HW2 PSTAT131

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```r
library(tidymodels)
```

```
## -- Attaching packages -------------------------------------- tidymodels 0.2.0 --

## v broom        0.7.12     v recipes      0.2.0
## v dials        0.1.1      v rsample      0.1.1
## v dplyr        1.0.8      v tibble       3.1.6
## v ggplot2      3.3.5      v tidyr        1.2.0
## v infer        1.0.0      v tune         0.2.0
## v modeldata    0.1.1      v workflows    0.2.6
## v parsnip      0.2.1      v workflowsets 0.2.1
## v purrr        0.3.4      v yardstick    0.0.9

## -- Conflicts ----------------------------------------- tidymodels_conflicts() --
## x purrr::discard() masks scales::discard()
## x dplyr::filter()  masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## x recipes::step()  masks stats::step()
## * Search for functions across packages at https://www.tidymodels.org/find/
```

```r
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --

## v readr   2.1.2     v forcats 0.5.1
## v stringr 1.4.0

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x readr::col_factor() masks scales::col_factor()
## x purrr::discard()    masks scales::discard()
## x dplyr::filter()     masks stats::filter()
## x stringr::fixed()    masks recipes::fixed()
## x dplyr::lag()        masks stats::lag()
## x readr::spec()       masks yardstick::spec()
```

```r
library(ggplot2)
# useless
abalone <- read.csv("abalone.csv")
head(abalone)
```

```
##   type longest_shell diameter height whole_weight shucked_weight viscera_weight
## 1    M         0.455    0.365  0.095       0.5140         0.2245         0.1010
## 2    M         0.350    0.265  0.090       0.2255         0.0995         0.0485
## 3    F         0.530    0.420  0.135       0.6770         0.2565         0.1415
## 4    M         0.440    0.365  0.125       0.5160         0.2155         0.1140
## 5    I         0.330    0.255  0.080       0.2050         0.0895         0.0395
## 6    I         0.425    0.300  0.095       0.3515         0.1410         0.0775
##   shell_weight rings
## 1        0.150    15
## 2        0.070     7
## 3        0.210     9
## 4        0.155    10
## 5        0.055     7
## 6        0.120     8
```

```
dim(abalone)
```

```
## [1] 4177    9
```

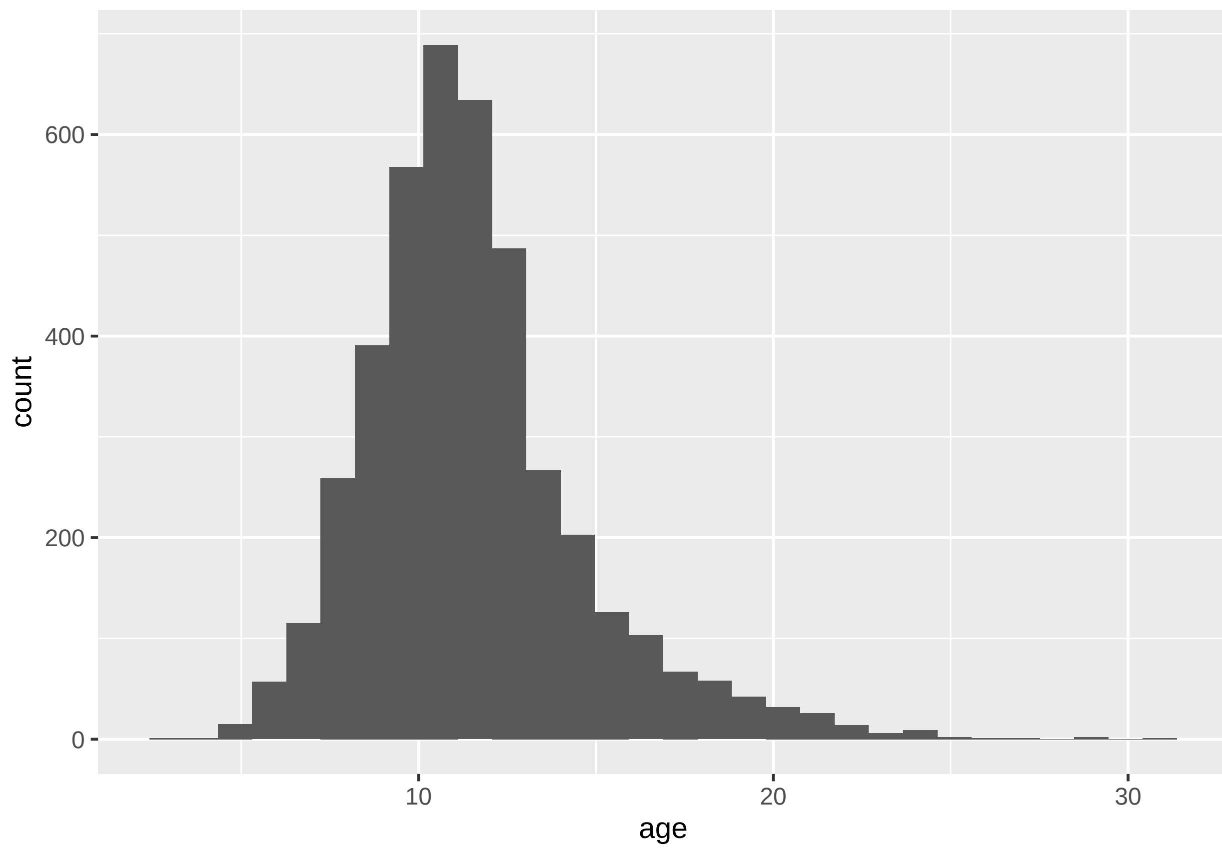
Question 1:

```
abalone<-
  abalone %>%
  mutate(age = rings + 1.5) %>%
  select(age, everything())
head(abalone)
```

```
##    age type longest_shell diameter height whole_weight shucked_weight
## 1 16.5    M         0.455    0.365  0.095       0.5140         0.2245
## 2  8.5    M         0.350    0.265  0.090       0.2255         0.0995
## 3 10.5    F         0.530    0.420  0.135       0.6770         0.2565
## 4 11.5    M         0.440    0.365  0.125       0.5160         0.2155
## 5  8.5    I         0.330    0.255  0.080       0.2050         0.0895
## 6  9.5    I         0.425    0.300  0.095       0.3515         0.1410
##   viscera_weight shell_weight rings
## 1         0.1010        0.150    15
## 2         0.0485        0.070     7
## 3         0.1415        0.210     9
## 4         0.1140        0.155    10
## 5         0.0395        0.055     7
## 6         0.0775        0.120     8
```

```
abalone %>%
  ggplot(aes(x = age)) +
  geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



As the histogram shown above, the distribution of age is approximately normal, with a tail on the right. And most of the abalone has the age around 10 in this data set.

Question 2:

```
set.seed(2216)

abalone_split <- initial_split(abalone, prop = 0.80)
abalone_train <- training(abalone_split)
abalone_test <- testing(abalone_split)
dim(abalone_train)
```

```
## [1] 3341   10
```

```
dim(abalone_test)
```

```
## [1] 836  10
```

Question 3:

```
head(abalone)
```

```
##    age type longest_shell diameter height whole_weight shucked_weight
## 1 16.5    M         0.455    0.365  0.095       0.5140         0.2245
## 2  8.5    M         0.350    0.265  0.090       0.2255         0.0995
## 3 10.5    F         0.530    0.420  0.135       0.6770         0.2565
## 4 11.5    M         0.440    0.365  0.125       0.5160         0.2155
## 5  8.5    I         0.330    0.255  0.080       0.2050         0.0895
## 6  9.5    I         0.425    0.300  0.095       0.3515         0.1410
##   viscera_weight shell_weight rings
## 1         0.1010        0.150    15
## 2         0.0485        0.070     7
## 3         0.1415        0.210     9
## 4         0.1140        0.155    10
## 5         0.0395        0.055     7
## 6         0.0775        0.120     8
```

```
abalone_recipe <-
  recipe(age ~
           type +
           longest_shell +
           diameter + height +
           whole_weight +
           shucked_weight +
           viscera_weight +
           shell_weight,
         data = abalone_train) %>%
  step_dummy(all_nominal_predictors()) %>%
  step_interact(~ starts_with("type"):shucked_weight) %>%
  step_interact(~ longest_shell:diameter) %>%
  step_interact(~ shucked_weight:shell_weight) %>%
  step_normalize()

abalone_recipe
```

```
## Recipe
##
## Inputs:
##
##       role #variables
##    outcome          1
##  predictor          8
##
## Operations:
##
## Dummy variables from all_nominal_predictors()
## Interactions with starts_with("type"):shucked_weight
## Interactions with longest_shell:diameter
## Interactions with shucked_weight:shell_weight
## Centering and scaling for <none>
```

```
# We should not include the predictor "rings",
# because the data of age is directly derived from rings;
# Thus, the training data would be 100% compatible with the testing data on the predictor of "rings"
```

QUestion 4:

```
lm_model <- linear_reg() %>%
  set_engine("lm")

#code is cited from lab2
```

Question 5:

```
lm_wflow <- workflow() %>%
  add_model(lm_model) %>%
  add_recipe(abalone_recipe)


#code is cited from lab2
```

QUestion 6:

```
lm_fit <- fit(lm_wflow, abalone_train)
hypo <- data.frame(type = "F",
                   longest_shell = 0.50,
                   diameter = 0.10,
                   height = 0.30,
                   whole_weight = 4,
                   shucked_weight = 1,
                   viscera_weight = 2,
                   shell_weight = 1)

# use predict() to predict the age of the hypothetical age of abalone:
predict(lm_fit,new_data = hypo)
```

```
## # A tibble: 1 x 1
##   .pred
##   <dbl>
## 1  23.4
```

QUestion 7:

```
abalone_train_res <- predict(lm_fit, new_data = abalone_train %>% select(-age))
abalone_train_res %>%
  head()
```

```
## # A tibble: 6 x 1
##   .pred
##   <dbl>
```

```
## 1 12.6
## 2  9.27
## 3 13.2
## 4 12.6
## 5 13.0
## 6 11.6
```

```r
abalone_train_res <- bind_cols(abalone_train_res, abalone_train %>% select(age))
abalone_train_res %>%
  head()
```

```
## # A tibble: 6 x 2
##   .pred   age
##   <dbl> <dbl>
## 1 12.6   11.5
## 2  9.27   9.5
## 3 13.2   12.5
## 4 12.6   12.5
## 5 13.0   13.5
## 6 11.6    9.5
```

```r
abalone_metrics <- metric_set(rmse, rsq, mae)
abalone_metrics(abalone_train_res, truth = age,
                estimate = .pred)
```

```
## # A tibble: 3 x 3
##   .metric .estimator .estimate
##   <chr>   <chr>          <dbl>
## 1 rmse    standard       2.13
## 2 rsq     standard       0.566
## 3 mae     standard       1.53
```

R-Squared means the proportion of the variance for a dependent variable that's explained by an independent variable or variables in a regression model.(cited from https://www.investopedia.com/terms/r/r-squared.asp)
Therefore, since the value of R-squared is 0.5639424, this means that 56.39424% of the response variable can be explained by predictor variables.