

Homework 4 Solution Script

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0. Loading Packages

```
rm(list=ls()) # Start clean: remove all objects from the workspace
## Libraries
library(foreign)
library(ggplot2)
library(dplyr)
library(ggpubr)
library(VGAM)
library(MASS)
library(GGally)
library(censReg)
library(sampleSelection)
library(tidyr)
library(mvtnorm)
library(AER)      # dispersiontest for Poisson overdispersion
library(MASS)     # glm.nb (Negative Binomial)
library(dplyr)    # data wrangling
library(tidyr)    # pivot_longer
library(ggplot2)  # plotting
library(stargazer) # model tables

## Working directory
setwd("/Users/songeunlee/Desktop/Ling/HW4")
#setwd("/Users/lingzhu/Dropbox/UH Teaching/POLS6382_2025/HW Assignments/2025 HW Review and Solution Scr

## Data
CESdata<-read.csv("CESdata.csv")
```

1. Analyzing 2022 Midterm Election Data

Question 1a and 1b: Data Preparation

```
# -----
# Question 1a:
# Download the 2022 CES post-election data from https://cces.gov.harvard.edu/
# This code cleans and recodes key variables for analysis.
# -----
# Load packages
```

```

library(dplyr)
library(tidyr)

# Remove missing cases only for the variables we need
CESdata <- CESdata %>%
  drop_na(race, birthyear, gender, party, votereg, vote, education)

# Recode variables
CESdata <- CESdata %>%
  mutate(
    white      = ifelse(race == 1, 1, 0),           # 1 = White, 0 = Non-White
    age        = 2022 - birthyear,                  # Age = 2022 minus birth year
    male       = ifelse(gender == 1, 1, 0),          # 1 = Male, 0 = Female/Other
    Democrat   = ifelse(party == 1, 1, 0),          # 1 = Democrat, 0 = Others
    votereg    = ifelse(votereg == 1, 1, 0),         # 1 = Registered, 0 = Not/Don't know
    vote       = ifelse(vote == 5, 1, 0),            # 1 = Voted, 0 = Did not vote
    college    = ifelse(education %in% c(3,4,5,6), 1, 0) # 1 = Some college or more
  )

# Keep only the variables needed for this exercise
data1 <- CESdata %>%
  dplyr::select(white, age, male, Democrat, votereg, vote, college)

# Check data summary
summary(data1) # Check the dataset with View(data1) or colnames(data1)

```

	white	age	male	Democrat
Min.	:0.0000	Min. :18.00	Min. :0.0000	Min. :0.0000
1st Qu.	:0.0000	1st Qu.:39.00	1st Qu.:0.0000	1st Qu.:0.0000
Median	:1.0000	Median :54.00	Median :1.0000	Median :0.0000
Mean	:0.7469	Mean :52.31	Mean :0.5241	Mean :0.3204
3rd Qu.	:1.0000	3rd Qu.:65.00	3rd Qu.:1.0000	3rd Qu.:1.0000
Max.	:1.0000	Max. :95.00	Max. :1.0000	Max. :1.0000
	votereg	vote	college	
Min.	:0.0000	Min. :0.000	Min. :0.0000	
1st Qu.	:1.0000	1st Qu.:1.000	1st Qu.:1.0000	
Median	:1.0000	Median :1.000	Median :1.0000	
Mean	:0.9753	Mean :0.802	Mean :0.7695	
3rd Qu.	:1.0000	3rd Qu.:1.000	3rd Qu.:1.0000	
Max.	:1.0000	Max. :1.000	Max. :1.0000	

```

# Save the cleaned dataset
write.csv(data1, "ces2022_clean.csv", row.names = FALSE)

```

Question 1c: Estimating a Standard Logit

```

# -----
# Question 1c: Predicting the Probability of Voting
# Estimate standard logit models using 2022 CES data
# -----

library(dplyr)
library(ggplot2)

```

```
# --- Model 1: Predict voting using demographics and partisanship ---
logit_model1 <- glm(vote ~ white + age + male + Democrat + college,
                     data = data1, family = binomial)

summary(logit_model1)          # Model summary (log-odds)
```

Call:
`glm(formula = vote ~ white + age + male + Democrat + college,
 family = binomial, data = data1)`

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.768356	0.091111	-30.38	<2e-16 ***
white	0.548546	0.048802	11.24	<2e-16 ***
age	0.050474	0.001502	33.60	<2e-16 ***
male	0.592213	0.045699	12.96	<2e-16 ***
Democrat	0.864663	0.053551	16.15	<2e-16 ***
college	1.138215	0.049065	23.20	<2e-16 ***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 15139 on 15209 degrees of freedom
Residual deviance: 12525 on 15204 degrees of freedom
AIC: 12537

Number of Fisher Scoring iterations: 5

```
exp(coef(logit_model1))          # Exponentiated coefficients (odds ratios)
```

(Intercept)	white	age	male	Democrat	college
0.06276513	1.73073411	1.05176904	1.80798522	2.37420573	3.12119299

```
# --- Model 2: Add voter registration as an additional predictor ---
logit_model2 <- glm(vote ~ white + age + male + Democrat + college + votereg,
                     data = data1, family = binomial)
```

```
summary(logit_model2)
```

Call:
`glm(formula = vote ~ white + age + male + Democrat + college +
 votereg, family = binomial, data = data1)`

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-4.983402	0.169777	-29.35	<2e-16 ***
white	0.539877	0.049750	10.85	<2e-16 ***
age	0.048461	0.001529	31.69	<2e-16 ***
male	0.587214	0.046604	12.60	<2e-16 ***
Democrat	0.829619	0.054450	15.24	<2e-16 ***
college	1.085820	0.050171	21.64	<2e-16 ***
votereg	2.443710	0.146225	16.71	<2e-16 ***

```

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 15139  on 15209  degrees of freedom
Residual deviance: 12163  on 15203  degrees of freedom
AIC: 12177

Number of Fisher Scoring iterations: 5
exp(coef(logit_model2))

(Intercept)      white        age       male   Democrat    college
0.006850715  1.715794995  1.049654065  1.798969006  2.292444068  2.961867321
voterreg
11.515685773

# -----
# Plotting Predicted Probabilities (Model 1)
# -----


# Calculate variable means for continuous and binary predictors
mean_white     <- mean(data1$white)
mean_age       <- mean(data1$age)
mean_male      <- mean(data1$male)
mean_Democrat <- mean(data1$Democrat)

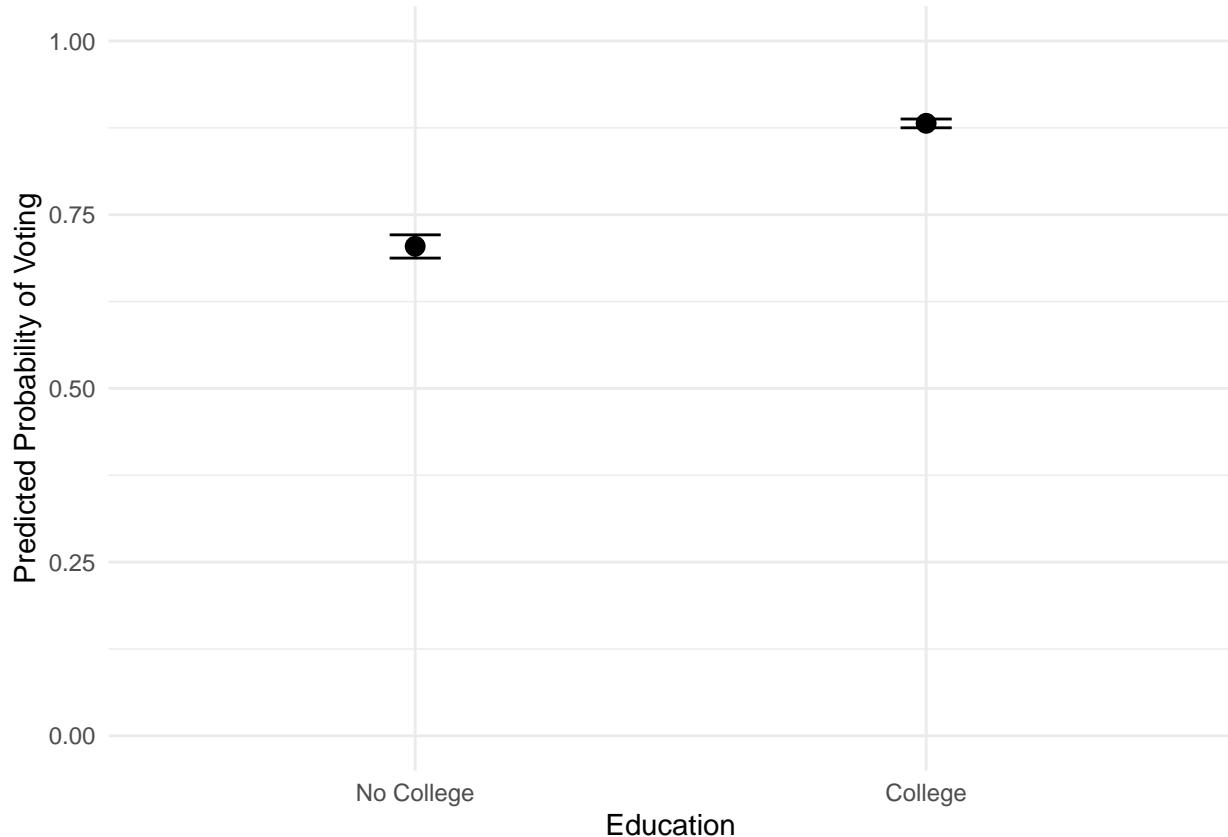
# Create a new dataset varying college (0 = No College, 1 = College)
new_data <- data.frame(
  white      = mean_white,
  age        = mean_age,
  male       = mean_male,
  Democrat   = mean_Democrat,
  college    = c(0, 1)
)

# Predict log-odds and convert to probabilities with 95% CI
pred <- predict(logit_model1, newdata = new_data, type = "link", se.fit = TRUE)
prob <- plogis(pred$fit)
lower <- plogis(pred$fit - 1.96 * pred$se.fit)
upper <- plogis(pred$fit + 1.96 * pred$se.fit)

plot_data <- data.frame(
  college = factor(new_data$college, labels = c("No College", "College")),
  prob = prob, lower = lower, upper = upper
)

# --- Plot predicted probabilities with confidence intervals ---
ggplot(plot_data, aes(x = college, y = prob)) +
  geom_point(size = 3) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.1) +
  labs(x = "Education", y = "Predicted Probability of Voting") +
  ylim(0, 1) +
  theme_minimal()

```



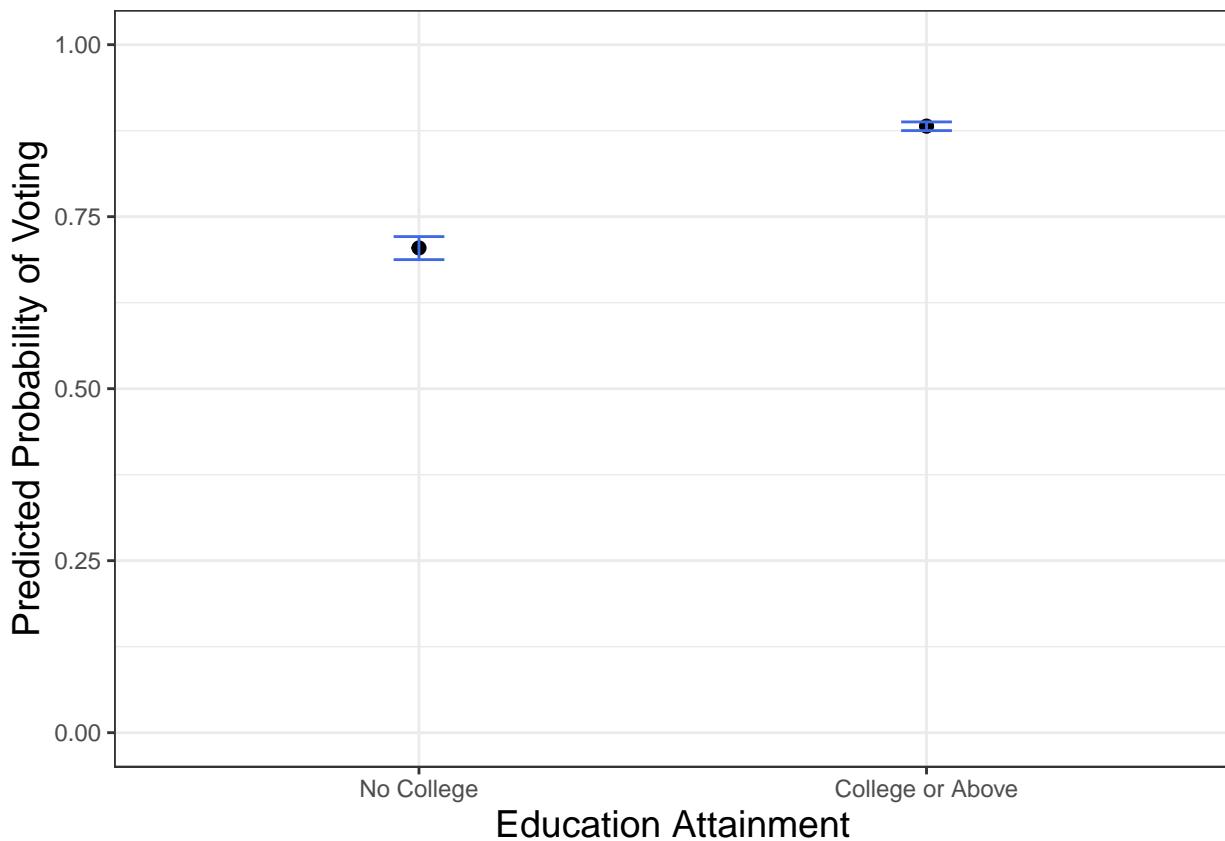
```

library(ggeffects)
pdturnout <- ggpredict(logit_model1, terms = "college [0,1]")

# make clean labels in the order you want
pdturnout$x <- factor(pdturnout$x,
                       levels = c(0, 1),
                       labels = c("No College", "College or Above"))

library(ggplot2)
ggplot(pdturnout, aes(x = x, y = predicted)) +
  geom_point(size = 2) +
  geom_errorbar(aes(ymin = conf.low, ymax = conf.high),
                width = 0.1, color = "royalblue") +
  labs(x = "Education Attainment",
       y = "Predicted Probability of Voting") +
  coord_cartesian(ylim = c(0, 1)) + # optional: clamp to [0,1]
  theme_bw() +
  theme(
    legend.position = "none",
    axis.title = element_text(size = 14)
  )

```



Question 1d: Estimating a Two-Step Heckman Selection Model

```
# Load the package for Heckman selection models
library(sampleSelection)

# Estimate the Heckman two-step selection model
selectionmodel1 <- selection(
  selection = voterreg ~ age + college,
  outcome   = vote ~ white + age + male + Democrat + college,
  data      = data1,
  method    = "2step"
)
```

```
# Display the model summary
summary(selectionmodel1)
```

```
Tobit 2 model (sample selection model)
2-step Heckman / heckit estimation
15210 observations (376 censored and 14834 observed)
12 free parameters (df = 15199)
Probit selection equation:
  Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.598875  0.075271  7.956  1.9e-15 ***
age         0.021775  0.001499 14.524  < 2e-16 ***
college     0.519222  0.047589 10.910  < 2e-16 ***
Outcome equation:
```

```

      Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.6414035  0.0268734 23.868 < 2e-16 ***
white        0.0756957  0.0060049 12.606 < 2e-16 ***
age          0.0021870  0.0003772  5.797 6.87e-09 ***
male         0.0759778  0.0058483 12.991 < 2e-16 ***
Democrat    0.0960684  0.0062953 15.260 < 2e-16 ***
college     0.0432011  0.0140258  3.080  0.00207 **
Multiple R-Squared:0.1565, Adjusted R-Squared:0.1561
Error terms:
      Estimate Std. Error t value Pr(>|t|)
invMillsRatio -1.8527      NaN      NaN      NaN
sigma          0.6922      NA       NA      NA
rho            -2.6766     NA       NA      NA
-----
# install.packages("GJRM")
library(GJRM)

# Ensure both dependent variables are coded as 0/1 integers (Bernoulli responses expected by probit link)
data1 <- transform(
  data1,
  votereg = as.integer(votereg %in% 1), # selection indicator: 1 = registered, 0 = not
  vote     = as.integer(vote %in% 1)      # outcome: 1 = voted, 0 = did not vote
)

# Specify the two equations:
# - eq_sel: selection (who is "in sample" for the outcome process-registered to vote)
# - eq_out: outcome (who votes among those eligible/selected)
eq_sel <- votereg ~ age + college
eq_out <- vote     ~ white + age + male + Democrat + college

# Fit a Bivariate Sample Selection (BSS) model:
# - FIML joint estimation of two Bernoulli-probit equations
# - Gaussian copula ties the latent errors, estimating their correlation (theta = rho)
# - margins = c("probit","probit") sets probit links for both equations
fit <- gjrm(
  list(eq_sel, eq_out),
  data    = data1,
  model   = "BSS",                      # bivariate probit selection model (FIML)
  margins = c("probit","probit")        # both equations are probit
)

# Summarize results:
# - Equation 1: probit coefficients for registration (selection)
# - Equation 2: probit coefficients for voting (outcome, conditional on selection)
# - theta: dependence parameter (latent error correlation = rho); tests endogenous selection
# - n / n.sel: total observations / number effectively in the selected regime
summary(fit)

```

COPULA: Gaussian
 MARGIN 1: Bernoulli
 MARGIN 2: Bernoulli

EQUATION 1

```

Link function for mui: probit
Formula: voterreg ~ age + college

Parametric coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.601032  0.075181  7.994  1.3e-15 ***
age         0.021683  0.001497 14.483  < 2e-16 ***
college     0.521414  0.047525 10.971  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

EQUATION 2

```

Link function for mu2: probit
Formula: vote ~ white + age + male + Democrat + college

```

```

Parametric coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.309701  0.078548 -16.67  <2e-16 ***
white        0.304783  0.028693  10.62  <2e-16 ***
age          0.026423  0.001051  25.14  <2e-16 ***
male         0.324174  0.026216  12.37  <2e-16 ***
Democrat    0.439978  0.029769  14.78  <2e-16 ***
college     0.590905  0.035141  16.82  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

theta = -0.452(-0.825,0.278)
n = 15210 n.sel = 14834
total edf = 10

```

Question 1e: Comparing Specifications

```
summary(logit_model1)
```

```

Call:
glm(formula = vote ~ white + age + male + Democrat + college,
     family = binomial, data = data1)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.768356  0.091111 -30.38  <2e-16 ***
white        0.548546  0.048802  11.24  <2e-16 ***
age          0.050474  0.001502  33.60  <2e-16 ***
male         0.592213  0.045699  12.96  <2e-16 ***
Democrat    0.864663  0.053551  16.15  <2e-16 ***
college     1.138215  0.049065  23.20  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

(Dispersion parameter for binomial family taken to be 1)

```

Null deviance: 15139 on 15209 degrees of freedom
Residual deviance: 12525 on 15204 degrees of freedom
AIC: 12537

```

Number of Fisher Scoring iterations: 5

```
summary(selectionmodel1)
```

```
-----
Tobit 2 model (sample selection model)
2-step Heckman / heckit estimation
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12 free parameters (df = 15199)
Probit selection equation:
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(Intercept) 0.598875  0.075271   7.956  1.9e-15 ***
age         0.021775  0.001499  14.524 < 2e-16 ***
college     0.519222  0.047589  10.910 < 2e-16 ***
Outcome equation:
      Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.6414035 0.0268734 23.868 < 2e-16 ***
white       0.0756957 0.0060049 12.606 < 2e-16 ***
age         0.0021870 0.0003772  5.797 6.87e-09 ***
male        0.0759778 0.0058483 12.991 < 2e-16 ***
Democrat    0.0960684 0.0062953 15.260 < 2e-16 ***
college     0.0432011 0.0140258  3.080  0.00207 **
Multiple R-Squared:0.1565, Adjusted R-Squared:0.1561
Error terms:
      Estimate Std. Error t value Pr(>|t|)
invMillsRatio -1.8527      NaN      NaN      NaN
sigma          0.6922      NA       NA      NA
rho            -2.6766      NA       NA      NA
-----
```

2. Analyzing Count Data

Question 2a and 2b: Estimating a Poisson Model

```
# Load the dataset (contains data on presidential vetoes)
load("vetos.RData")

# Load stargazer for formatted regression output tables
require(stargazer)

# (1) Poisson Regression Model (Full Specification)
# Dependent variable: never (number of vetoes)
# Includes multiple predictors: congressional experience, governor experience, presidential party,
# House majority, Senate majority, and presidential election proximity
poissonmod <- glm(
  never ~ congexpr + govexpr + prespty + hmajor + smajor + presepct,
  data = vetos,
  family = "poisson"    # Poisson regression for count data
)
```

```

# (2) Poisson Regression Model (Reduced Specification)
# A more parsimonious model including only key predictors
poissonmod2 <- glm(
  nover ~ congexpr + govexpr + prespty,
  data = vetos,
  family = "poisson"
)

# Display both models side-by-side in a formatted table
# Title indicates comparison between a full and reduced Poisson model
stargazer(
  poissonmod, poissonmod2,
  type = "text",
  title = "Poisson Regression Models Predicting the Number of Veto"
)

```

Poisson Regression Models Predicting the Number of Veto

Dependent variable:		
	nover	
	(1)	(2)
congexpr	2.225*** (0.778)	1.845** (0.739)
govexpr	1.584* (0.843)	1.388* (0.769)
prespty	-0.705* (0.423)	-0.698** (0.316)
hmajor	-1.025 (0.725)	
smajor	0.074 (0.618)	
presepct	0.024* (0.013)	
Constant	-2.069 (1.318)	-0.693 (0.707)
Observations	26	26
Log Likelihood	-42.126	-46.167
Akaike Inf. Crit.	98.252	100.334

Note: *p<0.1; **p<0.05; ***p<0.01

Question 2C: Methods of Substantively Interpreting Results

```

# --- Incidence Rate Ratios (IRRs) with 95% CIs -----
# Do NOT overwrite the base 'coef' function name; store into 'coef_ci' instead.
# 'confint(poissommod)' gives profile-likelihood CIs on the *log* scale.
# Exponentiating turns log-coefficients into IRRs and CIs onto the IRR scale.
coef_ci <- cbind(Estimate = coef(poissommod),
                   confint(poissommod)) # may profile; can be slow on big models
IRR <- exp(coef_ci)
IRR

      Estimate      2.5 %     97.5 %
(Intercept) 0.1262628 0.008146699 1.527394
congexpr     9.2530026 2.493316691 60.883153
govexpr      4.8735643 1.073307880 34.604845
prespty      0.4939730 0.207273235 1.103564
hmajor       0.3588653 0.084804432 1.502153
smajor       1.0763951 0.312913814 3.686567
presepct    1.0239137 0.999405144 1.050216

# --- Predicted counts across 'presepct' with 95% CI (on response scale) -----
# IMPORTANT: For GLMs, standard errors are returned on the *link* scale.
# So: predict on 'link', build CIs on link, then transform via inverse link (exp)
# to the response (mean count) scale.

# Build a prediction grid: vary 'presepct' 0..100, hold others at their medians
newdata <- data.frame(
  presepct = seq(0, 100, length = 30),
  govexpr  = median(vetos$govexpr, na.rm = TRUE),
  prespty   = median(vetos$prespty, na.rm = TRUE),
  congexpr  = median(vetos$congexpr, na.rm = TRUE),
  hmajor    = median(vetos$hmajor, na.rm = TRUE),
  smajor    = median(vetos$smajor, na.rm = TRUE)
)

# Predict on the LINK scale with SEs
pred_link <- predict(poissommod, newdata, type = "link", se.fit = TRUE)

# Transform to RESPONSE scale (mean counts) and build 95% CIs correctly
predicdata <- within(newdata, {
  eta   = pred_link$fit                         # linear predictor
  se    = pred_link$se.fit                        # its standard error
  LL    = exp(eta - 1.96 * se)                   # lower CI on response scale
  UL    = exp(eta + 1.96 * se)                   # upper CI on response scale
  fit   = exp(eta)                                # mean predicted counts
})

# --- Plot: predicted mean counts vs. 'presepct' with 95% CI errorbars -----
# Points + line for the mean, error bars for 95% CI, clean theme
library(ggplot2)

ggplot(predicdata, aes(x = presepct, y = fit)) +
  geom_point() +
  geom_line(size = 0.8) +
  geom_errorbar(aes(ymin = LL, ymax = UL), width = 1.5, size = 0.5, color = "gray50") +

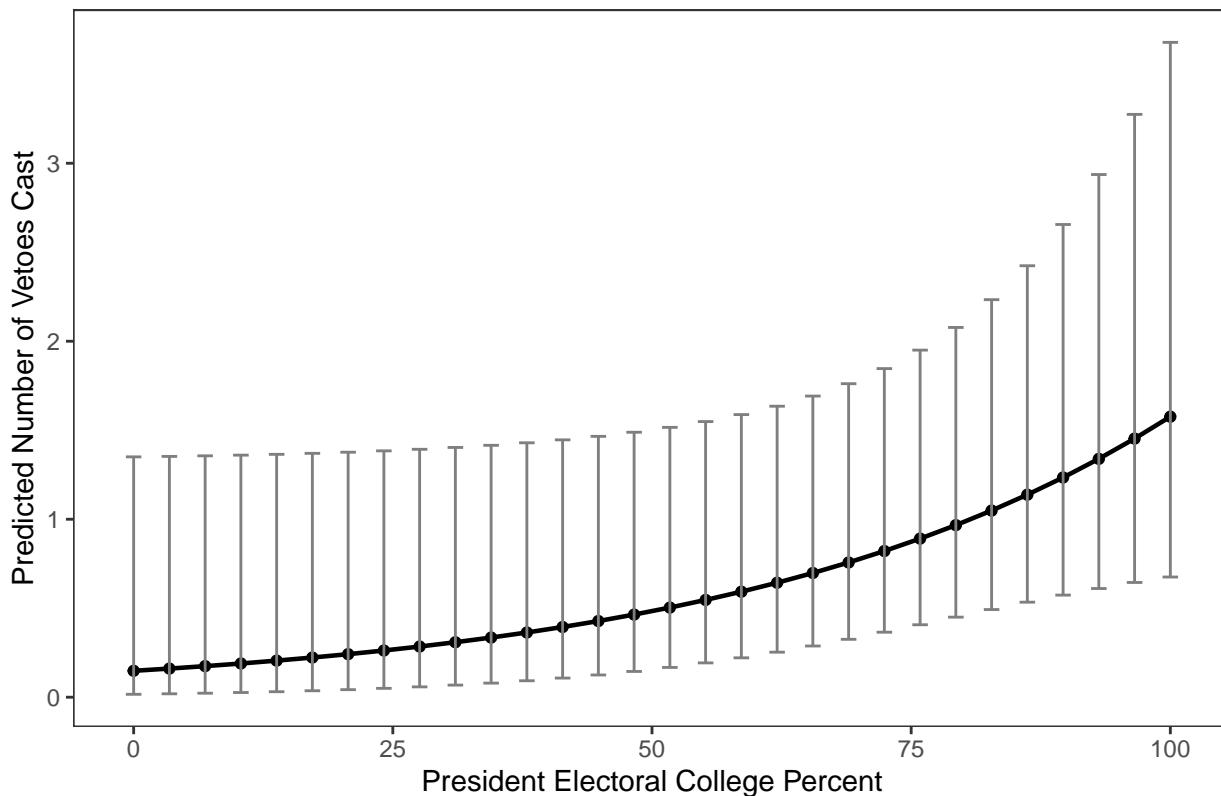
```

```

theme_bw() +
theme(panel.grid = element_blank()) +
labs(x = "President Electoral College Percent",
y = "Predicted Number of Veto Cast",
title = "Poisson GLM Predictions with 95% Confidence Intervals")

```

Poisson GLM Predictions with 95% Confidence Intervals



Question 2D: Testing for Overdispersion and Estimating a Negative Binomial Model

```

# --- Fit competing count models -----
# Poisson regression (PRM)
poissonmod <- glm(
  nover ~ conexpr + govexpr + prespty + hmajor + smajor + presepct,
  data   = vetos,
  family = poisson(link = "log")
)

# Overdispersion diagnostic for Poisson ( $H_0$ : equidispersion)
dispersiontest(poissonmod)

```

Overdispersion test

```

data: poissonmod
z = 1.693, p-value = 0.04523
alternative hypothesis: true dispersion is greater than 1

```

```

sample estimates:
dispersion
 1.377474

# Negative Binomial regression (accounts for overdispersion via theta)
negbinomod <- glm.nb(
  nover ~ congexpr + govexpr + prespty + hmajor + smajor + presepct,
  data = vetos
)

# Likelihood-based comparison (NB nests Poisson when theta)
anova(poissionmod, negbinomod, test = "Chisq")

```

Analysis of Deviance Table

```

Model 1: nover ~ congexpr + govexpr + prespty + hmajor + smajor + presepct
Model 2: nover ~ congexpr + govexpr + prespty + hmajor + smajor + presepct
Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1          19     39.904
2          19     32.534  0     7.3704

```

```

# --- Side-by-side model table -----
stargazer(
  poissionmod, negbinomod,
  type = "text",
  title = "Comparison of Poisson vs. Negative Binomial Regression for Veto Counts",
  dep.var.labels = "Number of Vetoes (nover)",
  covariate.labels = c("Congressional Experience",
                       "Governor Experience",
                       "President's Party (Indicator)",
                       "House Majority (President's Party)",
                       "Senate Majority (President's Party)",
                       "Pres. Electoral College %"),
  digits = 3
)

```

Comparison of Poisson vs. Negative Binomial Regression for Veto Counts

Dependent variable:		
	Poisson	negative binomial
	(1)	(2)
Congressional Experience	2.225*** (0.778)	2.103** (0.825)
Governor Experience	1.584* (0.843)	1.511* (0.906)
President's Party (Indicator)	-0.705* (0.423)	-0.681 (0.489)
House Majority (President's Party)	-1.025	-0.870

	(0.725)	(0.849)
Senate Majority (President's Party)	0.074 (0.618)	0.058 (0.733)
Pres. Electoral College %	0.024* (0.013)	0.020 (0.015)
Constant	-2.069 (1.318)	-1.806 (1.522)

Observations	26	26
Log Likelihood	-42.126	-42.779
theta		5.231 (7.358)
Akaike Inf. Crit.	98.252	99.559
=====		

Note: *p<0.1; **p<0.05; ***p<0.01

```
# --- Predicted values: Poisson vs. NB (Simple Version) -----
# Create a simple data frame with observed and predicted counts
compare <- data.frame(
  id          = seq_len(nrow(vetos)),
  never       = vetos$never,
  prmpredicted = round(fitted(poissonmod), 1),
  nbrmpredicted = round(fitted(negbinomod), 1)
)

# Convert to long format for ggplot (base R reshape)
compare_long <- reshape(
  compare,
  varying = c("never", "prmpredicted", "nbrmpredicted"),
  v.names = "Counts",
  timevar = "model",
  times = c("Observed", "Poisson Predicted", "NB Predicted"),
  direction = "long"
)
rownames(compare_long) <- NULL

# Make model a factor to control legend order/labels
compare_long$model <- factor(
  compare_long$model,
  levels = c("Observed", "Poisson Predicted", "NB Predicted")
)

# --- Plot observed vs. fitted (PRM vs. NB) -----
ggplot(compare_long, aes(x = id, y = Counts, color = model, group = model, shape = model)) +
  geom_line(linewidth = 1) +
  geom_point(size = 2) +
  scale_x_continuous(breaks = seq(1, max(compare_long$id), 2)) +
  labs(x = "Observation Index", y = "Counts",
       title = "Observed vs. Predicted Counts: Poisson vs. Negative Binomial") +
  theme_bw() +
  theme(
```

```

    panel.grid      = element_blank(),
    legend.position = "bottom",
    legend.background = element_rect(color = "grey80"),
    legend.title     = element_blank(),
    legend.text      = element_text(size = 12),
    axis.text        = element_text(size = 12),
    axis.title       = element_text(size = 12)
)

```

Observed vs. Predicted Counts: Poisson vs. Negative Binomial

