Predicting Legendary Status of Pokemon

Introduction

The aim of the project is to develop a model to predict if a Pokemon is going to be a Legendary based on its characteristics such as battle statistics and generation number.

The report will be split into 4 sections, the **introduction**, the **analysis**, the **results**, and the **conclusion** section.

Analysis

This section will involve a few key steps, namely **pre-processing**, **data visualization**, and **model development**.

Pre-processing

Before we start, we will import all relevant libraries. Then, we will save the Kaggle Pokemon dataset into our variable 'pokemon'.

```
pokemon <- read.csv('C:/Users/User/Documents/Pokemon.csv')
head(pokemon)
```

```
##   X.                  Name Type.1 Type.2 Total HP Attack Defense Sp..Atk
## 1  1             Bulbasaur  Grass Poison   318 45     49      49      65
## 2  2               Ivysaur  Grass Poison   405 60     62      63      80
## 3  3              Venusaur  Grass Poison   525 80     82      83     100
## 4  3 VenusaurMega Venusaur  Grass Poison   625 80    100     123     122
## 5  4            Charmander   Fire          309 39     52      43      60
## 6  5            Charmeleon   Fire          405 58     64      58      80
##   Sp..Def Speed Generation Legendary
## 1      65    45          1     False
## 2      80    60          1     False
## 3     100    80          1     False
## 4     120    80          1     False
## 5      50    65          1     False
## 6      65    80          1     False
```

For users who want to reference the original dataset, please feel free to use the link provided below:
https://www.kaggle.com/mlomuscio/pokemon

When we view the Pokemon dataset, we can see that our main outcome, the Legendary status, is in the form of a Boolean rather than a 1 or 0 factor. We thus must convert the entire data column before any of it becomes interpretable. The code is as follows:

```
pokemon$Legendary <- factor(pokemon$Legendary, levels = c("True", "False"), labels = c(1,
    0))
head(pokemon)
```

```
##   X.                  Name Type.1 Type.2 Total HP Attack Defense Sp..Atk
## 1  1             Bulbasaur  Grass Poison   318 45     49      49      65
## 2  2               Ivysaur  Grass Poison   405 60     62      63      80
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## 5  4            Charmander   Fire          309 39     52      43      60
## 6  5            Charmeleon   Fire          405 58     64      58      80
##   Sp..Def Speed Generation Legendary
## 1      65    45          1         0
## 2      80    60          1         0
## 3     100    80          1         0
## 4     120    80          1         0
## 5      50    65          1         0
## 6      65    80          1         0
```

We now need to split our dataset into training and test sets. For the purpose of this project, I have split the dataset into 3 partitions, 1 large training set subdivided into two - train_a and train_b - and 1 final test set to evaluate the true performance of my model.

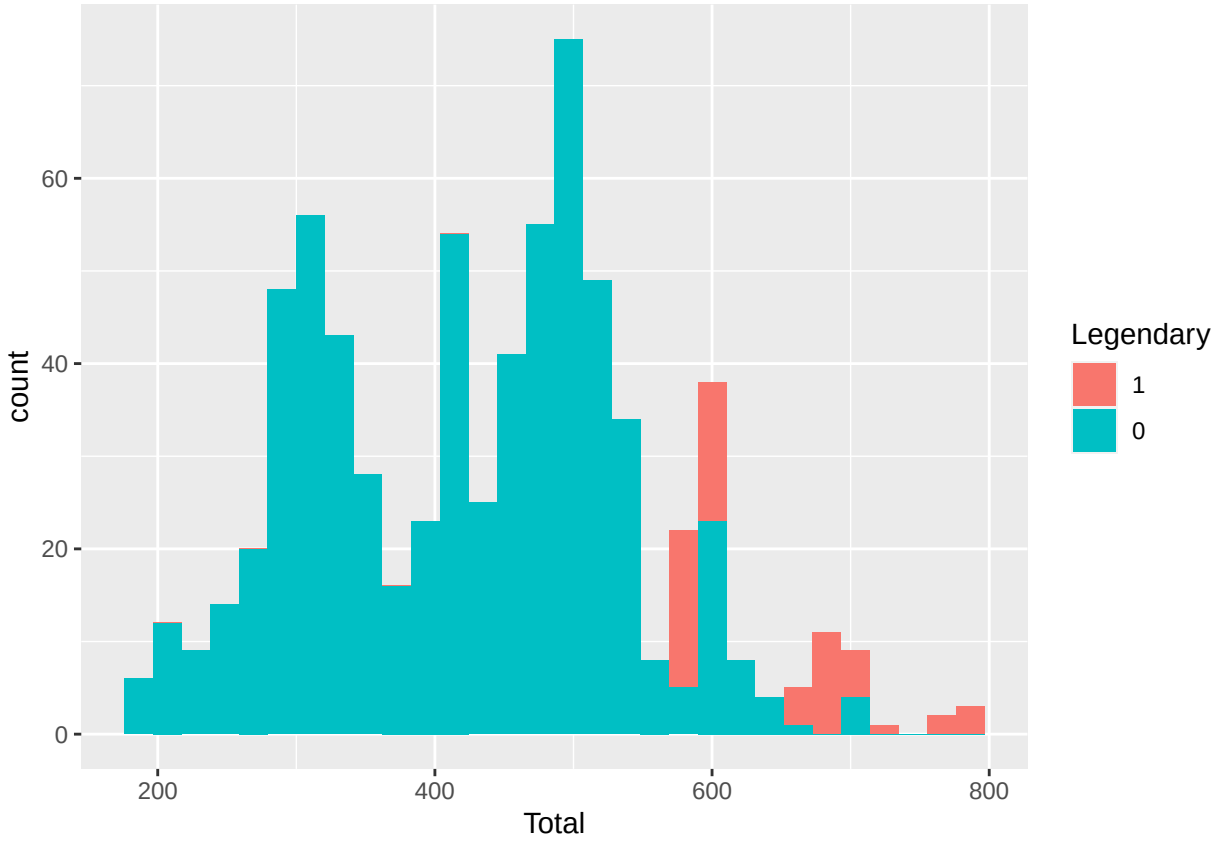
```
set.seed(1)
test_index <- createDataPartition(y = pokemon$Legendary, times = 1, p = 0.1, list = FALSE)
train_set <- pokemon[-test_index, ]
test_set <- pokemon[test_index, ]

train_index <- createDataPartition(y = train_set$Legendary, times = 1, p = 0.1, list = FALSE)
train_a <- train_set[-train_index, ]
train_b <- train_set[train_index, ]
```

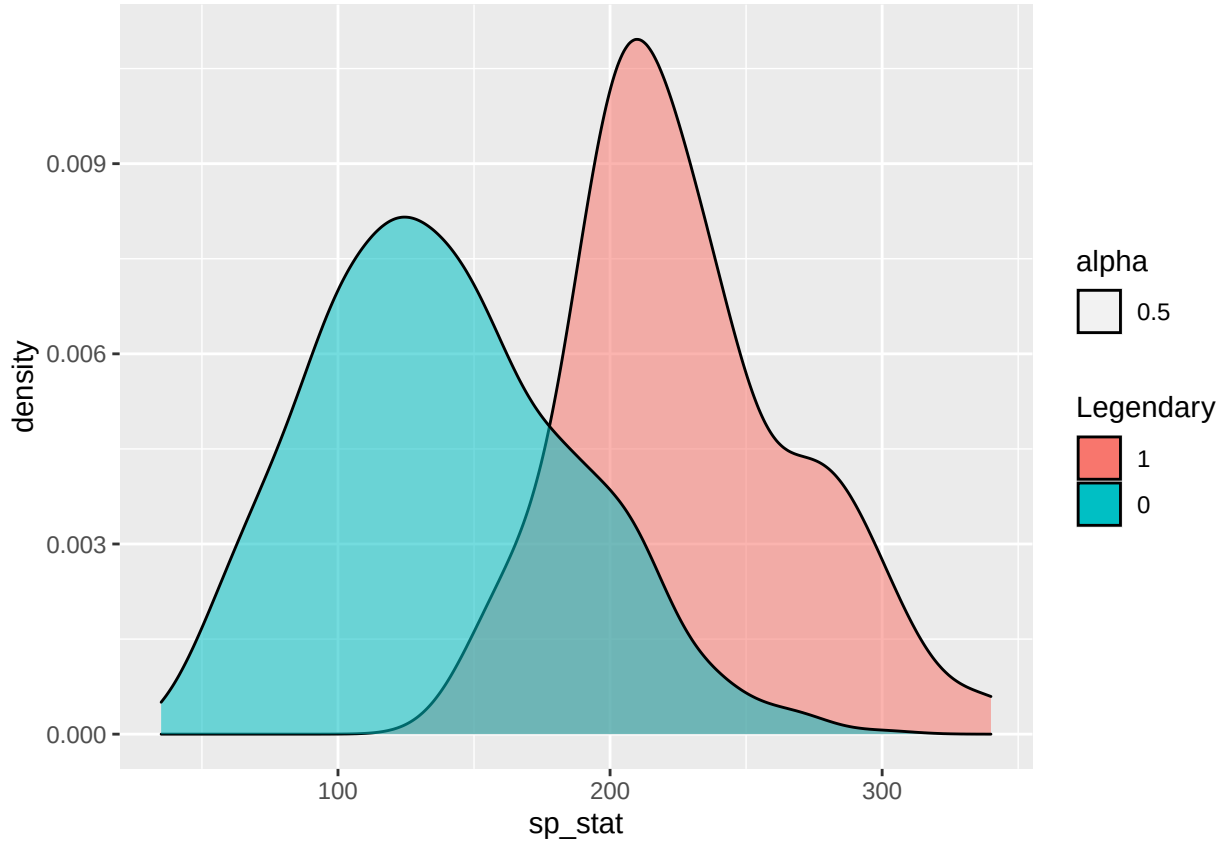
Data Visualization

We shall then proceed on to Data Visualization. For this section, I will only be using the training set so as to preserve the integrity of the final evaluation set.
First, we will analyse the relationship between a Pokemon's battle stats and its Legendary Status.

```
stat_effect <- train_set %>% ggplot(aes(x = Total, fill = Legendary)) + geom_histogram()
stat_effect
```



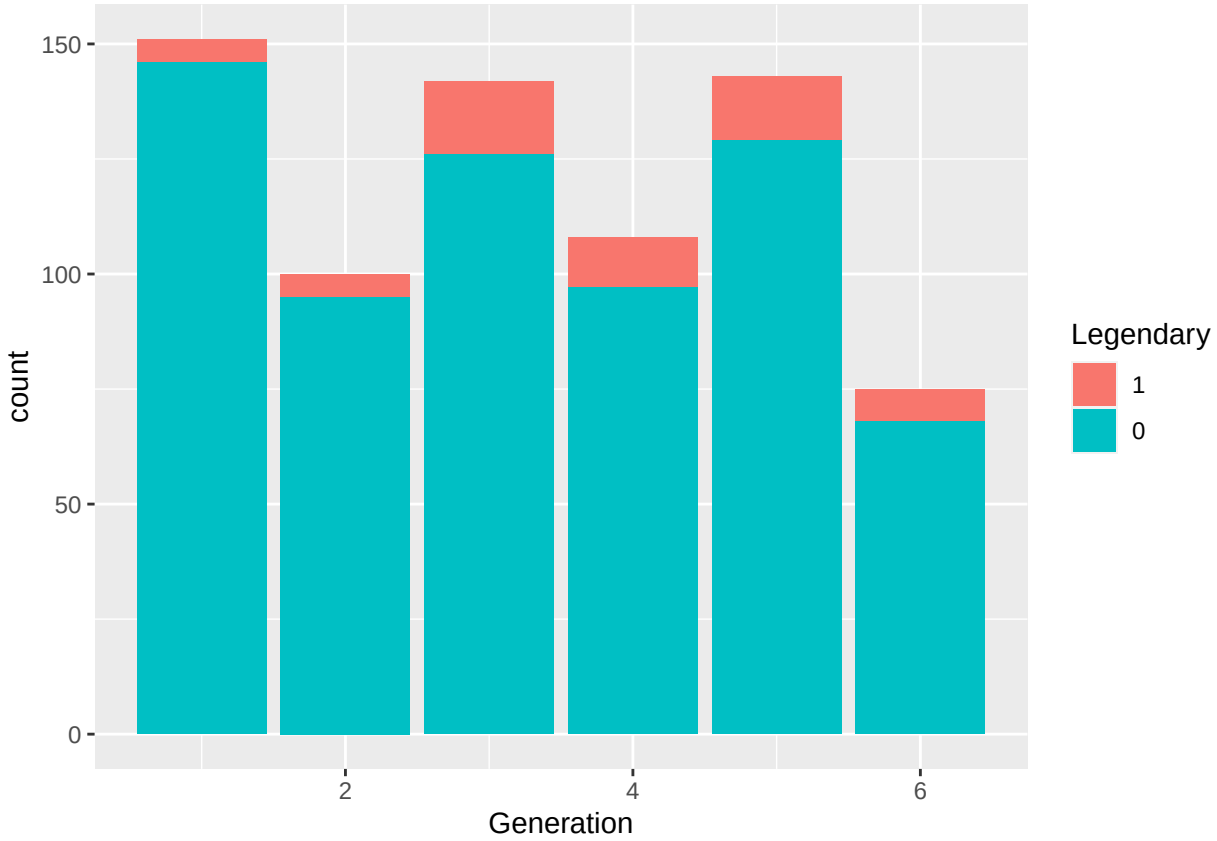

```
sp_effect <- train_set %>% mutate(sp_stat = round(Sp..Atk + Sp..Def)) %>% ggplot() +
    geom_density(aes(x = sp_stat, fill = Legendary, alpha = 0.5))
sp_effect
```



We can see that Legendary Pokemon exist with significantly higher total stat points. We go into even more detail by separating out the Special Attack and Special Defense points (sp_stat) to show how significant stat points are as a factor in determining a Pokemon's legendary status.

Next, we will consider the relationship between a Pokemon's generation and it's Legendary status.

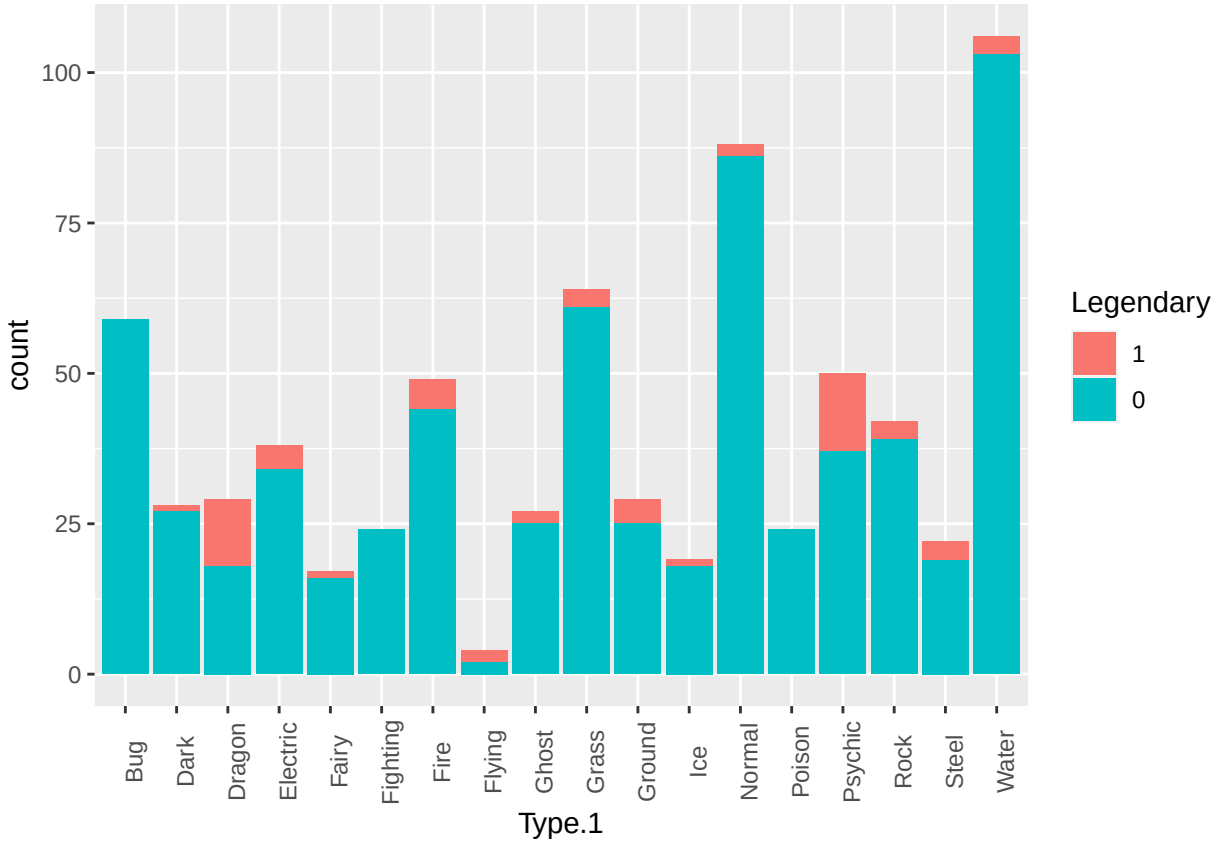
```
gen_effect <- train_set %>% ggplot(aes(x = Generation, fill = Legendary)) + geom_bar()
gen_effect
```



From the above barplot, we can see that the number of legendary pokemon are relatively constant across all the generations, with notable exceptions in only generation 3 and generation 5 with slightly more legendary pokemon.

Lastly, we shall consider the effect of the Pokemon's type on their status.

```
type_effect <- train_set %>% group_by(Type.1) %>% ggplot(aes(x = Type.1, fill = Legendary)) +
    geom_bar() + theme(axis.text.x = element_text(angle = 90))
type_effect
```



From this plot, we can see that only the 'Dragon' and 'Psychic' types have slightly more number of legendaries. The other types have relatively constant numbers of legendaries with some types even having none.

With this knowledge, we can proceed to develop our machine-learning algorithm to predict the legendary status of pokemon in the test set.

Model Development

To create my model, I intend to use an ensemble of different machine learning algorithms - K-Nearest Neighbors, Quadratic Discriminant Analysis, Linear Discriminant Analysis, Random Forests, and lastly a Generalized Additive Model using Locally Estimated Scatterplot Smoothing (LOESS).

I specifically chose to use the two Discriminant Analysis algorithms as they utilize the Naive Bayes model which performs well with predictions involving 2 categorical outcomes. Random forests was chosen over regression trees as it performs significantly better at predicting categorical outcomes by using more relevant optimizing metrics such as the Gini index. I chose random forests over decision trees due to its superior performance and stability by its random process of averaging multiple decision trees.

Lastly, for my tuning parameters and training controls, I used a 3-fold cross validation on the KNN and Random Forests model to improve their stability and accuracy.

Multiple tuning parameters were implemented for the KNN, random forests, and gamLoess models as well. The train function from the caret package will automatically select the best tuning parameter to be used for the model.

To generate the ensemble, each model's prediction is saved as a list of integer values of 1s and 0s, with a 1 representing a Legendary Pokemon.
As I assume that all the model's have equal weight, I will simply be taking the average of all the model's predictions to calculate the final prediction for the ensemble.

```
model_func <- function(test_set) {

    knn_control <- trainControl(method = "cv", number = 3, p = 0.9)
    knn_fit <- train(Legendary ~ HP + Attack + Defense + Sp..Atk + Sp..Def + Speed +
        Total + Generation, method = "knn", tuneGrid = data.frame(k = seq(1, 15,
        2)), trControl = knn_control, data = train_a)
    knn_y_hat <- predict(knn_fit, newdata = test_set, type = "raw")
    knn_y_hat <- ifelse(as.integer(knn_y_hat) == 2, 0, 1)


    qda_fit <- train(Legendary ~ HP + Attack + Defense + Sp..Atk + Sp..Def + Speed +
        Generation, method = "qda", data = train_a)
    qda_y_hat <- predict(qda_fit, test_set, type = "raw")
    qda_y_hat <- ifelse(as.integer(qda_y_hat) == 2, 0, 1)

    lda_fit <- train(Legendary ~ HP + Attack + Defense + Sp..Atk + Sp..Def + Speed +
        Generation, method = "lda", data = train_a)
    lda_y_hat <- predict(lda_fit, test_set, type = "raw")
    lda_y_hat <- ifelse(as.integer(lda_y_hat) == 2, 0, 1)

    rf_control <- trainControl(method = "cv", number = 3, p = 0.9)
    rf_grid <- expand.grid(minNode = c(1, 5), predFixed = c(5, 5, 5, 5, 5))
    rf_fit <- train(Legendary ~ HP + Attack + Defense + Sp..Atk + Sp..Def + Speed +
        Generation, method = "Rborist", ntree = 50, trControl = rf_control, tuneGrid = rf_grid,
        nSamp = 5000, data = train_a)
    rf_y_hat <- predict(rf_fit, test_set)
    rf_y_hat <- ifelse(as.integer(rf_y_hat) == 2, 0, 1)

    loess_fit <- train(Legendary ~ HP + Attack + Defense + Sp..Atk + Sp..Def + Speed +
        Generation, method = "gamLoess", tuneGrid = expand.grid(span = seq(0.2, 0.6,
        len = 2), degree = 1), data = train_a)
    loess_y_hat <- predict(loess_fit, test_set)
    loess_y_hat <- ifelse(as.integer(loess_y_hat) == 2, 0, 1)

    final_y_hat <- (knn_y_hat + qda_y_hat + lda_y_hat + rf_y_hat + loess_y_hat)/4
    final_y_hat <- ifelse(final_y_hat < 0.5, 0, 1)
    final_y_hat <- final_y_hat %>% factor(levels = levels(test_set$Legendary))
    return(confusionMatrix(data = final_y_hat, reference = test_set$Legendary)$overall["Accuracy"])

}
```

Results

Before I implemented the model on the final test set, I trialed it on the smaller train set, train_b, to fine-tune the code.

```
model_func(train_b)
```

```
##  Accuracy
## 0.9452055
```

```
model_func(test_set=test_set)
```

```
## Accuracy
## 0.962963
```

The accuracy from the train_b set is 0.959, while the accuracy from the final test set is 0.963. The ensemble model achieves close to 97% accuracy and therefore can be considered a good predictor of a Pokemon's Legendary status.

Conclusion

It is surprising that the accuracy on the final test set is higher than the accuracy of the training set. However, since the smaller train set was used in the same way as the final test set, we can argue that the difference in accuracy is due to random error from the sampling itself. Furthermore, the small size of the entire pokemon dataset ($\sim$ 800) entries, and the small size of the test set could have contribute to the variation as well.

All in all, the small size of the dataset poses a significant challenge to accuracy. We have tried to maintain a high accuracy through ensuring that the dataset used to train our model is as large as possible, while also using an ensemble of algorithms to predict the final outcome.

In the future, we could consider using other methods like Principal Component Analysis to elucidate further links between the different predictors.