PSTAT231 HW5 Cheng Ye

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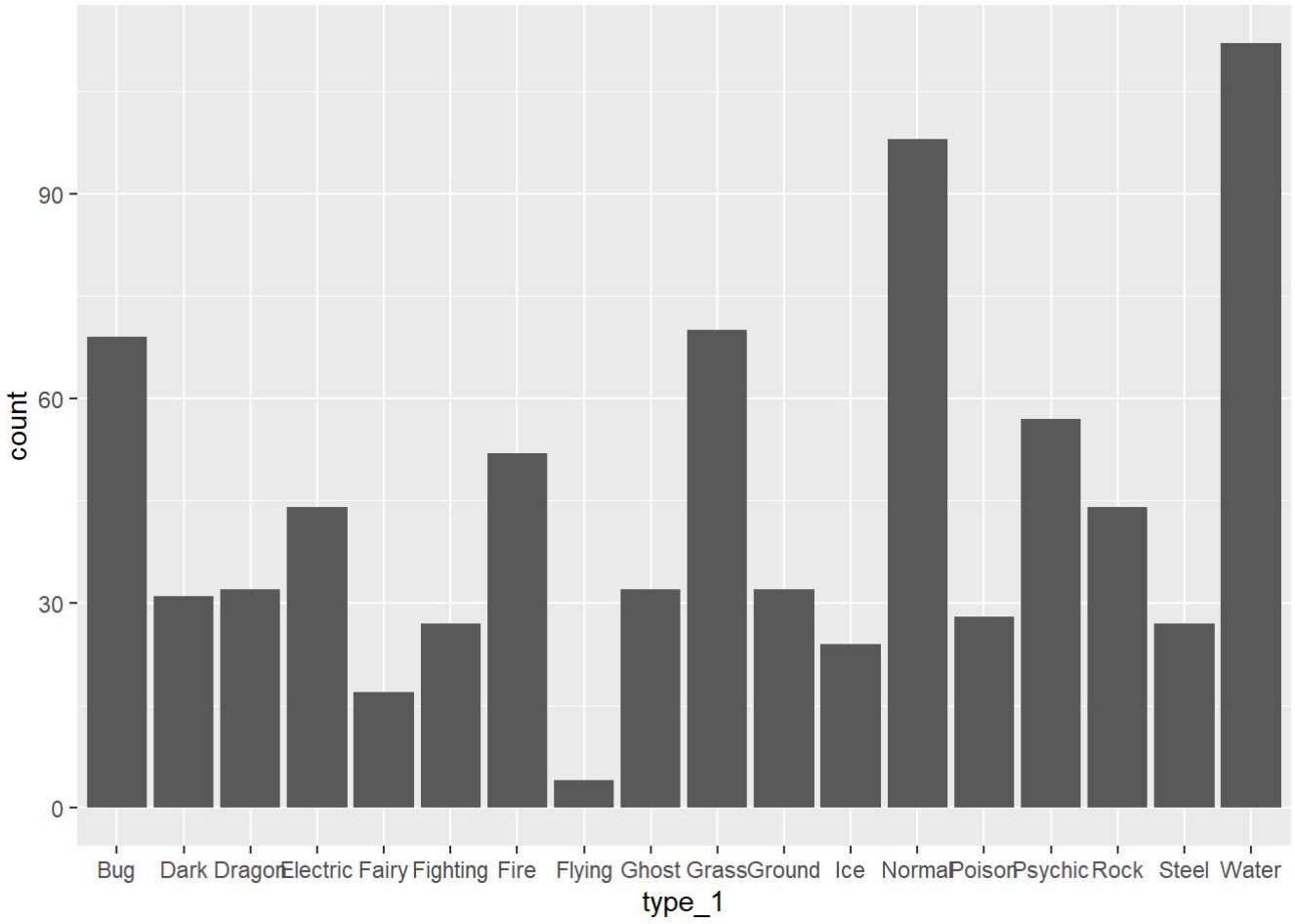
#Question 1

```
Pokemon_origin <- read.csv("C:/Cheng Ye/UCSB/PSTAT 231/HW/homework-5/homework-5/data/pokemon.csv")
#Pokemon_origin
Pokemon <- clean_names(Pokemon_origin)
#Pokemon

## From the description. By using clean_names(), the resulting column names are change to a format that only consist of the underscore, numbers, and letters. It is useful as in it makes calling variables easier and gets rid of unreadable characters.
```

#Question 2

```
Pokemon_plot <- ggplot(data=Pokemon, aes(x=type_1)) +
     geom_bar(stat = "count")
Pokemon_plot
```



```
Pokemon <- Pokemon[Pokemon$type_1 %in% c('Bug', 'Fire', 'Grass', 'Normal', 'Water', 'Psychic'),
 ]
Pokemon$type_1 = factor(Pokemon$type_1)
Pokemon$legendary = factor(Pokemon$legendary)
Pokemon$generation = factor(Pokemon$generation)

##There are 18 classes of outcome. There are very few pokemons belonging to the flying type.
```

#Question 3

```
set.seed(231)
Pokemon_split<-initial_split(Pokemon,strata = type_1,prop = 0.8)

Pokemon_train<-training(Pokemon_split)
Pokemon_test<-testing(Pokemon_split)
dim(Pokemon_train)
```

```
## [1] 364  13
```

```
dim(Pokemon_test)
```

```
## [1] 94 13
```

```
#From the results we could observe that the training and testing data sets have desired number o
f observations

#K-fold Cross Validation
Pokemon_folds<-vfold_cv(Pokemon_train, v = 5, strata = type_1)
#Stratifying the folds could be useful because it keeps the distribution, aka the proportion of
 variable types in each fold to be the same so that it is easier for us to analyze and avoid ove
rfitting.
```

#Question 4

```
Pokemon_recipe <-
  recipe(formula = type_1 ~ legendary + generation + sp_atk + attack + speed + defense + hp + sp
_def, data = Pokemon_train) %>%
  step_dummy(c('legendary', 'generation')) %>%
  step_normalize(all_predictors())
Pokemon_recipe %>%
  prep() %>%
  juice()
```

```
## # A tibble: 364 x 13
##    sp_atk attack   speed defense      hp sp_def type_1 legenda~1 gener~2 gener~3
##     <dbl>  <dbl>   <dbl>   <dbl>   <dbl>  <dbl> <fct>      <dbl>   <dbl>   <dbl>
##  1 -1.63  -1.36  -0.821   -1.15  -0.866  -1.75  Bug       -0.247  -0.417  -0.513
##  2 -1.48  -1.67  -1.34    -0.444 -0.690  -1.58  Bug       -0.247  -0.417  -0.513
##  3  0.565 -0.889  0.0367  -0.622 -0.338   0.353 Bug       -0.247  -0.417  -0.513
##  4 -1.63  -1.20  -0.650   -1.33  -1.04   -1.75  Bug       -0.247  -0.417  -0.513
##  5 -1.48  -1.52  -1.16    -0.622 -0.866  -1.58  Bug       -0.247  -0.417  -0.513
##  6 -0.848  0.524  0.208   -0.976 -0.162   0.353 Bug       -0.247  -0.417  -0.513
##  7 -1.79   2.41   2.61    -0.976 -0.162   0.353 Bug       -0.247  -0.417  -0.513
##  8 -0.848 -0.104 -1.51    -0.444 -1.22   -0.524 Bug       -0.247  -0.417  -0.513
##  9  0.565 -0.261  0.723   -0.267  0.0140  0.177 Bug       -0.247  -0.417  -0.513
## 10 -0.534  1.15   1.24     0.443  0.0140  0.353 Bug       -0.247  -0.417  -0.513
## # ... with 354 more rows, 3 more variables: generation_X4 <dbl>,
## #   generation_X5 <dbl>, generation_X6 <dbl>, and abbreviated variable names
## #   1: legendary_True, 2: generation_X2, 3: generation_X3
```

#Question 5

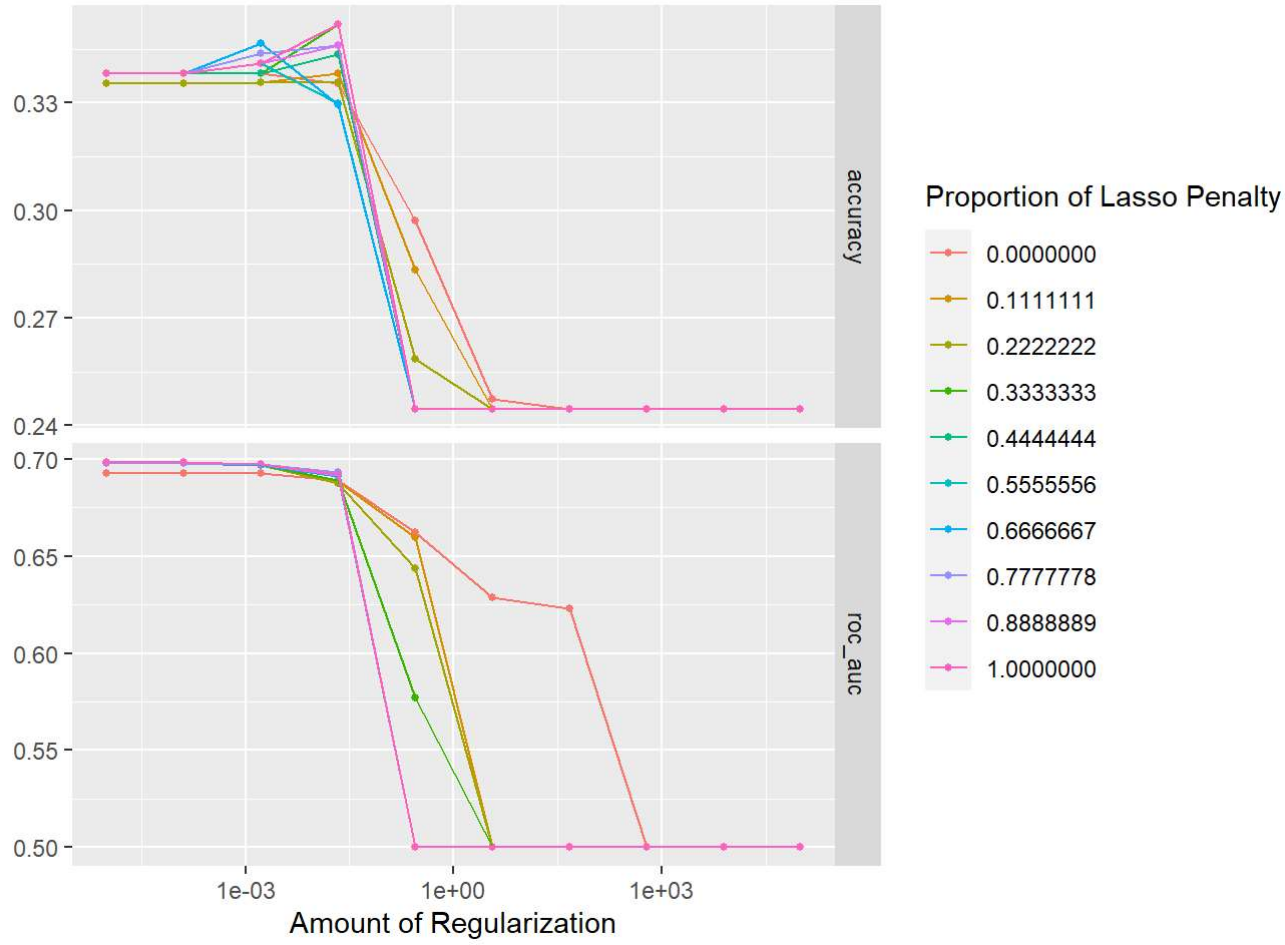
```
Mul_reg <- multinom_reg(penalty = tune(),mixture = tune()) %>%
  set_engine("glmnet")

Pokemon_wkflow <- workflow() %>%
  add_recipe(Pokemon_recipe) %>%
  add_model(Mul_reg)

Pokemon_grid <- grid_regular(penalty(range = c(-5, 5)),mixture(range=c(0,1)), levels = 10)
#Because the grid has 10 level penalty and 10 level mixture, and we set 5 folds, so there are 50
0 models to be fitted in total
```

#Question 6

```
Pokemon_tune <- tune_grid(object = Pokemon_wkflow,
  resamples = Pokemon_folds,
  grid = Pokemon_grid
)
autoplot(Pokemon_tune)
```




```
#From the results we could observe that the higher the penalty, the lower the accuracy. Larger/S
maller value of regularization determines ROC_AUC and accuracy
```

#Question 7

```
best_penalty <- select_best(Pokemon_tune, metric = "roc_auc")
final_flow <- finalize_workflow(Pokemon_wkflow, best_penalty)
final_fit <- fit(final_flow, data = Pokemon_train)
aug_fit <- augment(final_fit, new_data = Pokemon_test)
aug_fit
```

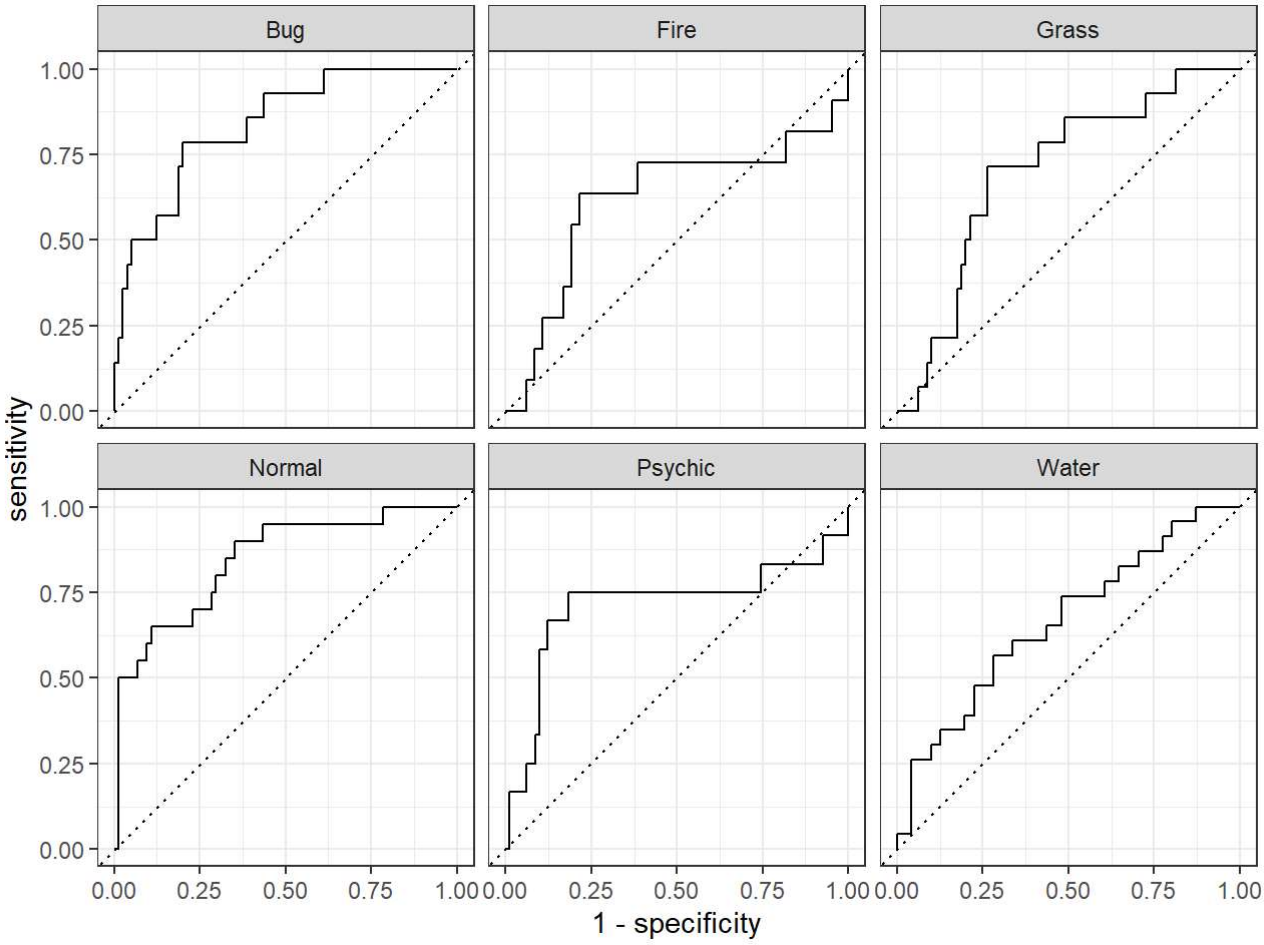
```
## # A tibble: 94 x 20
##        x name       type_1 type_2 total    hp attack defense sp_atk sp_def speed
##    <int> <chr>      <fct>  <chr>  <int> <int>  <int>   <int>  <int>  <int> <int>
##  1     1 Bulbasaur  Grass  "Pois~   318    45     49      49     65     65    45
##  2     3 VenusaurM~ Grass  "Pois~   625    80    100     123    122    120    80
##  3     5 Charmeleon Fire   ""       405    58     64      58     80     65    80
##  4     6 Charizard~ Fire   "Flyi~   634    78    104      78    159    115   100
##  5    22 Fearow     Normal "Flyi~   442    65     90      65     61     61   100
##  6    38 Ninetales  Fire   ""       505    73     76      75     81    100   100
##  7    45 Vileplume  Grass  "Pois~   490    75     80      85    110     90    50
##  8    47 Parasect   Bug    "Gras~   405    60     95      80     60     80    30
##  9    48 Venonat    Bug    "Pois~   305    60     55      50     40     55    45
## 10    69 Bellsprout Grass  "Pois~   300    50     75      35     70     30    40
## # ... with 84 more rows, and 9 more variables: generation <fct>,
## #   legendary <fct>, .pred_class <fct>, .pred_Bug <dbl>, .pred_Fire <dbl>,
## #   .pred_Grass <dbl>, .pred_Normal <dbl>, .pred_Psychic <dbl>,
## #   .pred_Water <dbl>
```

#Question 8

```
aug_fit <- augment(final_fit, new_data = Pokemon_test, type = "prob") %>%
  mutate(type_1 = as.factor(type_1))
Pokemon_roc <- roc_auc(aug_fit, truth = type_1 ,estimate = .pred_Bug:.pred_Water)
Pokemon_roc
```

```
## # A tibble: 1 x 3
##   .metric .estimator .estimate
##   <chr>   <chr>          <dbl>
## 1 roc_auc hand_till      0.727
```

```
roc_curve(aug_fit, truth = type_1, estimate=.pred_Bug:.pred_Water) %>%
  autoplot()
```

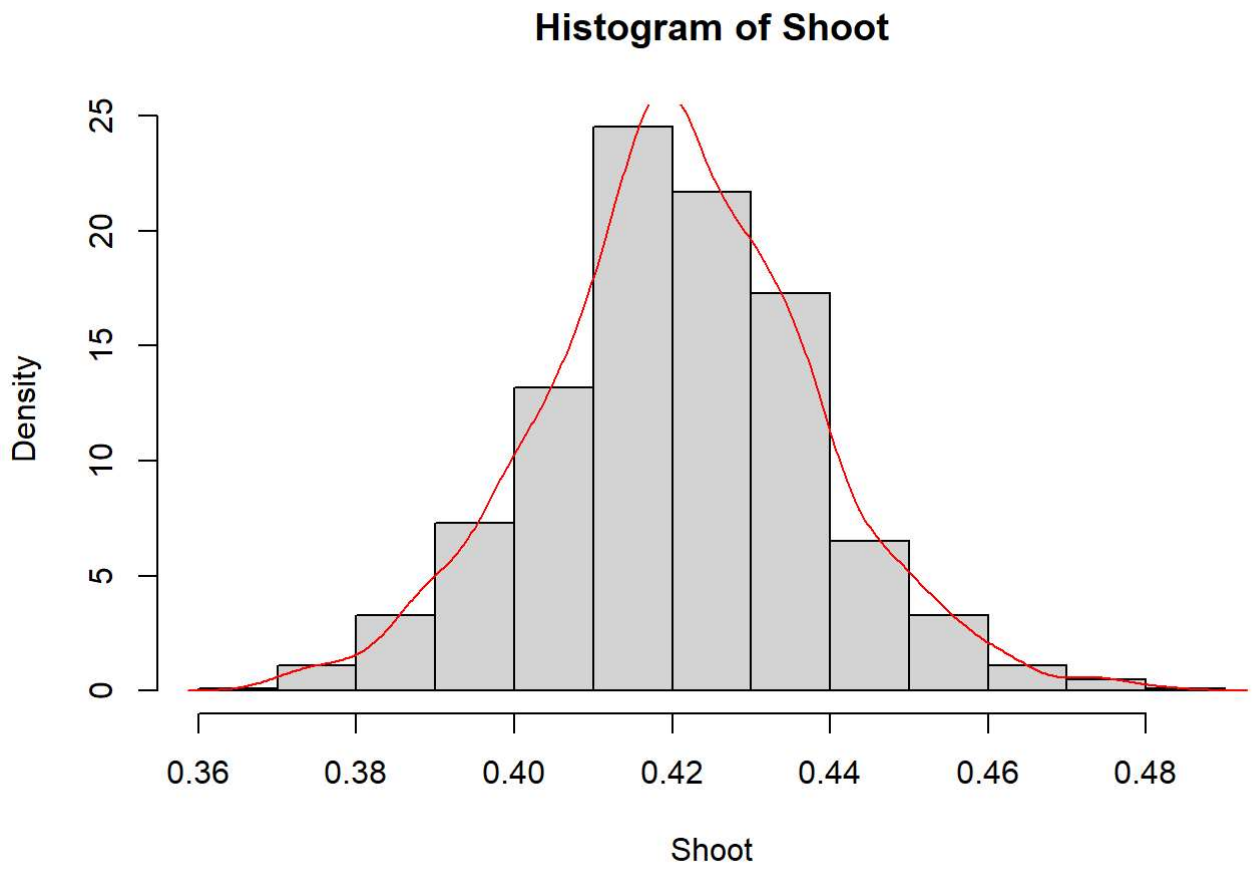



```
aug_fit %>%
  conf_mat(truth= type_1, estimate=.pred_class) %>%
  autoplot(type="heatmap")
```

#From the results, we could observe that the model performs poorly in predicting grass and fire types. From the heat map, the model doesn't perform well besides predicting the normal type. I think the independent variables have little correlations to the response variable so that we cannot come up with a logical prediction between them.

#Question 9

```
library(boot)
Curry_shot <- c(rep(1,337),rep(0,464))
Curry_shot_mean <- function(original_vector, resample_vector) {
    mean(original_vector[resample_vector])
}
Curry_shots <- boot(Curry_shot,Curry_shot_mean,R=1000)
Shoot<-Curry_shots$t
Nine_CI <- boot.ci(Curry_shots,conf = 0.99)
hist(Shoot,freq = F)
lines(density(Shoot), col="red")
```




```
Nine_CI$normal
```

```
##      conf
## [1,] 0.99 0.3759721 0.4653912
```

```
#From the results, we could observe that the 99%CI for boostrap is (0.3740969,0.4666422)
```