131-hw-3

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Q1

We want to use stratified sampling since the number of people who did or did not survive is uneven.

```
# set seed
set.seed(266)

# changing survived and pclass to factors
titanic$survived = factor(titanic$survived, levels = c('Yes','No'))
titanic$pclass = factor(titanic$pclass)
titanic$sex = factor(titanic$sex)

# split data, stratifying on survived
titanic_split <- initial_split(titanic, prop = 0.80, strata = survived)
titanic_train <- training(titanic_split)
titanic_test <- testing(titanic_split)

# checking missing values
sum(is.na(titanic_train))
```

```
## [1] 691
```

Our training set has 712 observations:

```
dim(titanic_train)
```

```
## [1] 712  12
```

Our test dataset has 179 observations:

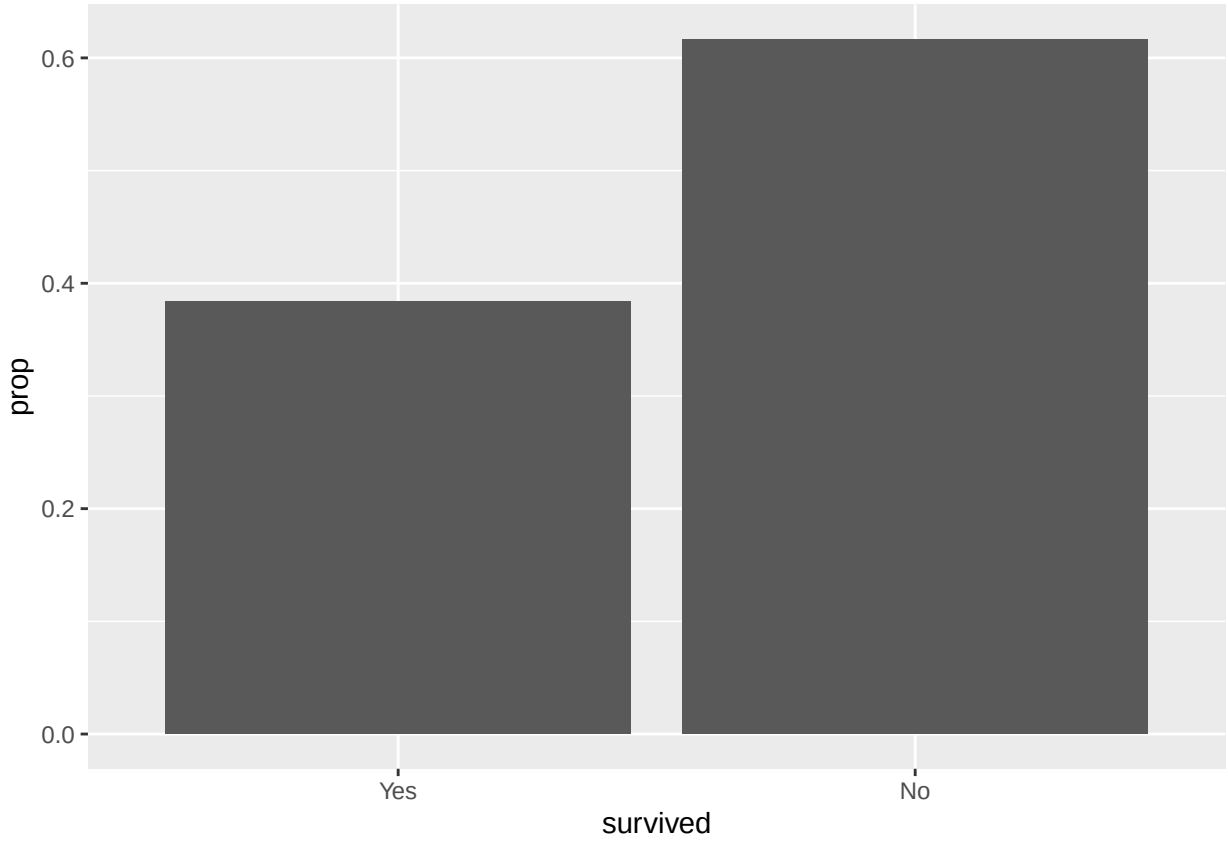
```
# get test dimensions
dim(titanic_test)
```

```
## [1] 179  12
```

Q2

Roughly 60% of passengers did not survivee.

```r
# plot of how many survived
titanic_train %>%
  ggplot(aes(x = survived)) +
  geom_bar(aes(y = ..prop.., group = 1))
```



Q3

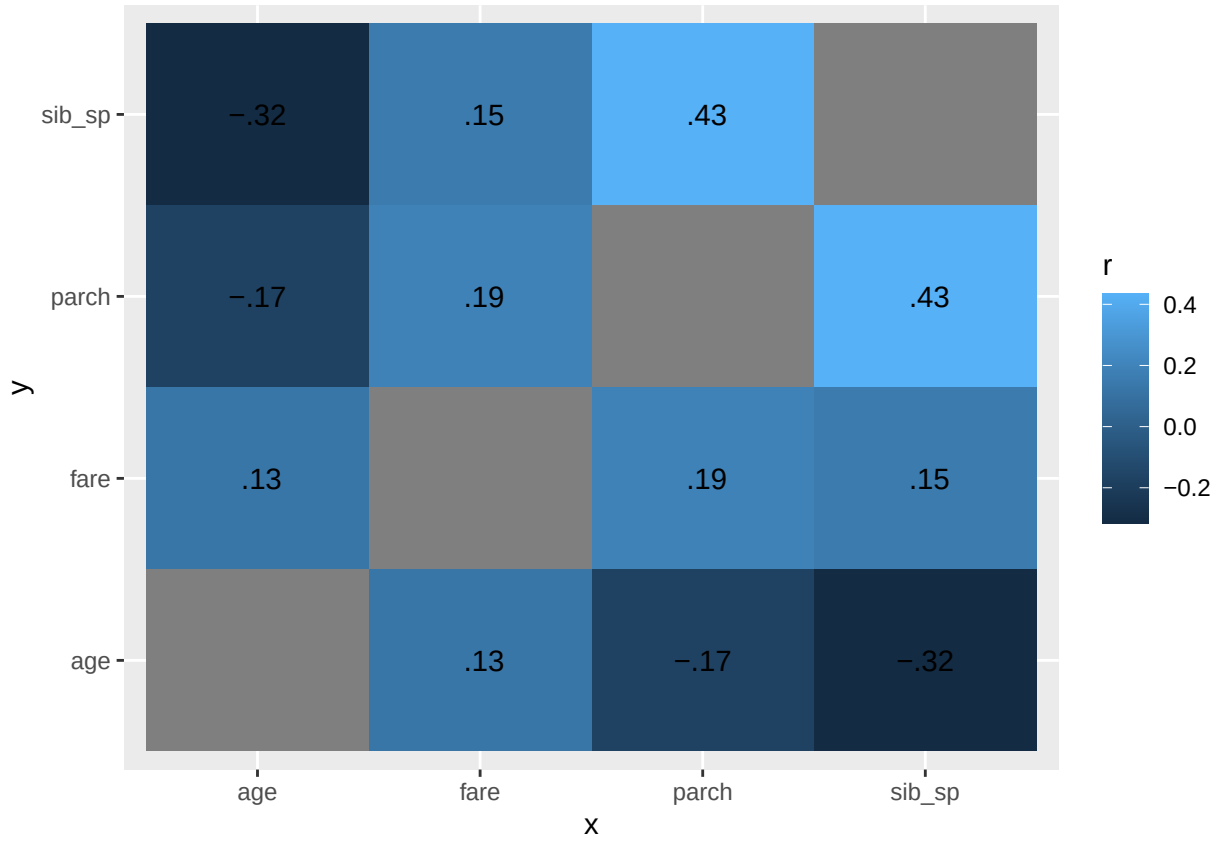
At most, there are weak to low correlations both positive and negative between the variables. Passenger id was removed because, despite being numeric, it is not meaningfully quantitative.

The strongest two correlations are 1) a low positive correlation between the number of siblings/spouses and the number of parents/children aboard and 2) a low negative correlation between number of siblings/spouses and age.

```r
# calculate corr matrix
cor_plot <- titanic_train %>%
  dplyr::select(-c(survived, pclass, name, sex, cabin, ticket, embarked, passenger_id)) %>%
  correlate(use = "pairwise.complete.obs", method = "pearson")
```

```
##
## Correlation method: 'pearson'
## Missing treated using: 'pairwise.complete.obs'
```

```
# visualize
cor_plot %>%
  stretch() %>%
  ggplot(aes(x, y, fill = r)) +
  geom_tile() +
  geom_text(aes(label = as.character(fashion(r))))
```



Q4

```
# creating a recipe predicting survived using training data
titanic_recipe <- recipe(survived ~ pclass + sex + age + sib_sp + parch + fare, data = titanic_train) %
  step_impute_linear(age) %>%
  step_dummy(all_nominal_predictors()) %>%
  step_interact(terms = ~ sex_male : fare) %>%
  step_interact(terms = ~ age : fare)

titanic_recipe
```

```
## Recipe
##
## Inputs:
##
```

```
##       role #variables
##    outcome          1
##  predictor          6
##
## Operations:
##
## Linear regression imputation for age
## Dummy variables from all_nominal_predictors()
## Interactions with sex_male:fare
## Interactions with age:fare
```

Q5

```
# specify model type and engine
log_reg <- logistic_reg() %>%
  set_engine('glm') %>%
  set_mode('classification')

# set up workflow
log_wkflow <- workflow() %>%
  add_model(log_reg) %>%
  add_recipe(titanic_recipe)

# fit model to training data
log_fit <- fit(log_wkflow, titanic_train)
```

Q6

```
# specify lda
lda_mod <- discrim_linear() %>%
  set_mode("classification") %>%
  set_engine("MASS")

# set lda workflow
lda_wkflow <- workflow() %>%
  add_model(lda_mod) %>%
  add_recipe(titanic_recipe)

# fit lda
lda_fit <- fit(lda_wkflow, titanic_train)
```

Q7

```
qda_mod <- discrim_quad() %>%
  set_mode("classification") %>%
  set_engine("MASS")
```

```
qda_wkflow <- workflow() %>%
  add_model(qda_mod) %>%
  add_recipe(titanic_recipe)

qda_fit <- fit(qda_wkflow, titanic_train)
```

Q8

```
nb_mod <- naive_Bayes() %>%
  set_mode("classification") %>%
  set_engine("klaR") %>%
  set_args(usekernel = FALSE)

nb_wkflow <- workflow() %>%
  add_model(nb_mod) %>%
  add_recipe(titanic_recipe)

nb_fit <- fit(nb_wkflow, titanic_train)
```

Q9

The logistic regression model performed the best on the training data.

```
pred_models = bind_cols(predict(log_fit, titanic_test),
                    predict(lda_fit, titanic_test),
                    predict(qda_fit, titanic_test),
                    predict(nb_fit, titanic_test))
colnames(pred_models) = c("log_pred","lda_pred","qda_pred", "nb_fit")

# calculate accuracies
log_reg_acc <- augment(log_fit, new_data = titanic_train) %>%
  accuracy(truth = survived, estimate = .pred_class)

lda_acc <- augment(lda_fit, new_data = titanic_train) %>%
  accuracy(truth = survived, estimate = .pred_class)

qda_acc <- augment(qda_fit, new_data = titanic_train) %>%
  accuracy(truth = survived, estimate = .pred_class)

nb_acc <- augment(nb_fit, new_data = titanic_train) %>%
  accuracy(truth = survived, estimate = .pred_class)

accuracies <- c(log_reg_acc$.estimate, lda_acc$.estimate,
                nb_acc$.estimate, qda_acc$.estimate)
models <- c("Logistic Regression", "LDA", "Naive Bayes", "QDA")
results <- tibble(accuracies = accuracies, models = models)
results %>%
  arrange(-accuracies)
```

```
## # A tibble: 4 x 2
##   accuracies models
##        <dbl> <chr>
## 1      0.819 Logistic Regression
## 2      0.805 LDA
## 3      0.794 QDA
## 4      0.770 Naive Bayes
```

Q10

The accuracy for the logistic regression was 0.8188 versus .8044 for the logistic regression. These values are quite close, so it seems our model is doing a good job of not overfitting.

Accuracy of testing data:

```
# fit
bind_cols(predict(log_fit, new_data = titanic_test), titanic_test %>% dplyr::select(survived))
```

```
## # A tibble: 179 x 2
##    .pred_class survived
##    <fct>       <fct>
##  1 Yes         Yes
##  2 Yes         Yes
##  3 No          No
##  4 Yes         Yes
##  5 No          No
##  6 No          No
##  7 No          No
##  8 No          No
##  9 No          No
## 10 Yes         No
## # ... with 169 more rows
```

```
# get accuracy
bind_cols(predict(log_fit, new_data = titanic_test), titanic_test %>% dplyr::select(survived)) %>% accu
```

```
## # A tibble: 1 x 3
##   .metric  .estimator .estimate
##   <chr>    <chr>          <dbl>
## 1 accuracy binary         0.804
```

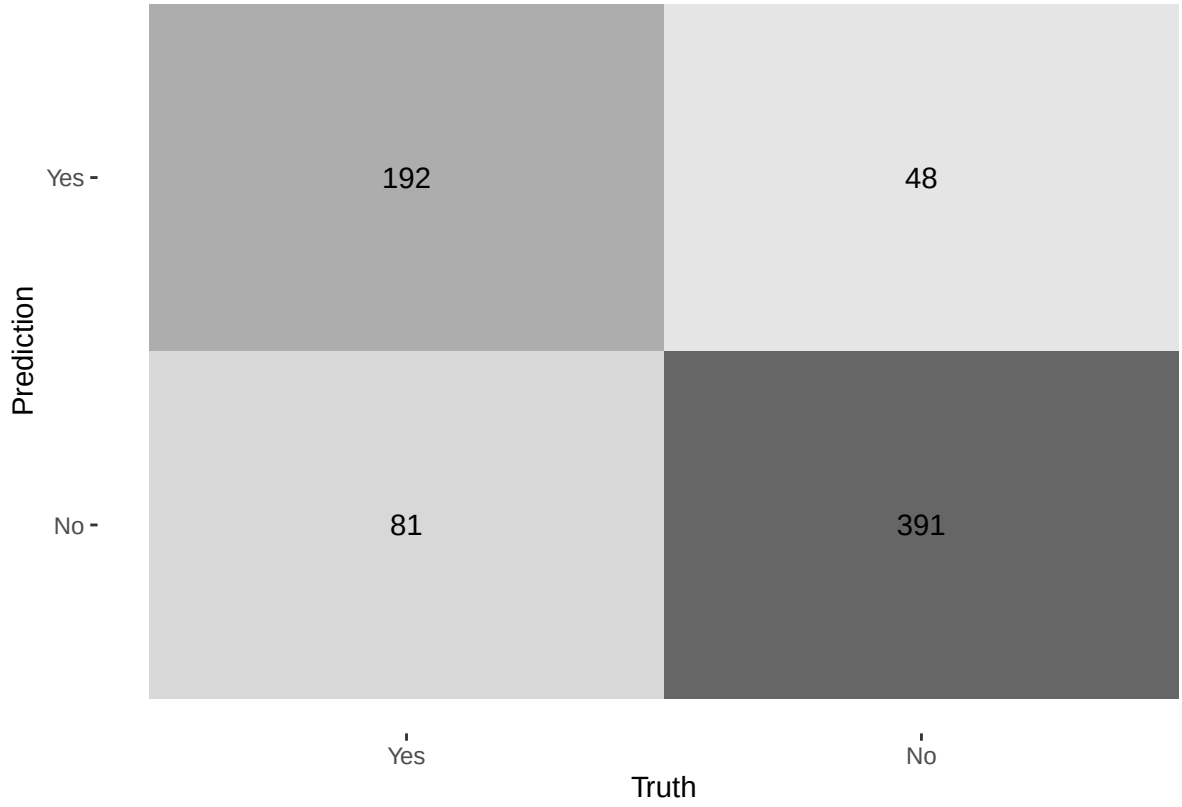
Confusion matrix heatmap:

```
predict(log_fit, titanic_test)
```

```
## # A tibble: 179 x 1
##    .pred_class
##    <fct>
##  1 Yes
##  2 Yes
##  3 No
```

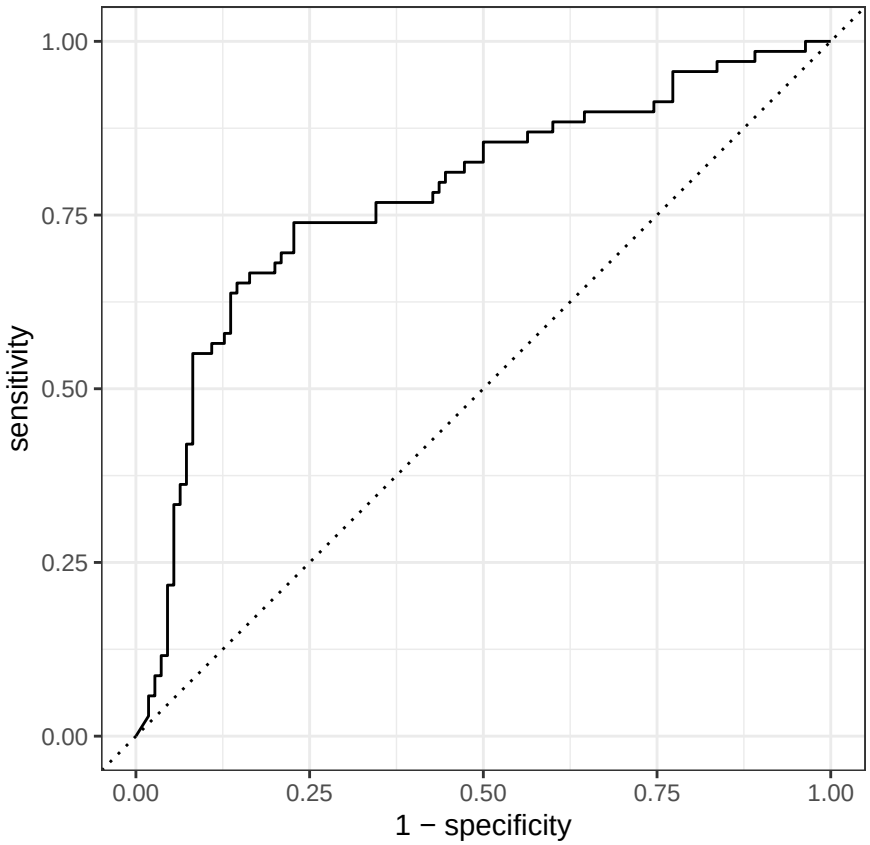
```
##  4 Yes
##  5 No
##  6 No
##  7 No
##  8 No
##  9 No
## 10 Yes
## # ... with 169 more rows
```

```
# visual representation of confusion matrix
augment(log_fit, new_data = titanic_train) %>%
  conf_mat(truth = survived, estimate = .pred_class) %>%
  autoplot(type = "heatmap")
```



ROC plot:

```
augment(nb_fit, new_data = titanic_test) %>%
  roc_curve(survived, .pred_Yes) %>%
  autoplot()
```



The AUC is 0.7781:

```
augment(nb_fit, new_data = titanic_test) %>%
  roc(survived, .pred_Yes)
```

```
##
## Call:
## roc.data.frame(data = ., response = survived, predictor = .pred_Yes)
##
## Data: .pred_Yes in 69 controls (survived Yes) > 110 cases (survived No).
## Area under the curve: 0.7781
```