# 131 Homework2

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Question1

```
library("tidyverse")
```

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

## v ggplot2 3.3.5     v purrr   0.3.4
## v tibble  3.1.6     v dplyr   1.0.8
## v tidyr   1.2.0     v stringr 1.4.0
## v readr   2.1.2     v forcats 0.5.1

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library("tidymodels")
```

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

## v broom        0.7.12     v rsample      0.1.1
## v dials        0.1.1      v tune         0.2.0
## v infer        1.0.0      v workflows    0.2.6
## v modeldata    0.1.1      v workflowsets 0.2.1
## v parsnip      0.2.1      v yardstick    0.0.9
## v recipes      0.2.0

## -- Conflicts ------------------------------------------ tidymodels_conflicts() --
## x scales::discard() masks purrr::discard()
## x dplyr::filter()   masks stats::filter()
## x recipes::fixed()  masks stringr::fixed()
## x dplyr::lag()      masks stats::lag()
## x yardstick::spec() masks readr::spec()
## x recipes::step()   masks stats::step()
## * Learn how to get started at https://www.tidymodels.org/start/
```

```
abalone=read_csv('abalone.csv')
```

```
## Rows: 4177 Columns: 9
```

```
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (1): type
## dbl (8): longest_shell, diameter, height, whole_weight, shucked_weight, visc...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

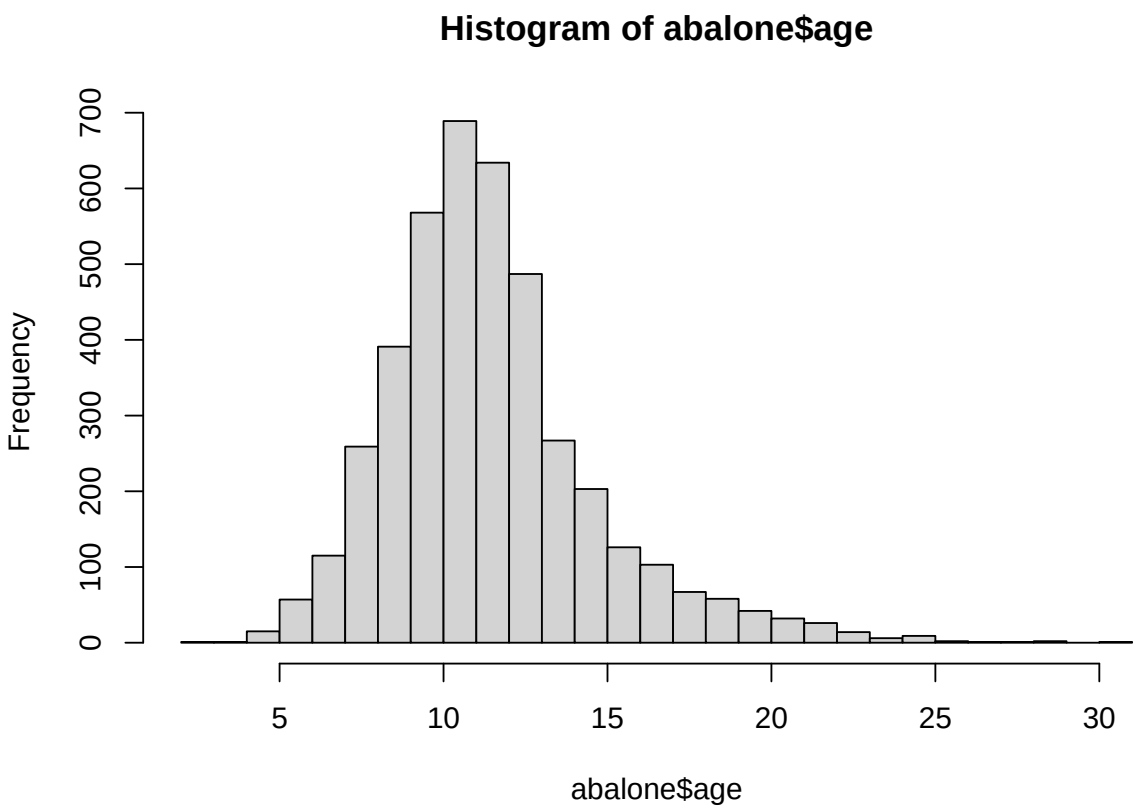
```
head(abalone)
```

```
## # A tibble: 6 x 9
##   type  longest_shell diameter height whole_weight shucked_weight viscera_weight
##   <chr>         <dbl>    <dbl>  <dbl>        <dbl>          <dbl>          <dbl>
## 1 M             0.455    0.365  0.095        0.514         0.224          0.101
## 2 M             0.35     0.265  0.09         0.226         0.0995         0.0485
## 3 F             0.53     0.42   0.135        0.677         0.256          0.142
## 4 M             0.44     0.365  0.125        0.516         0.216          0.114
## 5 I             0.33     0.255  0.08         0.205         0.0895         0.0395
## 6 I             0.425    0.3    0.095        0.352         0.141          0.0775
## # ... with 2 more variables: shell_weight <dbl>, rings <dbl>
```

```
abalone$age=abalone$rings+1.5
head(abalone)
```

```
## # A tibble: 6 x 10
##   type  longest_shell diameter height whole_weight shucked_weight viscera_weight
##   <chr>         <dbl>    <dbl>  <dbl>        <dbl>          <dbl>          <dbl>
## 1 M             0.455    0.365  0.095        0.514         0.224          0.101
## 2 M             0.35     0.265  0.09         0.226         0.0995         0.0485
## 3 F             0.53     0.42   0.135        0.677         0.256          0.142
## 4 M             0.44     0.365  0.125        0.516         0.216          0.114
## 5 I             0.33     0.255  0.08         0.205         0.0895         0.0395
## 6 I             0.425    0.3    0.095        0.352         0.141          0.0775
## # ... with 3 more variables: shell_weight <dbl>, rings <dbl>, age <dbl>
```

```
hist(abalone$age,breaks=20)
```




```
summary(abalone$age)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##     2.5     9.5    10.5    11.4    12.5    30.5
```

From the histogram above, we notice that the distribution of age is partially normal distributed, but slightly skewed to the right, with minimum 2.5, maximum 30.5, and mean 11.4.

Question2

```
set.seed(1234)
ab_split=initial_split(abalone,prop=0.80,strata=age)
ab_train=training(ab_split)
ab_test=testing(ab_split)
```

Question3

```
ab_recipe=recipe(age~type+longest_shell+diameter+height+whole_weight+shucked_weight+viscera_weight+shel
  step_dummy(all_nominal_predictors())%>%
  step_interact(terms=~type_I:shucked_weight+type_M:shucked_weight+longest_shell:diameter+shucked_weigh
  step_normalize(all_predictors())
```

We shouldn't use rings to predict age because age is depends on age, so we won't have the relation between age and other predictors.

Question4

```
lm_model=linear_reg()%>%
  set_engine("lm")
```

Question5

```
lm_wflow=workflow() %>%
  add_model(lm_model) %>%
  add_recipe(ab_recipe)
```

Question6

```
lm_fit=fit(lm_wflow,ab_train)

ab_test=data.frame("type"="F","longest_shell" = 0.50, "diameter" = 0.10, "height" = 0.30, "whole_weight

predict(lm_fit,new_data=ab_test)
```

```
## # A tibble: 1 x 1
##   .pred
##   <dbl>
## 1  23.5
```

Question7

```
ab_metric=metric_set(rsq,rmse,mae)
ab_pred=predict(lm_fit,new_data=ab_train%>%select(-age))
ab_pred=bind_cols(ab_pred,ab_train%>%select(age))
ab_pred
```

```
## # A tibble: 3,340 x 2
##    .pred   age
##    <dbl> <dbl>
##  1  9.33   9.5
##  2  9.83   8.5
##  3 10.1    9.5
##  4  6.32   6.5
##  5  5.82   6.5
##  6  5.95   5.5
##  7  8.56   8.5
##  8  7.72   7.5
##  9 10.2    8.5
## 10 12.7    9.5
## # ... with 3,330 more rows
```

```
ab_metric(ab_pred,truth=age,estimate=.pred)
```

```
## # A tibble: 3 x 3
##   .metric .estimator .estimate
##   <chr>   <chr>          <dbl>
## 1 rsq     standard       0.558
## 2 rmse    standard       2.15
## 3 mae     standard       1.55
```

The R-squared value we got is 0.55. It's a measure of how much variation of the response variable is explained by the predictors. In this case, we found that our model is not that good.