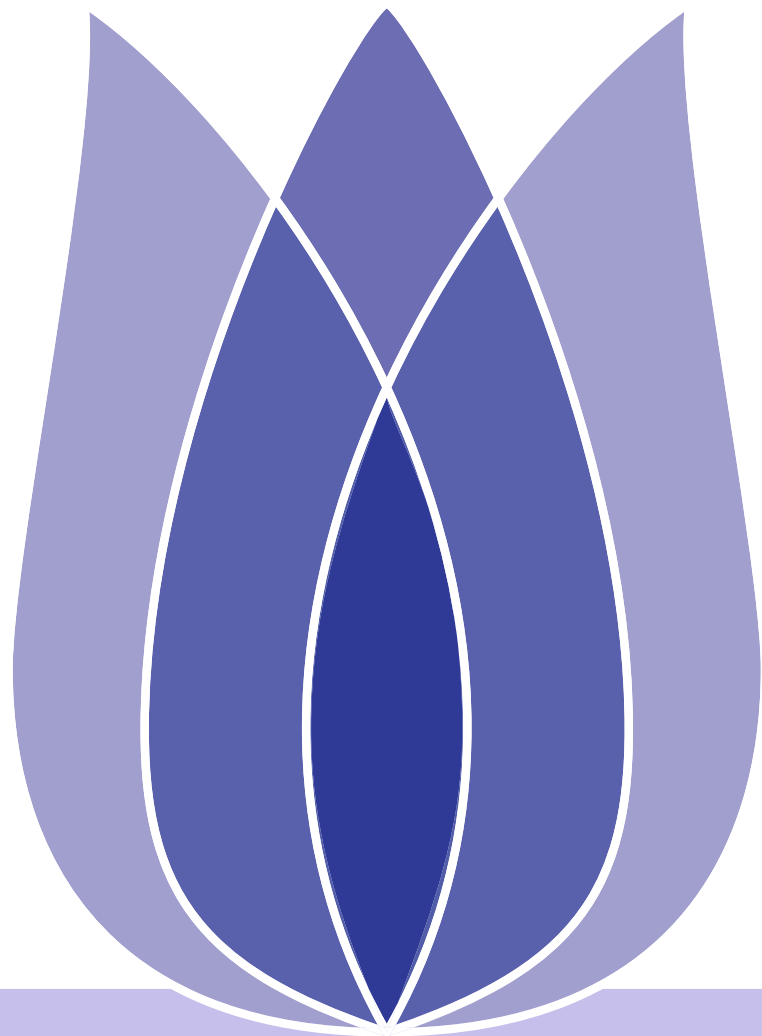




# Flip00 Project Final Presentation

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SouthEast University

2019-10-27





# Overview

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# Problem Statement

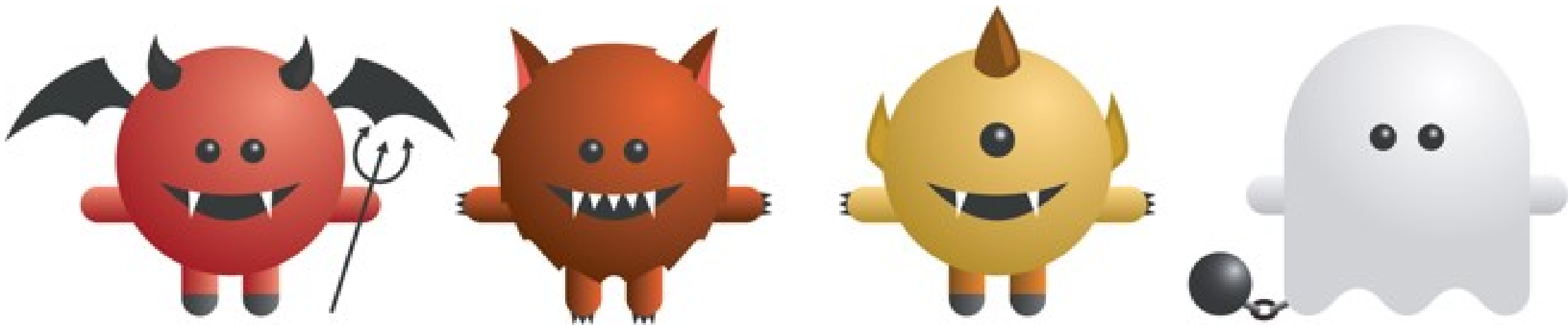


# Problem Definition

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Defn

After a month of making scientific observations and taking careful measurements, can determined that 900 **ghouls**, **ghosts**, and **goblins**. The raw dataset contains train set with **371** samples and **529** unlabeled samples as test set. Through the train data, find the relationship between the attributes and species, and then identify the ghastrly creatures in test data.





# Data Set

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Defn

There are 4 numerical variables and 1 categorical, and no missing values. Numerical columns are either normalized or show a percentage, so no need to scale them.

## ■ Data List

**id** id of the creature

**bone\_length** average length of bone in the creature, normalized between 0 and 1

**rotting\_flesh** percentage of rotting flesh in the creature

**hair\_length** average hair length, normalized between 0 and 1

**has\_soul** percentage of soul in the creature

**Color** dominant color of the creature: *white,black,clear, blue,green,blood*

**type** target variable: *Ghost, Goblin, and Ghoul*

## ■ Train Data and Test Data

Divide the raw train set into train data and test data, and the ratio is 8:2.



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# Exploratory Data Analysis



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Exp Use EDA to plot the distribution of the data, can observe the data intuitively and find the relation between the attribute values.

- Figures
  - ◆ Histogram
  - ◆ Boxplot
  - ◆ Pairplot
  - ◆ Correllogram



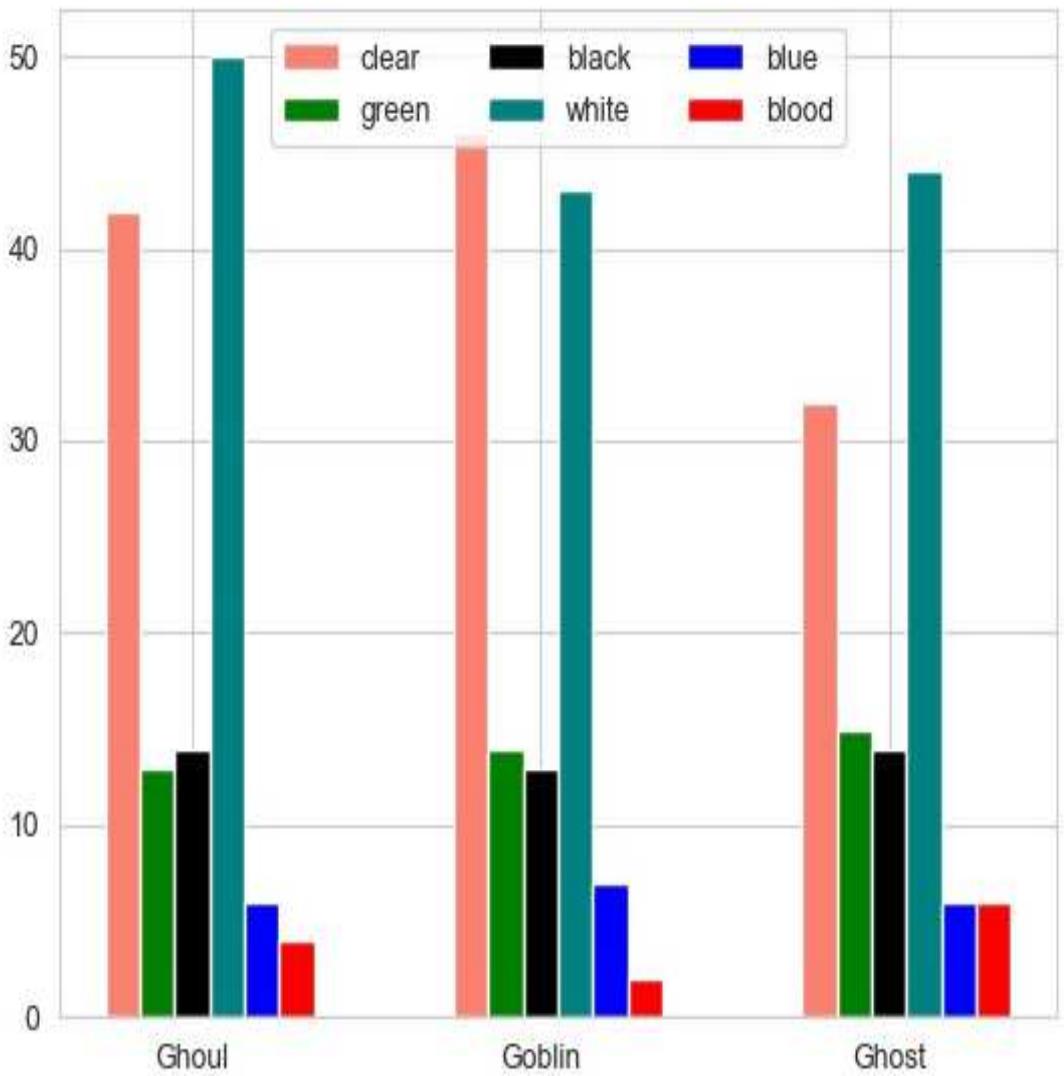
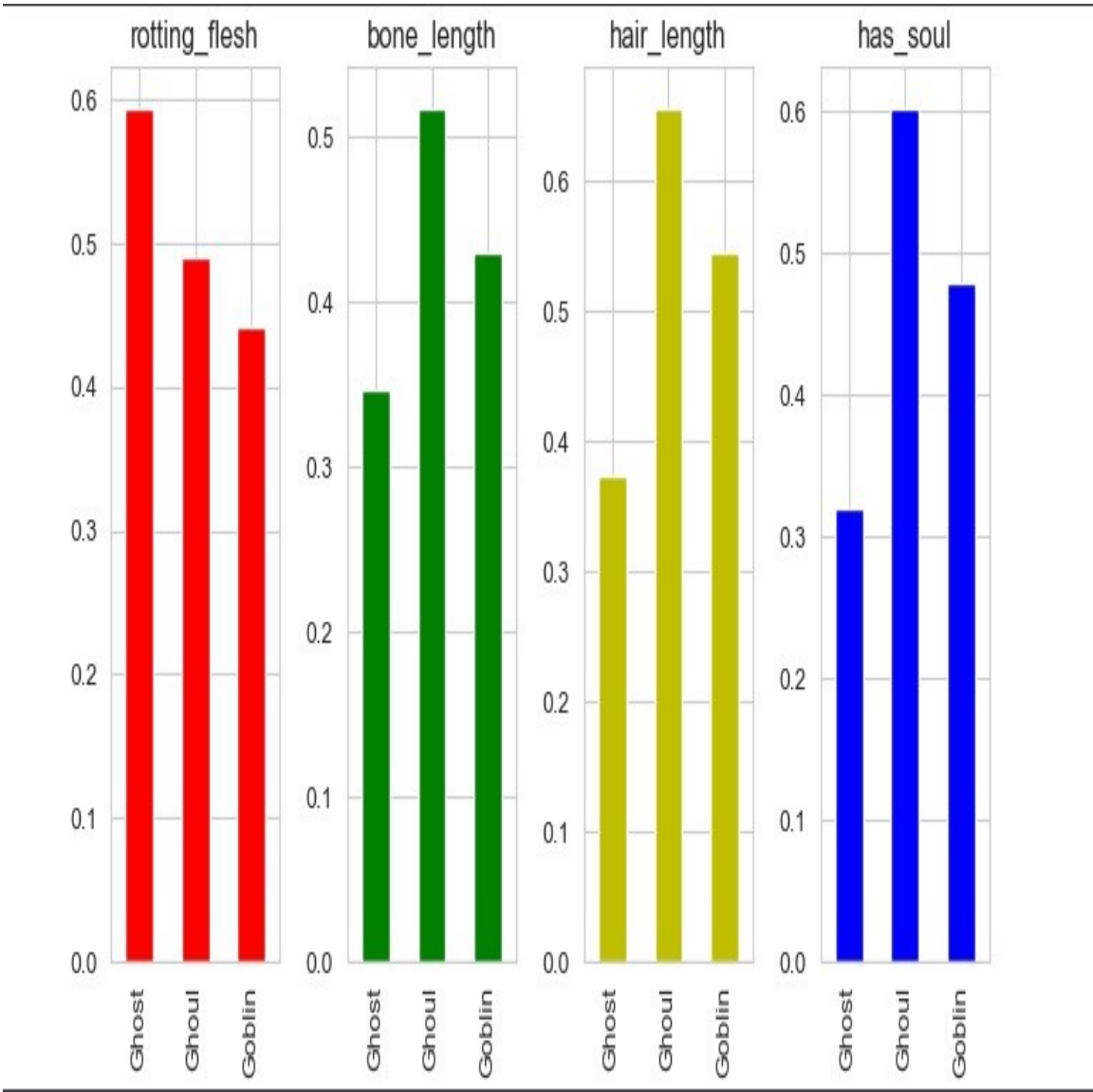


# Data Visualization

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Exp

It seems that all numerical features may be useful, but many colors are evenly distributed among the monsters, which means they maybe have little effect on classification.



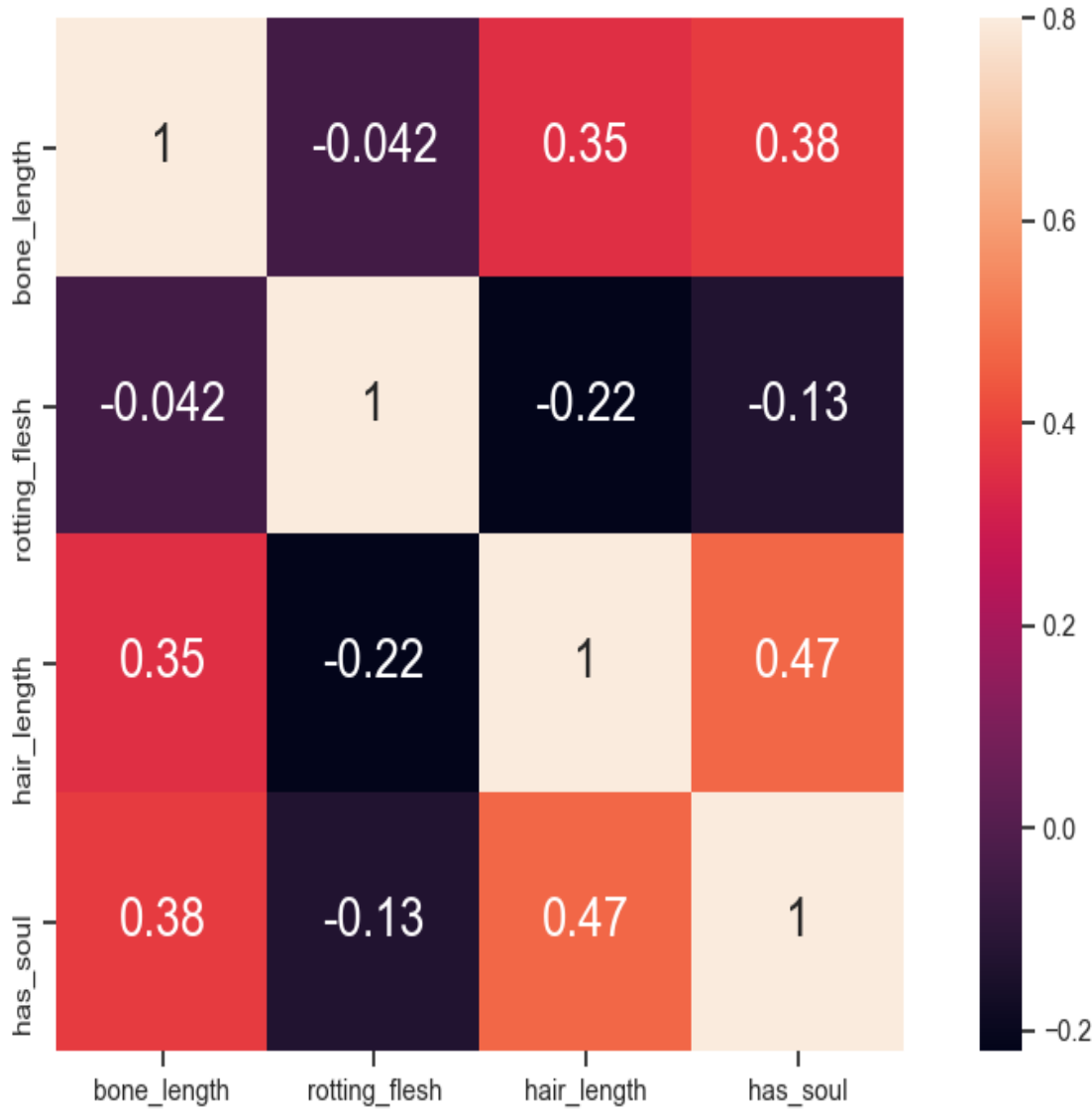
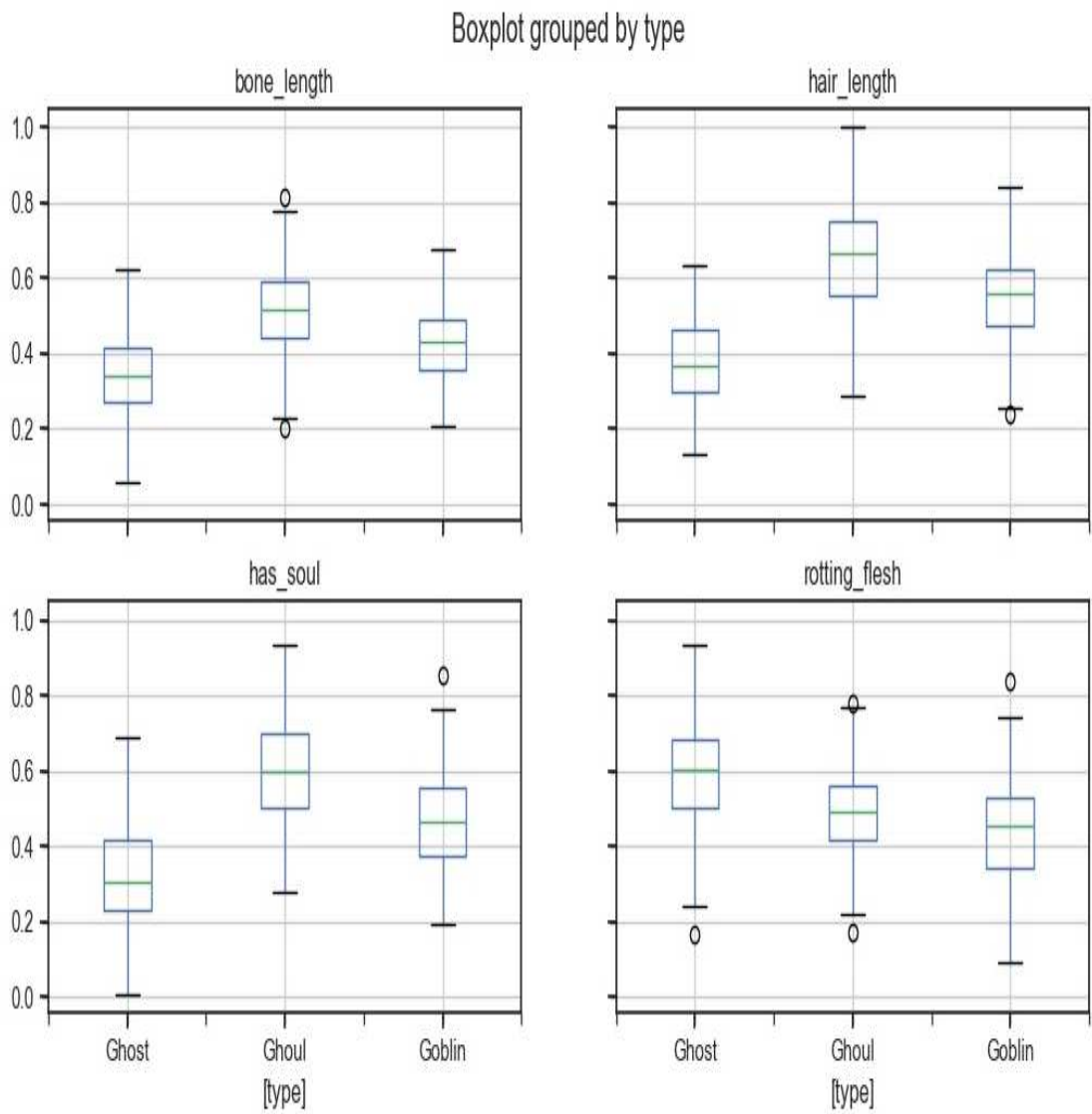


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Exp

Based on the above observation on boxplot, we guess that the predictive accuracy of Ghost and Ghoul will be better than Goblin. And the outliers are very small, which can be ignored. As for correllogram, can find that it is no obvious linear relationship between these variables.



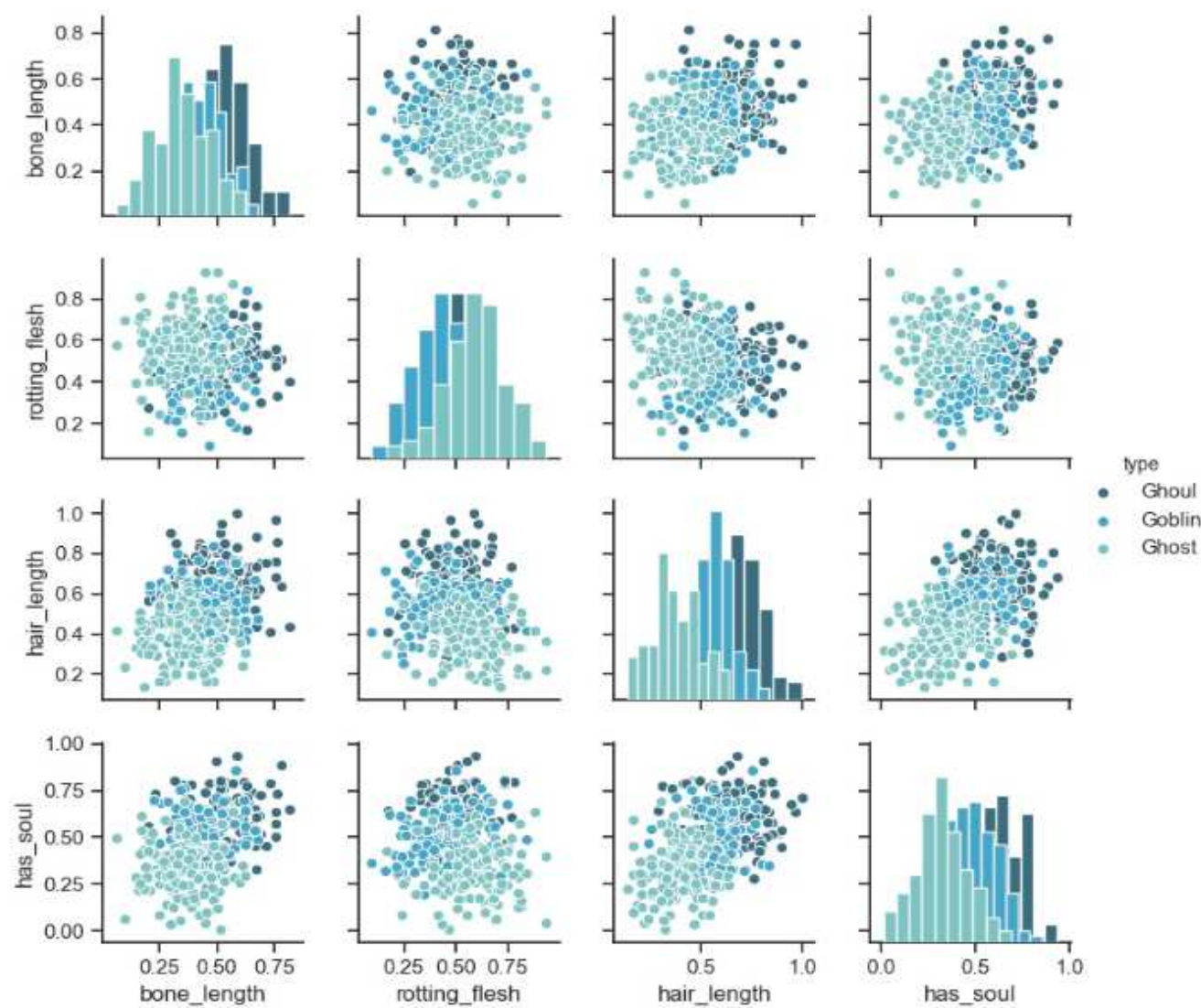


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Exp

This pairplot shows that data is distributed normally. And while most pairs are widely scattered (in relationship to the type), some of them show clusters: hair\_length and has\_soul, hair\_length and bone\_length. So it may need to reassemble the data.







# Data Engineering

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As it can be seen from the pairplot front the data is distributed normally. But some of them show clusters: hair\_length and has\_soul, hair\_length and bone\_length. So create new variables with multiplication of these columns:

- New Features

```
hair_soul  row[hair_length]*row[has_soul]
hair_bone  row[hair_length]*row[bone_length]
bone_soul  row[bone_length]*row[has_soul]
hair_soul_bone  row[hair_length]*row[has_soul]*row[bone_length]
```



# Features Selection

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**Require:** Features  $X = \{X_1, X_2, \dots, X_n\}$ , The number of tree node  $M$ ,  $GI_m$  Gini index of node  $m$ ,  $K$  the number of target,  $p_{mk}$  proportion of target  $k$  in node  $m$ ,  $VIM_{jm}^{(Gini)}$  the importance of feature  $X_j$  in node  $m$ ,  $n$  the tree number of RF.

**Ensure:** Variable Importance Measures  $VIM_j^{(Gini)}$ .

- 1: Initialize  $GI_m$ ,  $VIM_j^{(Gini)}$ ;
- 2: **for**  $m \leftarrow 1 \dots M$  **do**
- 3:     **for**  $k \leftarrow 1 \dots K$  **do**
- 4:         Compute the Gini index of node  $m$   $GI_m = \sum_{k=1}^{|K|} \sum_{k' \neq k} p_{mk} p_{mk'} = 1 - \sum_{k=1}^{|K|} p_{mk}^2$
- 5:     **end for**
- 6:     Divide node  $m$  into node  $r$  and node  $l$
- 7:     Compute the importance of feature  $X_j$  in node  $m$   $VIM_{jm}^{(Gini)} = GI_m - GI_l - GI_r$
- 8: **end for**
- 9: **for**  $i \leftarrow 1 \dots N$  **do**
- 10:     Compute variable importance measures  $VIM_j^{(Gini)} = VIM_j^{(Gini)} + VIM_{ij}^{(Gini)}$
- 11: **end for**
- 12: **return**  $VIM_j^{(Gini)}$

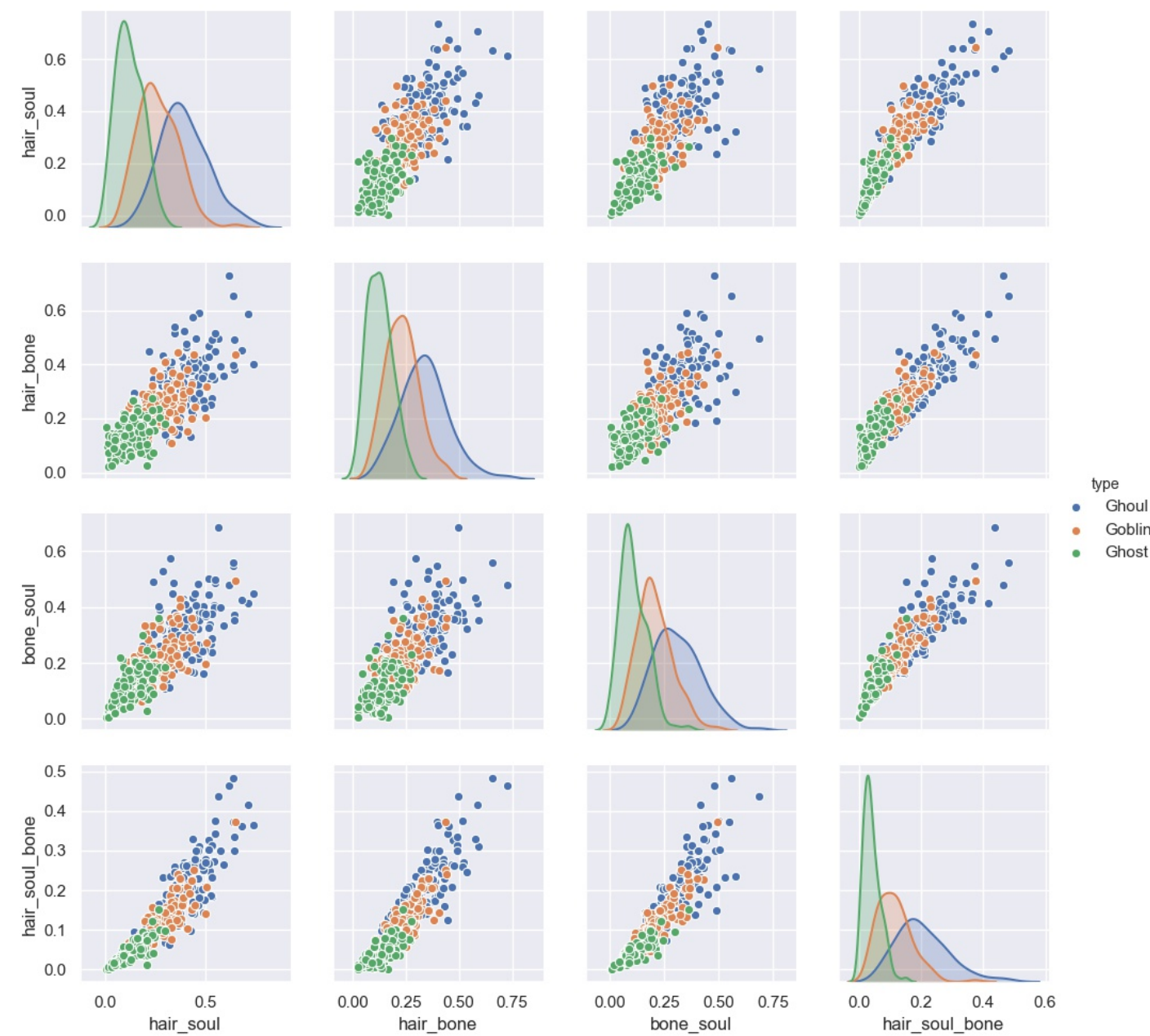
## Algorithm 1: Features Selection





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Analyse the new features in a pairplot, it can be seen from the picture that there is a clear linear relationship between the variables.

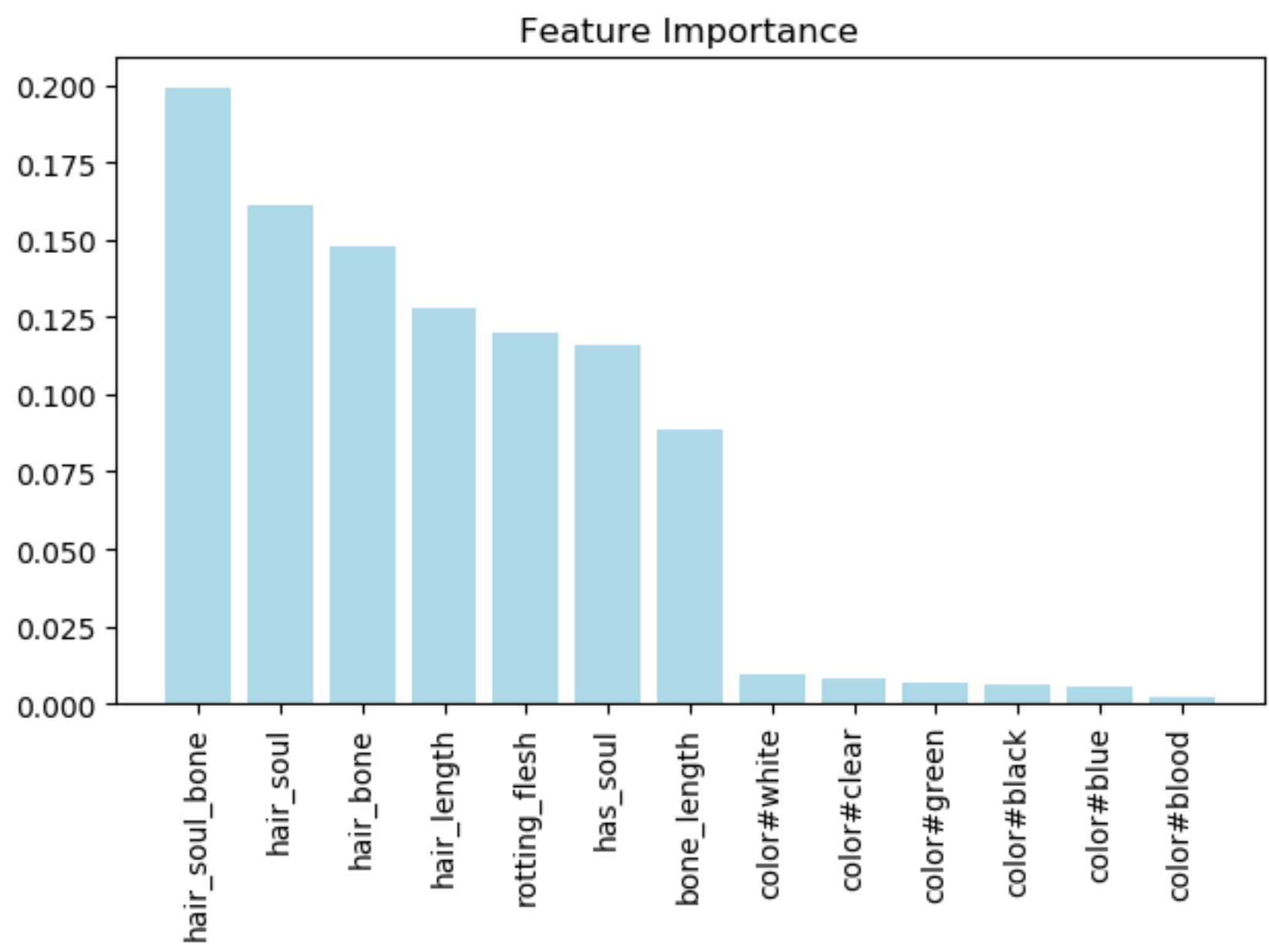




# New Train Data

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The following figure is a histogram ordered by feature importance. We take the top seven features with higher importance to form a new train data, the rest are discarded.





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# Methods





# Methods

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There are many machine learning algorithms, use the machine learning algorithms below as Ensemble Model's base models. Through Grid Search and ten-fold cross-validation to find the optimal parameters. Then use the ensemble model on test data.

- Base Models
  - ◆ RandomForest
  - ◆ LogisticRegression
  - ◆ SVC
  - ◆ KNeighbors
  - ◆ XGBoost
  - ◆ Netual Network
- Ensemble Model





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# Forecast Results



# Evaluation Methods

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- F1 Score
- Precision
- Recall



# Forecast Results

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The tables below are the metrics classification report of ensemble model in original and new train data.

■ Metrics Classification Report of Ensemble Model in original and new train data

	data	precision	recall	f1-score	support
Ghost	original	0.80	0.83	0.82	24
	new	0.84	0.88	0.86	24
Ghoul	original	0.88	0.79	0.84	29
	new	0.93	0.97	0.95	29
Goblin	original	0.67	0.73	0.70	22
	new	0.80	0.73	0.76	22
weighted avg	original	0.79	0.79	0.79	75
	new	0.86	0.87	0.86	75

It can be observed that ensemble model performaces better in new features.



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# Conclusion



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**Exploratory Data Analysis** It is an exploratory analysis of the data to provide the necessary conclusions for data processing and modeling.

**Data Preprocessing** This step contains dealing with missing data and outliers, changing categorical variable into one-hot code and so on.

**Feature Engineering** It’s the most important thing. Create as more as poossible features, then select the most useful features.

**Model Training** The models have many parameters, and can use Grid Search to find the optimal paratemers.



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