

hsls_MAR

```
library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
library(ggplot2)
```

Warning: package 'ggplot2' was built under R version 4.3.3

```
library(gridExtra)
```

Attaching package: 'gridExtra'

The following object is masked from 'package:dplyr':

combine

```
library(psych)
```

Warning: package 'psych' was built under R version 4.3.3

Attaching package: 'psych'

The following objects are masked from 'package:ggplot2':

`%+%`, `alpha`

```
library(tidyr)
```

Warning: package 'tidyr' was built under R version 4.3.2

```
dathsls <- haven::read_sav("HSLs6.11.21.sav")

hsls <- dathsls

hsls <- hsls %>%
  rename(stu_id = STU_ID, # change column names
         sch_id = SCH_ID,
         # excellentTests = S1MTESTS,
         # understandTexts = S1MTEXTBOOK,
         # masterSkills = S1MSKILLS,
         # excellentAssign = S1MASSEXCL,
         # sex = X1SEX,
         race = X1RACE,
         hispanic = X1HISPANIC,
         white = X1WHITE,
         black = X1BLACK,
         asian = X1ASIAN,
         pacificIsland = X1PACISLE,
         SES = X1SES,
         hsls_w_cohort_g9 = W1STUDENT,
         hsls_w_cohort_g12 = W2STUDENT)

hsls <- dathsls %>%
```

```

    rename(math_theta1 = X2TXMTH,
           math_theta2 = X1TXMTH)

na_proportions_gender_poverty <- hsls %>%
  filter(!is.na(S1MENJOYING)) %>%
  filter(!is.na(X1POVERTY)) %>%
  group_by(S1MENJOYING, X1SEX, X1POVERTY) %>%
  summarize(na_prop = mean(is.na(S2MTESTS))) %>%
  ungroup()

```

``summarise()`` has grouped output by 'S1MENJOYING', 'X1SEX'. You can override using the ``.groups`` argument.

```

na_proportions_gender <- hsls %>%
  filter(!is.na(S1MENJOYING)) %>%
  group_by(S1MENJOYING, X1SEX) %>%
  summarize(na_prop = mean(is.na(S2MTESTS))) %>%
  ungroup()

```

``summarise()`` has grouped output by 'S1MENJOYING'. You can override using the ``.groups`` argument.

```

likert_order <- c("Strongly disagree", "Disagree", "Agree", "Strongly agree")

# Create a bar plot
plot_prop_gender <- ggplot(na_proportions_gender, aes(x = as.factor(S1MENJOYING), y = na_p
  geom_line(size = 1.2) +
  geom_point(size = 3) +
  labs(x = "S1MENJOYING (Likert Response)", y = "Proportion of NA's in S2MTESTS", color =
  ggtitle("Proportion of NA's in S2MTESTS by S1MENJOYING Response and Gender") +
  theme_minimal()

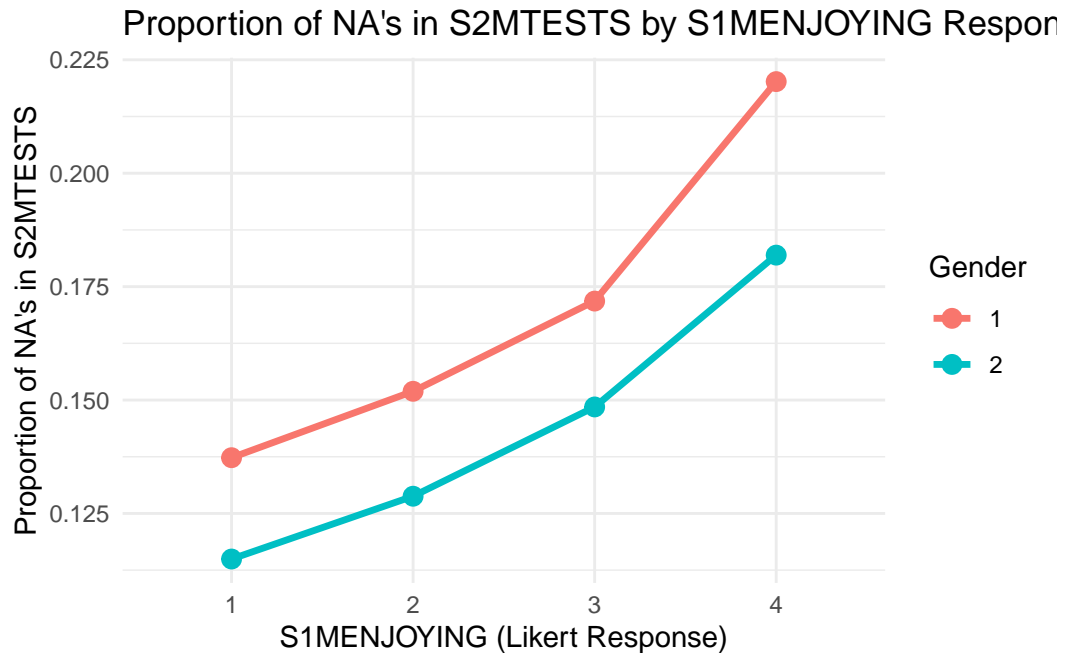
```

Warning: Using ``size`` aesthetic for lines was deprecated in ggplot2 3.4.0.
 i Please use ``linewidth`` instead.

```

plot_prop_gender

```



```
hsls$S2MTESTS_na <- ifelse(is.na(hsls$S2MTESTS), 1, 0)

log_reg_a <- glm(S2MTESTS_na ~ S1MENJOYING * X1SEX,
                 data = hsls,
                 family = "binomial")

summary(log_reg_a)
```

Call:

```
glm(formula = S2MTESTS_na ~ S1MENJOYING * X1SEX, family = "binomial",
    data = hsls)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.877104	0.183491	-10.230	<2e-16 ***
S1MENJOYING	0.181879	0.074138	2.453	0.0142 *
X1SEX	-0.185335	0.119999	-1.544	0.1225
S1MENJOYING:X1SEX	-0.004426	0.048473	-0.091	0.9272

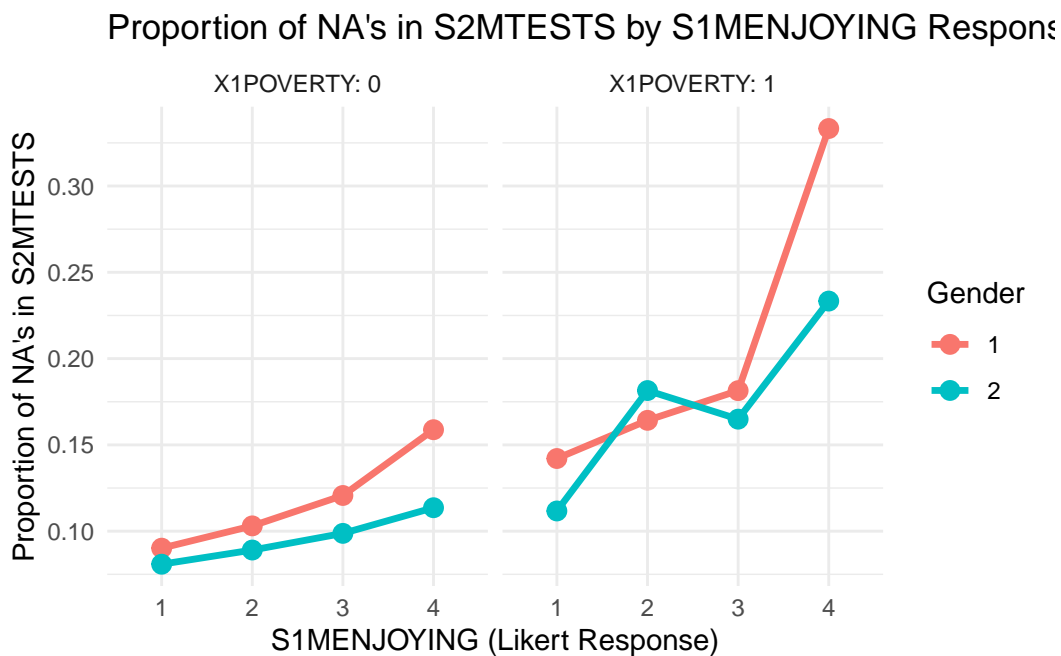
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 15991 on 19079 degrees of freedom
Residual deviance: 15916 on 19076 degrees of freedom
(6126 observations deleted due to missingness)
AIC: 15924

Number of Fisher Scoring iterations: 4

```
ggplot(na_proportions_gender_poverty, aes(x = as.factor(S1MENJOYING), y = na_prop, group =  
  geom_line(size = 1.2) +  
  geom_point(size = 3) +  
  labs(x = "S1MENJOYING (Likert Response)", y = "Proportion of NA's in S2MTESTS", color =  
  ggtitle("Proportion of NA's in S2MTESTS by S1MENJOYING Response, Gender, and Poverty Sta  
  theme_minimal() +  
  facet_wrap(~X1POVERTY, labeller = label_both)
```



```
log_reg_b <- glm(S2MTESTS_na ~ S1MENJOYING * X1SEX * X1POVERTY,  
  data = hsls,  
  family = "binomial")
```

```
summary(log_reg_b)
```

Call:

```
glm(formula = S2MTESTS_na ~ S1MENJOYING * X1SEX * X1POVERTY,  
     family = "binomial", data = hsls)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.548087	0.268577	-9.487	< 2e-16 ***
S1MENJOYING	0.282833	0.109254	2.589	0.00963 **
X1SEX	-0.007615	0.174762	-0.044	0.96524
X1POVERTY	0.049048	0.595850	0.082	0.93440
S1MENJOYING:X1SEX	-0.081161	0.071311	-1.138	0.25507
S1MENJOYING:X1POVERTY	0.170412	0.240465	0.709	0.47852
X1SEX:X1POVERTY	0.250598	0.383010	0.654	0.51293
S1MENJOYING:X1SEX:X1POVERTY	-0.052996	0.156194	-0.339	0.73439

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 10285 on 14743 degrees of freedom
Residual deviance: 10149 on 14736 degrees of freedom
(10462 observations deleted due to missingness)
AIC: 10165

Number of Fisher Scoring iterations: 5