Intro to R for Epidemiologists

Lab 8 (3/5/15)

Data

This lab will use the combined male and female diabetes dataset (from Homework 2). The full dataset can be found on the website under lab 8 as "diabetes.csv". This dataset also contains diabetes status as computed in homework 2.

Part 1. Multiple logistic regression

1. Read in the dataset "diabetes.csv"
2. Use multiple logistic regression (one regression model) to estimate the associations between a set of variables (total cholesterol, hdl cholesterol, age, height, and weight) and diabetes status.
3. Create a data frame as below of the variable name, odds ratio from multiple logistic regression, corresponding p-value from the regression, and lower and upper confidence bounds for a 95% confidence interval.

```
# Load libraries

# 1. Read in data
diabetes <- read.csv("diabetes.csv", stringsAsFactors = F)

# 2. Perform multiple logistic regression
glm1 <- glm(diab1 ~ chol + hdl + age + weight + height, data = diabetes,
  family = "binomial")

# 3. Create data frame

# a. get odds ratios
MLR_OR <- exp(glm1$coef)[-1]

# b. get p-values
sum_glm <- summary(glm1)$coef[-1, ]
MLR_pval <- sum_glm[, 4]

# c. get 95% confidence interval
confint1 <- exp(confint(glm1))[-1, ]

# d. get names of variables
Variable <- rownames(sum_glm)

# Create output data frame
OR_df <- data.frame(Variable, MLR_OR, MLR_pval, confint1)
# Name columns, not rows
colnames(OR_df)[-1] <- c("OR", "p-value", "LB", "UB")
rownames(OR_df) <- NULL
OR_df
```

```
##   Variable        OR      p-value        LB        UB
## 1     chol 1.0111629 1.422292e-03 1.0044689 1.0183326
## 2      hdl 0.9765422 2.421062e-02 0.9553714 0.9959181
## 3      age 1.0605720 1.032982e-07 1.0385658 1.0847577
## 4   weight 1.0118751 5.496561e-03 1.0034372 1.0204154
## 5   height 1.0125684 7.739832e-01 0.9297465 1.1031758
```

Part 2. Plotting regression results

Create the plot displaying the odds ratios from Part 1 and corresponding 95% confidence intervals as shown on the following page. The colors for this plot can be specified using: `cols <- c("blue", "red", "seagreen4", "slateblue", "sienna3" )`.

1. Plot the odds ratios. Be sure to label your axes.
   - Specify `ylim = c(0.92, 1.11)` and `axes = F`).
   - Your x values will be 1:5 and your y values will be the odds ratios.
2. Add the correct axes using the R function `axis`
3. Add a box around the plot using `box()`.
4. Add confidence intervals to each point using `segments`.
5. Add a horizontal dashed grey line (Hint: specify `lty = 2`)

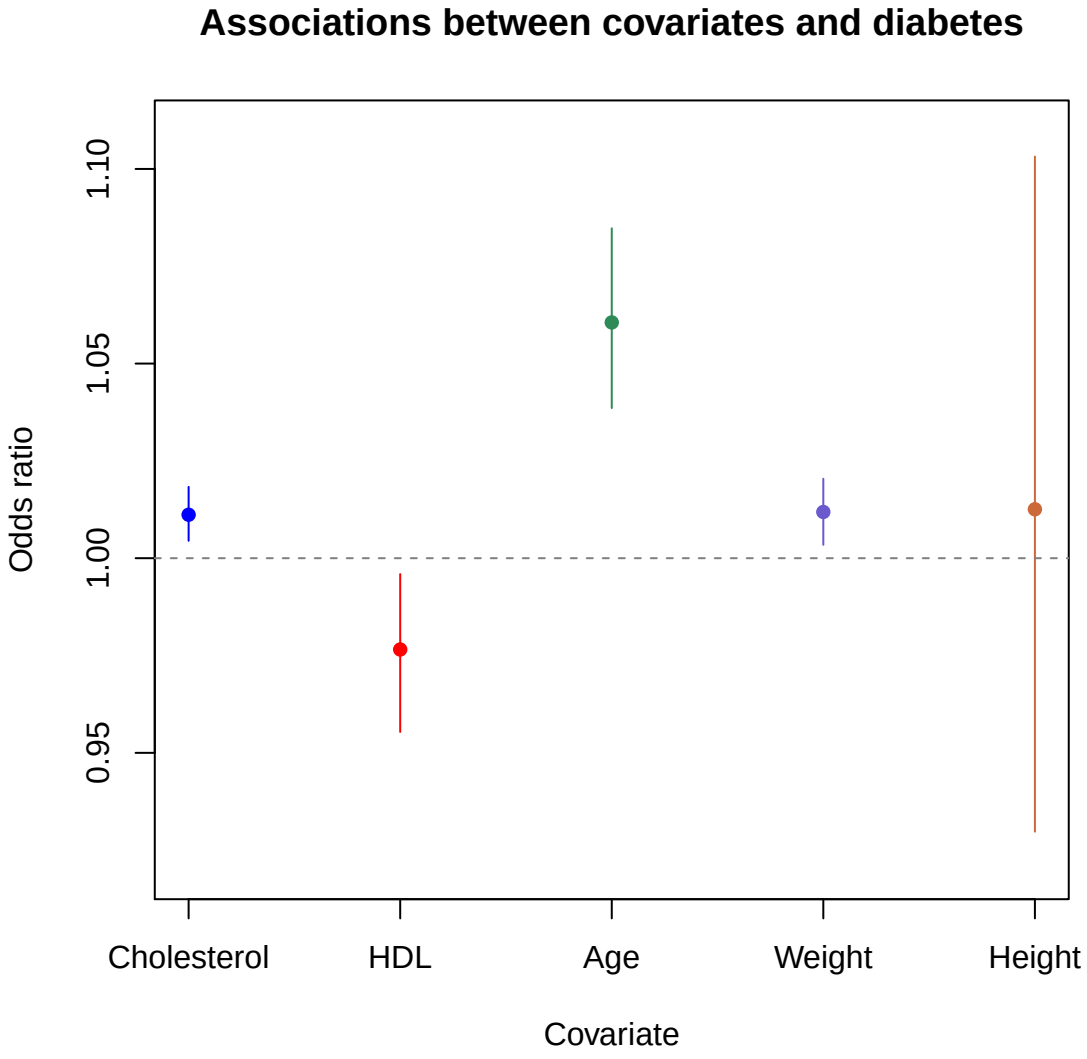
```r
# 1. First create empty plot
cols <- c("blue", "red", "seagreen4", "slateblue", "sienna3" )
plot(1 : 5, MLR_OR, xlab = "Covariate", ylab = "Odds ratio",
  main = "Associations between covariates and diabetes", pch = 16,
  axes = F, ylim = c(0.92, 1.11), col = cols)

# 2. Add axes
axis(2)
axis(1, at = 1 : 5, labels = c("Cholesterol", "HDL", "Age", "Weight",
  "Height"))

# 3. Add box
box()

# 3. Add confidence intervals
segments(1 : 5, confint1[, 1], 1 : 5, confint1[, 2], col = cols)

# 4. Add a horizontal grey line with lty
abline(h = 1, lty = 2, col = "grey50")
```



Part 3. Kaplan-Meier Curves

For this part, we will use the `kidney` dataset in the survival package, which gives recurrence times to infection for kidney patients.

1. Create a survival object for the data using `Surv` for time followed until recurrence.
2. Plot the Kaplan-Meier curves for time until recurrence by disease type.

```
library(survival)
# 1. Create survival object
surv_kidney <- Surv(time = kidney$time, event = kidney$status)


# 2. Get Kaplan-Meier estimates
surv1 <- survfit(surv_kidney ~ disease, data = kidney)


# 3. Plot curves
cols <- c("slateblue", "forestgreen", "black", "darkred")
```

```r
plot(surv1, main = "Survival Estimates for Kidney patients", xlab = "Time",
  ylab = "Proportion not recurred", col = cols)
# Get strata names
names1 <- sapply(strsplit(names(surv1$strata), "="), function(x) x[[2]])
# add legend
legend("topright", legend = names1, lty = 1, col = cols,
  title = "Disease type")
```