

**Class 8:
Chapter 9**

Min Lu

Object:

Logit Models for
Nominal Responses

Plot and Understand
Model Specification

R Exercise

Reshape Data and
Plot ROC Curve

Logit Model for
Nominal Responses

In class exercise

Take home exercise

Class 8: Chapter 9

EPH 705

Min Lu

Division of Biostatistics
University of Miami

Spring 2017

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Logit Models for Nominal Responses

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Multinomial logistic regression uses a linear predictor function $f(k, i)$ to predict the probability that observation i has outcome k , of the following form:

$$f(k, i) = \beta_{0,k} + \beta_{1,k}x_{1,i} + \beta_{2,k}x_{2,i} + \cdots + \beta_{M,k}x_{M,i},$$

where $\beta_{m,k}$ is a regression coefficient associated with the m th explanatory variable and the k th outcome. The regression coefficients and explanatory variables are normally grouped into vectors of size $M+1$, so that the predictor function can be written more compactly:

$$f(k, i) = \beta_k \cdot \mathbf{x}_i,$$

where β_k is the set of regression coefficients associated with outcome k , and \mathbf{x}_i (a row vector) is the set of explanatory variables associated with observation i .

Logit Models for Nominal Responses

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Using the fact that all K of the probabilities must sum to one, we find:

$$\Pr(Y_i = K) = \frac{1}{1 + \sum_{k=1}^{K-1} e^{\beta_k \cdot \mathbf{X}_i}}$$

We can use this to find the other probabilities:

The fact that we run multiple regressions reveals why the model relies on the assumption of independence of irrelevant alternatives described above.

Estimating response probabilities

$$\Pr(Y_i = 1) = \frac{e^{\beta_1 \cdot \mathbf{X}_i}}{1 + \sum_{k=1}^{K-1} e^{\beta_k \cdot \mathbf{X}_i}}$$

$$\Pr(Y_i = 2) = \frac{e^{\beta_2 \cdot \mathbf{X}_i}}{1 + \sum_{k=1}^{K-1} e^{\beta_k \cdot \mathbf{X}_i}}$$

.....

$$\Pr(Y_i = K - 1) = \frac{e^{\beta_{K-1} \cdot \mathbf{X}_i}}{1 + \sum_{k=1}^{K-1} e^{\beta_k \cdot \mathbf{X}_i}}$$

As a set of independent binary regressions

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One fairly simple way to arrive at the multinomial logit model is to imagine, for K possible outcomes, running $K - 1$ independent binary logistic regression models, in which one outcome is chosen as a "pivot" and then the other $K - 1$ outcomes are separately regressed against the pivot outcome. This would proceed as follows, if outcome K (the last outcome) is chosen as the pivot:

Baseline-category logits

$$\ln \frac{\Pr(Y_i = 1)}{\Pr(Y_i = K)} = \beta_1 \cdot \mathbf{X}_i$$

$$\ln \frac{\Pr(Y_i = 2)}{\Pr(Y_i = K)} = \beta_2 \cdot \mathbf{X}_i$$

.....

$$\ln \frac{\Pr(Y_i = K - 1)}{\Pr(Y_i = K)} = \beta_{K-1} \cdot \mathbf{X}_i$$

Note that we have introduced separate sets of regression coefficients, one for each possible outcome.

Model Specification Example

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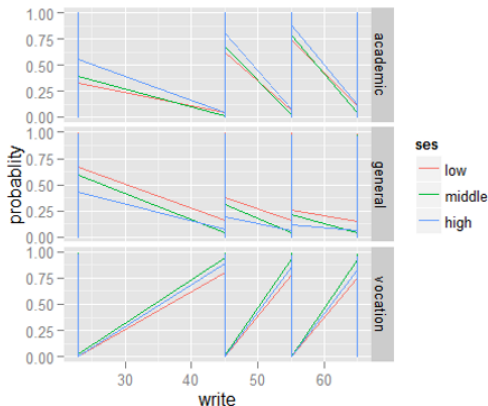
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The modeling of program choices made by high school students can be done using Multinomial logit. The program choices are general program, vocational program and academic program. Their choice can be modeled using their writing score and their social economic status.



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reshape a data into binary outcome

```
dat <- matrix(c(0, 10, 25, 0, 20, 35, 0, 21, 45, 7, 15, 55, 6, 11, 65, 17, 25, 75), 6, 3,
             byrow = T)
colnames(dat) <- c("disease", "n", "age")
dat <- as.data.frame(dat)
# mod=glm(formula = disease/n~age,weights=dat$n, family = binomial(link = logit), data
# = dat)

Melt <- function(data, yes, n) {
  x <- do.call(rbind, lapply(1:nrow(data), function(i) {
    cbind(data[i, -c(yes, n)], c(rep(1, data[i, yes]), rep(0, (data[i, n] - data[i, yes]))))
  }))
  colnames(x) = c(colnames(data)[-c(yes, n)], colnames(data)[yes])
  x
}
### yes=number of colume you want to covert to 1, no=.....0
head(Melt(data = dat, yes = 1, n = 2))
```

```
##      age disease
## [1,] 25        0
## [2,] 25        0
## [3,] 25        0
## [4,] 25        0
## [5,] 25        0
## [6,] 25        0
```

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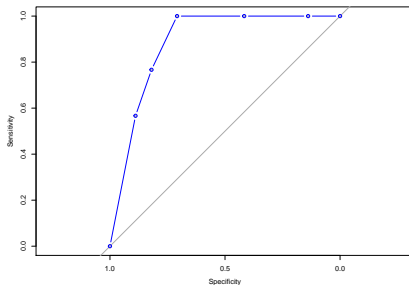
In class exercise

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ROC curve (only works for binary outcome)

```
dat1 <- as.data.frame(Melt(data = dat, yes = 1, n = 2))
mod <- glm(disease ~ age, family = binomial, data = dat1)

library(pROC)
rocobj <- plot.roc(dat1$disease, fitted(mod), type = "n")
lines(rocobj, type = "b", pch = 21, col = "blue", bg = "grey")
```



Western Collaborative Group Study data

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Data: The Western Collaborative Group Study (WCGS), a prospective cohort study, recruited middle-aged men (ages 39 to 59) who were employees of 10 California companies and collected data on 3154 individuals during the years 1960-1961. These subjects were primarily selected to study the relationship between behavior pattern and the risk of coronary heart disease (CHD). A number of other risk factors were also measured.

variable name	discreption
id	Subject ID:
age0	Age: age in years
height0	Height: height in inches
weight0	Weight: weight in pounds
sbp0	Systolic blood pressure: mm Hg
dbp0	Diastolic blood pressure: mm Hg
chol0	Cholesterol: mg/100 ml
behpat0	Behavior pattern:
ncigs0	Smoking: Cigarettes/day
dibpat0	Dichotomous behavior pattern: 0 = Type B; 1 = Type A
chd69	Coronary heart disease event: 0 = none; 1 = yes
typechd	to be done
time169	Observation (follow up) time: Days
arcus0	Corneal arcus: 0 = none; 1 = yes

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Logistic regression for nominal outcome

```
wcgs <- read.csv("wcgs.csv")[,-1]
library("nnet")
wcgs$behpat0 <- as.factor(wcgs$behpat0)
wcgs$chd69 <- as.factor(wcgs$chd69)
wcgs$behpat1 <- relevel(wcgs$behpat0, ref = "1")
model <- multinom(behpat1 ~ age0 + chd69, data = wcgs)

## # weights: 16 (9 variable)
## initial value 4372.372415
## iter 10 value 3707.459619
## final value 3698.301245
## converged
summary(model)

## Call:
## multinom(formula = behpat1 ~ age0 + chd69, data = wcgs)
##
## Coefficients:
## (Intercept)          age0          chd691
## 2    3.017701  -0.02995064   0.04913322
## 3    3.984092  -0.05135421  -0.77081969
## 4    3.046124  -0.05818738  -0.72683151
##
## Std. Errors:
## (Intercept)          age0          chd691
## 2    0.5637161  0.01186314  0.2146806
## 3    0.5719645  0.01207527  0.2365233
## 4    0.6939913  0.01481671  0.3125612
##
## Residual Deviance: 7396.602
## AIC: 7414.602
```

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Logistic regression for nominal outcome

```
beta <- summary(model)$coefficients
beta.se <- summary(model)$standard.errors
colnames(beta.se) <- paste(colnames(beta), ".SE", sep = "")
round(cbind(beta, beta.se), 2)
```

```
## (Intercept) age0 chd691 (Intercept).SE age0.SE chd691.SE
## 2      3.02 -0.03  0.05      0.56  0.01  0.21
## 3      3.98 -0.05 -0.77      0.57  0.01  0.24
## 4      3.05 -0.06 -0.73      0.69  0.01  0.31
```

```
## p value for the coefficients
1 - pnorm(abs(beta/beta.se))
```

```
## (Intercept)      age0      chd691
## 2 4.319943e-08 5.790182e-03 0.4094863045
## 3 1.634692e-12 1.055377e-05 0.0005591098
## 4 5.686254e-06 4.297988e-05 0.0100251449
```

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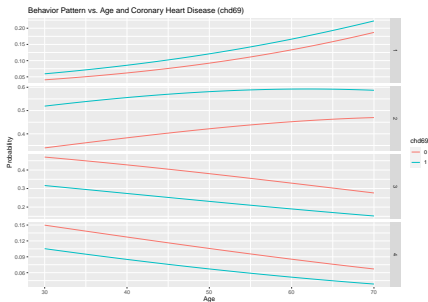
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GGplot Logistic regression for nominal outcome

```
xx <- data.frame(chd69 = rep(as.factor(c(0, 1)), each = 41), age0 = rep(c(30:70),2))
pp.xx <- cbind(xx, predict(model, type = "probs", newdata = xx, se = TRUE)) #
library("reshape")
lpp <- melt(pp.xx, id.vars = c("age0","chd69"), value.name = "probability")
library("ggplot2")
ggplot(lpp, aes(x = age0, y = value, colour = chd69)) + geom_line() + facet_grid(variable ~., scales = "free")+ labs(lines= "Nitrogen",
x = "Age",
y = "Probability",
title = "Behavior Pattern vs. Age and Coronary Heart Disease (chd69)")
```



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Use the wchs data and plot Figure 1.6 but substitute variable chd69 with arcus0.

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Use the `wcgs` data, choose your own outcome and predictors, conduct a Logit Model for Nominal Responses and make two plots: one from model with main effects only and the other from model with interaction.

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