Methods_hw4

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2018-11-12

Problem 2

```
heartdisease_data = read_csv("./data/HeartDisease.csv")
```

```
## Parsed with column specification:
## cols(
##   id = col_integer(),
##   totalcost = col_double(),
##   age = col_integer(),
##   gender = col_integer(),
##   interventions = col_integer(),
##   drugs = col_integer(),
##   ERvisits = col_integer(),
##   complications = col_integer(),
##   comorbidities = col_integer(),
##   duration = col_integer()
## )
```

a)

Description of the Data Set

The main outcome is `totalcost` of patients diagnosed with heart disease. The main predictor is `ERvisits`, which is number of emergency room visits. Other important covariates are `age`, `gender`, `complications` and `duration`. `interventions`, `drugs` and `comorbidities` are potential covariates.

Descriptive Statistics for all Variables of Interest

Descriptive statistics for continous variables of interest:

```
heartdisease_data %>%
  select(totalcost, ERvisits, age, complications, duration) %>%
  summary() %>%
  knitr::kable(digits = 1)
```

totalcost	ERvisits	age	complications	duration
Min. : 0.0	Min. : 0.000	Min. :24.00	Min. :0.00000	Min. : 0.00
1st Qu.: 161.1	1st Qu.: 2.000	1st Qu.:55.00	1st Qu.:0.00000	1st Qu.: 41.75
Median : 507.2	Median : 3.000	Median :60.00	Median :0.00000	Median :165.50
Mean : 2800.0	Mean : 3.425	Mean :58.72	Mean :0.05711	Mean :164.03
3rd Qu.: 1905.5	3rd Qu.: 5.000	3rd Qu.:64.00	3rd Qu.:0.00000	3rd Qu.:281.00
Max. :52664.9	Max. :20.000	Max. :70.00	Max. :3.00000	Max. :372.00

Descriptive statistics for categorical variable of interest:

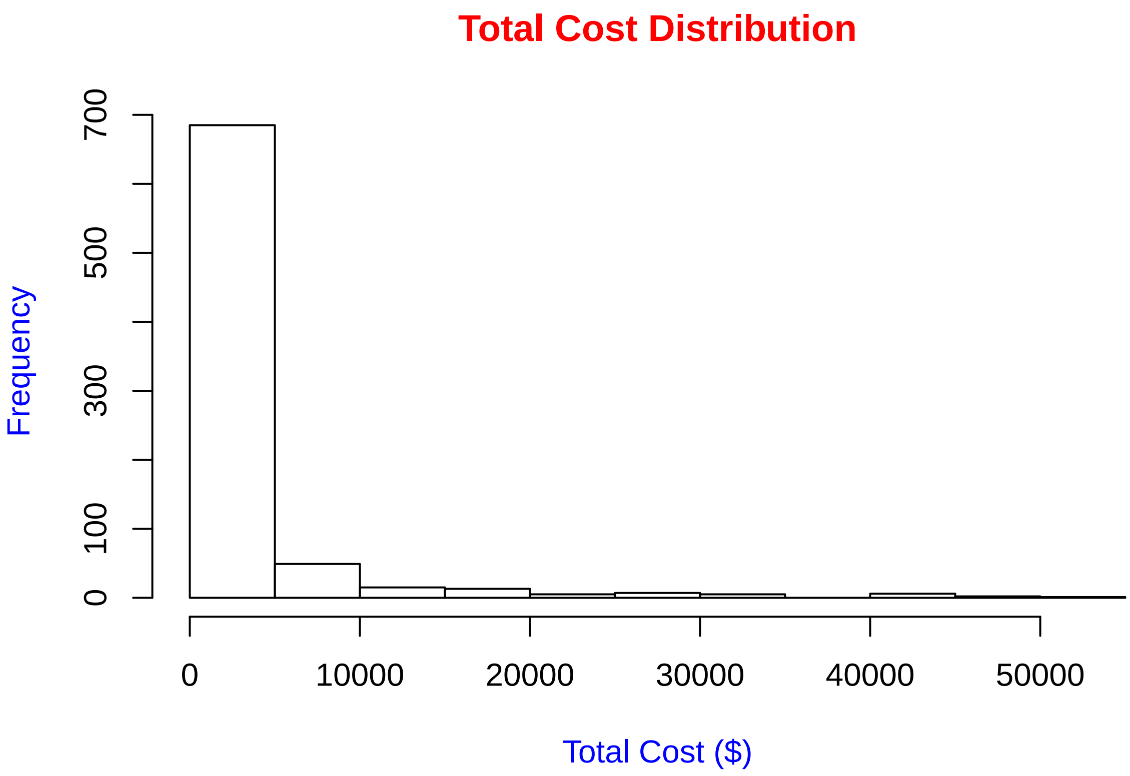
```
table(factor(heartdisease_data$gender, levels = c(1, 0), labels = c('Male', 'Female'))) %>%
  addmargins() %>%
  knitr::kable(digits = 1)
```

Var1	Freq
Male	180
Female	608
Sum	788

b)

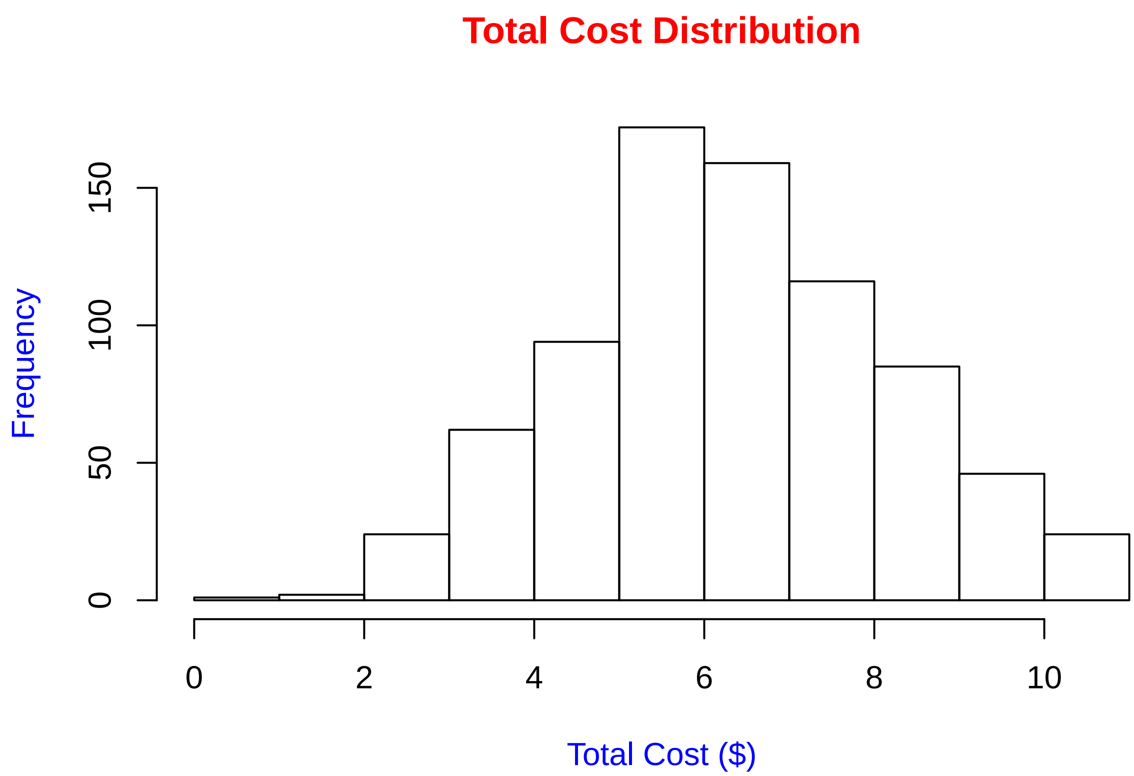
Plot the distribution for variable `totalcost`:

```
hist(heartdisease_data$totalcost, main = "Total Cost Distribution", xlab = "Total Cost ($)", col.main =
```



Use log transformation:

```
hist(log(heartdisease_data$totalcost), main = "Total Cost Distribution", xlab = "Total Cost ($)", col.ma
```



c)

Create a new variable called `comp_bin` by dichotomizing `complications`: 0 if no complications, and 1 otherwise.

```
new_heartdisease_data = heartdisease_data %>%
  mutate(comp_bin = as.factor(ifelse(complications == 0, 0, 1))) %>%
  mutate(gender = as.factor(gender))
```

d)

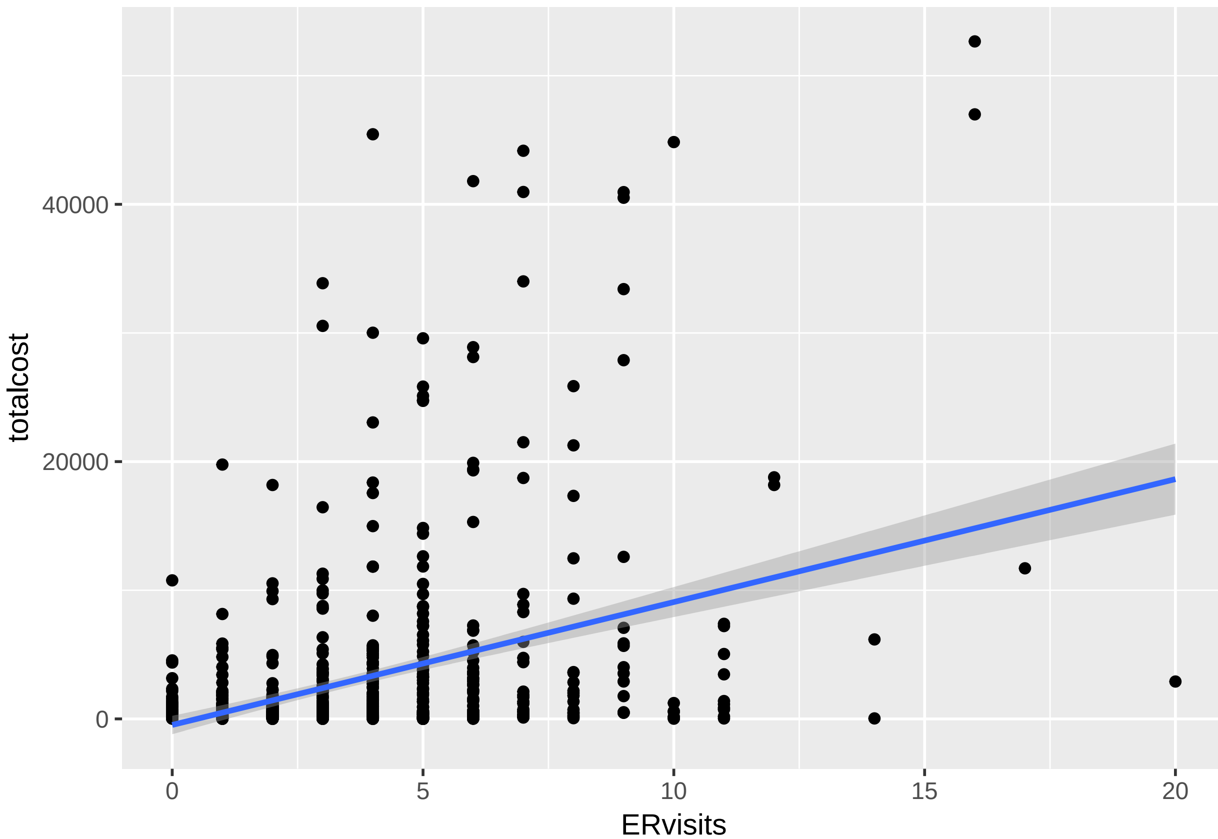
Fit a simple linear regression between the original `totalcost` and predictor `ERvisits`.

Ho: beta_ERvisits = 0

Ha: beta_ERvisits != 0

Model: totolcost = beta_0 + beta_ERvisits * ERvisits

```
ggplot(heartdisease_data, aes(x = ERvisits, y = totalcost)) +
  geom_point() +
  geom_smooth(method = 'lm', formula = y~x)
```




```r
reg_original_slr = lm(totalcost ~ ERvisits, heartdisease_data)
summary(reg_original_slr)
```

```
##
## Call:
## lm(formula = totalcost ~ ERvisits, data = heartdisease_data)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -15733  -2353  -1062    185  42098
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -472.54     362.24  -1.304    0.192
## ERvisits      955.44      83.81  11.399   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6201 on 786 degrees of freedom
## Multiple R-squared:  0.1419, Adjusted R-squared:  0.1408
## F-statistic: 129.9 on 1 and 786 DF,  p-value: < 2.2e-16
```

Comments on significance and interpretation of the slope:

- From the p-value of the F test, we can conclude that the test is significant and there is a linear relationship between `totalcost` and `ERvisits`, and `ERvisits` is a significant predictor of `totalcost`. But only 14% of variation of `totalcost` around its mean can be explained by the model.

- We expect the total cost will increase $955.44 on average if the number of emergency room (ER) visits increase 1 more time.

Fit a simple linear regression between the transformed `totalcost` and predictor `ERvisits`.

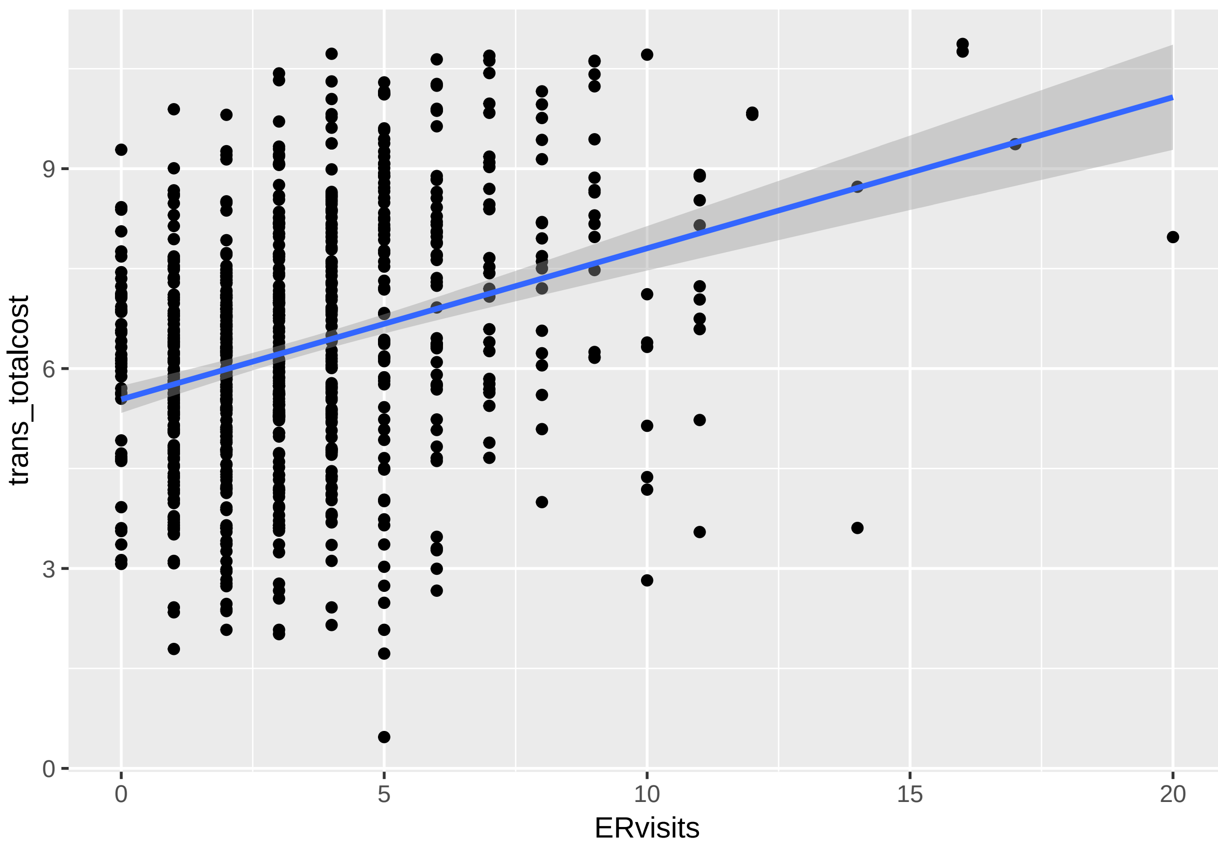
Ho: beta_ERvisits = 0

Ha: beta_ERvisits != 0

Model: trans_totolcost = beta_0 + beta_ERvisits * ERvisits

```
trans_heartdisease_data = heartdisease_data %>%
  filter(totalcost != 0) %>%
  mutate(trans_totalcost = log(totalcost)) %>%
  mutate(comp_bin = as.factor(ifelse(complications == 0, 0, 1))) %>%
  mutate(gender = as.factor(gender))

ggplot(trans_heartdisease_data, aes(x = ERvisits, y = trans_totalcost)) +
  geom_point() +
  geom_smooth(method = 'lm', formula = y~x)
```




```
reg_trans_slr = lm(trans_totalcost ~ ERvisits, trans_heartdisease_data)
summary(reg_trans_slr)
```

```
##
## Call:
## lm(formula = trans_totalcost ~ ERvisits, data = trans_heartdisease_data)
##
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -6.2013 -1.1265  0.0191  1.2668  4.2797
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  5.53771    0.10362   53.44   <2e-16 ***
## ERvisits     0.22672    0.02397    9.46   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.772 on 783 degrees of freedom
## Multiple R-squared:  0.1026, Adjusted R-squared:  0.1014
## F-statistic:  89.5 on 1 and 783 DF,  p-value: < 2.2e-16
```

Comments on significance and interpretation of the slope:

- From the p-value of the F test, we can conclude that the test is significant and there is a linear relationship between the transformed `totalcost` and `ERvisits`, and `ERvisits` is a significant predictor of the transformed `totalcost`. But only 10% of variation of the transformed `totalcost` around its mean can be explained by the model.
- We expect the total cost will increase $\exp(0.23 + 5.54) = \$321$ on average if the number of emergency room (ER) visits increase 1 more time.

e)

Fit a multiple linear regression with `comp_bin` and `ERvisits` as predictors.

Ho: beta_ERvisits = beta_comp_bin = 0

Ha: at lease one beta is not 0

Model: trans_totolcost = beta_0 + beta_ERvisits * ERvisits + beta_comp_bin * comp_bin

```
reg_trans_mlr = lm(trans_totalcost ~ ERvisits + comp_bin, trans_heartdisease_data)
summary(reg_trans_mlr)
```

```
##
## Call:
## lm(formula = trans_totalcost ~ ERvisits + comp_bin, data = trans_heartdisease_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.0741 -1.0737 -0.0181  1.1810  4.3848
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.5211     0.1013  54.495  < 2e-16 ***
## ERvisits      0.2046     0.0237   8.633  < 2e-16 ***
## comp_bin1     1.6859     0.2749   6.132 1.38e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.732 on 782 degrees of freedom
## Multiple R-squared:  0.1437, Adjusted R-squared:  0.1416
## F-statistic: 65.64 on 2 and 782 DF,  p-value: < 2.2e-16
```

I)

Test if `comp_bin` is an effect modifier of the relationship between `totalcost` and `ERvisits`.

Ho: beta_ERvisits = beta_comp_bin = beta_ERvisits&comp_bin = 0

Ha: at lease one beta is not 0

Model: trans_totolcost = beta_0 + beta_ERvisits * ERvisits + beta_comp_bin * comp_bin + beta_ERvisits&comp_bin * ERvisits&comp_bin

```
reg_interaction = lm(trans_totalcost ~ ERvisits + comp_bin + ERvisits * comp_bin, trans_heartdisease_da
summary(reg_interaction)
```

```
##
## Call:
## lm(formula = trans_totalcost ~ ERvisits + comp_bin + ERvisits *
##     comp_bin, data = trans_heartdisease_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.0852 -1.0802 -0.0078  1.1898  4.3803
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         5.49899    0.10349  53.138  < 2e-16 ***
## ERvisits            0.21125    0.02453   8.610  < 2e-16 ***
## comp_bin1           2.17969    0.54604   3.992 7.17e-05 ***
## ERvisits:comp_bin1 -0.09927    0.09483  -1.047    0.296
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.732 on 781 degrees of freedom
## Multiple R-squared:  0.1449, Adjusted R-squared:  0.1417
## F-statistic: 44.13 on 3 and 781 DF,  p-value: < 2.2e-16
```

Comment

Since the p-value of 'ERvisits:comp_bin1' is greater than 0.05, `comp_bin` is not an effect modifier of the relationship between `totalcost` and `ERvisits`

II)

Test if `comp_bin` is a confounder of the relationship between `totalcost` and `ERvisits`.

|beta_ERvisits_slr - beta_ERvisits_mlr| / beta_ERvisits_slr = |0.23 - 0.20| / 0.23 = 0.13, which is greater than 10%, so `comp_bin` is a confounder of the relationship between `totalcost` and `ERvisits`.

III)

Decide if `comp_bin` should be included along with 'ERvisits.

Ho: beta_comp_bin = 0

Ha: beta_comp_bin != 0

```r
anova(reg_trans_slr, reg_trans_mlr)
```

```
## Analysis of Variance Table
##
## Model 1: trans_totalcost ~ ERvisits
## Model 2: trans_totalcost ~ ERvisits + comp_bin
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1    783 2459.8
## 2    782 2347.0  1    112.84 37.598 1.379e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Reason

`comp_bin` should be included along with 'ERvisits because the p-value of the F test is less than 0.05 and it indicates that beta_camp_bin is not equal to 0 and `comp_bin` is significant to predict `totalcost`.

f)

I)

Use the model in part e) and add additional covariates and fit MLR.

Ho: beta_ERvisits = beta_comp_bin = beta_age = beta_gender = beta_duration = 0

Ha: at lease one beta is not 0

Model: trans_totolcost = beta_0 + beta_ERvisits * ERvisits + beta_comp_bin * comp_bin + beta_age * age + beta_gender * gender + beta_duration * duration

```r
full_model = lm(trans_totalcost ~ ERvisits + comp_bin + age + gender + duration, trans_heartdisease_data
summary(full_model)
```

```
##
## Call:
## lm(formula = trans_totalcost ~ ERvisits + comp_bin + age + gender +
##     duration, data = trans_heartdisease_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.0823 -1.0555 -0.1352  0.9533  4.3462
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  6.0449619  0.5063454  11.938  < 2e-16 ***
## ERvisits     0.1757486  0.0223189   7.874 1.15e-14 ***
## comp_bin1    1.4921110  0.2554883   5.840 7.65e-09 ***
## age         -0.0221376  0.0086023  -2.573   0.0103 *
## gender1     -0.1176181  0.1379809  -0.852   0.3942
## duration     0.0055406  0.0004848  11.428  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 1.605 on 779 degrees of freedom
## Multiple R-squared:  0.268,  Adjusted R-squared:  0.2633
## F-statistic: 57.03 on 5 and 779 DF,  p-value: < 2.2e-16
```

Comment

- From the p-value of the F test, we can conclude that the test is significant and there is a linear relationship between the transformed `totalcost` and `ERvisits`, `comp_bin`, `age`, `gender`, `duration`.
- `ERvisits`, `comp_bin`, `age`, and `duration` are significant predictors of the transformed `totalcost`. But `gender` is not significant predictors of the transformed `totalcost`.
- 27% of the variation of the transformed `totalcost` around its mean can be explained by the multiple linear regression model.

II)

Ho: beta_comp_bin = beta_age = beta_gender = beta_duration = 0

Ha: at lease one beta is not 0

```
anova(reg_trans_slr, full_model)
```

```
## Analysis of Variance Table
##
## Model 1: trans_totalcost ~ ERvisits
## Model 2: trans_totalcost ~ ERvisits + comp_bin + age + gender + duration
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1    783 2459.8
## 2    779 2006.5  4     453.3 43.996 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

I should use MLR than SLR because:

- More variation of the transformed `totalcost` around its mean can be explained by the multiple linear regression model.
- Since the p-value of F test is less than 0.05, there is at least one beta not equal to 0 among beta_camp_bin, beta_age, beta_gender, and beta_duration.

Problem 3

```
patsatisfaction_data = readxl::read_excel("./data/PatSatisfaction.xlsx") %>%
  janitor::clean_names()
```

a)

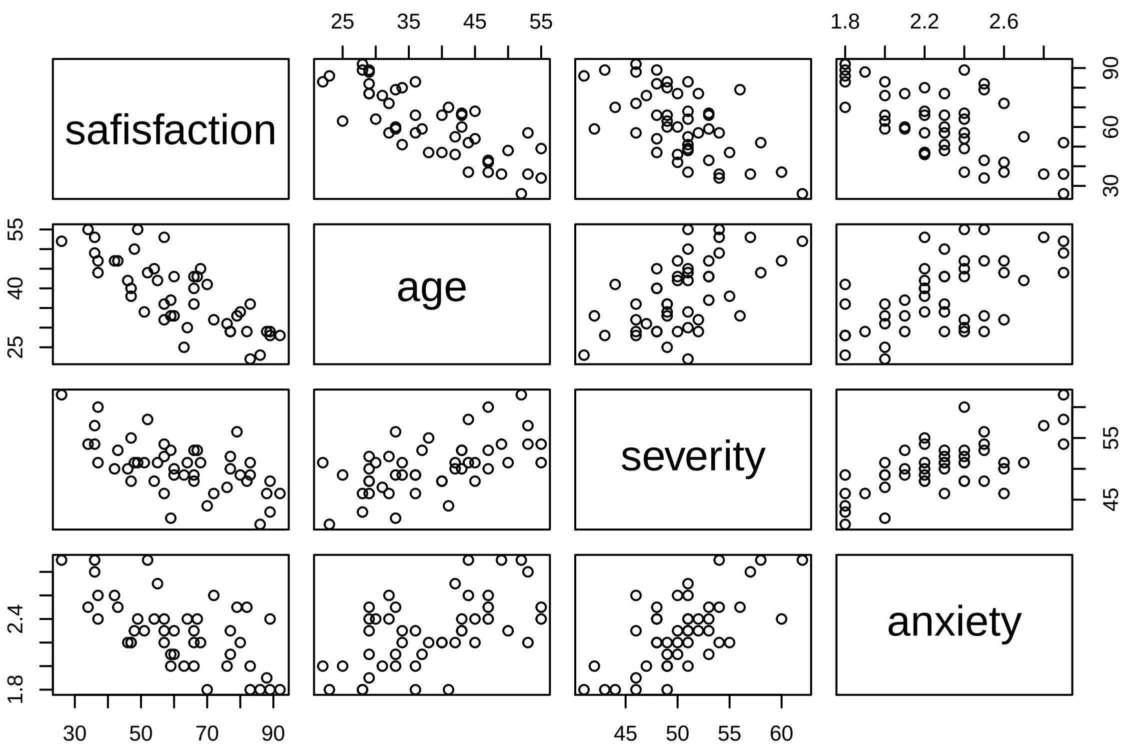
Create a correlation matrix

```
Hmisc::rcorr(as.matrix(patsatisfaction_data))
```

```
##              safisfaction   age severity anxiety
## safisfaction         1.00 -0.79    -0.60   -0.64
## age                 -0.79  1.00     0.57    0.57
```

```
## severity           -0.60  0.57     1.00    0.67
## anxiety            -0.64  0.57     0.67    1.00
##
## n= 46
##
##
## P
##              safisfaction age severity anxiety
## safisfaction              0   0        0
## age           0               0        0
## severity      0           0            0
## anxiety       0           0   0
```

```
pairs(patsatisfaction_data)
```



Initial Findings

- Satisfaction and age have the strong negative association. Satisfication has the moderately strong negative association with both severity and anxiety.
- Anxiety and severity have the moderately strong positive association, we might want to check **collinearity** later.
- Severity and age have the moderately strong positive association, which is the same as the association between anxiety and age.

b)

Fit a multiple regression model and test whether there is a regression relation and test whether there is a regression relation.

Ho: beta_age = beta_severity = beta_anxiety = 0

Ha: at lease one beta is not 0

Model: satification = beta_0 + beta_age * age + beta_severity * severity + beta_anxiety * anxiety

```
reg_mlr = lm(safisfaction ~ age + severity + anxiety, patsatisfaction_data)
summary(reg_mlr)
```

```
##
## Call:
## lm(formula = safisfaction ~ age + severity + anxiety, data = patsatisfaction_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.3524  -6.4230   0.5196   8.3715  17.1601
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 158.4913    18.1259   8.744 5.26e-11 ***
## age          -1.1416     0.2148  -5.315 3.81e-06 ***
## severity     -0.4420     0.4920  -0.898   0.3741
## anxiety     -13.4702     7.0997  -1.897   0.0647 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.06 on 42 degrees of freedom
## Multiple R-squared:  0.6822, Adjusted R-squared:  0.6595
## F-statistic: 30.05 on 3 and 42 DF,  p-value: 1.542e-10
```

State the hypotheses, decision rule and conclusion.

Ho: beta_age = beta_severity = beta_anxiety = 0

Ha: at least one beta is not 0

If the p-value is less than 0.05, we reject Ho and conclude that at least one beta is not 0 and there is a regression relation. If not, we do not reject Ho and conclude that beta_age = beta_severity = beta_anxiety = 0 and there is not a regression relation.

Since p-value is far less than 0.05, we reject Ho and conclude that at least one beta is not 0 and there is a regression relation.

c)

```
confint(reg_mlr, level = 0.95) %>%
  knitr::kable(digits = 1)
```

	2.5 %	97.5 %
(Intercept)	121.9	195.1
age	-1.6	-0.7
severity	-1.4	0.6
anxiety	-27.8	0.9

- The 95% CI for beta_0 is (121.9, 195.1).

- The 95% CI for beta_age is (-1.6, -0.7).
- The 95% CI for beta_severity is (-1.4, 0.6).
- The 95% CI for beta_anxiety is (-27.8, 0.9).

Interpret the coefficient and 95% CI associated with `severity`.

- The coefficient of `severity`: satisfaction will decrease by 0.442 units on average if severity increases by 1 unit adjusting age and anxiety constant.
- We are 95% confident that satisfaction will differ between -1.4 units and 0.6 units on average if severity increases by 1 unit adjusting age and anxiety constant.

d)

Obtain an interval estimate for a new patient's satisfaction when Age = 35, Severity = 42, Anxiety = 2.1.

```
input_data = data.frame(age = 35, severity = 42, anxiety = 2.1)
predict(reg_mlr, input_data, interval = "predict")
```

```
##        fit      lwr      upr
## 1 71.68332 50.06237 93.30426
```

(beta_0 + beta_age * age + beta_severity * severity + beta_anxiety * anxiety) +- t(alpha, n - 2) * sqrt(MSE(1 + 1/n + (xh - xbar)^2 / sum((xi - xbar)^2)))

After pluging in the value, we have 95% prediction CI (50, 93).

Interpret

We are 95% confident that the next new satisfaction observation with age = 35, severity = 42, and anxiety = 2.1 is between 50 and 93.

e)

Test whether `anxiety` can be dropped from the regression model, given the other two covariates are retained.

For linear model:

Ho: beta_age = beta_age = beta_severity = 0

Ha: at least one beta is not 0

Model: safisfaction = beta_0 + beta_age * age + beta_severity * severity

For ANOVA model:

Ho: beta_anxiety = 0

Ha: beta_anxiety != 0

```
reg_mlr_sub = lm(safisfaction ~ age + severity, patsatisfaction_data)
summary(reg_mlr_sub)
```

```
##
## Call:
## lm(formula = safisfaction ~ age + severity, data = patsatisfaction_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.1662  -8.5462  -0.4595   7.1342  17.2364
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 156.6719    18.6396   8.405 1.27e-10 ***
## age          -1.2677     0.2104  -6.026 3.35e-07 ***
## severity     -0.9208     0.4349  -2.117   0.0401 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.36 on 43 degrees of freedom
## Multiple R-squared:  0.655,  Adjusted R-squared:  0.6389
## F-statistic: 40.81 on 2 and 43 DF,  p-value: 1.16e-10
```

```r
anova(reg_mlr_sub, reg_mlr)
```

```
## Analysis of Variance Table
##
## Model 1: safisfaction ~ age + severity
## Model 2: safisfaction ~ age + severity + anxiety
##   Res.Df    RSS Df Sum of Sq      F  Pr(>F)
## 1     43 4613.0
## 2     42 4248.8  1    364.16 3.5997 0.06468 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

State the hypotheses, decision rule and conclusion.

Ho: beta_anxiety = 0

Ha: beta_anxiety != 0

If the p-value is less than 0.05, we reject Ho and conclude that beta_anxiety is not 0 and we can't drop the variable anxiety from the regression model. If not, we do not reject Ho and conclude that beta_anxiety is 0 and we can drop the variable anxiety from the regression model.

Since p-value is greater than 0.05, we don't reject Ho and conclude that beta_anxiety is 0 and we can drop the variable anxiety from the regression model.