

Week 9 - Homework

STAT 420, Fall 2024, Banghao Chi

10/28/2024

Exercise 1 (EPA Emissions Data)

For this exercise, we will use the data stored in [epa2017.csv](#). It contains detailed descriptions of vehicles manufactured in 2017 that were used for fuel economy testing [as performed by the Environment Protection Agency](#). The variables in the dataset are:

- **Make** - Manufacturer
- **Model** - Model of vehicle
- **ID** - Manufacturer defined vehicle identification number within EPA's computer system (not a VIN number)
- **disp** - Cubic inch displacement of test vehicle
- **type** - Car, truck, or both (for vehicles that meet specifications of both car and truck, like smaller SUVs or crossovers)
- **horse** - Rated horsepower, in foot-pounds per second
- **cyl** - Number of cylinders
- **lockup** - Vehicle has transmission lockup; N or Y
- **drive** - Drivetrain system code
 - A = All-wheel drive
 - F = Front-wheel drive
 - P = Part-time 4-wheel drive
 - R = Rear-wheel drive
 - 4 = 4-wheel drive
- **weight** - Test weight, in pounds
- **axleratio** - Axle ratio
- **nvratio** - n/v ratio (engine speed versus vehicle speed at 50 mph)
- **THC** - Total hydrocarbons, in grams per mile (g/mi)
- **CO** - Carbon monoxide (a regulated pollutant), in g/mi
- **CO2** - Carbon dioxide (the primary byproduct of all fossil fuel combustion), in g/mi
- **mpg** - Fuel economy, in miles per gallon

We will attempt to model **CO2** using both **horse** and **type**. In practice, we would use many more predictors, but limiting ourselves to these two, one numeric and one factor, will allow us to create a number of plots.

Load the data, and check its structure using `str()`. Verify that **type** is a factor; if not, coerce it to be a factor.

```
data = read.csv("epa2017.csv")
data$type = as.factor(data$type)
levels(data$type)
```

```
## [1] "Both" "Car"  "Truck"
```

```

colors = c("Both" = "pink", "Car" = "dodgerblue", "Truck" = "orange")
pchs = c("Both" = 2, "Car" = 0, "Truck" = 1)
str(data)

## 'data.frame': 4037 obs. of 18 variables:
## $ Make : chr "Aston Martin" "Aston Martin" "Aston Martin" "Aston Martin" ...
## $ Model : chr "Rapide S" "Rapide S" "V12 Vantage S" "V12 Vantage S" ...
## $ ID : chr "410TT4202" "410TT4202" "288TT2087" "288TT2087" ...
## $ disp : num 6 6 6 6 6 ...
## $ type : Factor w/ 3 levels "Both","Car","Truck": 2 2 2 2 2 2 2 2 2 ...
## $ horse : int 552 552 565 565 568 568 568 568 211 211 ...
## $ cyl : int 12 12 12 12 12 12 12 12 4 4 ...
## $ gears : int 8 8 7 7 7 7 8 8 6 6 ...
## $ lockup : chr "Y" "Y" "Y" "Y" ...
## $ drive : chr "R" "R" "R" "R" ...
## $ weight : int 4750 4750 4250 4250 4250 4250 4500 4500 3875 3875 ...
## $ axleratio: num 2.73 2.73 3.73 3.73 3.73 3.73 2.73 2.73 3.69 3.69 ...
## $ nvratio : num 22.4 22.4 33.6 33.6 33.6 33.6 23.2 23.2 31.2 31.2 ...
## $ THC : num 0.0269 0.0008 0.0248 0.0005 0.0413 ...
## $ CO : num 0.5 0.06 0.61 0.05 0.68 ...
## $ CO2 : num 512 297 603 353 720 ...
## $ NOx : num 0.009 0.001 0.011 0.002 0.014 0.003 0.0141 0.00179 0.016 0.034 ...
## $ mpg : num 17.3 29.9 14.8 25.3 12.3 22.4 16.5 28.7 24.1 24.1 ...

```

(a) Do the following:

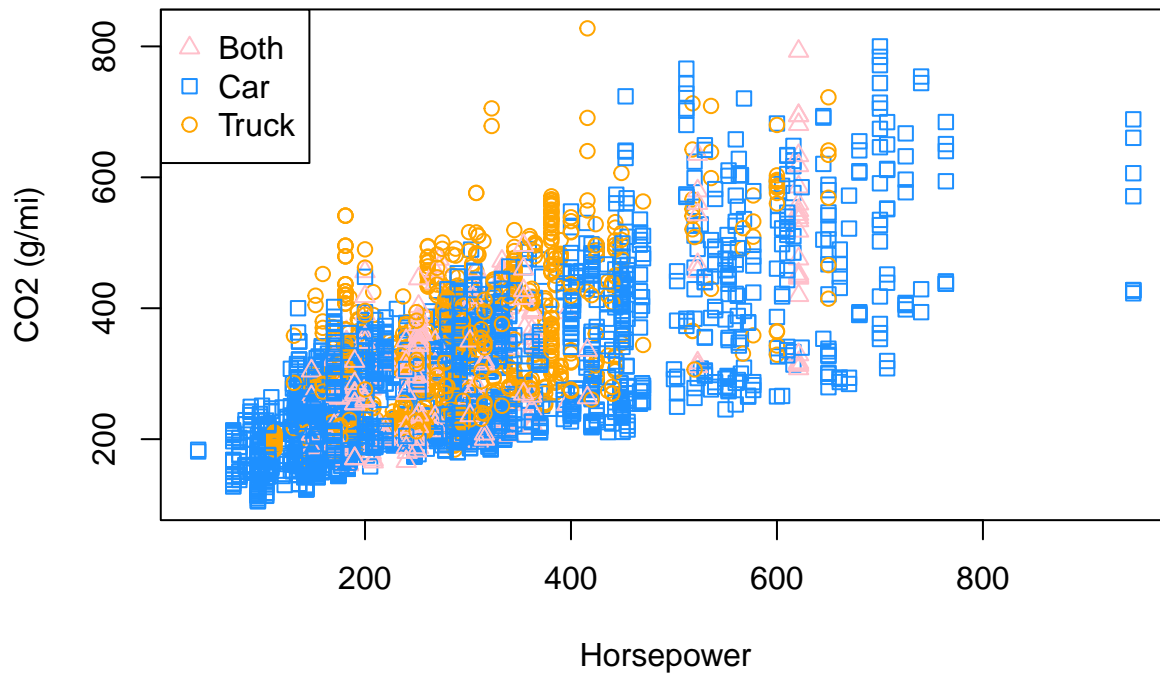
- Make a scatterplot of CO2 versus horse. Use a different color point for each vehicle type.

```

plot(CO2~horse, data = data,
     col = colors[type],
     xlab = "Horsepower",
     ylab = "CO2 (g/mi)",
     main = "CO2 vs Horsepower",
     pch = pchs[type],
     cex = 1
)
legend("topleft",
     legend = levels(data$type),
     col = c("pink", "dodgerblue", "orange"),
     pch = c(2, 0, 1),
     cex = 1)

```

CO2 vs Horsepower

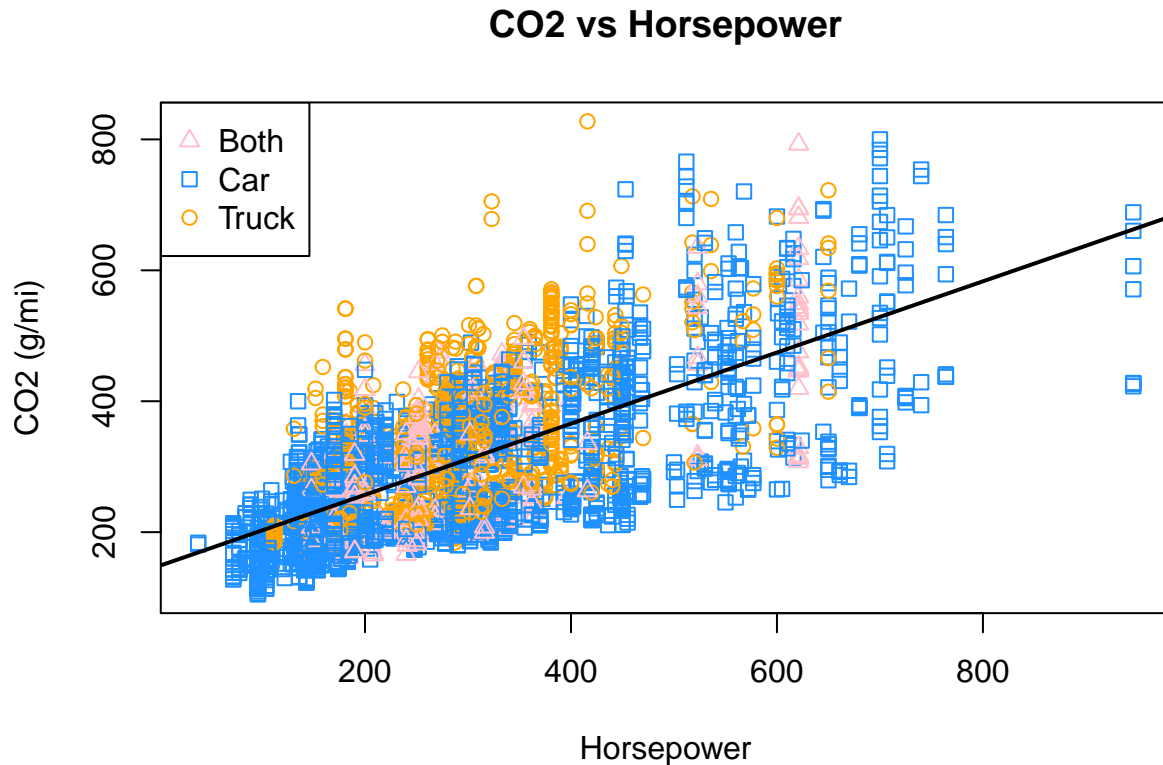


- Fit a simple linear regression model with CO2 as the response and only `horse` as the predictor.

```
model_a = lm(CO2 ~ horse, data = data)
```

- Add the fitted regression line to the scatterplot. Comment on how well this line models the data.

```
plot(CO2~horse, data = data,
     col = colors[type],
     xlab = "Horsepower",
     ylab = "CO2 (g/mi)",
     main = "CO2 vs Horsepower",
     pch = pchs[type],
     cex = 1
)
legend("topleft",
     legend = levels(data$type),
     col = c("pink", "dodgerblue", "orange"),
     pch = c(2, 0, 1),
     cex = 1)
abline(model_a, col = "black", lwd = 2)
```



The regression line shows a positive relationship between horsepower and CO2 emissions. It models well as for the relationship between CO2 and Both, and CO2 and Car, but the tendency of Truck mostly fall above the line.

- Give an estimate for the average change in C02 for a one foot-pound per second increase in `horse` for a vehicle of type `car`.

```
coef(model_a)
```

```
## (Intercept)      horse
##    148.3228      0.5436
```

```
coef_a = coef(model_a)[2]
```

The estimate for the average change in C02 for a one foot-pound per second increase in `horse` for a vehicle of type `car` is 0.5436.

- Give a 90% prediction interval using this model for the C02 of a Subaru Impreza Wagon, which is a vehicle with 148 horsepower and is considered type `Both`. (Interestingly, the dataset gives the wrong drivetrain for most Subarus in this dataset, as they are almost all listed as F, when they are in fact all-wheel drive.)

```
new_data_a = data.frame(horse = 148)
pred_int_a = predict(model_a, newdata = new_data_a, interval = "prediction", level = 0.90)
pred_int_a
```

```
##      fit  lwr upr
## 1 228.8 91.5 366
```

```
pre_int_a_lwr = pred_int_a[2]
pre_int_a_upr = pred_int_a[3]
```

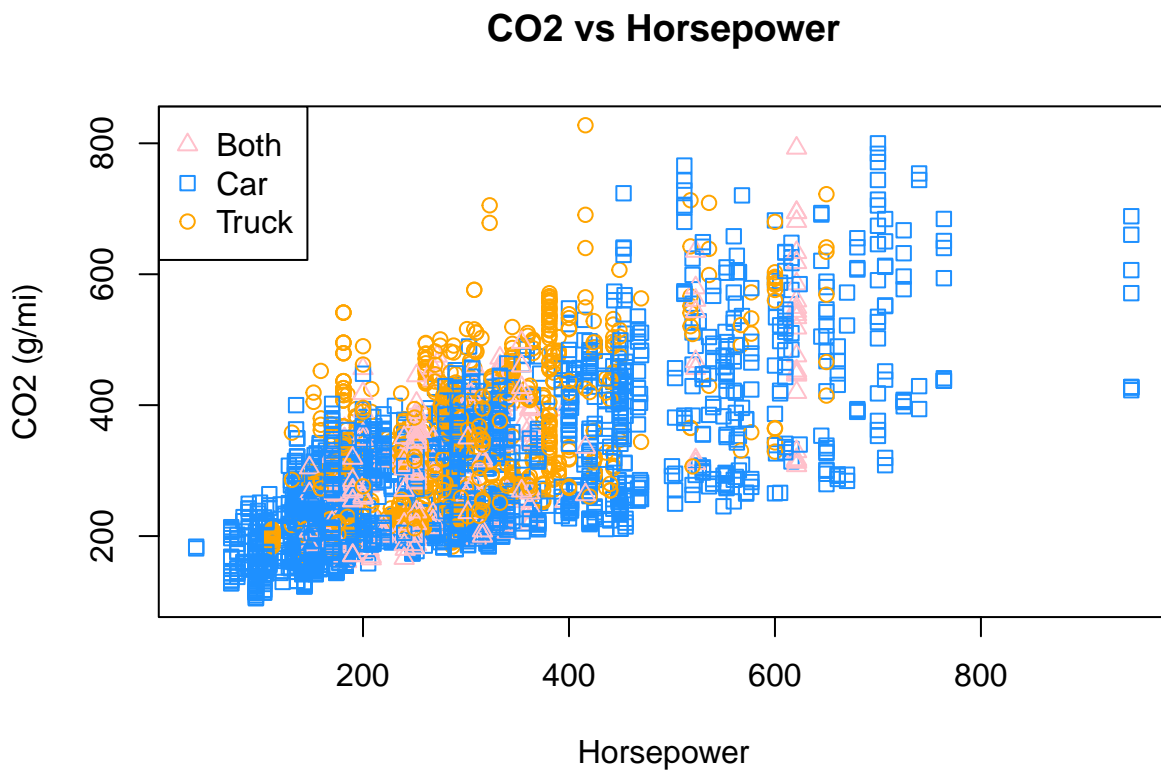
The 90% prediction interval using this model for the C02 of a Subaru Impreza Wagon is between 91.5033 and

366.0446.

(b) Do the following:

- Make a scatterplot of CO2 versus `horse`. Use a different color point for each vehicle `type`.

```
plot(CO2~horse, data = data,
     col = colors[type],
     xlab = "Horsepower",
     ylab = "CO2 (g/mi)",
     main = "CO2 vs Horsepower",
     pch = pchs[type],
     cex = 1
)
legend("topleft",
      legend = levels(data$type),
      col = c("pink", "dodgerblue", "orange"),
      pch = c(2, 0, 1),
      cex = 1)
```



- Fit an additive multiple regression model with CO2 as the response and `horse` and `type` as the predictors.

```
model_b = lm(CO2 ~ horse + type, data = data)
```

- Add the fitted regression “lines” to the scatterplot with the same colors as their respective points (one line for each vehicle type). Comment on how well this line models the data.

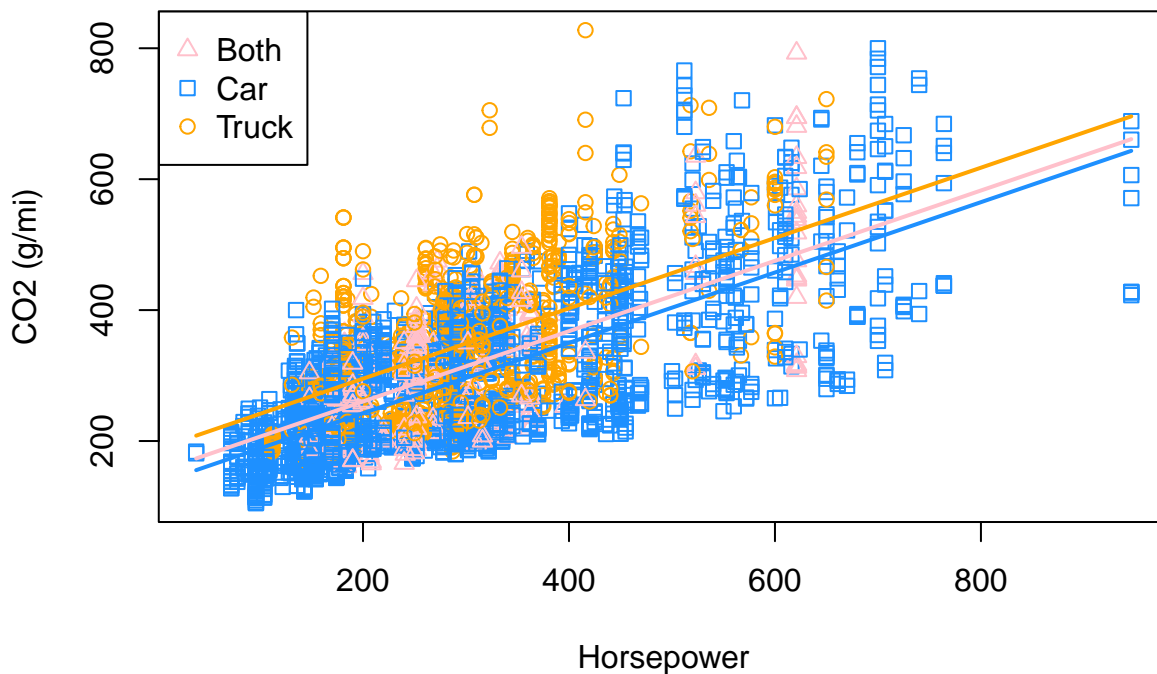
```
plot(CO2~horse, data = data,
     col = colors[type],
     xlab = "Horsepower",
     ylab = "CO2 (g/mi)",
     main = "CO2 vs Horsepower",
     pch = pchs[type],
```

```

    cex = 1
  )
  legend("topleft",
        legend = levels(data$type),
        col = c("pink", "dodgerblue", "orange"),
        pch = c(2, 0, 1),
        cex = 1)
  horse_seq = seq(min(data$horse), max(data$horse), length.out = 100)
  for(type in levels(data$type)) {
    pred_data = data.frame(horse = horse_seq, type = type)
    pred = predict(model_b, newdata = pred_data)
    lines(horse_seq, pred, col = colors[type], lwd = 2)
  }

```

CO2 vs Horsepower



The regression line shows a positive relationship between horsepower and CO2 emissions. The regression line did a pretty good job modeling the data, however, it would be better if the slope can be different, so that the line can fit better using the data.

- Give an estimate for the average change in CO2 for a one foot-pound per second increase in `horse` for a vehicle of type `car`.

```
coef_b = coef(model_b)[2]
```

The estimate for the average change in CO2 for a one foot-pound per second increase in `horse` for a vehicle of type `car` is 0.5372.

- Give a 90% prediction interval using this model for the CO2 of a Subaru Impreza Wagon, which is a vehicle with 148 horsepower and is considered type `Both`.

```

new_data_b = data.frame(horse = 148, type = "Both")
pred_int_b = predict(model_b, newdata = new_data_b, interval = "prediction", level = 0.90)
pred_int_b

```

```
##      fit lwr   upr
## 1 232.4 100 364.9

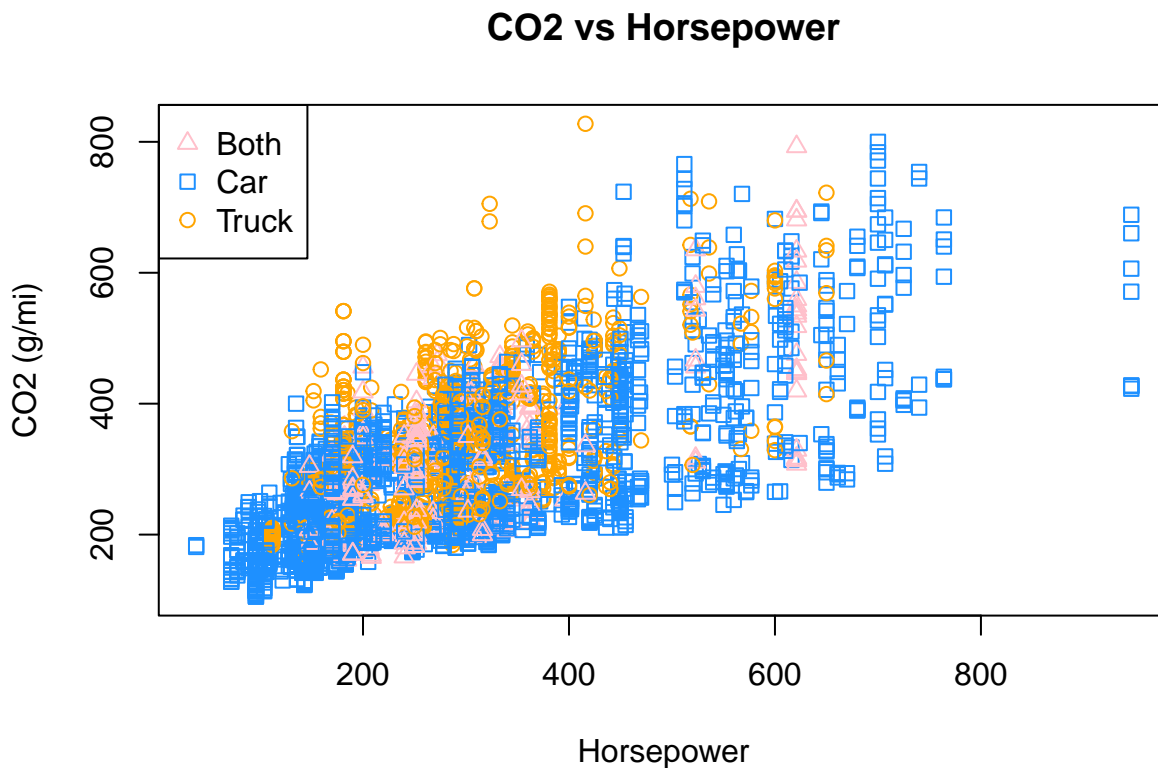
pre_int_b_lwr = pred_int_b[2]
pre_int_b_upr = pred_int_b[3]
```

The 90% prediction interval using this model for the C02 of a Subaru Impreza Wagon is between 100.0012 and 364.8952.

(c) Do the following:

- Make a scatterplot of C02 versus `horse`. Use a different color point for each vehicle `type`.

```
plot(C02~horse, data = data,
     col = colors[type],
     xlab = "Horsepower",
     ylab = "C02 (g/mi)",
     main = "C02 vs Horsepower",
     pch = pchs[type],
     cex = 1
)
legend("topleft",
     legend = levels(data$type),
     col = c("pink", "dodgerblue", "orange"),
     pch = c(2, 0, 1),
     cex = 1)
```



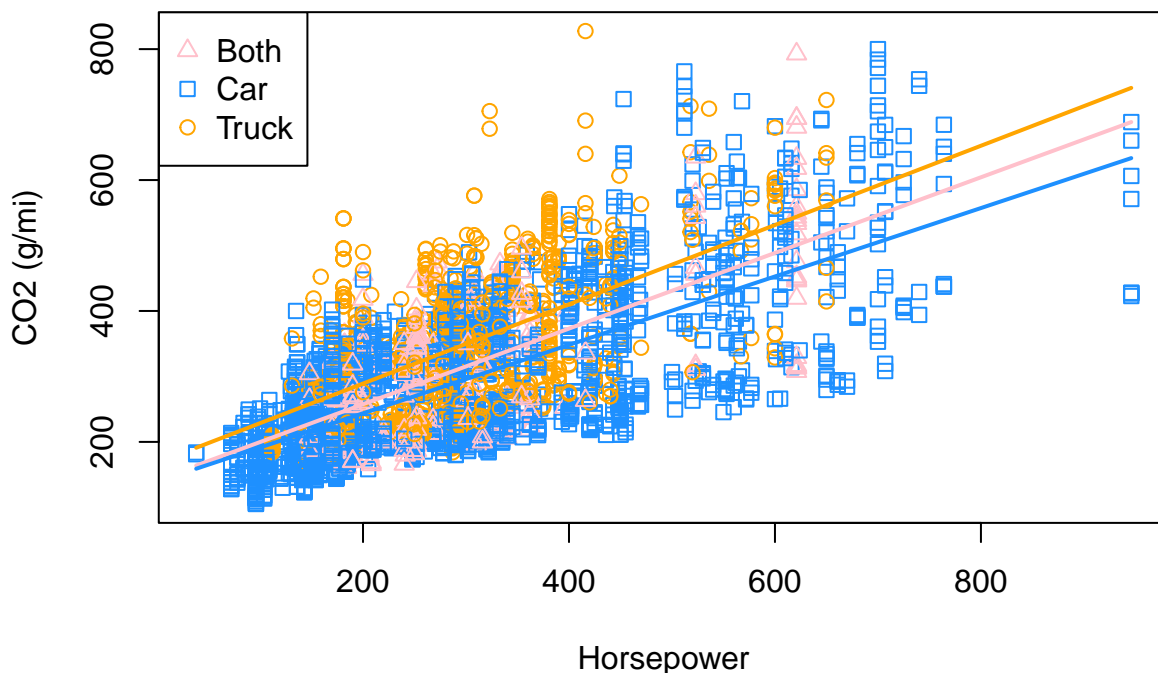
- Fit an interaction multiple regression model with C02 as the response and `horse` and `type` as the predictors.

```
model_c = lm(CO2 ~ horse * type, data = data)
```

- Add the fitted regression “lines” to the scatterplot with the same colors as their respective points (one line for each vehicle type). Comment on how well this line models the data.

```
plot(CO2~horse, data = data,
     col = colors[type],
     xlab = "Horsepower",
     ylab = "CO2 (g/mi)",
     main = "CO2 vs Horsepower",
     pch = pchs[type],
     cex = 1
)
legend("topleft",
      legend = levels(data$type),
      col = c("pink", "dodgerblue", "orange"),
      pch = c(2, 0, 1),
      cex = 1)
for(type in levels(data$type)) {
  pred_data = data.frame(horse = horse_seq, type = type)
  pred = predict(model_c, newdata = pred_data)
  lines(horse_seq, pred, col = colors[type], lwd = 2)
}
```

CO2 vs Horsepower



The regression line shows a positive relationship between horsepower and CO2 emissions. The regression line did a pretty good job modeling the data, with different slopes and different intercept.

- Give an estimate for the average change in CO2 for a one foot-pound per second increase in `horse` for a vehicle of type `car`.


```
coef_c = coef(model_c)[2] + coef(model_c)[5]
```

The estimate for the average change in CO₂ for a one foot-pound per second increase in `horse` for a vehicle of type `car` is 0.5226.

- Give a 90% prediction interval using this model for the CO₂ of a Subaru Impreza Wagon, which is a vehicle with 148 horsepower and is considered type `Both`.

```
new_data_c = data.frame(horse = 148, type = "Both")
pred_int_c = predict(model_c, newdata = new_data_c, interval = "prediction", level = 0.90)
pred_int_c
```

```
##      fit    lwr upr
## 1 227.5 95.01 360
```

```
pre_int_c_lwr = pred_int_c[2]
pre_int_c_upr = pred_int_c[3]
```

The 90% prediction interval using this model for the CO₂ of a Subaru Impreza Wagon is between 95.0055 and 359.9619.

(d) Based on the previous plots, you probably already have an opinion on the best model. Now use an ANOVA F -test to compare the additive and interaction models. Based on this test and a significance level of $\alpha = 0.10$, which model is preferred?

```
anova_test = anova(model_b, model_c)
anova_test
```

```
## Analysis of Variance Table
##
## Model 1: CO2 ~ horse + type
## Model 2: CO2 ~ horse * type
##   Res.Df      RSS Df Sum of Sq   F Pr(>F)
## 1    4033 26073761
## 2    4031 26007441   2    66320 5.14 0.0059 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Since p-value, which is 0.0059 according to the ANOVA table, $< \alpha = 0.10$, we reject the null hypothesis, meaning that interaction model is preferred.

Exercise 2 (Hospital SUPPORT Data, White Blood Cells)

For this exercise, we will use the data stored in [hospital.csv](#). It contains a random sample of 580 seriously ill hospitalized patients from a famous study called “SUPPORT” (Study to Understand Prognoses Preferences Outcomes and Risks of Treatment). As the name suggests, the purpose of the study was to determine what factors affected or predicted outcomes, such as how long a patient remained in the hospital. The variables in the dataset are:

- `Days` - Days to death or hospital discharge
- `Age` - Age on day of hospital admission
- `Sex` - Female or male
- `Comorbidity` - Patient diagnosed with more than one chronic disease
- `EdYears` - Years of education
- `Education` - Education level; high or low
- `Income` - Income level; high or low
- `Charges` - Hospital charges, in dollars

- Care - Level of care required; high or low
- Race - Non-white or white
- Pressure - Blood pressure, in mmHg
- Blood - White blood cell count, in gm/dL
- Rate - Heart rate, in bpm

For this exercise, we will use Age, Education, Income, and Sex in an attempt to model Blood. Essentially, we are attempting to model white blood cell count using only demographic information.

(a) Load the data, and check its structure using `str()`. Verify that Education, Income, and Sex are factors; if not, coerce them to be factors. What are the levels of Education, Income, and Sex?

```
data = read.csv("hospital.csv")
str(data)

## 'data.frame':    580 obs. of  13 variables:
## $ Days      : int  8 14 21 4 11 9 25 26 9 16 ...
## $ Age       : num  42.3 63.7 41.5 42 52.1 ...
## $ Sex       : chr   "female" "female" "male" "male" ...
## $ Comorbidity: chr   "no" "no" "yes" "yes" ...
## $ EdYears   : int  11 22 18 16 8 12 12 13 16 30 ...
## $ Education : chr   "low" "high" "high" "high" ...
## $ Income    : chr   "high" "high" "high" "high" ...
## $ Charges   : num  9914 283303 320843 4173 13414 ...
## $ Care      : chr   "low" "high" "high" "low" ...
## $ Race      : chr   "non-white" "white" "white" "white" ...
## $ Pressure  : int  84 69 66 97 89 57 99 115 93 102 ...
## $ Blood     : num  11.3 30.1 0.2 10.8 6.4 ...
## $ Rate      : int  94 108 130 88 92 114 150 132 86 90 ...
```

```
data$Sex = as.factor(data$Sex)
data$Education = as.factor(data$Education)
data$Income = as.factor(data$Income)
levels(data$Sex)
```

```
## [1] "female" "male"
```

```
levels(data$Education)
```

```
## [1] "high" "low"
```

```
levels(data$Income)
```

```
## [1] "high" "low"
```

(b) Fit an additive multiple regression model with Blood as the response using Age, Education, Income, and Sex as predictors. What does R choose as the reference level for Education, Income, and Sex?

```
model_add = lm(Blood ~ Age + Education + Income + Sex, data = data)
coef(model_add)
```

```
## (Intercept)      Age Educationlow      Incomelow      Sexmale
##    10.86624     0.02828     0.59667     0.18667    -1.87144
```

According to the `coef()` of the model, R choose "high", "high", "female" as the reference level for Education, Income, and Sex.

(c) Fit a multiple regression model with Blood as the response. Use the main effects of Age, Education, Income, and Sex, as well as the interaction of Sex with Age and the interaction of Sex and Income. Use a statistical test to compare this model to the additive model using a significance level of $\alpha = 0.10$. Which do you prefer?

```
model_int = lm(Blood ~ Age + Education + Income + Sex + Sex:Age + Sex:Income, data = data)
anova(model_add, model_int)
```

```
## Analysis of Variance Table
##
## Model 1: Blood ~ Age + Education + Income + Sex
## Model 2: Blood ~ Age + Education + Income + Sex + Sex:Age + Sex:Income
##   Res.Df  RSS Df Sum of Sq   F Pr(>F)
## 1     575 35694
## 2     573 35423   2      271 2.19  0.11
p_value = anova(model_add, model_int)[["Pr(>F)"]][2]
p_value
```

```
## [1] 0.1128
```

I'd prefer the additive model, since the p-value $0.1128 > \alpha = 0.10$, we fail to reject the null hypothesis, meaning that the smaller model is better, which is exactly the additive model.

(d) Fit a model similar to that in (c), but additionally add the interaction between **Income** and **Age** as well as a three-way interaction between **Age**, **Income**, and **Sex**. Use a statistical test to compare this model to the preferred model from (c) using a significance level of $\alpha = 0.10$. Which do you prefer?

```
model_full = lm(Blood ~ Age + Education + Income + Sex + Sex:Age + Sex:Income + Income:Age + Age:Income +
anova(model_int, model_full)
```

```
## Analysis of Variance Table
##
## Model 1: Blood ~ Age + Education + Income + Sex + Sex:Age + Sex:Income
## Model 2: Blood ~ Age + Education + Income + Sex + Sex:Age + Sex:Income +
##   Income:Age + Age:Income:Sex
##   Res.Df  RSS Df Sum of Sq   F Pr(>F)
## 1     573 35423
## 2     571 35166   2      257 2.08  0.13
p_value = anova(model_add, model_full)[["Pr(>F)"]][2]
p_value
```

```
## [1] 0.07439
```

I'd prefer the new model, since the p-value $0.0744 < \alpha = 0.10$, we reject the null hypothesis, meaning that the larger model is better, which is exactly the new model in the current question.

(e) Using the model in (d), give an estimate of the change in average Blood for a one-unit increase in **Age** for a highly educated, low income, male patient.

```
coefs = coef(model_full)
coefs
```

```
##           (Intercept)                Age           Educationlow
##           14.34808         -0.01748             0.56459
##           Incomelow           Sexmale           Age:Sexmale
##           -8.32364         -5.62832             0.04237
##           Incomelow:Sexmale      Age:Incomelow Age:Incomelow:Sexmale
##           10.94854             0.11488             -0.13447
```

```
est = coefs[2] + coefs[6] + coefs[8] + coefs[9]
```

The estimate of the change in average Blood for a one-unit increase in **Age** for a highly educated, low income, male patient is 0.0053.

Exercise 3 (Hospital SUPPORT Data, Stay Duration)

For this exercise, we will again use the data stored in [hospital.csv](#). It contains a random sample of 580 seriously ill hospitalized patients from a famous study called “SUPPORT” (Study to Understand Prognoses Preferences Outcomes and Risks of Treatment). As the name suggests, the purpose of the study was to determine what factors affected or predicted outcomes, such as how long a patient remained in the hospital. The variables in the dataset are:

- **Days** - Days to death or hospital discharge
- **Age** - Age on day of hospital admission
- **Sex** - Female or male
- **Comorbidity** - Patient diagnosed with more than one chronic disease
- **EdYears** - Years of education
- **Education** - Education level; high or low
- **Income** - Income level; high or low
- **Charges** - Hospital charges, in dollars
- **Care** - Level of care required; high or low
- **Race** - Non-white or white
- **Pressure** - Blood pressure, in mmHg
- **Blood** - White blood cell count, in gm/dL
- **Rate** - Heart rate, in bpm

For this exercise, we will use **Blood**, **Pressure**, and **Rate** in an attempt to model **Days**. Essentially, we are attempting to model the time spent in the hospital using only health metrics measured at the hospital.

Consider the model

$$Y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_1 x_2 + \beta_5 x_1 x_3 + \beta_6 x_2 x_3 + \beta_7 x_1 x_2 x_3 + \epsilon,$$

where

- Y is **Days**
- x_1 is **Blood**
- x_2 is **Pressure**
- x_3 is **Rate**.

(a) Fit the model above. Also fit a smaller model using the provided R code.

```
days_full = lm(Days ~ Blood * Pressure * Rate, data = data)
days_add = lm(Days ~ Pressure + Blood + Rate, data = data)
anova_table = anova(days_add, days_full)
anova_table
```

```
## Analysis of Variance Table
##
## Model 1: Days ~ Pressure + Blood + Rate
## Model 2: Days ~ Blood * Pressure * Rate
##   Res.Df    RSS Df Sum of Sq   F Pr(>F)
## 1      576 279493
## 2      572 275557   4      3936 2.04 0.087 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

f_test = anova_table[["F"]][2]
f_test
```

```
## [1] 2.043
```

```
p_value = anova_table[["Pr(>F)"]][2]
p_value
```

```
## [1] 0.08705
```

Use a statistical test to compare the two models. Report the following:

- The null and alternative hypotheses in terms of the model given in the exercise description
 - $H_0 : \beta_4 = \beta_5 = \beta_6 = \beta_7 = 0$ (interaction terms are not needed)
 - $H_1 : \text{At least one of } \beta_4, \beta_5, \beta_6, \beta_7 \neq 0$ (at least one interaction term is needed)
- The value of the test statistic is 2.0426
- The p-value of the test is 0.087
- A statistical decision using a significance level of $\alpha = 0.10$
 - Since p-value $0.087 < \alpha = 0.10$, we reject the null hypothesis.
- Which model you prefer:
 - Since the null hypothesis is rejected, I prefer the larger model.

(b) Give an expression based on the model in the exercise description for the true change in length of hospital stay in days for a 1 bpm increase in **Rate** for a patient with a **Pressure** of 139 mmHg and a **Blood** of 10 gm/dL. Your answer should be a linear function of the β s.

$$\frac{\partial Y}{\partial x_3} = \beta_3 + \beta_5 x_1 + \beta_6 x_2 + \beta_7 x_1 x_2$$

Plugging in the value of Rate, Pressure and Blood, we have:

$$\frac{\partial Y}{\partial x_3} = \beta_3 + 10\beta_5 + 139\beta_6 + 1390\beta_7$$

(c) Give an expression based on the additive model in part (a) for the true change in length of hospital stay in days for a 1 bpm increase in **Rate** for a patient with a **Pressure** of 139 mmHg and a **Blood** of 10 gm/dL. Your answer should be a linear function of the β s.

$$\frac{\partial Y}{\partial x_3} = \beta_3$$

Exercise 4 (*t*-test Is a Linear Model)

In this exercise, we will try to convince ourselves that a two-sample *t*-test assuming equal variance is the same as a *t*-test for the coefficient in front of a single two-level factor variable (dummy variable) in a linear model.

First, we set up the data frame that we will use throughout.

```
n = 30

sim_data = data.frame(
  groups = c(rep("A", n / 2), rep("B", n / 2)),
  values = rep(0, n))
str(sim_data)
```

```
## 'data.frame':   30 obs. of  2 variables:
## $ groups: chr   "A" "A" "A" "A" ...
## $ values: num   0 0 0 0 0 0 0 0 0 0 ...
```

We will use a total sample size of 30, 15 for each group. The `groups` variable splits the data into two groups, A and B, which will be the grouping variable for the t -test and a factor variable in a regression. The `values` variable will store simulated data.

We will repeat the following process a number of times.

```
set.seed(20)
sim_data$values = rnorm(n, mean = 42, sd = 3.5) # simulate response data
summary(lm(values ~ groups, data = sim_data))

##
## Call:
## lm(formula = values ~ groups, data = sim_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
##    -9.04    -1.11    -0.14     2.23     7.33
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   40.922      0.950   43.07  <2e-16 ***
## groupsB        0.029      1.344    0.02    0.98
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.68 on 28 degrees of freedom
## Multiple R-squared:  1.66e-05,    Adjusted R-squared:  -0.0357
## F-statistic: 0.000465 on 1 and 28 DF,  p-value: 0.983
t.test(values ~ groups, data = sim_data, var.equal = TRUE)

##
## Two Sample t-test
##
## data:  values by groups
## t = -0.022, df = 28, p-value = 1
## alternative hypothesis: true difference in means between group A and group B is not equal to 0
## 95 percent confidence interval:
##  -2.781  2.723
## sample estimates:
## mean in group A mean in group B
##           40.92           40.95
```

We use `lm()` to test

$$H_0 : \beta_1 = 0$$

for the model

$$Y = \beta_0 + \beta_1 x_1 + \epsilon$$

where Y is the values of interest, and x_1 is a dummy variable that splits the data in two. We will let `R` take care of the dummy variable.

We use `t.test()` to test

$$H_0 : \mu_A = \mu_B$$

where μ_A is the mean for the A group, and μ_B is the mean for the B group.

The following code sets up some variables for storage.

```
num_sims = 300
lm_t = rep(0, num_sims)
lm_p = rep(0, num_sims)
tt_t = rep(0, num_sims)
tt_p = rep(0, num_sims)
```

- `lm_t` will store the test statistic for the test $H_0 : \beta_1 = 0$.
- `lm_p` will store the p-value for the test $H_0 : \beta_1 = 0$.
- `tt_t` will store the test statistic for the test $H_0 : \mu_A = \mu_B$.
- `tt_p` will store the p-value for the test $H_0 : \mu_A = \mu_B$.

The variable `num_sims` controls how many times we will repeat this process, which we have chosen to be 300.

(a) Set a seed equal to your birthday. (Month and day are sufficient without year.) Then write code that repeats the above process 300 times. Each time, store the appropriate values in `lm_t`, `lm_p`, `tt_t`, and `tt_p`. Specifically, each time you should use `sim_data$values = rnorm(n, mean = 42, sd = 3.5)` to update the data. The grouping will always stay the same.

```
set.seed(1023)

for(i in 1:num_sims) {
  sim_data$values = rnorm(n, mean = 42, sd = 3.5)

  lm_fit = lm(values ~ groups, data = sim_data)
  lm_summary = summary(lm_fit)

  tt_result = t.test(values ~ groups, data = sim_data, var.equal = TRUE)

  lm_t[i] = lm_summary$coefficients["groupsB", "t value"]
  lm_p[i] = lm_summary$coefficients["groupsB", "Pr(>|t|)"]
  tt_t[i] = tt_result$statistic
  tt_p[i] = tt_result$p.value
}
```

(b) Report the value obtained by running `mean(lm_t == tt_t)`, which tells us what proportion of the test statistics is equal. The result may be extremely surprising!

```
mean(lm_t == tt_t)
```

```
## [1] 0
```

(c) Report the value obtained by running `mean(lm_p == tt_p)`, which tells us what proportion of the p-values is equal. The result may be extremely surprising!

```
mean(lm_p == tt_p)
```

```
## [1] 0.02333
```

(d) If you have done everything correctly so far, your answers to the last two parts won't indicate the equivalence we want to show! What the heck is going on here? The first issue is one of using a computer to do calculations. When a computer checks for equality, it demands **equality**; nothing can be different. However, when a computer performs calculations, it can only do so with a certain level of precision. So, if we calculate two quantities we know to be analytically equal, they can differ numerically. Instead of `mean(lm_p`

`== tt_p)` run `all.equal(lm_p, tt_p)`. This will perform a similar calculation, but with a very small error tolerance for each equality. What is the result of running this code? What does it mean?

```
all.equal(lm_p, tt_p)
```

```
## [1] TRUE
```

We get TRUE. This means that while the values aren't exactly equal when compared with `==`, they are equal within a small numerical tolerance.

(e) Your answer in (d) should now make much more sense. Then what is going on with the test statistics? Look at the values stored in `lm_t` and `tt_t`. What do you notice? Is there a relationship between the two? Can you explain why this is happening?

```
head(lm_t, 10)
```

```
## [1] 0.13612 -0.56579 -0.10257 -0.13934 0.04301 0.62926 2.29215 -1.84315
## [9] -0.25745 0.06684
```

```
head(tt_t, 10)
```

```
## [1] -0.13612 0.56579 0.10257 0.13934 -0.04301 -0.62926 -2.29215 1.84315
## [9] 0.25745 -0.06684
```

They're actually the same in absolute value but with opposite signs. This is because:

- t test on the model:
 - When it is group A ($x_1 = 0$), $Y = \beta_0 + \epsilon$
 - When it is group B ($x_1 \neq 0$), $Y = \beta_0 + \beta_1 + \epsilon$
 - Meaning that the difference of the mean of B minus A equals β_1 .
- t test on mean:
 - $t = (\text{mean_A} - \text{mean_B}) / \text{SE}$

As the sign of B minus A is opposite to `mean_A - mean_B`, we observe opposite sign in these two variables.