# Day8 exercise solutions

Ali Movasati, Isabelle Caroline Rose Cretton, Tristan Koning

Oct. 4th, 2024

```
# Set global code chunk options
knitr::opts_chunk$set(warning = FALSE)

# load required libraries
library("skimr")
library("dplyr")
library("magrittr")
library("ggplot2")

# define functions
`%notin%` <- Negate(`%in%`)</pre>
```

### Problem 1

```
data(bliss, package = "faraway")
bliss %<>% mutate(ratio = dead/(alive + dead))
```

### 1.A)

```
skim(bliss)
```

Table 1: Data summary

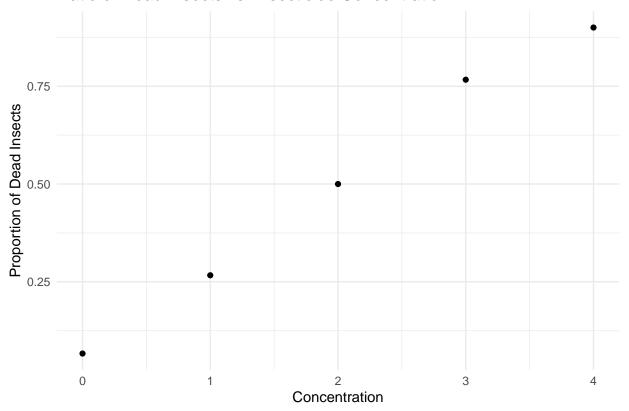
Name	bliss
Number of rows	5
Number of columns	4
Column type frequency:	
numeric	4
Group variables	None

### Variable type: numeric

skim_variable	n_missing	$complete\_rate$	mean	$\operatorname{sd}$	p0	p25	p50	p75	p100	hist
dead	0	1	15.0	10.32	2.00	8.00	15.0	23.00	27.0	
alive	0	1	15.0	10.32	3.00	7.00	15.0	22.00	28.0	
conc	0	1	2.0	1.58	0.00	1.00	2.0	3.00	4.0	
ratio	0	1	0.5	0.34	0.07	0.27	0.5	0.77	0.9	

#### head(bliss) ## dead alive conc ratio ## 1 2 28 0 0.06666667 ## 2 22 1 0.26666667 8 ## 3 15 2 0.50000000 15 ## 4 23 3 0.76666667 7 ## 5 27 4 0.90000000 # Load the data data(bliss, package = "faraway") # Calculate total insects and ratio bliss\$ratio <- bliss\$dead / (bliss\$dead + bliss\$alive)</pre> # Plot the ratio vs concentration ggplot(bliss, aes(x = conc, y = ratio)) + geom\_point() + labs(title = "Ratio of Dead Insects vs. Insecticide Concentration", x = "Concentration",y = "Proportion of Dead Insects") + theme\_minimal()

### Ratio of Dead Insects vs. Insecticide Concentration



### 1.B)

```
logit_model <- glm(cbind(dead,alive)~conc, family = binomial(link=logit), data = bliss)</pre>
```

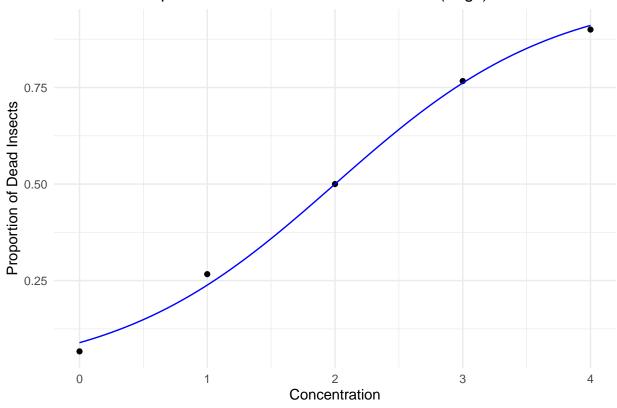
```
summary(logit_model)
##
## Call:
## glm(formula = cbind(dead, alive) ~ conc, family = binomial(link = logit),
      data = bliss)
##
## Deviance Residuals:
      1 2
                          3
## -0.4510 0.3597 0.0000 0.0643 -0.2045
##
## Coefficients:
              Estimate Std. Error z value Pr(>|z|)
##
## (Intercept) -2.3238 0.4179 -5.561 2.69e-08 ***
## conc
              1.1619
                           0.1814 6.405 1.51e-10 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 64.76327 on 4 degrees of freedom
## Residual deviance: 0.37875 on 3 degrees of freedom
## AIC: 20.854
## Number of Fisher Scoring iterations: 4
1.C)
# Calculate predicted values manually
coeffs <- coef(logit model)</pre>
linear_pred <- coeffs[1] + coeffs[2] * bliss$conc</pre>
manual_pred <- exp(linear_pred) / (1 + exp(linear_pred))</pre>
# Compare with fitted values
fitted_pred <- fitted(logit_model)</pre>
# Compare results
comparison_df <- data.frame(</pre>
 concentration = bliss$conc,
 manual = manual_pred,
 fitted = fitted_pred,
 difference = abs(manual_pred - fitted_pred)
print(comparison_df)
## concentration
                      manual
                               fitted difference
## 1
              0 0.08917177 0.08917177
## 2
               1 0.23832314 0.23832314
                                                 0
## 3
               2 0.50000000 0.50000000
## 4
               3 0.76167686 0.76167686
## 5
                4 0.91082823 0.91082823
```

### 1.D)

```
# Create prediction grid
pred_grid <- data.frame(conc = seq(min(bliss$conc), max(bliss$conc), length.out = 100))
pred_grid$pred <- predict(logit_model, newdata = pred_grid, type = "response")

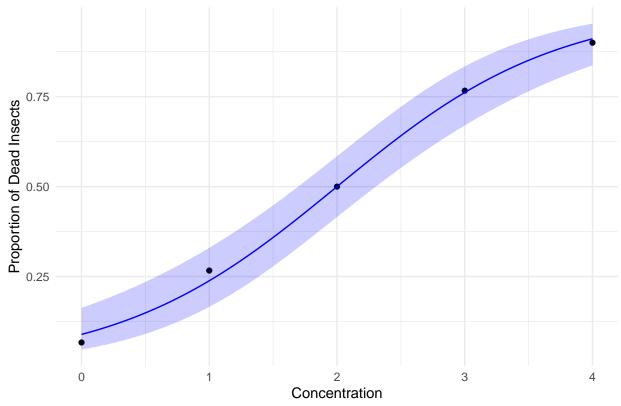
ggplot() +
    geom_point(data = bliss, aes(x = conc, y = ratio)) +
    geom_line(data = pred_grid, aes(x = conc, y = pred), color = "blue") +
    labs(title = "Observed Proportions and Predicted Probabilities (Logit)",
        x = "Concentration",
        y = "Proportion of Dead Insects") +
    theme_minimal()</pre>
```

# Observed Proportions and Predicted Probabilities (Logit)



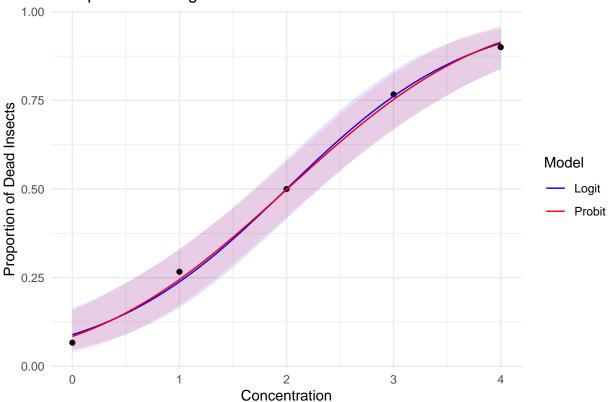
### 1.E)

### Logistic Regression with 90% Confidence Interval



```
newdata = pred_grid,
                    type = "link",
                    se.fit = TRUE)
pred_grid$probit_lower <- pnorm(probit_ci$fit - 1.645 * probit_ci$se.fit)</pre>
pred_grid$probit_upper <- pnorm(probit_ci$fit + 1.645 * probit_ci$se.fit)</pre>
# Plot both models
ggplot() +
 geom_point(data = bliss, aes(x = conc, y = ratio)) +
  geom_line(data = pred_grid, aes(x = conc, y = pred, color = "Logit")) +
  geom_line(data = pred_grid, aes(x = conc, y = probit_pred, color = "Probit")) +
  geom_ribbon(data = pred_grid,
              aes(x = conc, ymin = lower, ymax = upper),
              alpha = 0.1, fill = "blue",
              fill = "blue") +
  geom_ribbon(data = pred_grid,
              aes(x = conc, ymin = probit_lower, ymax = probit_upper),
              alpha = 0.1, fill = "red") +
  scale_color_manual(values = c("blue", "red")) +
  labs(title = "Comparison of Logit and Probit Models",
       x = "Concentration",
       y = "Proportion of Dead Insects",
       color = "Model") +
  theme_minimal()
```

## Comparison of Logit and Probit Models



### Problem 2: Exponential Family

The exponential family has the form:

$$f(y;\theta,\phi) = \exp((y\theta - b(\theta))/\phi + c(y,\phi))$$

#### (a) Exponential Distribution

The probability density function is:  $f(y; \lambda) = \lambda e^{-\lambda y}$ 

We can rewrite this as:  $f(y; \lambda) = exp(log(\lambda) - \lambda y) = exp(-\lambda y + log(\lambda))$ 

This belongs to the exponential family with:

- $\theta = -\lambda$
- $\phi = 1$
- $b(\theta) = -log(-\theta)$
- $c(y, \phi) = 0$

### (b) Binomial Distribution

The probability density function is:  $f(y;\pi) = \binom{n}{y} \pi^y (1-\pi)^{n-y}$ 

We can rewrite this as:  $f(y;\pi) = \exp(ylog(\pi/(1-\pi)) + nlog(1-\pi) + log(\binom{n}{y})) \\ = \exp(y\theta - nlog(1+e^{\theta}) + log(\binom{n}{y}))$ 

where  $\theta = log(\pi/(1-\pi))$ 

This belongs to the exponential family with:

- $\theta = log(\pi/(1-\pi))$
- $\phi = 1$
- $b(\theta) = nlog(1 + e^{\theta})$
- $c(y,\phi) = log(\binom{n}{y})$

#### (c) Uniform Distribution

- version 1

The probability density function is:  $f(y; \theta) = 1/\theta$ ,  $0 < y < \theta$ 

This cannot be written in exponential family form because the support of y depends on  $\theta$ .

- version 2

The probability density function is: The continuous uniform distribution  $\operatorname{Uniform}(a,b)$  has the following probability density function:

$$p(x \mid a, b) = \frac{1}{b-a}, \quad x \in [a, b].$$

where:

- 1. Sufficient statistic  $\phi$ : Since the distribution is constant over [a, b], it does not depend on x. Thus, we set  $\phi = 0$ .
- 2. Natural parameter  $\theta$ : The natural parameter,  $\theta$ , is also zero, as there's no variation in x in the density.
- 3. Base measure  $c(y,\phi)$ : This is the constant  $c(y,\phi)=\frac{1}{b-a}$ , representing the flat density within the interval [a,b].

4. Log-partition function  $b(\theta)$ : Since there's no dependence on x or  $\theta$ , we have  $b(\theta) = 0$ .

### (d) Normal Distribution (known variance)

The probability density function is:  $f(y; \mu, \sigma^2) = (1/\sqrt{2\pi\sigma^2}) exp(-(y-\mu)^2/(2\sigma^2))$ 

We can rewrite this as:  $f(y;\mu,\sigma^2)=exp(y\mu/\sigma^2-\mu^2/(2\sigma^2)-y^2/(2\sigma^2)-(1/2)log(2\pi\sigma^2))$ 

#### - Version 1

This belongs to the exponential family with:

- $\begin{array}{ll} \bullet & \theta = \mu \\ \bullet & \phi = \sigma^2 \end{array}$
- $b(\theta) = \theta^2/2$   $c(y,\phi) = -y^2/(2\phi) (1/2)log(2\pi\phi)$

#### - Version 2

- Natural parameter:  $\theta=\frac{\mu}{\sigma^2}$  Dispersion parameter:  $\phi=\sigma^2$  Function  $b(\theta)$ :  $b(\theta)=\frac{\mu^2}{2\sigma^2}$  Function  $c(y,\phi)$ :  $c(y,\phi)=-\frac{y^2}{2\phi^2}-\frac{1}{2}\ln(2\pi\phi^2)$