PSTAT131HW4

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Resampling

For this assignment, we will continue working with part of a Kaggle data set that was the subject of a machine learning competition and is often used for practicing ML models. The goal is classification; specifically, to predict which passengers would survive the Titanic shipwreck.

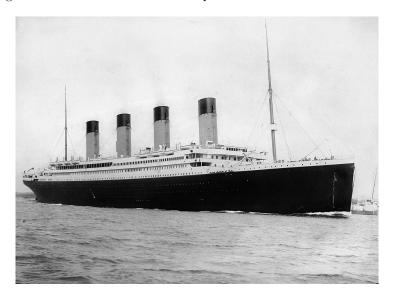


Figure 1: Fig. 1: RMS Titanic departing Southampton on April 10, 1912.

Load the data from $\mathtt{data/titanic.csv}$ into R and familiarize yourself with the variables it contains using the codebook $\mathtt{(data/titanic_codebook.txt)}$.

Notice that survived and pclass should be changed to factors. When changing survived to a factor, you may want to reorder the factor so that "Yes" is the first level.

Make sure you load the tidyverse and tidymodels!

Remember that you'll need to set a seed at the beginning of the document to reproduce your results.

Create a recipe for this dataset identical to the recipe you used in Homework 3.

Loading Packages

```
library(tidymodels)
library(tidyverse)
library(dplyr)
library(corrr)
library(klaR)
library(MASS)
library(discrim)
library(poissonreg)

tidymodels_prefer()

titanic <- read_csv("data/titanic.csv")
titanic$survived <- factor(titanic$survived)
titanic$survived <- relevel(titanic$survived, "Yes")
titanic$pclass <- factor(titanic$pclass)
head(titanic)</pre>
```

```
## # A tibble: 6 x 12
    passenger_id survived pclass name sex
                                            age sib_sp parch ticket fare cabin
##
          <dbl> <fct>
                        <fct> <chr> <dbl> <dbl> <dbl> <chr> <dbl> <chr>
## 1
              1 No
                         3
                               Brau~ male
                                             22
                                                    1
                                                          0 A/5 2~ 7.25 <NA>
## 2
              2 Yes
                              Cumi~ fema~
                                             38
                                                    1
                                                          0 PC 17~ 71.3 C85
                        1
## 3
              3 Yes
                        3
                             Heik~ fema~
                                             26
                                                    0
                                                          0 STON/~ 7.92 <NA>
## 4
              4 Yes
                        1
                              Futr~ fema~
                                             35
                                                    1
                                                          0 113803 53.1 C123
## 5
              5 No
                         3
                               Alle~ male
                                             35
                                                    0
                                                          0 373450 8.05 <NA>
## 6
              6 No
                        3
                              Mora~ male
                                             NA
                                                    0
                                                          0 330877 8.46 <NA>
## # ... with 1 more variable: embarked <chr>
```

Question 1

Split the data, stratifying on the outcome variable, survived. You should choose the proportions to split the data into. Verify that the training and testing data sets have the appropriate number of observations.

```
titanic_split <- initial_split(titanic, prop = 0.7, strata = survived)

# The training data sets can be materialized using the training() functions
titanic_train <- training(titanic_split)

# The testing data sets can be materialized using the testing() functions
titanic_test <- testing(titanic_split)

# use dim() to verify that the correct number of observations are now in each data set
dim(titanic_train)</pre>
```

```
## [1] 623 12
```

```
dim(titanic_test)
## [1] 268 12
Question 2
Fold the training data. Use k-fold cross-validation, with k = 10.
poly_tuned_rec <-</pre>
  recipe(survived ~ pclass+sex+age+sib_sp+parch+fare, data = titanic_train) %>%
  step_impute_linear(age) %>%
  step_dummy(all_nominal_predictors()) %>%
  step_interact(~ starts_with("sex"):fare + age:fare)
poly_tuned_rec
## Recipe
##
## Inputs:
##
##
         role #variables
##
      outcome
##
   predictor
## Operations:
##
## Linear regression imputation for age
```

```
lm_spec <- linear_reg() %>%
  set_mode("regression") %>%
  set_engine("lm")

poly_tuned_wf <- workflow() %>%
  add_recipe(poly_tuned_rec) %>%
  add_model(lm_spec)

Auto_folds <- vfold_cv(titanic_train, v = 10)
Auto_folds</pre>
```

```
## # 10-fold cross-validation
## # A tibble: 10 x 2
## splits id
## tist> chr>
## 1 <split [560/63]> Fold01
## 2 <split [560/63]> Fold02
## 3 <split [560/63]> Fold03
## 4 <split [561/62]> Fold04
## 5 <split [561/62]> Fold05
## 6 <split [561/62]> Fold06
```

Dummy variables from all_nominal_predictors()

Interactions with starts_with("sex"):fare + age:fare

```
## 7 <split [561/62]> Fold07
## 8 <split [561/62]> Fold08
## 9 <split [561/62]> Fold09
## 10 <split [561/62]> Fold10
```

Question 3

In your own words, explain what we are doing in Question 2. What is k-fold cross-validation? Why should we use it, rather than simply fitting and testing models on the entire training set? If we **did** use the entire training set, what resampling method would that be?

In order to solve the shortcomings of simple cross-validation, I think we need use k-fold cross-validation. Divide the dataset into different k segments, select one segment as the validation set in each cycle of k times, and use all the remaining segments as the training set. It may be less computationally-expensive than other procedures, can be useful if we have limited data. Randomly initialize the weights to train the model.

Question 4

Set up workflows for 3 models:

- 1. A logistic regression with the glm engine;
- 2. A linear discriminant analysis with the MASS engine;
- 3. A quadratic discriminant analysis with the MASS engine.

How many models, total, across all folds, will you be fitting to the data? To answer, think about how many folds there are, and how many models you'll fit to each fold.

```
log_reg <- logistic_reg() %>%
  set_engine("glm") %>%
  set_mode("classification")
log_workflow <- workflow() %>%
  add_model(log_reg) %>%
  add_recipe(poly_tuned_rec)
lda_mod <- discrim_linear() %>%
  set_mode("classification") %>%
  set_engine("MASS")
lda_workflow <- workflow() %>%
  add_model(lda_mod) %>%
  add_recipe(poly_tuned_rec)
qda_mod <- discrim_quad() %>%
  set_mode("classification") %>%
  set_engine("MASS")
qda workflow <- workflow() %>%
  add_model(qda_mod) %>%
  add_recipe(poly_tuned_rec)
```

There are a total of 30 models, 10 for each engine, corresponding to 10-fold. For each of the 10 folds, we will be fitting the 3 models to the 9 other folds combined as training data. Ends up as 30 models fitted.

Question 5

Fit each of the models created in Question 4 to the folded data.

IMPORTANT: Some models may take a while to run – anywhere from 3 to 10 minutes. You should NOT re-run these models each time you knit. Instead, run them once, using an R script, and store your results; look into the use of loading and saving. You should still include the code to run them when you knit, but set **eval** = FALSE in the code chunks.

```
log_fit <- log_workflow %>%
  fit_resamples(resamples = Auto_folds)

lda_fit <- lda_workflow %>%
  fit_resamples(resamples = Auto_folds)

qda_fit <- qda_workflow %>%
  fit_resamples(resamples = Auto_folds)
```

Question 6

Use collect_metrics() to print the mean and standard errors of the performance metric accuracy across all folds for each of the four models.

Decide which of the 3 fitted models has performed the best. Explain why. (Note: You should consider both the mean accuracy and its standard error.)

```
collect_metrics(log_fit)
```

The logistic regression has an accuracy of 0.824 and a standard error of 0.0157.

```
collect_metrics(lda_fit)
```

The logistic regression has an accuracy of 0.804 and a standard error of 0.0192.

```
collect_metrics(qda_fit)
```

The logistic regression has an accuracy of 0.766 and a standard error of 0.0209.

So, the logistic regression model performed the best because it had the highest accuracy and smallest standard error.

Question 7

Now that you've chosen a model, fit your chosen model to the entire training dataset (not to the folds).

```
final_fit <- fit(log_workflow, titanic_train)
final_fit</pre>
```

```
## Preprocessor: Recipe
## Model: logistic_reg()
##
## -- Preprocessor ------
## 3 Recipe Steps
##
## * step_impute_linear()
## * step_dummy()
## * step_interact()
## -- Model -----
##
## Call: stats::glm(formula = ..y ~ ., family = stats::binomial, data = data)
##
## Coefficients:
##
     (Intercept)
                                   sib\_sp
                                                 parch
                        age
##
      -4.479635
                    0.065303
                                 0.591529
                                              0.131192
##
                                 pclass_X3
                                              sex_male
                   pclass_X2
          fare
##
      -0.007895
                    0.932520
                                 2.216490
                                              2.530135
## sex_male_x_fare
                   fare_x_age
##
       0.014305
                   -0.000260
##
## Degrees of Freedom: 622 Total (i.e. Null); 613 Residual
## Null Deviance:
                  829.6
## Residual Deviance: 522.8
                        AIC: 542.8
```

Question 8

Finally, with your fitted model, use predict(), bind_cols(), and accuracy() to assess your model's performance on the testing data!

Compare your model's testing accuracy to its average accuracy across folds. Describe what you see.

```
predict(final_fit, new_data = titanic_test) %>% bind_cols(titanic_test%>% dplyr::select(survived)) %>%
```

we can be seen that the logistic regression model is better than the test set. does not have very high variance nor bias.	Using the k-fold cross validation