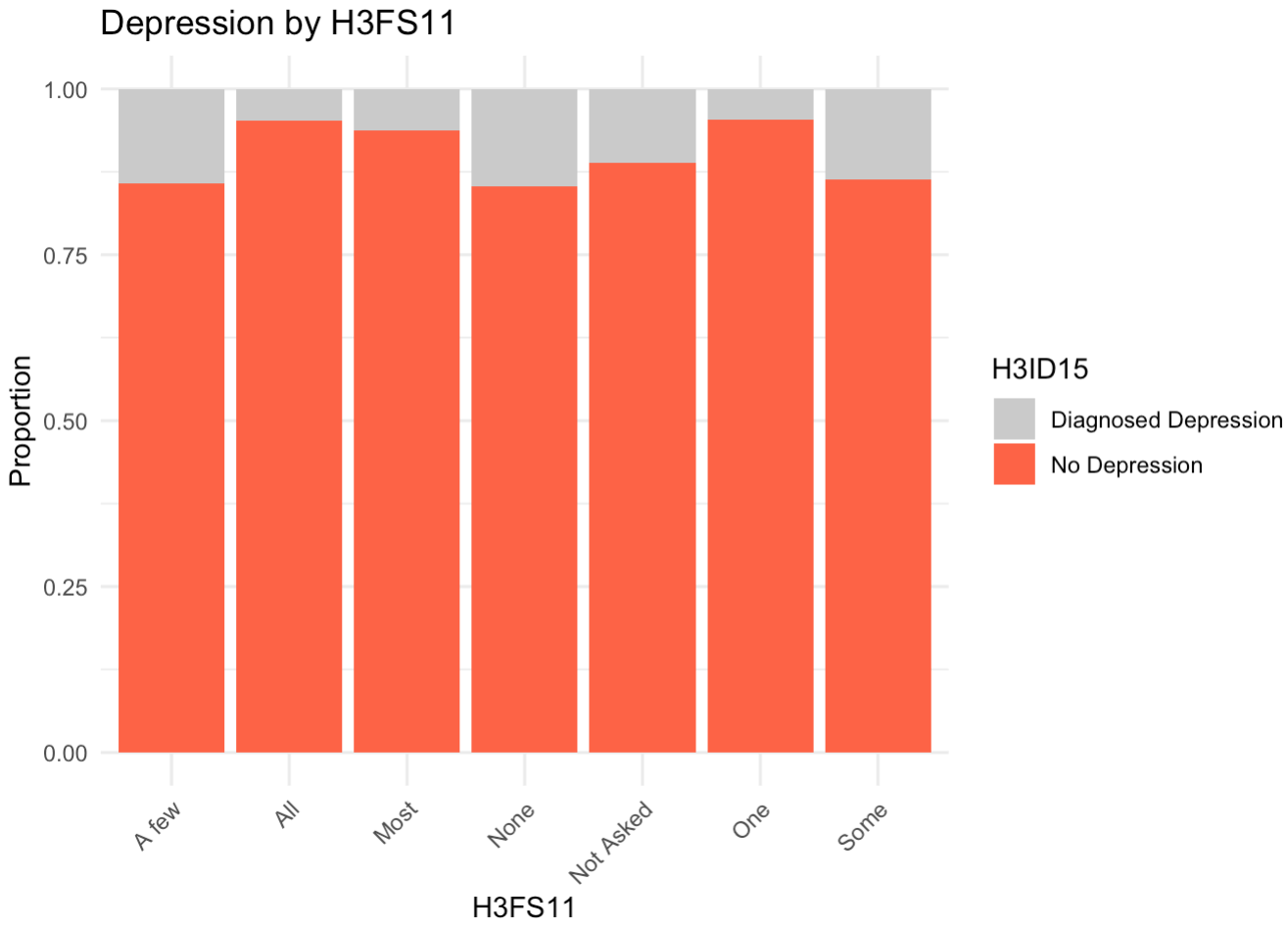
```
# Step 1: Read and clean the dataset
data <- read.csv("complete_addhealth_data.csv", stringsAsFactors = TRUE)
names(data) <- gsub("_recode$", "", names(data))

# Step 2: Make sure key variables are treated as factors
categorical_vars <- c("H3ID15", "BIO_SEX3", "H3FS11", "H3FS12", "H3SP6",
                      "H3WP46", "H3WP53", "H3WP57", "H3DA28", "H3EC7", "H3EC3",
                      "H3DA36", "H3EC26", "H3EC38", "H3OD4A")

data[categorical_vars] <- lapply(data[categorical_vars], as.factor)

# Step 3: Summary stats for numeric variable
summary(data$H3DA15)
```

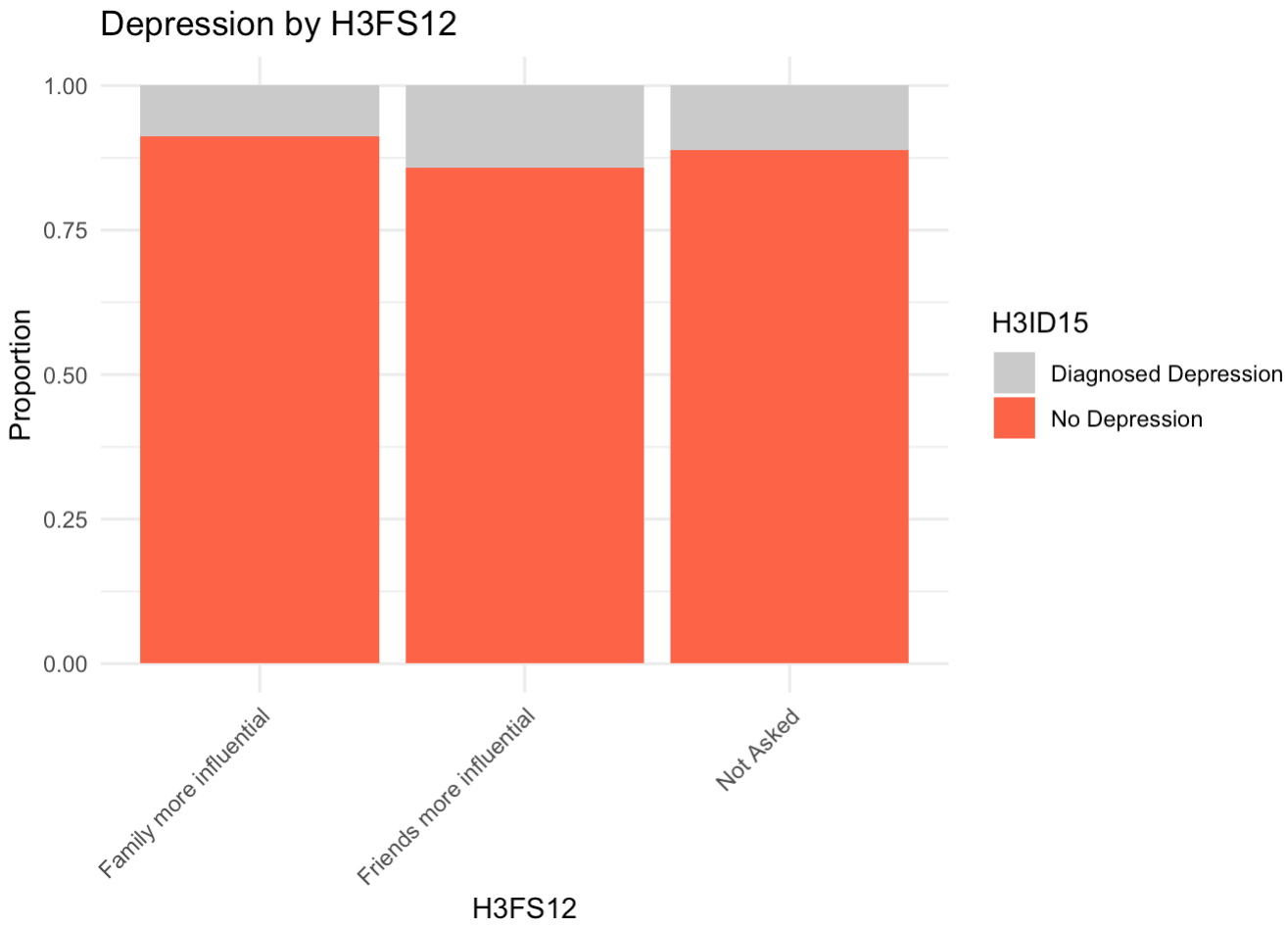
```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   3.000   4.000   4.389   7.000   7.000
```

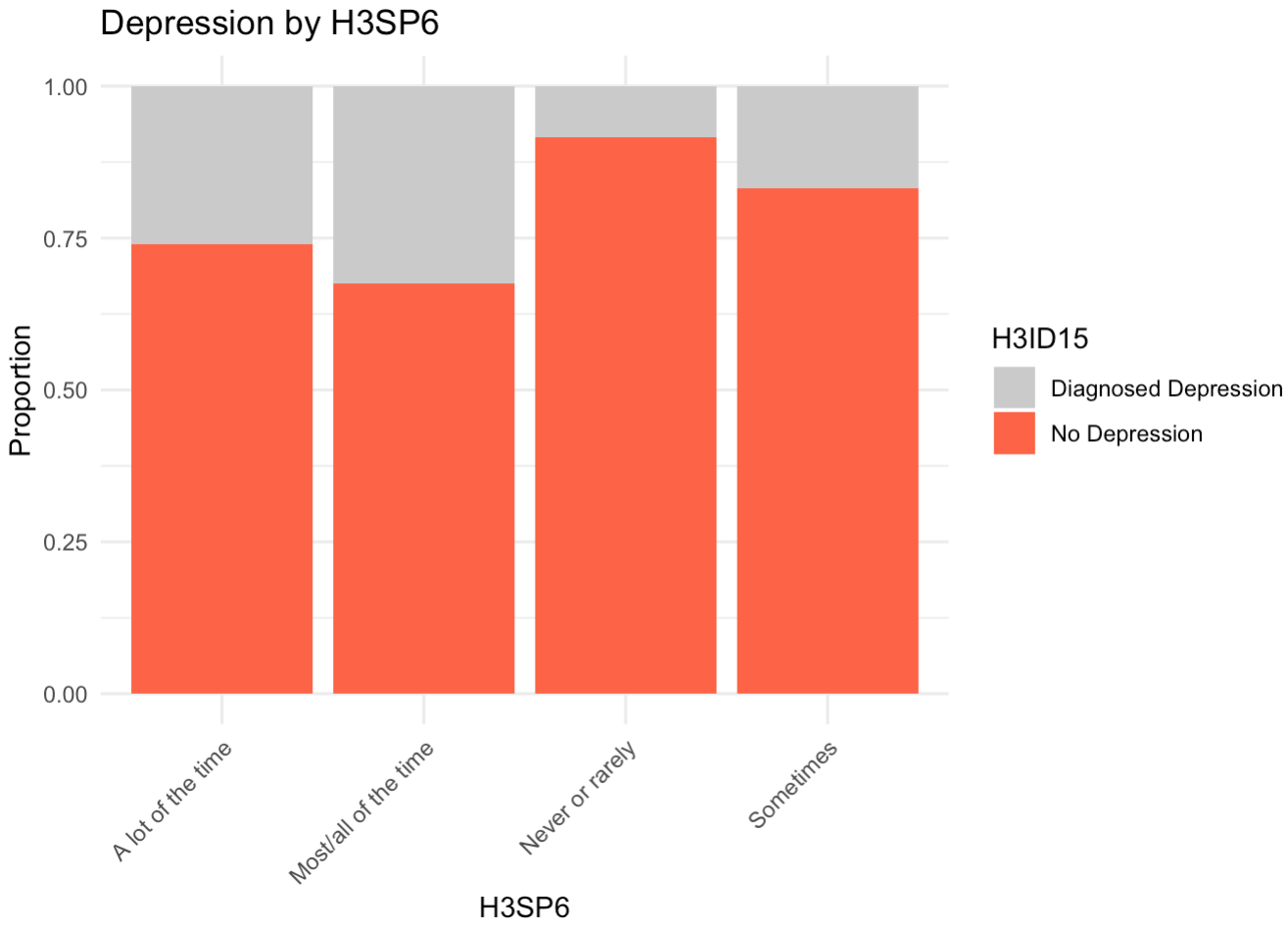
```
# Step 4: Bar plots – Bivariate with Depression
plot_vars <- categorical_vars[categorical_vars != "H3ID15"]  # exclude target

for (var in plot_vars) {
  print(
    ggplot(data, aes_string(x = var, fill = "H3ID15")) +
      geom_bar(position = "fill") +
      labs(title = paste("Depression by", var),
           x = var, y = "Proportion") +
      scale_fill_manual(values = c("gray80", "tomato")) +
      theme_minimal() +
      theme(axis.text.x = element_text(angle = 45, hjust = 1))
  )
}
```

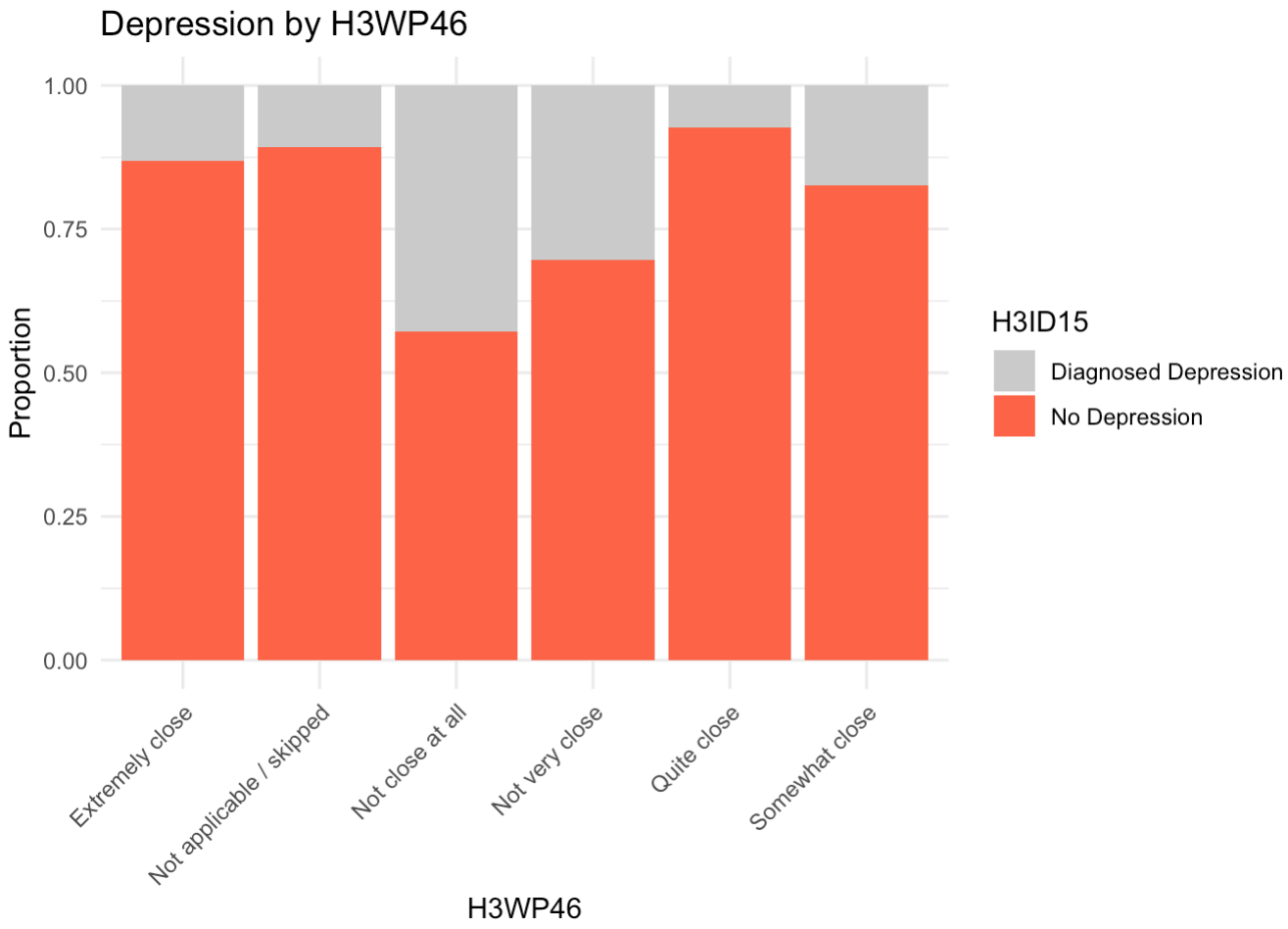
```
## Warning: `aes_string()` was deprecated in ggplot2 3.0.0.
## ℹ Please use tidy evaluation idioms with `aes()`.
## ℹ See also `vignette("ggplot2-in-packages")` for more information.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```


Depression by BIO_SEX3
1.00
0.75
0.50
0.25
0.00
Proportion
Female
Male
BIO_SEX3
H3ID15
Diagnosed Depression
No Depression

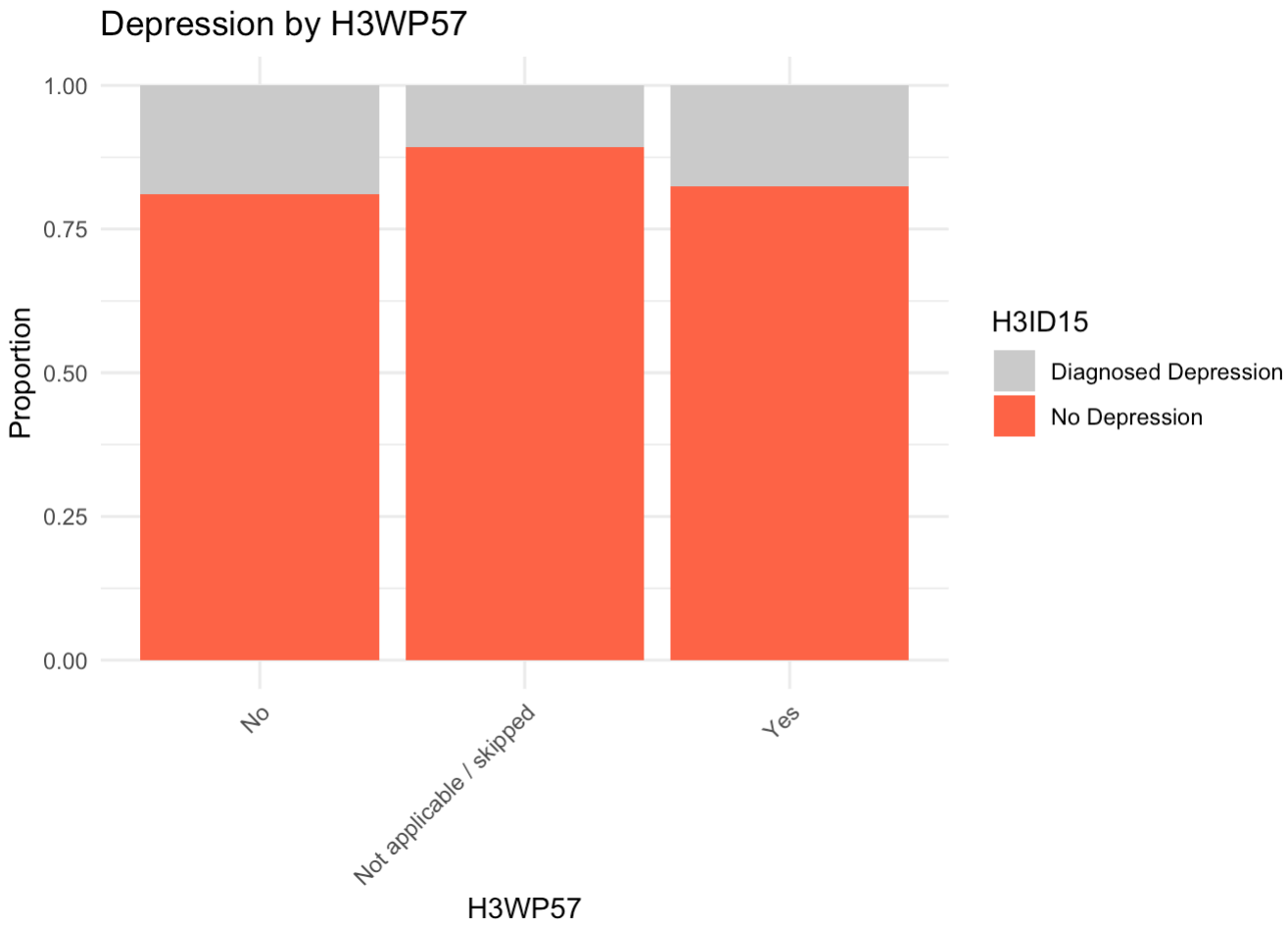

Depression by H3FS11
1.00
0.75
0.50
0.25
0.00
Proportion
A few
All
Most
None
Not Asked
One
Some
H3FS11
H3ID15
Diagnosed Depression
No Depression

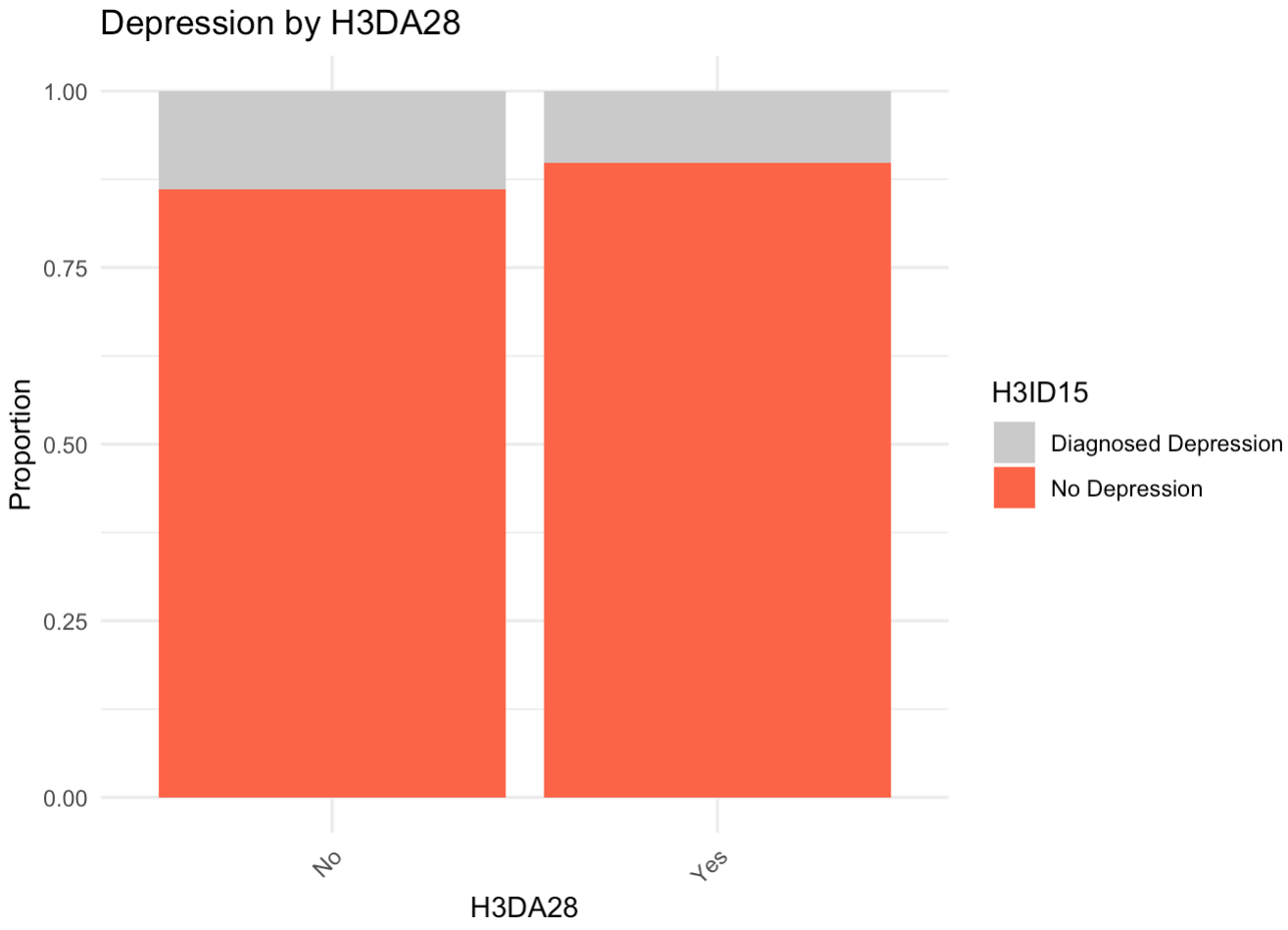

Depression by H3FS12
1.00
0.75
0.50
0.25
0.00
Proportion
Family more influential
Friends more influential
Not Asked
H3FS12
H3ID15
Diagnosed Depression
No Depression

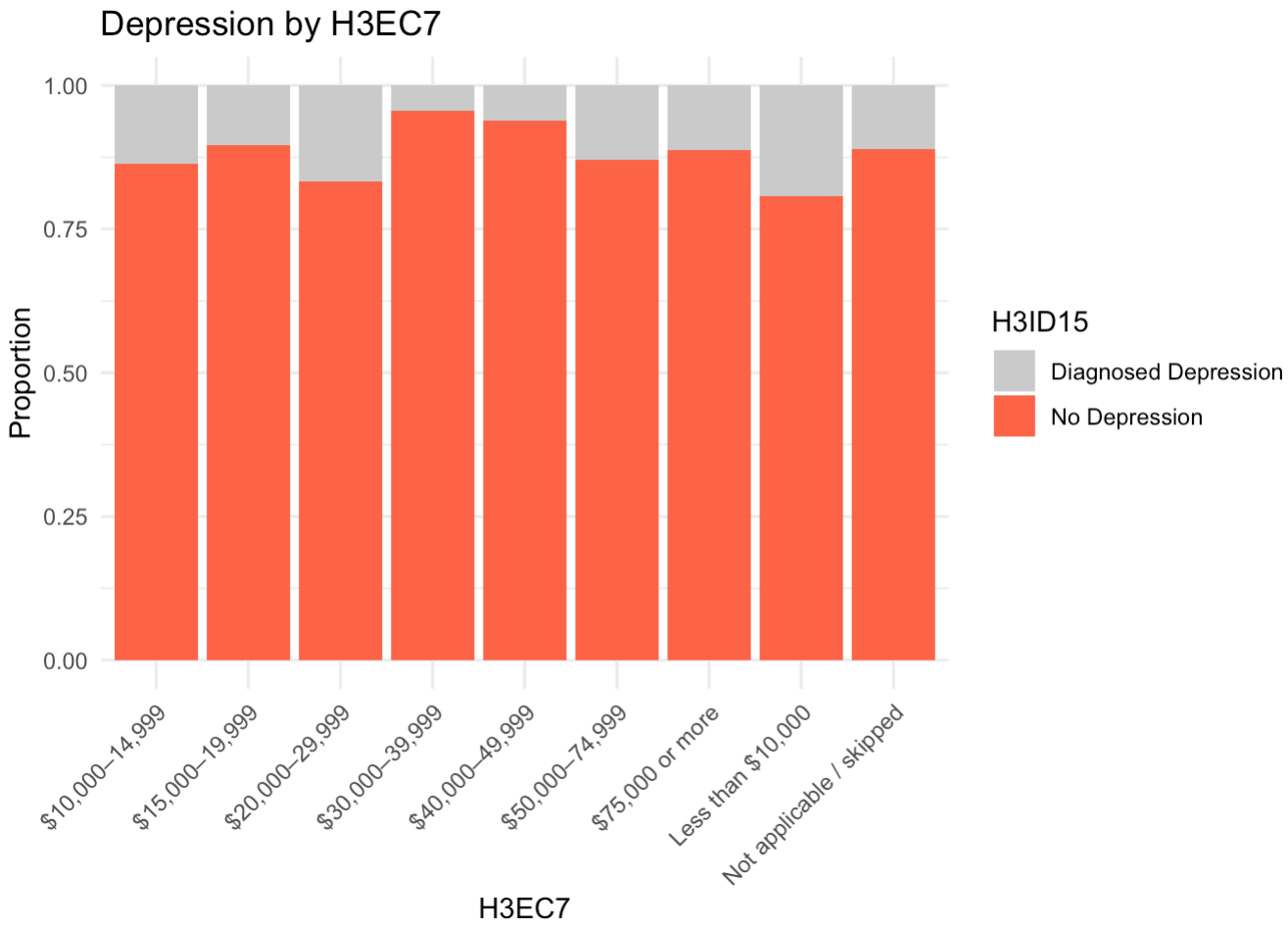

Depression by H3SP6
1.00
0.75
0.50
0.25
0.00
Proportion
A lot of the time
Most/all of the time
Never or rarely
Sometimes
H3SP6
H3ID15
Diagnosed Depression
No Depression

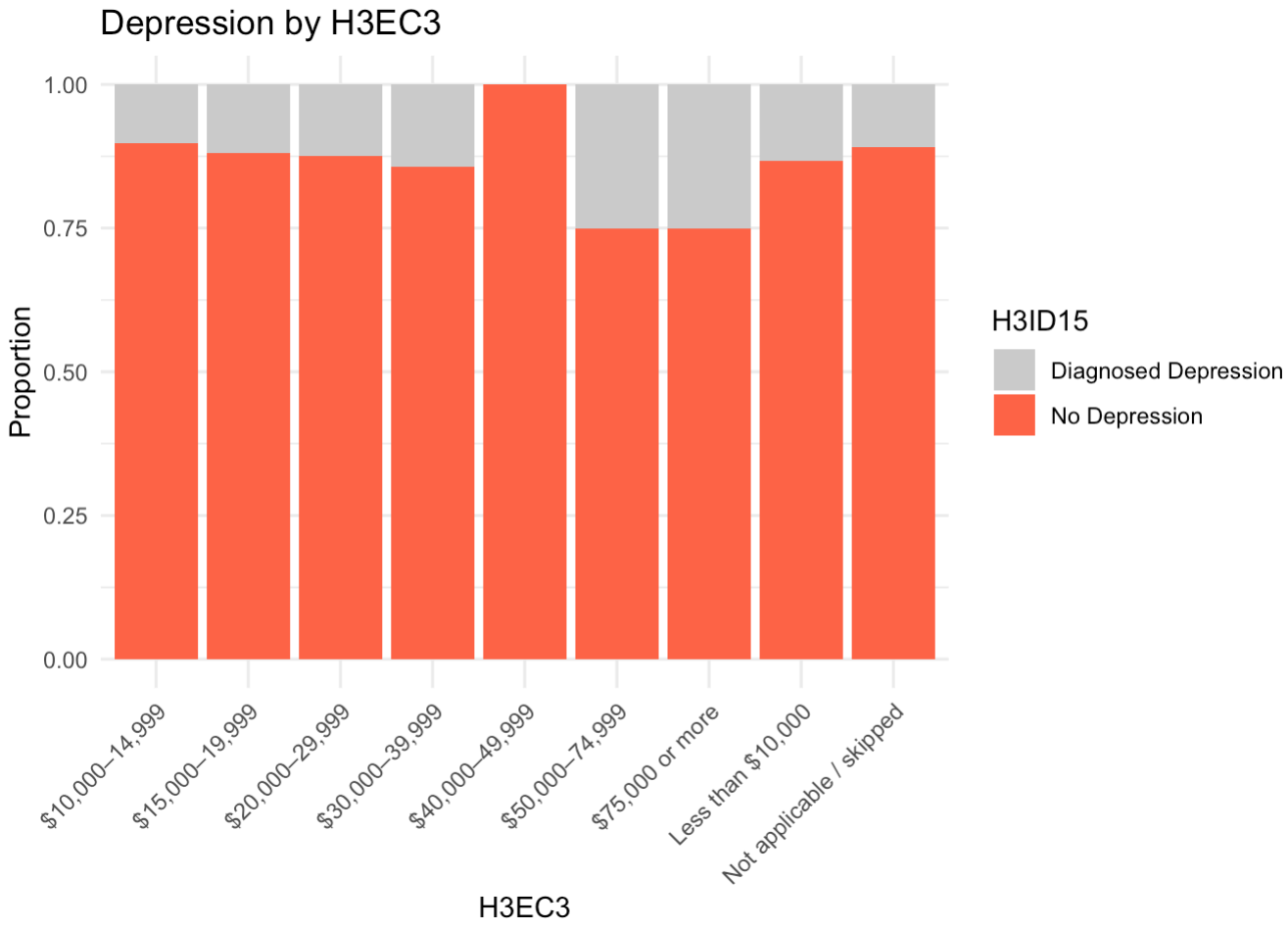

Depression by H3WP46
1.00
0.75
0.50
0.25
0.00
Proportion
Extremely close
Not applicable / skipped
Not close at all
Not very close
Quite close
Somewhat close
H3WP46
H3ID15
Diagnosed Depression
No Depression

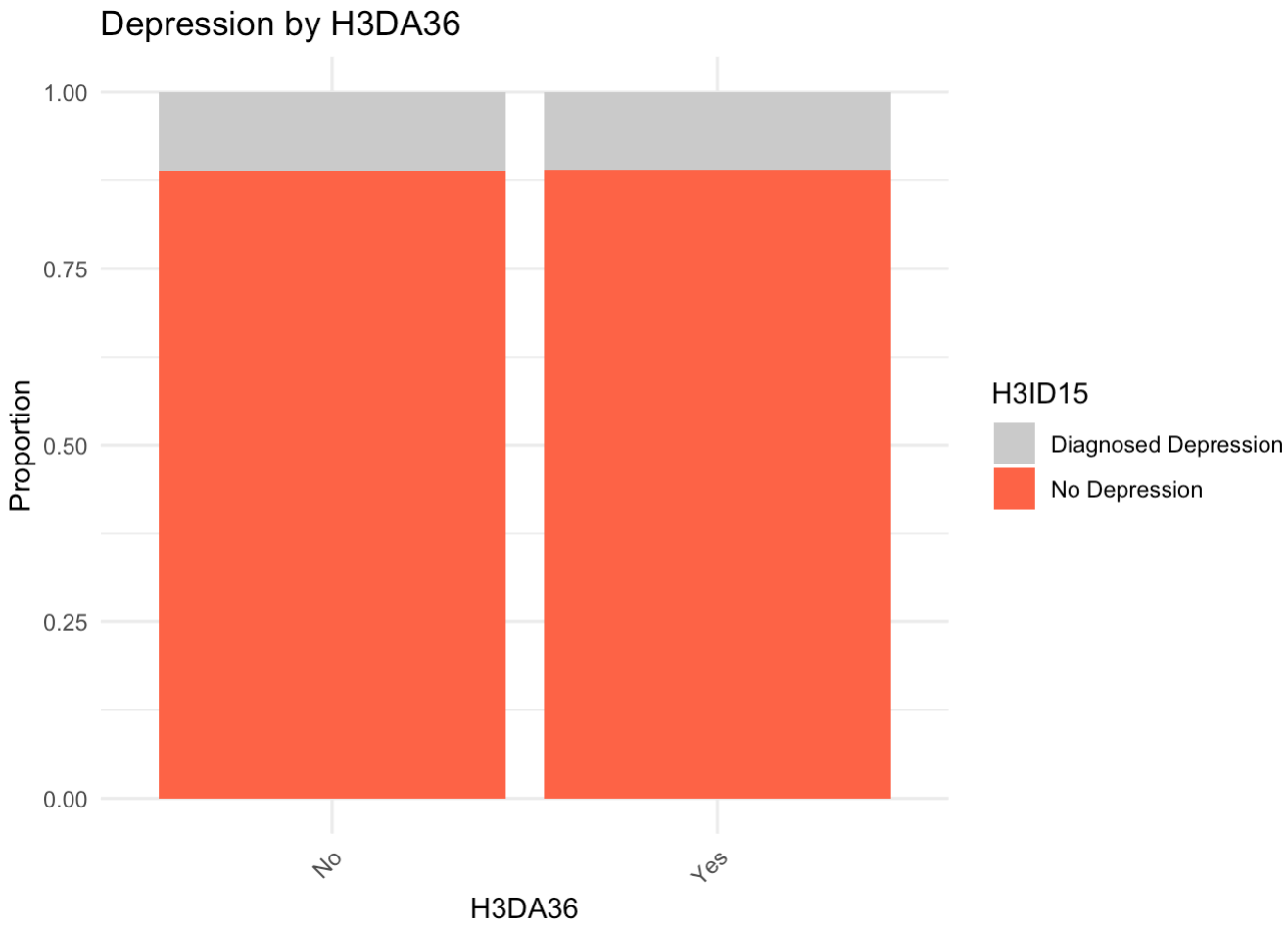

Depression by H3WP53
1.00
0.75
0.50
0.25
0.00
Proportion
Extremely close
Not applicable / skipped
Not close at all
Not very close
Quite close
Somewhat close
H3WP53
H3ID15
Diagnosed Depression
No Depression

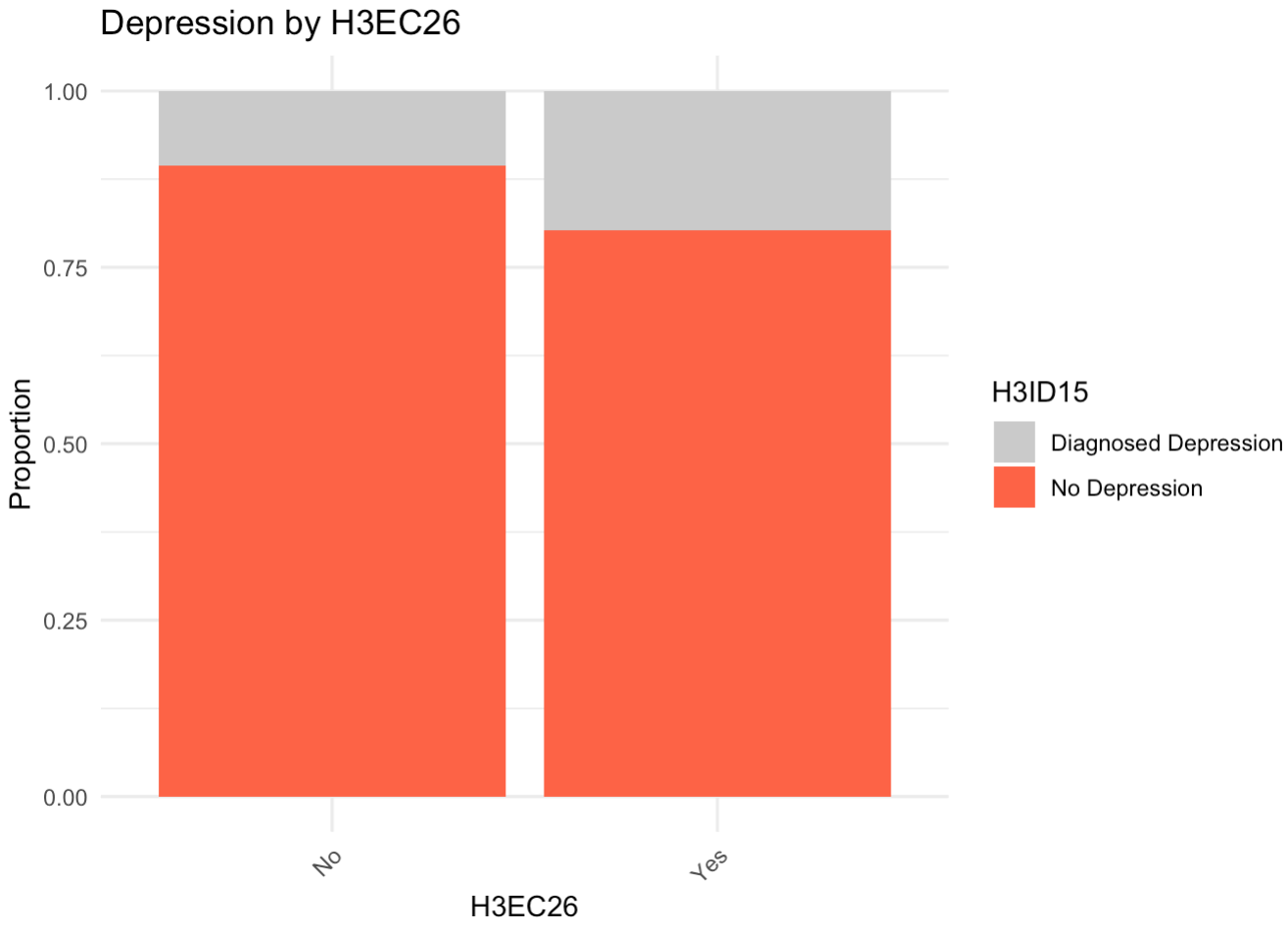

Depression by H3WP57
1.00
0.75
0.50
0.25
0.00
Proportion
No
Not applicable / skipped
Yes
H3WP57
H3ID15
Diagnosed Depression
No Depression

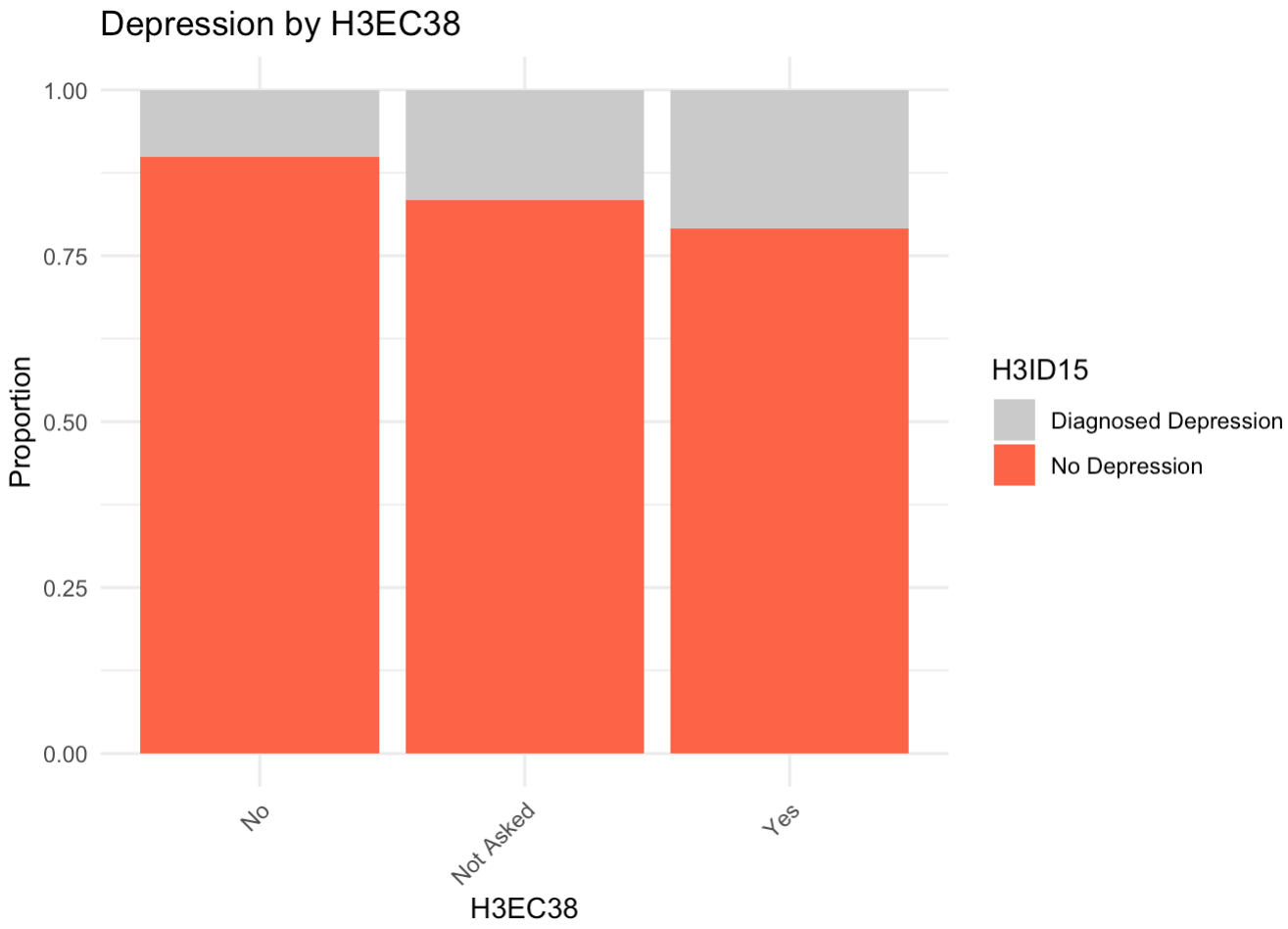

Depression by H3DA28
1.00
0.75
0.50
0.25
0.00
Proportion
No
Yes
H3DA28
H3ID15
Diagnosed Depression
No Depression


Depression by H3EC7
1.00
0.75
0.50
0.25
0.00
Proportion
$10,000–14,999
$15,000–19,999
$20,000–29,999
$30,000–39,999
$40,000–49,999
$50,000–74,999
$75,000 or more
Less than $10,000
Not applicable / skipped
H3EC7
H3ID15
Diagnosed Depression
No Depression


Depression by H3EC3
1.00
0.75
0.50
0.25
0.00
Proportion
$10,000–14,999
$15,000–19,999
$20,000–29,999
$30,000–39,999
$40,000–49,999
$50,000–74,999
$75,000 or more
Less than $10,000
Not applicable / skipped
H3EC3
H3ID15
Diagnosed Depression
No Depression

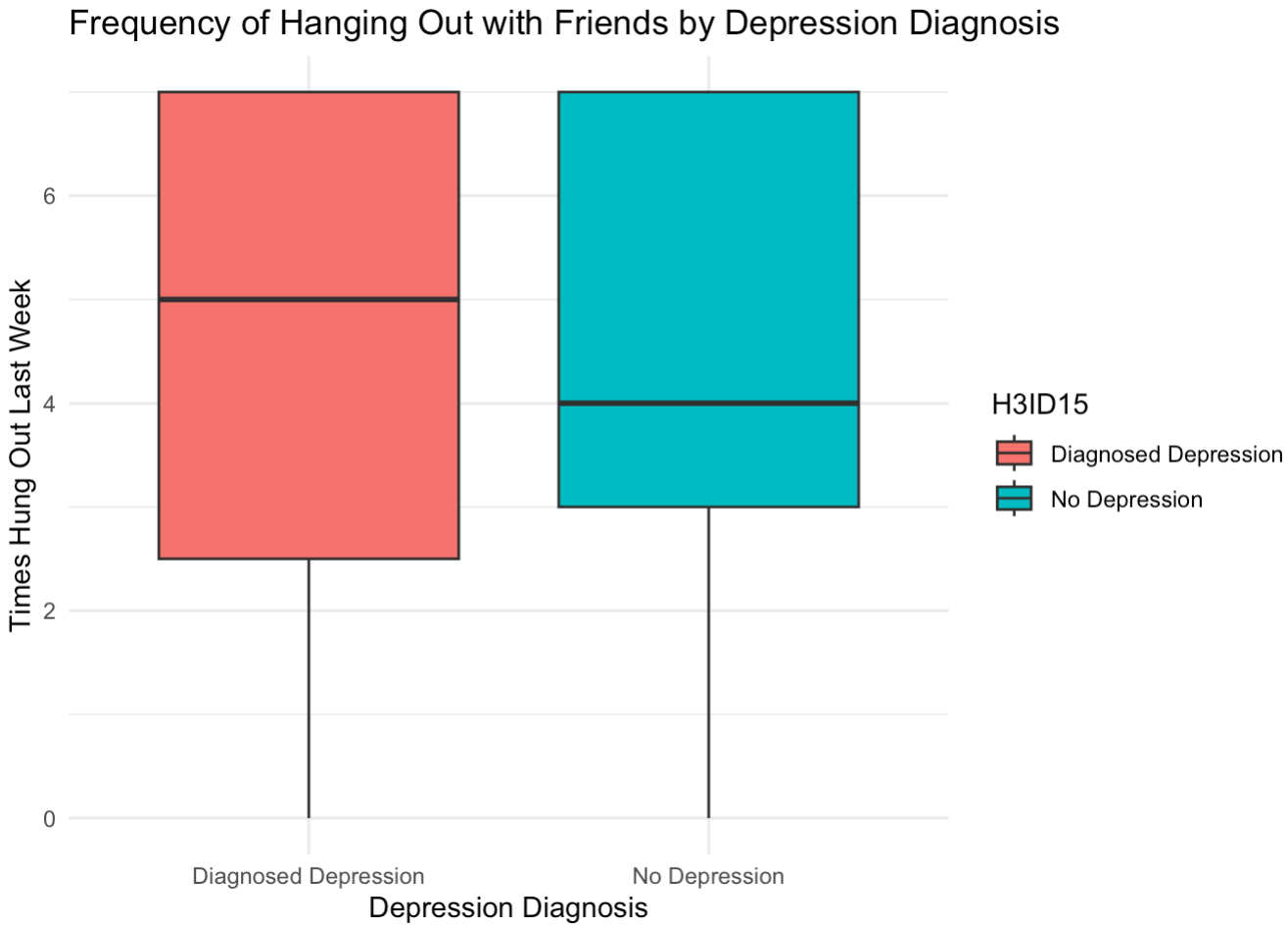

Depression by H3DA36
1.00
0.75
0.50
0.25
0.00
Proportion
No
Yes
H3DA36
H3ID15
Diagnosed Depression
No Depression


Depression by H3EC26
1.00
0.75
0.50
0.25
0.00
Proportion
No
Yes
H3EC26
H3ID15
Diagnosed Depression
No Depression


Depression by H3EC38
1.00
0.75
0.50
0.25
0.00
Proportion
No
Not Asked
Yes
H3EC38
H3ID15
Diagnosed Depression
No Depression


Depression by H3OD4A
1.00
0.75
0.50
0.25
0.00
Proportion
Not White
White
H3OD4A
H3ID15
Diagnosed Depression
No Depression

```
# Step 5: Boxplot – Numeric Predictor vs Target
ggplot(data, aes(x = H3ID15, y = H3DA15, fill = H3ID15)) +
  geom_boxplot() +
  labs(title = "Frequency of Hanging Out with Friends by Depression Diagnosis",
       x = "Depression Diagnosis", y = "Times Hung Out Last Week") +
  theme_minimal()
```




```
# Step 6: Cross-tabs

# Peer support vs Depression
print("Depression by Peer Interaction:")
```

```
## [1] "Depression by Peer Interaction:"
```

```
print(prop.table(table(data$H3DA15, data$H3ID15), margin = 1))
```

```
##
##     Diagnosed Depression No Depression
##   0           0.13068182    0.86931818
##   1           0.11312217    0.88687783
##   2           0.10389610    0.89610390
##   3           0.08253968    0.91746032
##   4           0.10101010    0.89898990
##   5           0.11389522    0.88610478
##   6           0.10849057    0.89150943
##   7           0.12254570    0.87745430
```

```
# Income vs Depression
print("Depression by Household Income:")
```

```
## [1] "Depression by Household Income:"
```

```
print(prop.table(table(data$H3EC7, data$H3ID15), margin = 1))
```

```
##
##                             Diagnosed Depression No Depression
##   $10,000–14,999                        0.13636364    0.86363636
##   $15,000–19,999                        0.10344828    0.89655172
##   $20,000–29,999                        0.16666667    0.83333333
##   $30,000–39,999                        0.04347826    0.95652174
##   $40,000–49,999                        0.06153846    0.93846154
##   $50,000–74,999                        0.12871287    0.87128713
##   $75,000 or more                       0.11188811    0.88811189
##   Less than $10,000                     0.19354839    0.80645161
##   Not applicable / skipped              0.11052770    0.88947230
```

```
# Gender vs Depression
print("Depression by Gender:")
```

```
## [1] "Depression by Gender:"
```

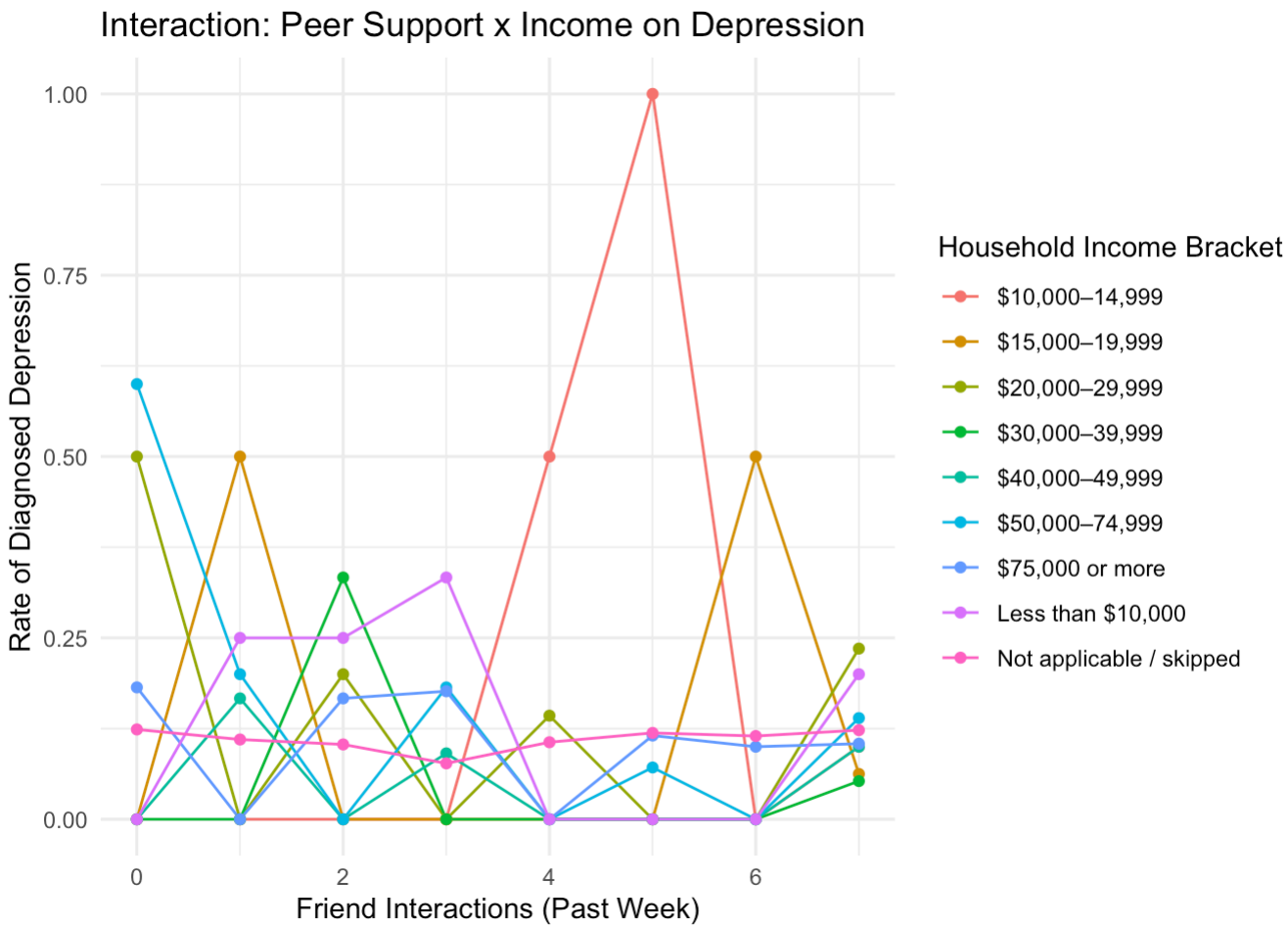
```
print(prop.table(table(data$BIO_SEX3, data$H3ID15), margin = 1))
```

```
##
##          Diagnosed Depression No Depression
##   Female           0.14693172    0.85306828
##   Male             0.06838906    0.93161094
```

```
library(dplyr)

# Collapse to average depression rate
interaction_summary <- data %>%
  group_by(H3DA15, H3EC7) %>%
  summarise(depression_rate = mean(H3ID15 == "Diagnosed Depression"))
```

```
## `summarise()` has grouped output by 'H3DA15'. You can override using the
## `.groups` argument.
```

```
# Plot
ggplot(interaction_summary, aes(x = H3DA15, y = depression_rate, color = H3EC7)) +
  geom_line() +
  geom_point() +
  labs(title = "Interaction: Peer Support x Income on Depression",
       x = "Friend Interactions (Past Week)",
       y = "Rate of Diagnosed Depression",
       color = "Household Income Bracket") +
  theme_minimal()
```

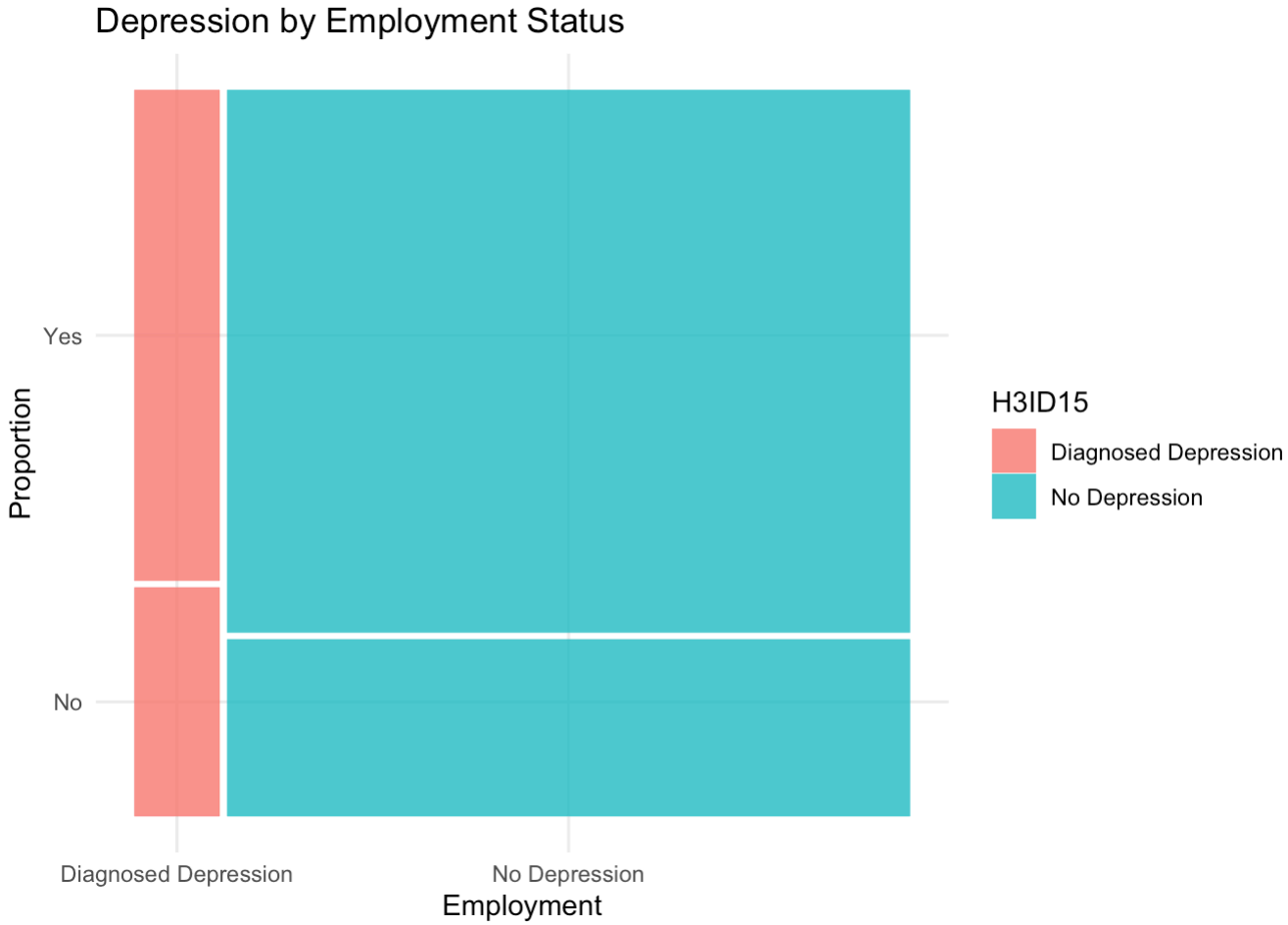



```
library(ggmosaic)

ggplot(data = data) +
  geom_mosaic(aes(weight = 1, x = product(H3DA28, H3ID15), fill = H3ID15)) +
  labs(title = "Depression by Employment Status",
       x = "Employment", y = "Proportion") +
  theme_minimal()
```

```
## Warning: The `scale_name` argument of `continuous_scale()` is deprecated as of ggp
lot2
## 3.5.0.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## Warning: The `trans` argument of `continuous_scale()` is deprecated as of ggplot2
3.5.0.
## ℹ Please use the `transform` argument instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

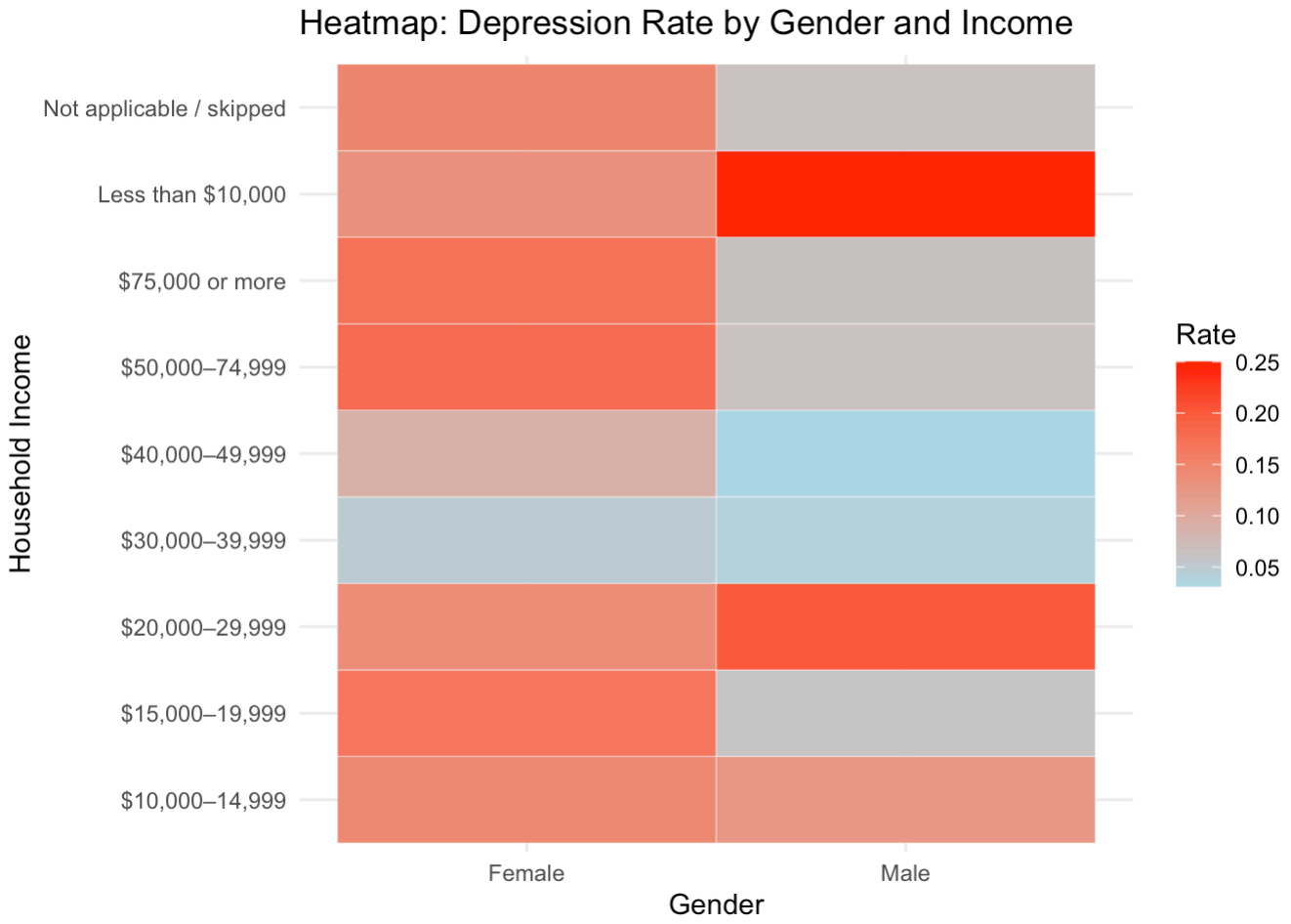
```
## Warning: `unite_()` was deprecated in tidyr 1.2.0.
## ℹ Please use `unite()` instead.
## ℹ The deprecated feature was likely used in the ggmosaic package.
##   Please report the issue at <https://github.com/haleyjeppson/ggmosaic>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```




```
heat_data <- data %>%
  group_by(BIO_SEX3, H3EC7) %>%
  summarise(depression_rate = mean(H3ID15 == "Diagnosed Depression"))
```

```
## `summarise()` has grouped output by 'BIO_SEX3'. You can override using the
## `.groups` argument.
```

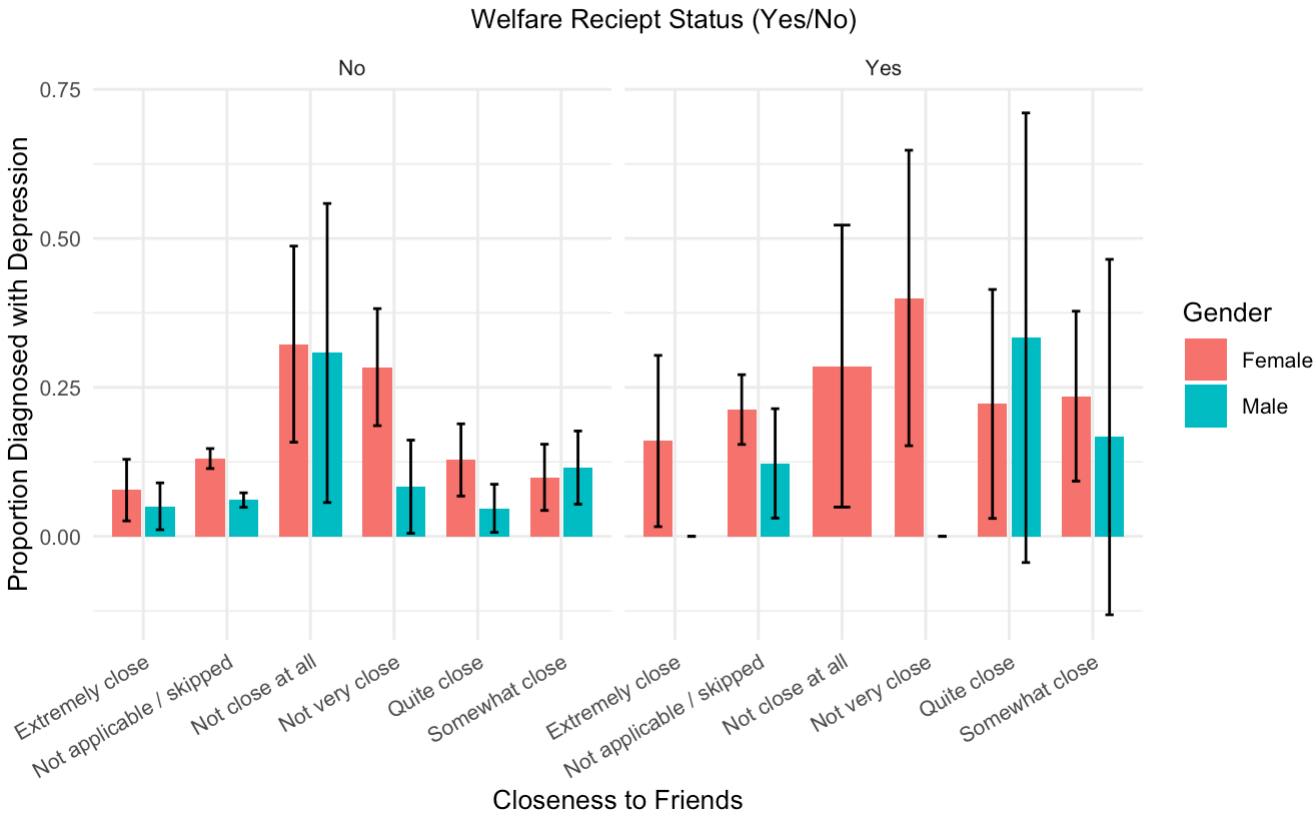
```
ggplot(heat_data, aes(x = BIO_SEX3, y = H3EC7, fill = depression_rate)) +
  geom_tile(color = "white") +
  scale_fill_gradient(low = "lightblue", high = "red") +
  labs(title = "Heatmap: Depression Rate by Gender and Income",
       x = "Gender", y = "Household Income", fill = "Rate") +
  theme_minimal()
```



```r
# Filter out non-responses and prepare data
plot_df <- data %>%
  filter(H3WP53 != "Not Asked", H3EC38 != "Not Asked") %>%
  group_by(H3WP53, H3EC38, BIO_SEX3) %>%
  summarise(
    DepressionRate = mean(H3ID15 == "Diagnosed Depression", na.rm = TRUE),
    N = n(),
    SE = sqrt((DepressionRate * (1 - DepressionRate))/N),
    .groups = "drop"
  )

# Plot
ggplot(plot_df, aes(x = H3WP53, y = DepressionRate, fill = BIO_SEX3)) +
  geom_col(position = position_dodge(width = 0.8), width = 0.7) +
  geom_errorbar(
    aes(ymin = DepressionRate - 1.96 * SE, ymax = DepressionRate + 1.96 * SE),
    width = 0.2, position = position_dodge(width = 0.8)
  ) +
  facet_wrap(~H3EC38) +
  labs(
    title = "Depression Diagnosis by Closeness to Friends, Income, and Gender ",
    subtitle = "Higher closeness is associated with lower depression rates across gen
ders and income groups \n\n
                                                    Welfare Reciept Status (Yes/No)",
    x = "Closeness to Friends",
    y = "Proportion Diagnosed with Depression",
    fill = "Gender"
  ) +
  theme_minimal(base_size = 10) +
  theme(axis.text.x = element_text(angle = 30, hjust = 1))
```

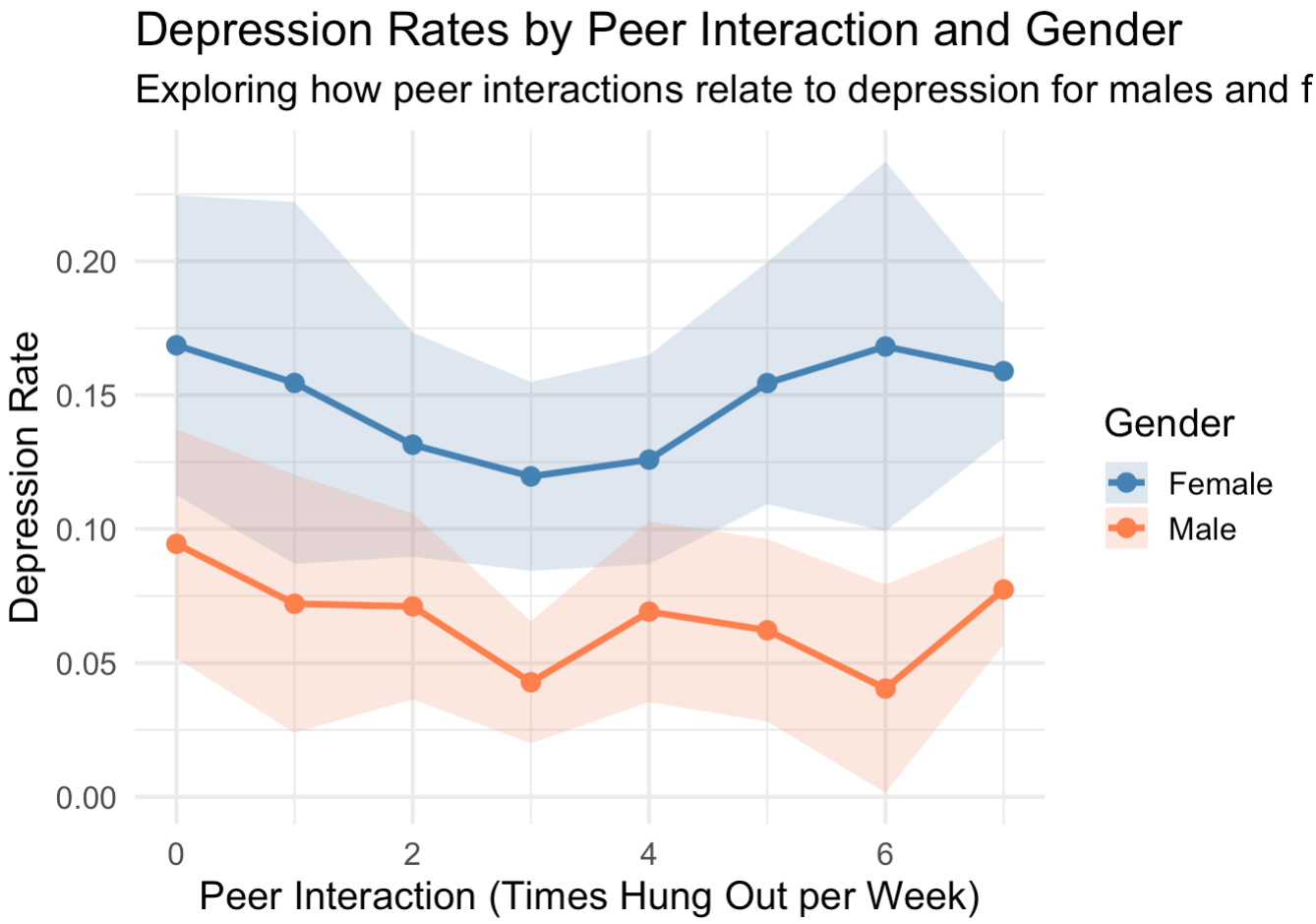
Depression Diagnosis by Closeness to Friends, Income, and Gender

Higher closeness is associated with lower depression rates across genders and income groups

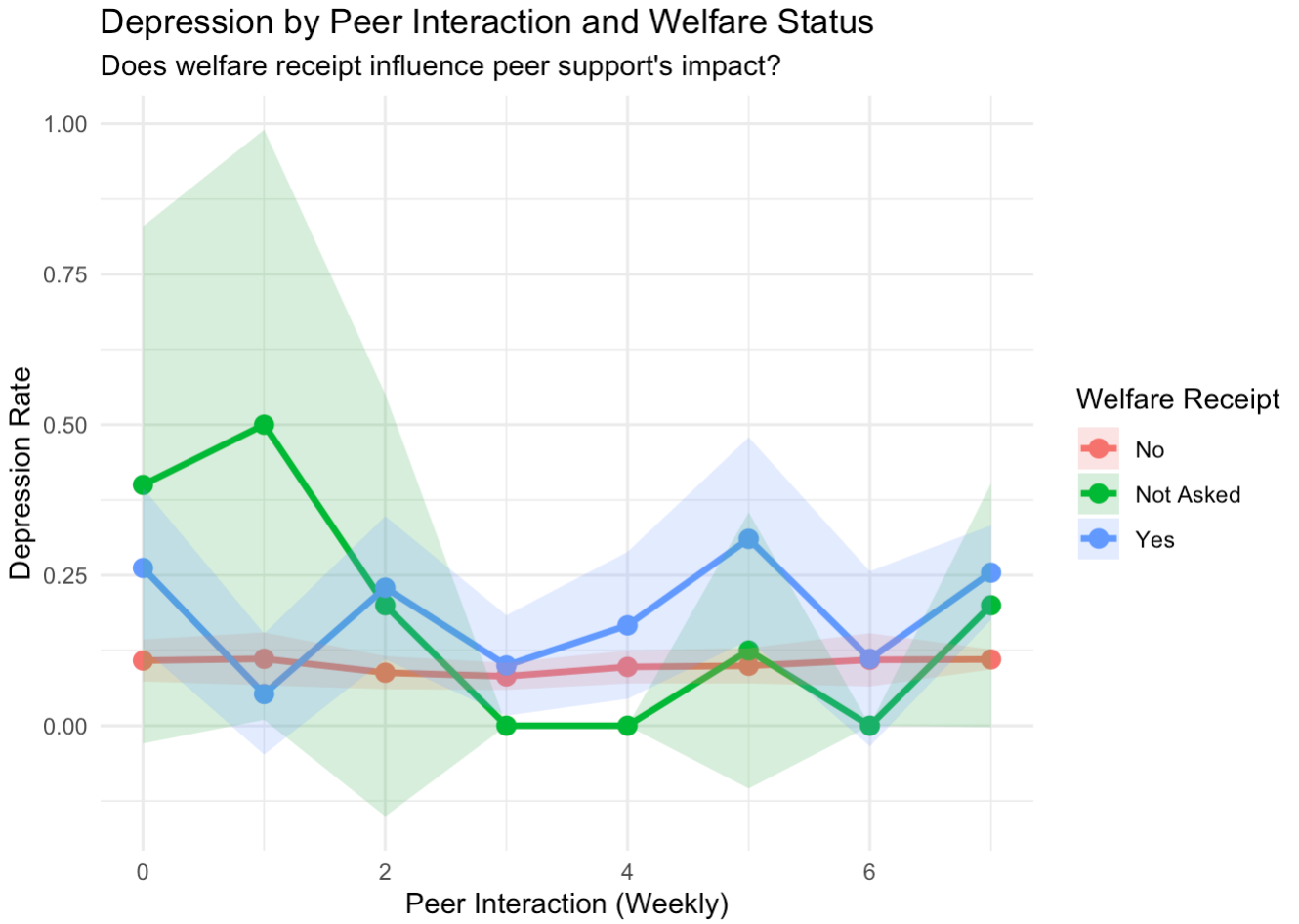


```r
library(dplyr)

plot_data <- data %>%
  group_by(H3DA15, BIO_SEX3) %>%
  summarise(DepressionRate = mean(H3ID15 == "Diagnosed Depression"),
            N = n(),
            SE = sqrt((DepressionRate * (1 - DepressionRate)) / N),
            .groups = 'drop')

# Add confidence intervals
plot_data <- plot_data %>%
  mutate(lower = DepressionRate - 1.96 * SE,
         upper = DepressionRate + 1.96 * SE)

library(ggplot2)

ggplot(plot_data, aes(x = H3DA15, y = DepressionRate, color = BIO_SEX3, group = BIO_S
EX3)) +
  geom_line(size = 1.2) +
  geom_point(size = 3) +
  geom_ribbon(aes(ymin = lower, ymax = upper, fill = BIO_SEX3), alpha = 0.2, color =
NA) +
  scale_color_manual(values = c("steelblue", "coral")) +
  scale_fill_manual(values = c("steelblue", "coral")) +
  labs(
    title = "Depression Rates by Peer Interaction and Gender",
    subtitle = "Exploring how peer interactions relate to depression for males and fe
males",
    x = "Peer Interaction (Times Hung Out per Week)",
    y = "Depression Rate",
    color = "Gender",
    fill = "Gender"
  ) +
  theme_minimal(base_size = 15)
```

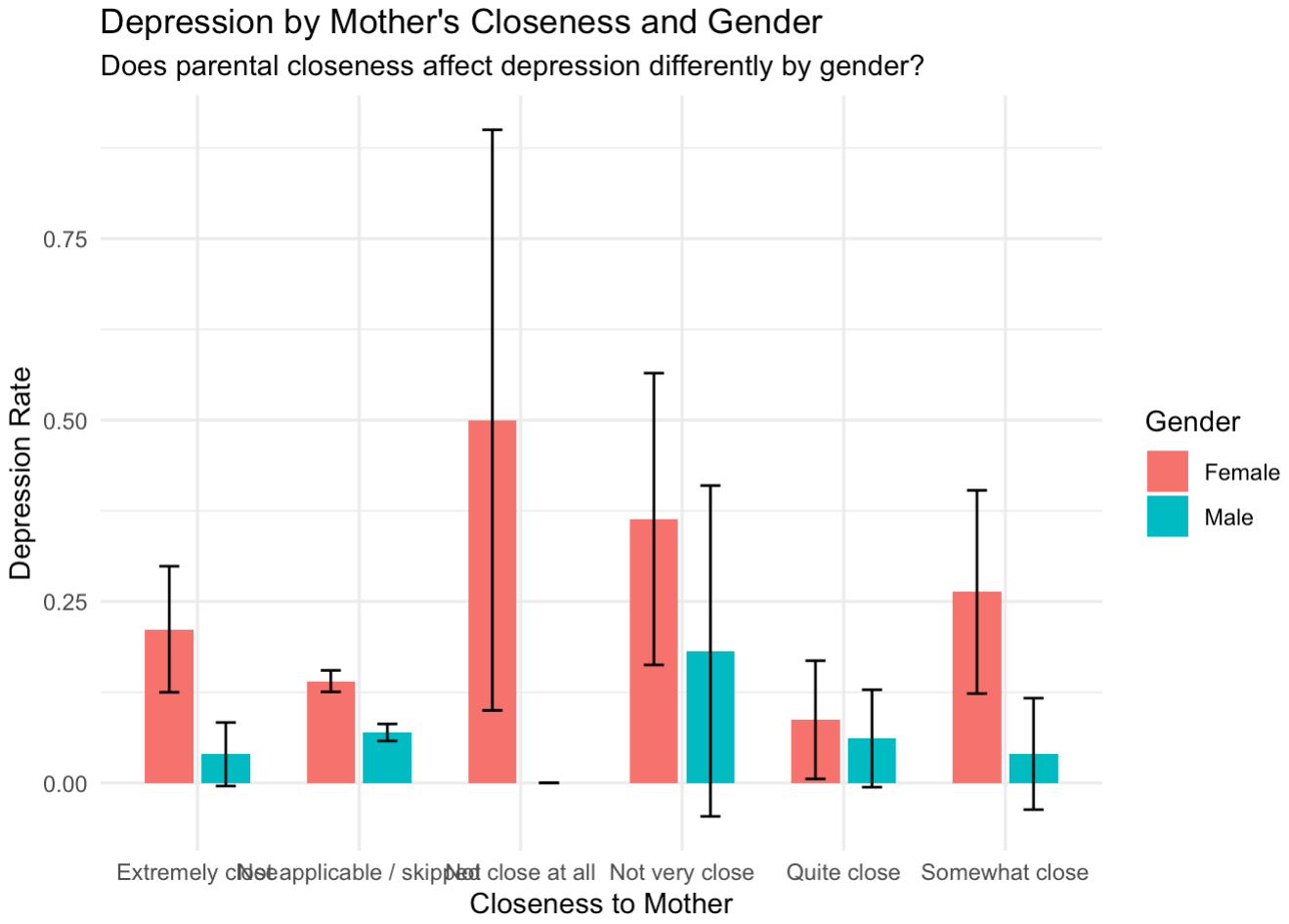
```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## ℹ Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



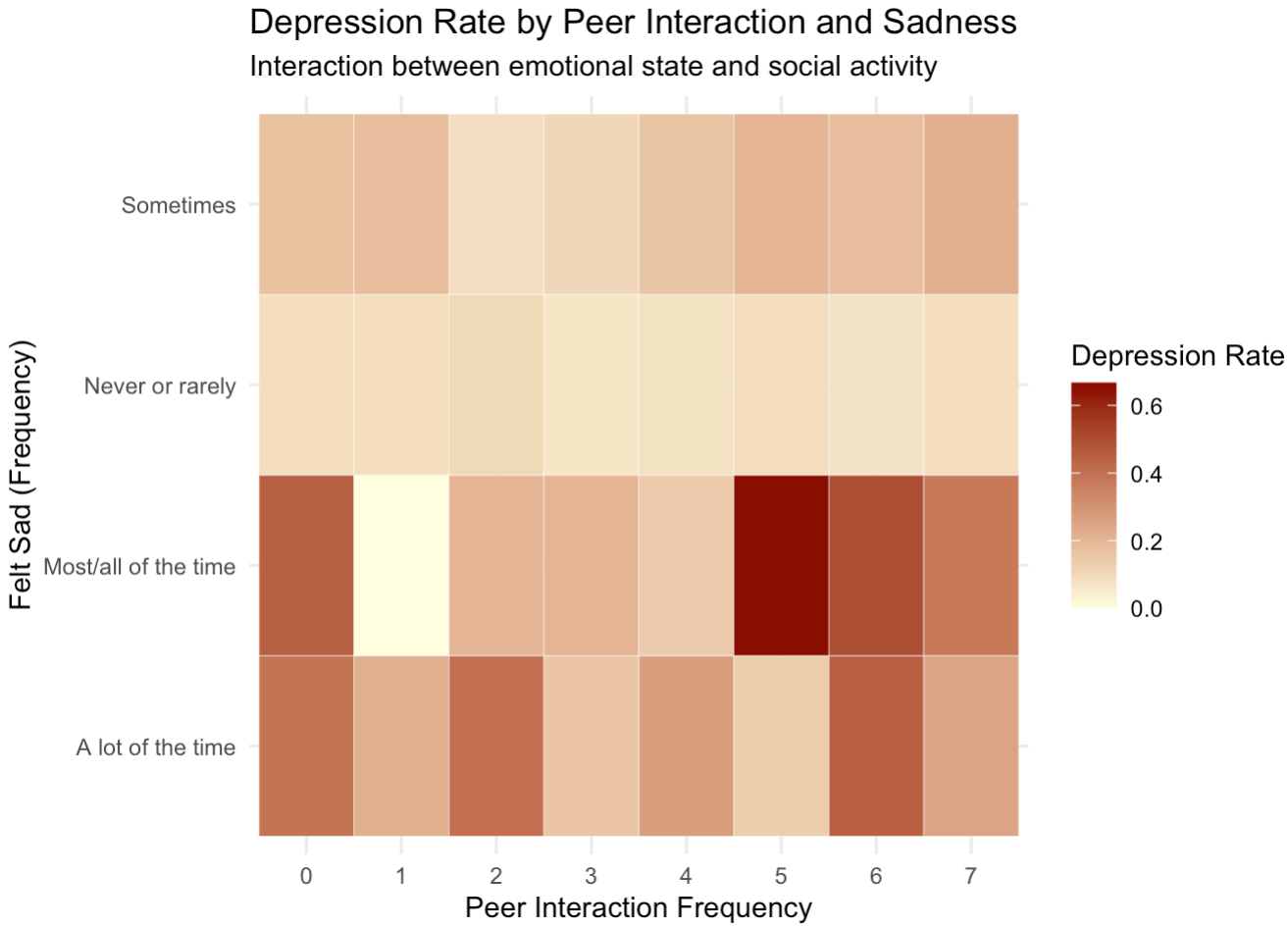

```
library(dplyr)
library(ggplot2)

plot_data_welfare <- data %>%
  group_by(H3DA15, H3EC38) %>%
  summarise(DepressionRate = mean(H3ID15 == "Diagnosed Depression"),
            N = n(),
            SE = sqrt((DepressionRate * (1 - DepressionRate))/N),
            .groups = 'drop')

ggplot(plot_data_welfare, aes(x = H3DA15, y = DepressionRate, color = H3EC38, group =
H3EC38)) +
  geom_line(size = 1.2) +
  geom_point(size = 3) +
  geom_ribbon(aes(ymin = DepressionRate - 1.96*SE, ymax = DepressionRate + 1.96*SE, f
ill = H3EC38), alpha = 0.2, color = NA) +
  labs(title = "Depression by Peer Interaction and Welfare Status",
       subtitle = "Does welfare receipt influence peer support's impact?",
       x = "Peer Interaction (Weekly)",
       y = "Depression Rate",
       color = "Welfare Receipt",
       fill = "Welfare Receipt") +
  theme_minimal()
```



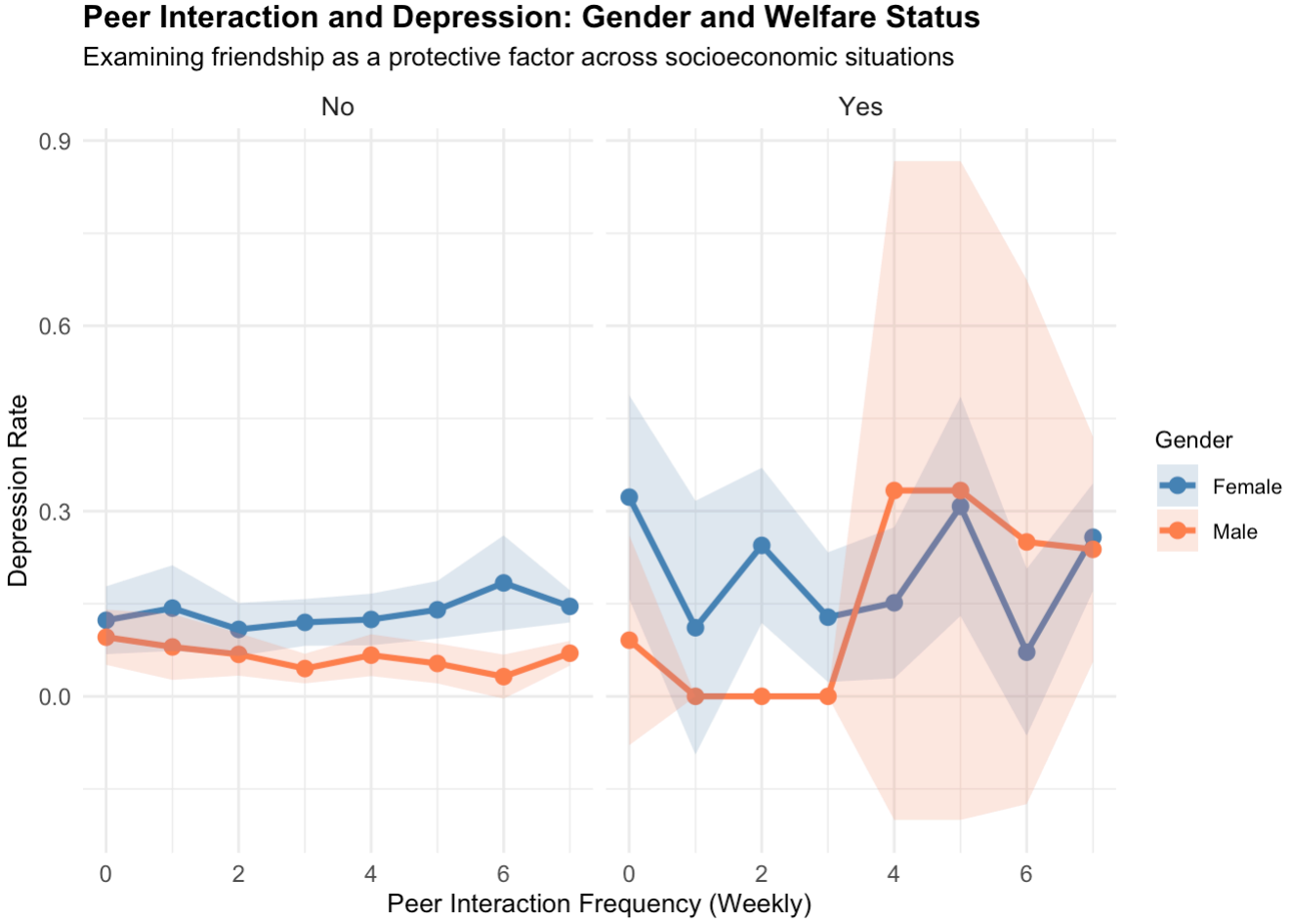

```
plot_data_parents <- data %>%
  group_by(H3WP46, BIO_SEX3) %>%  # Using mother's closeness here; you can replicate
for father
  summarise(DepressionRate = mean(H3ID15 == "Diagnosed Depression"),
            N = n(),
            SE = sqrt((DepressionRate * (1 - DepressionRate))/N),
            .groups = 'drop')

ggplot(plot_data_parents, aes(x = H3WP46, y = DepressionRate, group = BIO_SEX3, fill
= BIO_SEX3)) +
  geom_bar(stat = "identity", position = position_dodge(width = 0.7), width=0.6) +
  geom_errorbar(aes(ymin = DepressionRate - 1.96*SE, ymax = DepressionRate + 1.96*S
E),
                position = position_dodge(width = 0.7), width = 0.25) +
  labs(title = "Depression by Mother's Closeness and Gender",
       subtitle = "Does parental closeness affect depression differently by gender?",
       x = "Closeness to Mother",
       y = "Depression Rate",
       fill = "Gender") +
  theme_minimal()
```




```
library(ggplot2)
library(dplyr)

heatmap_data <- data %>%
  group_by(H3DA15, H3SP6) %>%
  summarise(DepressionRate = mean(H3ID15 == "Diagnosed Depression"), .groups = 'dro
p')

ggplot(heatmap_data, aes(x = factor(H3DA15), y = H3SP6, fill = DepressionRate)) +
  geom_tile(color = "white") +
  scale_fill_gradient(low = "lightyellow", high = "darkred") +
  labs(title = "Depression Rate by Peer Interaction and Sadness",
       subtitle = "Interaction between emotional state and social activity",
       x = "Peer Interaction Frequency",
       y = "Felt Sad (Frequency)",
       fill = "Depression Rate") +
  theme_minimal()
```


Depression Rate by Peer Interaction and Sadness
Interaction between emotional state and social activity
Felt Sad (Frequency)
Sometimes
Never or rarely
Most/all of the time
A lot of the time
0
1
2
3
4
5
6
7
Peer Interaction Frequency
Depression Rate
0.6
0.4
0.2
0.0

```r
library(dplyr)
library(ggplot2)

# Exclude 'Not Asked'
plot_main <- data %>%
  filter(H3EC38 != "Not Asked") %>%
  group_by(H3DA15, BIO_SEX3, H3EC38) %>%
  summarise(DepressionRate = mean(H3ID15 == "Diagnosed Depression"),
            N = n(),
            SE = sqrt((DepressionRate * (1 - DepressionRate))/N),
            .groups = 'drop')

# Plot with smaller text sizes
ggplot(plot_main, aes(x = H3DA15, y = DepressionRate, color = BIO_SEX3, group = BIO_S
EX3)) +
  geom_line(size = 1.1) +
  geom_point(size = 2.5) +
  geom_ribbon(aes(ymin = DepressionRate - 1.96*SE, ymax = DepressionRate + 1.96*SE, f
ill = BIO_SEX3), alpha = 0.2, color = NA) +
  facet_wrap(~H3EC38) +
  scale_color_manual(values = c("steelblue", "coral")) +
  scale_fill_manual(values = c("steelblue", "coral")) +
  labs(
    title = "Peer Interaction and Depression: Gender and Welfare Status",
    subtitle = "Examining friendship as a protective factor across socioeconomic situ
ations",
    x = "Peer Interaction Frequency (Weekly)",
    y = "Depression Rate",
    color = "Gender",
    fill = "Gender"
  ) +
  theme_minimal(base_size = 10) +  # Reduce base text size
  theme(
    plot.title = element_text(size = 12, face = "bold"),
    plot.subtitle = element_text(size = 10),
    axis.title = element_text(size = 10),
    axis.text = element_text(size = 9),
    strip.text = element_text(size = 10),
    legend.title = element_text(size = 9),
    legend.text = element_text(size = 8)
  )
```



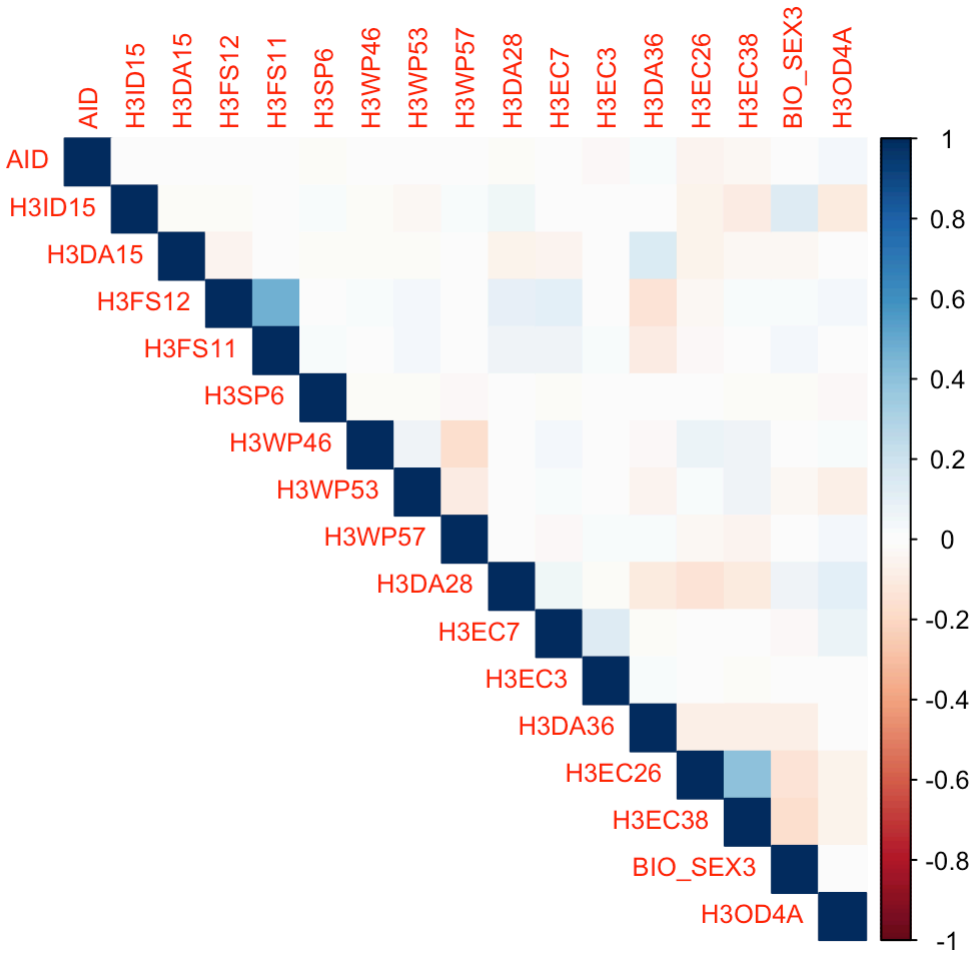
###Part 3 - Regressions

Correlation Matrix:

```
# Load libraries
library(tidyverse)
library(corrplot)
```

```
## corrplot 0.95 loaded
```

```
# Read and clean data
data <- read.csv("complete_addhealth_data.csv", stringsAsFactors = TRUE)
names(data) <- gsub("_recode$", "", names(data))

# Encode factors as numeric for correlation
data_corr <- data
for (col in names(data_corr)) {
  if (is.factor(data_corr[[col]]) || is.character(data_corr[[col]])) {
    data_corr[[col]] <- as.numeric(as.factor(data_corr[[col]]))
  }
}

# Plot correlation matrix
cor_matrix <- cor(data_corr, use = "complete.obs")
corrplot(cor_matrix, method = "color", type = "upper", tl.cex = 0.8)
```



Baseline Regression Model:

```
# Make sure variables are factors where needed
factor_vars <- c("H3ID15", "BIO_SEX3", "H3DA28", "H3DA36", "H3OD4A", "H3EC7", "H3EC
3")
data[factor_vars] <- lapply(data[factor_vars], as.factor)

# Baseline model with only SES + demographic predictors
baseline_model <- glm(H3ID15 ~ H3EC3 + H3EC7 + H3DA28 + H3DA36 + BIO_SEX3 + H3OD4A,
                      data = data, family = binomial)

summary(baseline_model)
```

```
##
## Call:
## glm(formula = H3ID15 ~ H3EC3 + H3EC7 + H3DA28 + H3DA36 + BIO_SEX3 +
##     H3OD4A, family = binomial, data = data)
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                     2.0059     0.7097   2.826 0.004709 **
## H3EC3$15,000–19,999            -0.4479     0.4879  -0.918 0.358636
## H3EC3$20,000–29,999            -0.5133     0.4750  -1.081 0.279819
## H3EC3$30,000–39,999            -0.6891     0.6397  -1.077 0.281335
## H3EC3$40,000–49,999            11.9528   260.8805   0.046 0.963456
## H3EC3$50,000–74,999            -1.5048     1.2388  -1.215 0.224472
## H3EC3$75,000 or more           -1.4505     1.2306  -1.179 0.238535
## H3EC3Less than $10,000         -0.2761     0.3675  -0.751 0.452530
## H3EC3Not applicable / skipped  -0.1923     0.3301  -0.582 0.560277
## H3EC7$15,000–19,999             0.2259     0.8906   0.254 0.799760
## H3EC7$20,000–29,999            -0.2564     0.7654  -0.335 0.737633
## H3EC7$30,000–39,999             1.1271     0.9677   1.165 0.244129
## H3EC7$40,000–49,999             0.9564     0.8256   1.158 0.246708
## H3EC7$50,000–74,999             0.2023     0.7078   0.286 0.775018
## H3EC7$75,000 or more            0.2734     0.6947   0.394 0.693910
## H3EC7Less than $10,000         -0.4803     0.7946  -0.604 0.545521
## H3EC7Not applicable / skipped   0.3610     0.6421   0.562 0.573950
## H3DA28Yes                       0.3974     0.1093   3.637 0.000276 ***
## H3DA36Yes                       0.1107     0.1040   1.064 0.287140
## BIO_SEX3Male                    0.8652     0.1087   7.959 1.73e-15 ***
## H3OD4AWhite                    -0.9325     0.1322  -7.056 1.72e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2985.6  on 4287  degrees of freedom
## Residual deviance: 2836.2  on 4267  degrees of freedom
## AIC: 2878.2
##
## Number of Fisher Scoring iterations: 13
```

Full Model

```r
# Ensure factor encoding for relevant variables
factor_vars <- c("H3ID15", "BIO_SEX3", "H3DA28", "H3DA36", "H3OD4A",
                 "H3EC7", "H3EC3", "H3FS12", "H3FS11", "H3SP6",
                 "H3WP46", "H3WP53", "H3WP57", "H3EC26", "H3EC38")
data[factor_vars] <- lapply(data[factor_vars], as.factor)

# Fit the full model
full_model <- glm(H3ID15 ~ H3FS12 + H3FS11 + H3SP6 + H3WP46 + H3WP53 + H3WP57 +
                    H3DA15 + H3DA28 + H3DA36 + H3EC7 + H3EC3 + H3EC26 + H3EC38 +
                    BIO_SEX3 + H3OD4A,
                  data = data,
                  family = binomial)

# View summary
summary(full_model)
```

```
##
## Call:
## glm(formula = H3ID15 ~ H3FS12 + H3FS11 + H3SP6 + H3WP46 + H3WP53 +
##     H3WP57 + H3DA15 + H3DA28 + H3DA36 + H3EC7 + H3EC3 + H3EC26 +
##     H3EC38 + BIO_SEX3 + H3OD4A, family = binomial, data = data)
##
## Coefficients: (1 not defined because of singularities)
##                                Estimate Std. Error z value Pr(>|z|)
## (Intercept)                     1.85679    0.87326   2.126  0.03348 *
## H3FS12Friends more influential -0.42142    0.22121  -1.905  0.05677 .
## H3FS12Not Asked                -0.21419    0.21730  -0.986  0.32428
## H3FS11All                       0.98530    0.76752   1.284  0.19923
## H3FS11Most                      0.60785    0.30961   1.963  0.04961 *
## H3FS11None                     -0.32705    0.41821  -0.782  0.43419
## H3FS11Not Asked                      NA         NA      NA       NA
## H3FS11One                       0.55973    0.75849   0.738  0.46054
## H3FS11Some                     -0.10794    0.27011  -0.400  0.68943
## H3SP6Most/all of the time      -0.33855    0.32061  -1.056  0.29098
## H3SP6Never or rarely            1.27747    0.20774   6.149 7.78e-10 ***
## H3SP6Sometimes                  0.50124    0.22018   2.276  0.02282 *
## H3WP46Not applicable / skipped -0.01928    0.31095  -0.062  0.95056
## H3WP46Not close at all         -1.26003    0.89413  -1.409  0.15877
## H3WP46Not very close           -0.68161    0.50380  -1.353  0.17608
## H3WP46Quite close               0.90025    0.48230   1.867  0.06196 .
## H3WP46Somewhat close           -0.11284    0.44370  -0.254  0.79925
## H3WP53Not applicable / skipped -0.40227    0.26763  -1.503  0.13282
## H3WP53Not close at all         -1.57468    0.39576  -3.979 6.92e-05 ***
## H3WP53Not very close           -1.16842    0.33242  -3.515  0.00044 ***
## H3WP53Quite close              -0.39348    0.33433  -1.177  0.23924
## H3WP53Somewhat close           -0.51437    0.32426  -1.586  0.11267
## H3WP57Not applicable / skipped  0.55520    0.34646   1.602  0.10905
## H3WP57Yes                       0.09226    0.50458   0.183  0.85492
## H3DA15                         -0.03106    0.02222  -1.398  0.16216
## H3DA28Yes                       0.33311    0.11547   2.885  0.00392 **
## H3DA36Yes                      -0.03152    0.11085  -0.284  0.77614
## H3EC7$15,000–19,999             0.41120    0.92216   0.446  0.65566
## H3EC7$20,000–29,999            -0.42385    0.79055  -0.536  0.59185
## H3EC7$30,000–39,999             1.12181    0.99544   1.127  0.25976
## H3EC7$40,000–49,999             0.75476    0.84960   0.888  0.37434
## H3EC7$50,000–74,999             0.10759    0.73420   0.147  0.88349
## H3EC7$75,000 or more            0.11557    0.71820   0.161  0.87216
## H3EC7Less than $10,000         -0.46176    0.82989  -0.556  0.57793
## H3EC7Not applicable / skipped   0.29100    0.66489   0.438  0.66163
## H3EC3$15,000–19,999            -0.48037    0.51578  -0.931  0.35168
## H3EC3$20,000–29,999            -0.46785    0.49984  -0.936  0.34927
## H3EC3$30,000–39,999            -0.74911    0.65527  -1.143  0.25295
## H3EC3$40,000–49,999            11.89368  253.80613   0.047  0.96262
## H3EC3$50,000–74,999            -1.67275    1.30285  -1.284  0.19917
## H3EC3$75,000 or more           -2.04968    1.24262  -1.649  0.09905 .
## H3EC3Less than $10,000         -0.40141    0.38516  -1.042  0.29733
## H3EC3Not applicable / skipped  -0.30255    0.34766  -0.870  0.38417
## H3EC26Yes                      -0.22082    0.22370  -0.987  0.32360
## H3EC38Not Asked                -0.86712    0.40539  -2.139  0.03244 *
## H3EC38Yes                      -0.45899    0.17169  -2.673  0.00751 **
## BIO_SEX3Male                    0.68594    0.11358   6.040 1.55e-09 ***
```

```
## H3OD4AWhite                     -1.13867    0.14088  -8.083 6.33e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2985.6  on 4287  degrees of freedom
## Residual deviance: 2658.2  on 4241  degrees of freedom
## AIC: 2752.2
##
## Number of Fisher Scoring iterations: 13
```

Step-Wise Regression Model

```
# Full model with all variables
full_model <- glm(H3ID15 ~ ., data = data, family = binomial)

# Stepwise model selection
step_model <- step(full_model, direction = "both")
```

```
## Start:  AIC=2754.01
## H3ID15 ~ AID + H3DA15 + H3FS12 + H3FS11 + H3SP6 + H3WP46 + H3WP53 +
##     H3WP57 + H3DA28 + H3EC7 + H3EC3 + H3DA36 + H3EC26 + H3EC38 +
##     BIO_SEX3 + H3OD4A
##
##            Df Deviance    AIC
## - H3EC3     8   2664.7 2744.7
## - H3EC7     8   2665.5 2745.5
## - H3DA36    1   2658.1 2752.1
## - AID       1   2658.2 2752.2
## - H3WP57    2   2660.7 2752.7
## - H3EC26    1   2659.0 2753.0
## - H3FS11    5   2667.2 2753.2
## - H3DA15    1   2659.9 2753.9
## <none>          2658.0 2754.0
## - H3WP46    5   2668.1 2754.1
## - H3FS12    1   2661.7 2755.7
## - H3DA28    1   2666.1 2760.1
## - H3EC38    2   2668.4 2760.4
## - H3WP53    5   2684.4 2770.4
## - BIO_SEX3  1   2696.3 2790.3
## - H3OD4A    1   2735.8 2829.8
## - H3SP6     3   2743.3 2833.3
##
## Step:  AIC=2744.71
## H3ID15 ~ AID + H3DA15 + H3FS12 + H3FS11 + H3SP6 + H3WP46 + H3WP53 +
##     H3WP57 + H3DA28 + H3EC7 + H3DA36 + H3EC26 + H3EC38 + BIO_SEX3 +
##     H3OD4A
##
##            Df Deviance    AIC
## - H3EC7     8   2672.5 2736.5
## - H3DA36    1   2664.7 2742.7
## - AID       1   2664.8 2742.8
## - H3WP57    2   2667.3 2743.3
## - H3EC26    1   2665.7 2743.7
## - H3FS11    5   2673.9 2743.9
## - H3WP46    5   2674.5 2744.5
## - H3DA15    1   2666.6 2744.6
## <none>          2664.7 2744.7
## - H3FS12    1   2668.5 2746.5
## - H3DA28    1   2672.4 2750.4
## - H3EC38    2   2674.9 2750.9
## + H3EC3     8   2658.0 2754.0
## - H3WP53    5   2691.1 2761.1
## - BIO_SEX3  1   2703.4 2781.4
## - H3OD4A    1   2741.4 2819.4
## - H3SP6     3   2750.8 2824.8
##
## Step:  AIC=2736.54
## H3ID15 ~ AID + H3DA15 + H3FS12 + H3FS11 + H3SP6 + H3WP46 + H3WP53 +
##     H3WP57 + H3DA28 + H3DA36 + H3EC26 + H3EC38 + BIO_SEX3 + H3OD4A
##
##            Df Deviance    AIC
## - H3DA36    1   2672.6 2734.6
## - AID       1   2672.7 2734.7
```

```
## - H3WP57    2   2675.1 2735.1
## - H3EC26    1   2673.6 2735.6
## - H3FS11    5   2681.6 2735.6
## - H3WP46    5   2682.3 2736.3
## - H3DA15    1   2674.3 2736.3
## <none>          2672.5 2736.5
## - H3FS12    1   2676.2 2738.2
## - H3EC38    2   2682.6 2742.6
## - H3DA28    1   2680.7 2742.7
## + H3EC7     8   2664.7 2744.7
## + H3EC3     8   2665.5 2745.5
## - H3WP53    5   2698.8 2752.8
## - BIO_SEX3  1   2710.5 2772.5
## - H3OD4A    1   2748.7 2810.7
## - H3SP6     3   2759.9 2817.9
##
## Step:  AIC=2734.56
## H3ID15 ~ AID + H3DA15 + H3FS12 + H3FS11 + H3SP6 + H3WP46 + H3WP53 +
##     H3WP57 + H3DA28 + H3EC26 + H3EC38 + BIO_SEX3 + H3OD4A
##
##            Df Deviance    AIC
## - AID       1   2672.7 2732.7
## - H3WP57    2   2675.1 2733.1
## - H3EC26    1   2673.6 2733.6
## - H3FS11    5   2681.6 2733.6
## - H3WP46    5   2682.3 2734.3
## - H3DA15    1   2674.4 2734.4
## <none>          2672.6 2734.6
## - H3FS12    1   2676.2 2736.2
## + H3DA36    1   2672.5 2736.5
## - H3EC38    2   2682.6 2740.6
## - H3DA28    1   2680.8 2740.8
## + H3EC7     8   2664.7 2742.7
## + H3EC3     8   2665.6 2743.6
## - H3WP53    5   2698.8 2750.8
## - BIO_SEX3  1   2711.0 2771.0
## - H3OD4A    1   2748.7 2808.7
## - H3SP6     3   2760.1 2816.1
##
## Step:  AIC=2732.7
## H3ID15 ~ H3DA15 + H3FS12 + H3FS11 + H3SP6 + H3WP46 + H3WP53 +
##     H3WP57 + H3DA28 + H3EC26 + H3EC38 + BIO_SEX3 + H3OD4A
##
##            Df Deviance    AIC
## - H3WP57    2   2675.3 2731.3
## - H3EC26    1   2673.7 2731.7
## - H3FS11    5   2681.7 2731.7
## - H3WP46    5   2682.5 2732.5
## - H3DA15    1   2674.6 2732.6
## <none>          2672.7 2732.7
## - H3FS12    1   2676.3 2734.3
## + AID       1   2672.6 2734.6
## + H3DA36    1   2672.7 2734.7
## - H3EC38    2   2682.8 2738.8
## - H3DA28    1   2681.0 2739.0
## + H3EC7     8   2664.9 2740.9
```

```
## + H3EC3     8   2665.8 2741.8
## - H3WP53    5   2698.9 2748.9
## - BIO_SEX3  1   2711.1 2769.1
## - H3OD4A    1   2749.0 2807.0
## - H3SP6     3   2760.2 2814.2
##
## Step:  AIC=2731.27
## H3ID15 ~ H3DA15 + H3FS12 + H3FS11 + H3SP6 + H3WP46 + H3WP53 +
##     H3DA28 + H3EC26 + H3EC38 + BIO_SEX3 + H3OD4A
##
##            Df Deviance    AIC
## - H3FS11    5   2684.2 2730.2
## - H3EC26    1   2676.3 2730.3
## - H3DA15    1   2677.1 2731.1
## <none>          2675.3 2731.3
## + H3WP57    2   2672.7 2732.7
## - H3WP46    5   2686.8 2732.8
## - H3FS12    1   2679.0 2733.0
## + AID       1   2675.1 2733.1
## + H3DA36    1   2675.2 2733.2
## - H3DA28    1   2683.5 2737.5
## - H3EC38    2   2685.7 2737.7
## + H3EC7     8   2667.5 2739.5
## + H3EC3     8   2668.4 2740.4
## - H3WP53    5   2702.1 2748.1
## - BIO_SEX3  1   2713.6 2767.6
## - H3OD4A    1   2752.5 2806.5
## - H3SP6     3   2763.2 2813.2
##
## Step:  AIC=2730.2
## H3ID15 ~ H3DA15 + H3FS12 + H3SP6 + H3WP46 + H3WP53 + H3DA28 +
##     H3EC26 + H3EC38 + BIO_SEX3 + H3OD4A
##
##            Df Deviance    AIC
## - H3EC26    1   2685.2 2729.2
## - H3DA15    1   2686.0 2730.0
## <none>          2684.2 2730.2
## - H3FS12    2   2689.0 2731.0
## + H3FS11    5   2675.3 2731.3
## + H3WP57    2   2681.7 2731.7
## + AID       1   2684.0 2732.0
## - H3WP46    5   2696.1 2732.1
## + H3DA36    1   2684.2 2732.2
## - H3DA28    1   2692.1 2736.1
## - H3EC38    2   2694.9 2736.9
## + H3EC7     8   2676.6 2738.6
## + H3EC3     8   2677.3 2739.3
## - H3WP53    5   2711.4 2747.4
## - BIO_SEX3  1   2724.4 2768.4
## - H3OD4A    1   2763.1 2807.1
## - H3SP6     3   2774.2 2814.2
##
## Step:  AIC=2729.17
## H3ID15 ~ H3DA15 + H3FS12 + H3SP6 + H3WP46 + H3WP53 + H3DA28 +
##     H3EC38 + BIO_SEX3 + H3OD4A
##
```

```
##            Df Deviance    AIC
## - H3DA15    1   2686.8 2728.8
## <none>          2685.2 2729.2
## - H3FS12    2   2689.8 2729.8
## + H3EC26    1   2684.2 2730.2
## + H3FS11    5   2676.3 2730.3
## + H3WP57    2   2682.7 2730.7
## + AID       1   2685.0 2731.0
## + H3DA36    1   2685.2 2731.2
## - H3WP46    5   2697.2 2731.2
## - H3DA28    1   2693.8 2735.8
## + H3EC7     8   2677.5 2737.5
## + H3EC3     8   2678.3 2738.3
## - H3EC38    2   2699.7 2739.7
## - H3WP53    5   2712.5 2746.5
## - BIO_SEX3  1   2726.1 2768.1
## - H3OD4A    1   2763.3 2805.3
## - H3SP6     3   2775.7 2813.7
##
## Step:  AIC=2728.77
## H3ID15 ~ H3FS12 + H3SP6 + H3WP46 + H3WP53 + H3DA28 + H3EC38 +
##     BIO_SEX3 + H3OD4A
##
##            Df Deviance    AIC
## <none>          2686.8 2728.8
## + H3DA15    1   2685.2 2729.2
## - H3FS12    2   2691.4 2729.4
## + H3FS11    5   2677.9 2729.9
## + H3EC26    1   2686.0 2730.0
## + H3WP57    2   2684.3 2730.3
## + AID       1   2686.6 2730.6
## - H3WP46    5   2698.7 2730.7
## + H3DA36    1   2686.7 2730.7
## - H3DA28    1   2695.5 2735.5
## + H3EC7     8   2679.2 2737.2
## + H3EC3     8   2679.9 2737.9
## - H3EC38    2   2700.7 2738.7
## - H3WP53    5   2713.6 2745.6
## - BIO_SEX3  1   2728.2 2768.2
## - H3OD4A    1   2764.5 2804.5
## - H3SP6     3   2777.0 2813.0
```

```
# Summary of selected model
summary(step_model)
```

```
##
## Call:
## glm(formula = H3ID15 ~ H3FS12 + H3SP6 + H3WP46 + H3WP53 + H3DA28 +
##     H3EC38 + BIO_SEX3 + H3OD4A, family = binomial, data = data)
##
## Coefficients:
##                                Estimate Std. Error z value Pr(>|z|)
## (Intercept)                     1.9588     0.4219   4.643 3.44e-06 ***
## H3FS12Friends more influential -0.4218     0.2160  -1.953 0.050795 .
## H3FS12Not Asked                -0.3043     0.1633  -1.864 0.062362 .
## H3SP6Most/all of the time      -0.3105     0.3181  -0.976 0.329062
## H3SP6Never or rarely            1.3151     0.2050   6.414 1.42e-10 ***
## H3SP6Sometimes                  0.5252     0.2176   2.413 0.015806 *
## H3WP46Not applicable / skipped  0.1898     0.2577   0.737 0.461390
## H3WP46Not close at all         -1.2005     0.8492  -1.414 0.157442
## H3WP46Not very close           -0.7283     0.4878  -1.493 0.135433
## H3WP46Quite close               0.8826     0.4791   1.842 0.065452 .
## H3WP46Somewhat close           -0.2108     0.4364  -0.483 0.628979
## H3WP53Not applicable / skipped -0.3043     0.2583  -1.178 0.238730
## H3WP53Not close at all         -1.5129     0.3902  -3.877 0.000106 ***
## H3WP53Not very close           -1.0974     0.3280  -3.346 0.000819 ***
## H3WP53Quite close              -0.3333     0.3309  -1.007 0.313905
## H3WP53Somewhat close           -0.4753     0.3199  -1.486 0.137345
## H3DA28Yes                       0.3396     0.1132   3.000 0.002703 **
## H3EC38Not Asked                -0.8125     0.3972  -2.046 0.040776 *
## H3EC38Yes                      -0.5263     0.1550  -3.395 0.000685 ***
## BIO_SEX3Male                    0.7007     0.1117   6.274 3.52e-10 ***
## H3OD4AWhite                    -1.1196     0.1386  -8.079 6.56e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2985.6  on 4287  degrees of freedom
## Residual deviance: 2686.8  on 4267  degrees of freedom
## AIC: 2728.8
##
## Number of Fisher Scoring iterations: 5
```

Regression By Gender

```
# Load necessary library
library(dplyr)

# Filter data into male and female subsets
male_data <- filter(data, BIO_SEX3 == "Male")
female_data <- filter(data, BIO_SEX3 == "Female")

# Run logistic regression for males
male_model <- glm(H3ID15 ~ H3FS12 + H3SP6 + H3WP53 +
                    H3DA28 + H3EC38 + H3OD4A,
                  family = binomial, data = male_data)
summary(male_model)
```

```
##
## Call:
## glm(formula = H3ID15 ~ H3FS12 + H3SP6 + H3WP53 + H3DA28 + H3EC38 +
##     H3OD4A, family = binomial, data = male_data)
##
## Coefficients:
##                                Estimate Std. Error z value Pr(>|z|)
## (Intercept)                     2.60630    0.64052   4.069 4.72e-05 ***
## H3FS12Friends more influential -0.31600    0.42404  -0.745 0.456146
## H3FS12Not Asked                -0.41325    0.32011  -1.291 0.196707
## H3SP6Most/all of the time      -0.40417    0.57430  -0.704 0.481580
## H3SP6Never or rarely            1.37105    0.36677   3.738 0.000185 ***
## H3SP6Sometimes                  0.66992    0.39725   1.686 0.091718 .
## H3WP53Not applicable / skipped -0.02455    0.43814  -0.056 0.955324
## H3WP53Not close at all         -1.98211    0.75217  -2.635 0.008409 **
## H3WP53Not very close           -0.25378    0.68556  -0.370 0.711255
## H3WP53Quite close              -0.03774    0.58267  -0.065 0.948354
## H3WP53Somewhat close           -0.70892    0.52784  -1.343 0.179252
## H3DA28Yes                       0.49182    0.20899   2.353 0.018609 *
## H3EC38Not Asked                -1.66290    0.58713  -2.832 0.004622 **
## H3EC38Yes                      -0.66702    0.39926  -1.671 0.094793 .
## H3OD4AWhite                    -1.21154    0.26566  -4.560 5.10e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 984.84  on 1973  degrees of freedom
## Residual deviance: 913.10  on 1959  degrees of freedom
## AIC: 943.1
##
## Number of Fisher Scoring iterations: 6
```

```
# Run logistic regression for females
female_model <- glm(H3ID15 ~ H3FS12 + H3SP6 + H3WP53 +
                      H3DA28 + H3EC38 + H3OD4A,
                    family = binomial, data = female_data)
summary(female_model)
```

```
##
## Call:
## glm(formula = H3ID15 ~ H3FS12 + H3SP6 + H3WP53 + H3DA28 + H3EC38 +
##     H3OD4A, family = binomial, data = female_data)
##
## Coefficients:
##                                Estimate Std. Error z value Pr(>|z|)
## (Intercept)                     2.1784     0.4314   5.050 4.42e-07 ***
## H3FS12Friends more influential  -0.4834     0.2510  -1.926 0.054073 .
## H3FS12Not Asked                 -0.2702     0.1895  -1.426 0.153979
## H3SP6Most/all of the time       -0.3469     0.3790  -0.915 0.359957
## H3SP6Never or rarely             1.2780     0.2463   5.188 2.12e-07 ***
## H3SP6Sometimes                   0.4509     0.2593   1.739 0.082062 .
## H3WP53Not applicable / skipped  -0.3334     0.3102  -1.075 0.282524
## H3WP53Not close at all          -1.3622     0.4491  -3.033 0.002421 **
## H3WP53Not very close            -1.3113     0.3827  -3.426 0.000612 ***
## H3WP53Quite close               -0.3728     0.3955  -0.943 0.345869
## H3WP53Somewhat close            -0.1962     0.3949  -0.497 0.619268
## H3DA28Yes                        0.2822     0.1338   2.109 0.034926 *
## H3EC38Not Asked                 -0.4148     0.5222  -0.794 0.426996
## H3EC38Yes                       -0.5239     0.1666  -3.145 0.001659 **
## H3OD4AWhite                     -1.0926     0.1622  -6.738 1.61e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1931.5  on 2313  degrees of freedom
## Residual deviance: 1773.7  on 2299  degrees of freedom
## AIC: 1803.7
##
## Number of Fisher Scoring iterations: 5
```

Regression by Income

```
# Create binary variable: 1 = Low income, 0 = Others
data$LowIncome <- ifelse(data$H3EC3 %in% c("Less than $10,000", "$10,000–14,999", "$1
5,000–19,999"), 1, 0)

interaction_model <- glm(H3ID15 ~ H3SP6 * LowIncome + H3FS12 + H3DA28 +
                         H3EC38 + BIO_SEX3 + H3OD4A,
                         family = binomial, data = data)

summary(interaction_model)
```

```
##
## Call:
## glm(formula = H3ID15 ~ H3SP6 * LowIncome + H3FS12 + H3DA28 +
##     H3EC38 + BIO_SEX3 + H3OD4A, family = binomial, data = data)
##
## Coefficients:
##                                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)                          1.7352     0.2748   6.315 2.70e-10 ***
## H3SP6Most/all of the time           -0.1725     0.3396  -0.508 0.611444
## H3SP6Never or rarely                 1.4026     0.2131   6.580 4.70e-11 ***
## H3SP6Sometimes                       0.5135     0.2260   2.272 0.023062 *
## LowIncome                            0.2792     0.6420   0.435 0.663594
## H3FS12Friends more influential      -0.4787     0.2144  -2.233 0.025558 *
## H3FS12Not Asked                     -0.3610     0.1620  -2.229 0.025811 *
## H3DA28Yes                            0.3135     0.1123   2.791 0.005253 **
## H3EC38Not Asked                     -0.8029     0.3980  -2.018 0.043639 *
## H3EC38Yes                           -0.5698     0.1514  -3.763 0.000168 ***
## BIO_SEX3Male                         0.7397     0.1112   6.655 2.84e-11 ***
## H3OD4AWhite                         -1.0695     0.1358  -7.876 3.39e-15 ***
## H3SP6Most/all of the time:LowIncome -1.0275     0.9238  -1.112 0.266049
## H3SP6Never or rarely:LowIncome      -0.5000     0.6669  -0.750 0.453444
## H3SP6Sometimes:LowIncome             0.1528     0.7231   0.211 0.832662
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 2985.6  on 4287  degrees of freedom
## Residual deviance: 2720.9  on 4273  degrees of freedom
## AIC: 2750.9
##
## Number of Fisher Scoring iterations: 5
```