Set R04 - Categorical explanatory variables

STAT 401 (Engineering) - Iowa State University

March 27, 2017

Binary explanatory variable

Recall the simple linear regression model

$$Y_i \stackrel{ind}{\sim} N(\beta_0 + \beta_1 X_i, \sigma^2).$$

If we have a binary explanatory variable (i.e. the explanatory variable only has two values), we can code it as

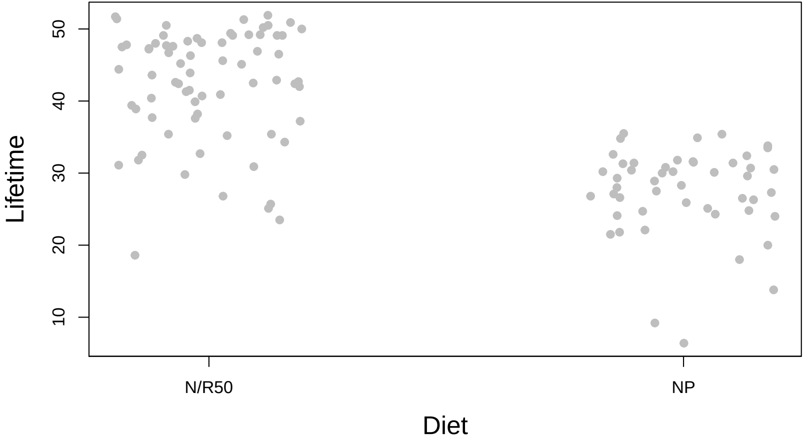
$$\begin{aligned} X_i &= \begin{cases} 1 & \text{obseration } i \text{ is one state} \\ 0 & \text{observation } i \text{ is the other state} \end{cases} \\ &= \mathrm{I}(\text{observation } i \text{ is ``one state''}) \end{aligned}$$

where $\mathrm{I}(A)$ is an indicator function that is 1 when A is true and 0 otherwise. Then

- β_0 is the expected response for the "other state",
- $\beta_0 + \beta_1$ is the expected response for the "one state", and therefore
- β_1 is the expected difference ("one state" minus "other state") in lifetimes.

Mice lifetimes

Reconsider the mice lifetime data set but only consider the diets NP and $N/R50$:



Regression model for mice lifetimes

Considering only the NP and N/R50 diets. Let

$$Y_i \stackrel{ind}{\sim} N(\beta_0 + \beta_1 X_i, \sigma^2)$$

where Y_i is the lifetime of the ith mouse and

$$X_i = \mathrm{I}(Diet_i == \text{N/R50}) = \begin{cases} 1 & i\text{th mouse diet is N/R50} \\ 0 & i\text{th mouse diet is NP} \end{cases}$$

then

$$\begin{array}{lll} E[\text{Lifetime}|\text{NP}] & = E[Y_i|X_i = 0] & = \beta_0 \\ E[\text{Lifetime}|\text{N/R50}] & = E[Y_i|X_i = 1] & = \beta_0 + \beta 1 \end{array}$$

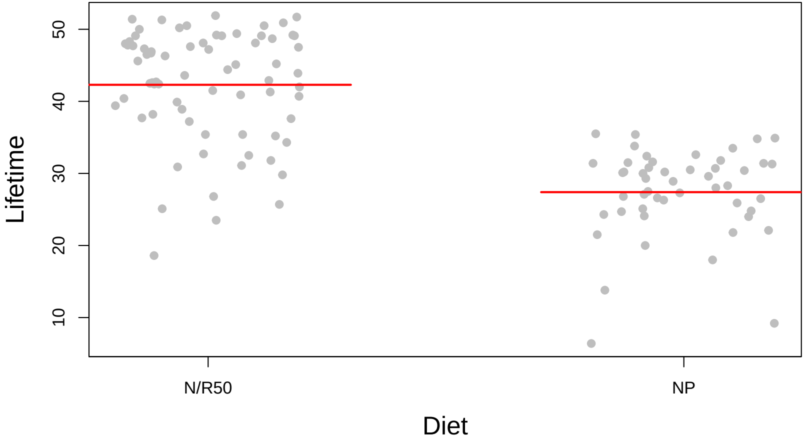
and

$$\begin{array}{ll} E[\text{Lifetime difference}] & = E[\text{Lifetime}|\text{N/R50}] - E[\text{Lifetime}|\text{NP}] \\ & = (\beta_0 + \beta_1) - \beta_0 = \beta_1. \end{array}$$

R code

```
case0501$X <- case0501$Diet == "N/R50"
(m <- lm(Lifetime ~ X, data = case0501, subset = Diet %in% c("NP","N/R50")))


Call:
lm(formula = Lifetime ~ X, data = case0501, subset = Diet %in%
    c("NP", "N/R50"))

Coefficients:
(Intercept)        XTRUE
       27.4         14.9


confint(m)


               2.5 %   97.5 %
(Intercept) 25.37974 29.42434
XTRUE       12.26605 17.52424


predict(m, data.frame(X=TRUE), interval = "confidence") # Expected lifetime on N/R50


       fit      lwr     upr
1 42.29718 40.61717 43.9772
```

Mice lifetimes



Equivalence to model for two-sample t-test

Recall that our two-sample t-test had the model

$$Y_{ij} \stackrel{ind}{\sim} N(\mu_j, \sigma^2)$$

for groups $j = 0, 1$. This is equivalent to our current regression model where

$$\begin{aligned} \mu_0 &= \beta_0 \\ \mu_1 &= \beta_0 + \beta_1 \end{aligned}$$

assuming

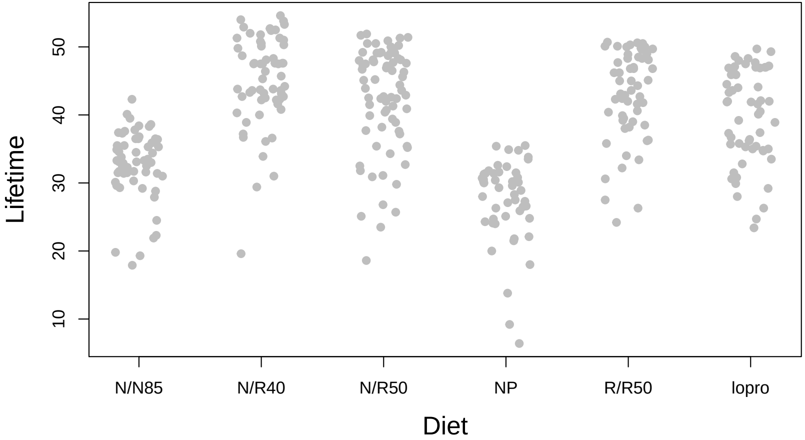
- μ_0 represents the mean for the NP group and
- μ_1 represents the mean for N/R50 group.

When the models are effectively the same, but have different parameters we call it a reparameterization.

Equivalence

```
summary(m)$coefficients[2,4] # p-value

[1] 2.534716e-20

confint(m)

               2.5 %   97.5 %
(Intercept) 25.37974 29.42434
XTRUE       12.26605 17.52424

t.test(Lifetime ~ Diet, data = case0501, subset = Diet %in% c("NP","N/R50"), var.equal=TRUE)

Two Sample t-test

data:  Lifetime by Diet
t = 11.219, df = 118, p-value < 2.2e-16
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 12.26605 17.52424
sample estimates:
mean in group N/R50    mean in group NP
           42.29718            27.40204
```

Using a categorical variable as an explanatory variable.



Regression with a categorical variable

- Choose one of the levels as the reference level, e.g. N/N85
- Construct dummy variables using indicator functions, i.e.

$$\mathrm{I}(A) = \begin{cases} 1 & A \text{ is TRUE} \\ 0 & A \text{ is FALSE} \end{cases}$$

for the other levels, e.g.

$$\begin{aligned} X_{i,1} &= \mathrm{I}(\text{diet for observation } i \text{ is N/R40}) \\ X_{i,2} &= \mathrm{I}(\text{diet for observation } i \text{ is N/R50}) \\ X_{i,3} &= \mathrm{I}(\text{diet for observation } i \text{ is NP}) \\ X_{i,4} &= \mathrm{I}(\text{diet for observation } i \text{ is R/R50}) \\ X_{i,5} &= \mathrm{I}(\text{diet for observation } i \text{ is lopro}) \end{aligned}$$

- Estimate the parameters of a multiple regression model using these dummy variables.

R code

```
case0501 <- case0501 %>%
  mutate(X1 = Diet == "N/R40",
         X2 = Diet == "N/R50",
         X3 = Diet == "NP",
         X4 = Diet == "R/R50",
         X5 = Diet == "lopro")

m <- lm(Lifetime ~ X1 + X2 + X3 + X4 + X5, data= case0501)
m


Call:
lm(formula = Lifetime ~ X1 + X2 + X3 + X4 + X5, data = case0501)

Coefficients:
(Intercept)       X1TRUE       X2TRUE       X3TRUE       X4TRUE       X5TRUE
     32.691       12.425        9.606       -5.289       10.194        6.994


confint(m)


                2.5 %    97.5 %
(Intercept) 30.951394 34.431062
X1TRUE       9.995893 14.854984
X2TRUE       7.269897 11.942013
X3TRUE      -7.848142 -2.730232
X4TRUE       7.723030 12.665943
X5TRUE       4.523030  9.465943
```

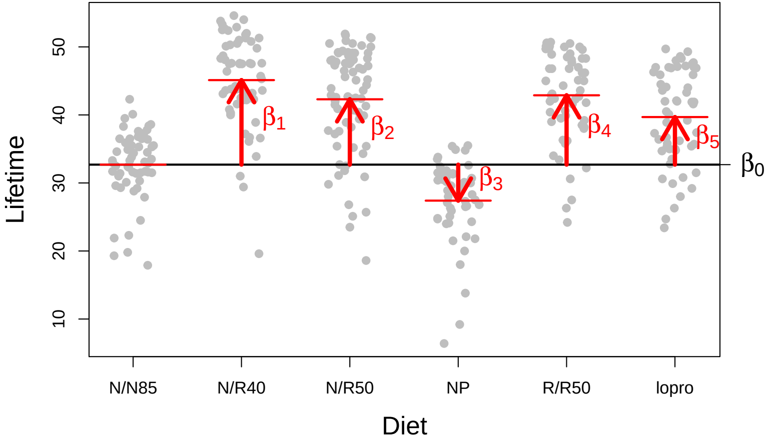
Interpretation

- $\beta_0 = E[Y_i|\text{reference level}]$, i.e. expected response for the reference level
  Note: the only way $X_{i,1} = \cdots = X_{i,p} = 0$ is if all indicators are zero, i.e. at the reference level.
- $\beta_p, p > 0$: expected change in the response moving from the reference level to the level associated with the p^{th} dummy variable
  Note: the only way for $X_{i,p}$ to increase by one is if initially $X_{i,1} = \cdots = X_{i,p} = 0$ and now $X_{i,p} = 1$

For example,

- The expected lifetime for mice on the N/N85 diet is 32.7 (31.0,34.4) weeks.
- The expected increase in lifetime for mice on the N/R40 diet compared to the N/N85 diet is 12.4 (10.0,14.9) weeks.
- The model explains 45% of the variability in mice lifetimes.

Using a categorical variable as an explanatory variable.



Equivalence to multiple group model

Recall that we had a multiple group model

$$Y_{ij} \stackrel{ind}{\sim} N(\mu_j, \sigma^2)$$

for groups $j = 0, 1, 2, \ldots, 5$. This is equivalent to our current regression model where

$$\begin{aligned} \mu_0 &= \beta_0 \\ \mu_1 &= \beta_0 + \beta_1 \\ \mu_2 &= \beta_0 + \beta_2 \\ \mu_3 &= \beta_0 + \beta_3 \\ \mu_4 &= \beta_0 + \beta_4 \\ \mu_5 &= \beta_0 + \beta_5 \end{aligned}$$

assuming the groups are labeled appropriately.