BIOST 546 HW 1

My-Anh Doan

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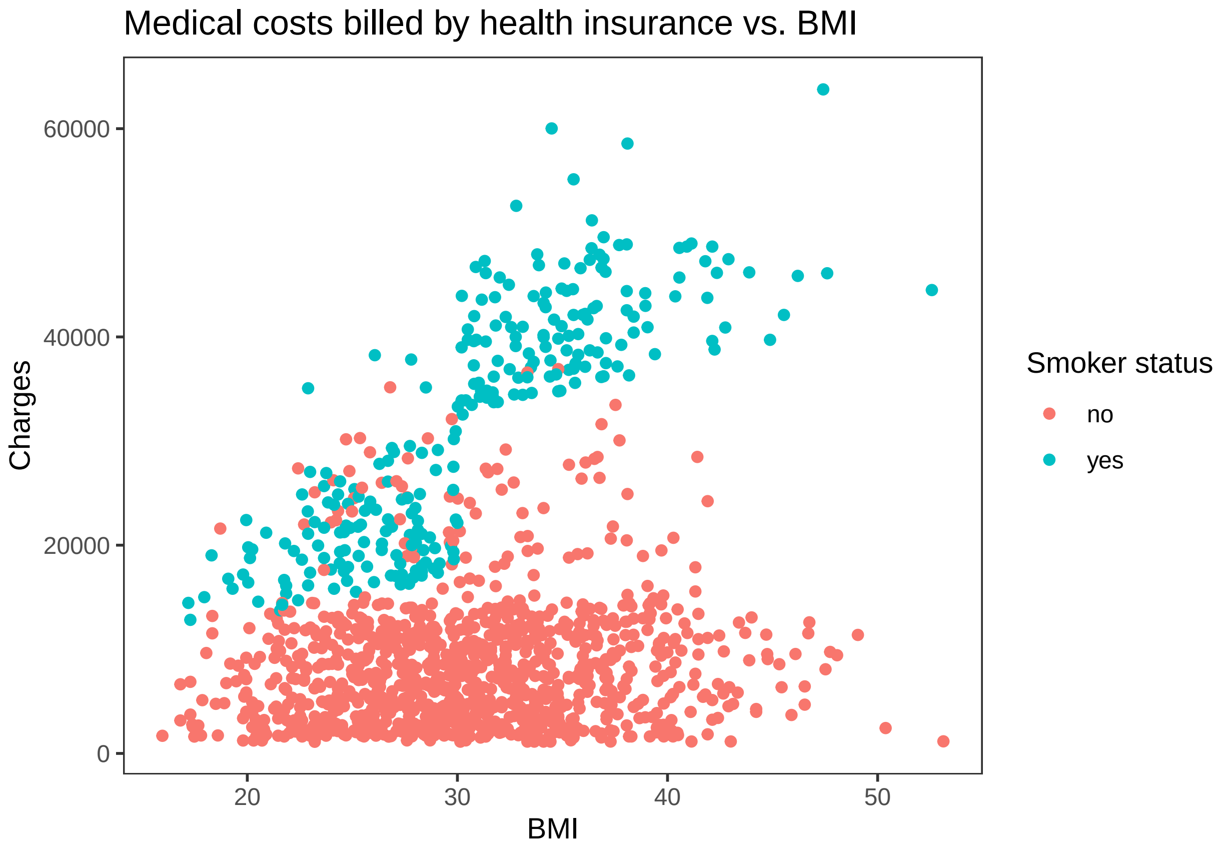
Q1. In this problem, we will make use of the data set `Medical_Cost_2.RData`.

(a) Load the data set with the command `load` and check if there are missing data.
(b) If any, remove the missing data using the command `na.omit`.

```r
# load data to environment
load("./dataset/Medical_Cost_2.RData")
str(df)
## 'data.frame':    1338 obs. of  7 variables:
##  $ age     : int  19 18 28 33 32 31 46 37 37 60 ...
##  $ sex     : Factor w/ 2 levels "female","male": 1 2 2 2 2 1 1 1 2 1 ...
##  $ bmi     : num  27.9 33.8 33 22.7 28.9 ...
##  $ children: int  0 1 3 0 0 0 1 3 2 0 ...
##  $ smoker  : Factor w/ 2 levels "no","yes": 2 1 1 1 1 1 1 1 1 1 ...
##  $ region  : Factor w/ 4 levels "northeast","northwest",..: 4 3 3 2 2 3 3 2 1 2 ...
##  $ charges : num  16885 1726 4449 21984 3867 ...

# check for missing data in `df`
# if returned value is non-zero, there are missing data
sum(is.na(df) == TRUE)
## [1] 60

# remove the missing data from `df`
df <- na.omit(df)
str(df)
## 'data.frame':    1278 obs. of  7 variables:
##  $ age     : int  19 18 28 33 32 31 46 37 37 60 ...
##  $ sex     : Factor w/ 2 levels "female","male": 1 2 2 2 2 1 1 1 2 1 ...
##  $ bmi     : num  27.9 33.8 33 22.7 28.9 ...
##  $ children: int  0 1 3 0 0 0 1 3 2 0 ...
##  $ smoker  : Factor w/ 2 levels "no","yes": 2 1 1 1 1 1 1 1 1 1 ...
##  $ region  : Factor w/ 4 levels "northeast","northwest",..: 4 3 3 2 2 3 3 2 1 2 ...
##  $ charges : num  16885 1726 4449 21984 3867 ...
##  - attr(*, "na.action")= 'omit' Named int [1:60] 22 37 39 40 84 111 129 193 248 252 ...
##   ..- attr(*, "names")= chr [1:60] "22" "37" "39" "40" ...
```

(c) We decide to focus on the outcome variable `charges` (individual medical costs billed by health insurance) and the predictors `bmi` (body mass index) and `smoker` (whether the subjects is a smoker or not). Make a scatter plot with `bmi` on the x-axis, `charges` on the y-axis, and with the color of each dot representing whether the subject is a smoker or not.

```
library(ggplot2)

q1c_plot <- ggplot(df, aes(x = bmi, y = charges)) +
  geom_point(aes(color = smoker)) +
  labs(title = "Medical costs billed by health insurance vs. BMI",
       x = "BMI",
       y = "Charges",
       color = "Smoker status") +
  theme_bw() +
  theme(panel.grid.minor = element_blank(),
        panel.grid.major = element_blank())
q1c_plot
```



(d) Fit a least-squares linear model, with intercept, in order to predict:

- `charges` using `bmi` as the only predictor;
- `charges` using `bmi` and `smoker` as predictors;
- `charges` using `bmi` and `smoker` as in the previous model; but allowing for an interaction term between the variables `bmi` and `smoker`

For each of the three models:

- Present your results in the form of a table where you report the estimated regression coefficients and their interpretations (be careful with the dummy variables);

- Report the 95% confidence interval for the coefficient of the variable `bmi`, and provide a sentence explaining the meaning of this confidence interval;
- Draw the regression line(s) of the model on the scatter plot produced in point (c);
- Report the (training set) mean squared error of the model;
- Predict the medical costs billed by the health insurance company to a smoker with a `bmi` that is 29 and 31.5;
- Compute the predicted difference in charges between a smoker with `bmi` 31.5 and one with `bmi` 29. Do the same for non-smokers. Comment on the results

```r
results_table <- function(linear_model) {
  coeffs <- as.data.frame(summary(linear_model)$coefficients)
  colnames(coeffs) <- c("Estimate", "Std. Error", "t-value", "p-value")
  coeffs <- coeffs %>%
    mutate(Estimate = round(Estimate, 2),
           `Std. Error` = round(`Std. Error`, 2),
           `t-value` = round(`t-value`, 3),
           `p-value` = format(`p-value`, scientific = TRUE, digits = 3))
  coeffs
}
```

```r
# linear model using `bmi` as the only predictor
charges_lm1 <- lm(charges ~ bmi, data = df)
results_table(charges_lm1)
##             Estimate Std. Error t-value  p-value
## (Intercept)   938.44    1682.00   0.558 5.77e-01
## bmi           402.65      53.85   7.478 1.40e-13
```

```r
# linear model using `bmi` and `smoker` as predictors
charges_lm2 <- lm(charges ~ bmi + smoker, data = df)
results_table(charges_lm2)
##             Estimate Std. Error t-value   p-value
## (Intercept) -3711.68    1018.78  -3.643  2.80e-04
## bmi           398.47      32.46  12.275  8.12e-33
## smokeryes   23218.77     491.04  47.285 1.02e-282
```

```r
# linear model using `bmi` and `smoker` as predictors but also allowing for an
# interaction term between predictors `bmi` and `smoker`
charges_lm3 <- lm(charges ~ bmi + smoker + bmi*smoker , data = df)
results_table(charges_lm3)
##                Estimate Std. Error t-value  p-value
## (Intercept)     5750.97     991.45   5.801 8.33e-09
## bmi               89.47      31.76   2.817 4.92e-03
## smokeryes     -20008.39    2122.67  -9.426 1.94e-20
## bmi:smokeryes   1410.05      67.84  20.784 7.42e-83
```

(e) Now define and add to the data set a new Boolean variable `smoker_bmi30p` that is `True` only if the subject is a smoker **and** has a `bmi` greater than 30. Use this newly defined variable, together with `bmi` and `smoker`, to fit the linear model represented in Figure 1 by carefully defining the interaction terms (allow each of the three straight lines to have their own intercept and slope, but use the command `lm` only once).

- Present your results in the form of one table where you report the estimated coefficients of the model.

- For each predictor, comment on whether you can reject the null hypothesis that there is no (linear) association between that predictor and `charges`, conditional on the other predictors in the model.
- Explain the interpretation of the non-significant variables in the model ($p > 0.05$) and explain how Figure 1 would change if we were to discard those variables, i.e., perform variable selection.
- According to this newly defined model, compute the predicted difference in `charges` between a smoker with `bmi` 31.5 and one with `bmi` 29. Do the same for non-smokers. Compare the analogous results in point (d) and comment on the results.

Q2. This problem has to do with the notation of bias-variance trade-off. For (a) and (b), it's okay to submit hand-sketched plots: this is a conceptual exercise.

(a) Make a plot, like the one we saw in class, with "flexibility" on the x-axis. Sketch the following curves: squared bias, variance, irreducible error, expected prediction error. Be sure to label each curve. Indicate which level of flexibility is *best*.
(b) Make a plot with "flexibility" on the x-axis. Sketch curves corresponding to the training error and the test error. Be sure to label each curve. Indicate which level of flexibility is "best".

Q3. This problem has to do with numerical explorations of the bias-variance trade-off phenomenon. You will generate simulated data, and will use these data to perform **linear regression**. Set the seed with `set.seed(0)` before you begin.

(a) Use the `rnorm()` function to generate a predictor vector `X` of length $n = 30$, and use `runif()` to generate a noise vector ϵ of length $n = 30$.
(b) Generate a response vector Y of length $n = 30$ according to the model