```
In [1]:
         import tensorflow as tf
         from tensorflow.keras.models import Sequential
         from tensorflow.keras.layers import Dense
         import pandas as pd
         import numpy as np
         import matplotlib.pyplot as plt
         import pandas as pd
         import seaborn as sns
         import matplotlib.pyplot as plt
         from sklearn.ensemble import RandomForestClassifier
         from sklearn.metrics import accuracy_score, classification_report
         from sklearn.metrics import mean_squared_error, mean_absolute_error
         from sklearn.naive_bayes import GaussianNB
         from sklearn.ensemble import RandomForestClassifier
         from sklearn.metrics import accuracy_score
         from sklearn.model_selection import train_test_split, GridSearchCV
         from sklearn.preprocessing import StandardScaler, PolynomialFeatures
         from sklearn.pipeline import Pipeline
         from sklearn.ensemble import RandomForestRegressor
         from sklearn.metrics import mean_squared_error, mean_absolute_error
         from sklearn.model_selection import cross_val_score
         from sklearn.metrics import roc_auc_score
         from sklearn.naive_bayes import GaussianNB
         from sklearn.model_selection import KFold
         from tensorflow.keras.models import Sequential
         from tensorflow.keras.layers import Dense
         from tensorflow.keras.callbacks import EarlyStopping
```

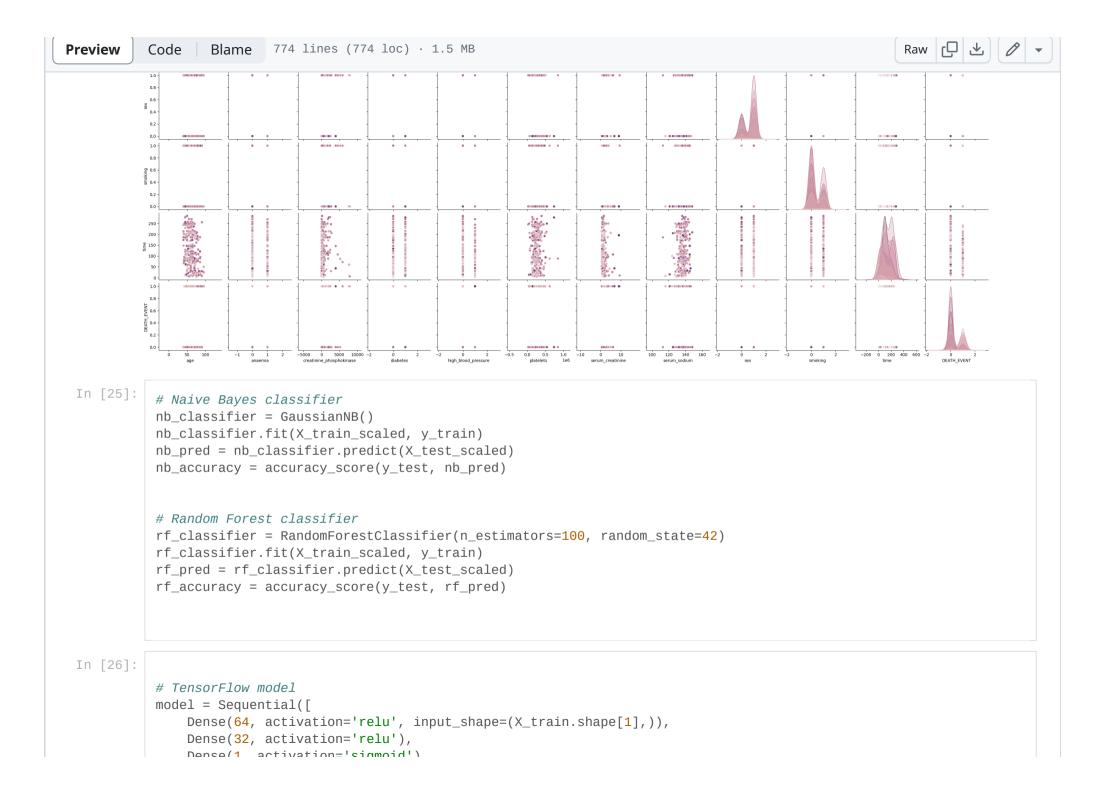
```
In [3]: data.describe()
```

data = pd.read_csv("/content/heart_failure_clinical_records_dataset.csv")

In [2]:

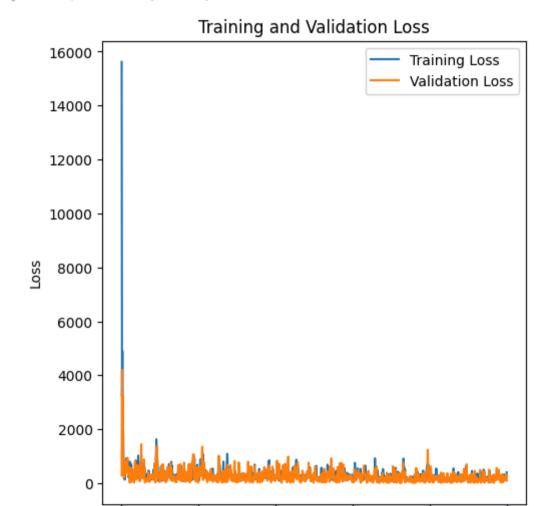
```
Out[3]:
                               anaemia creatinine phosphokinase
                                                                  diabetes ejection fraction high blood pressure
                                                                                                                     platelets serum (
                       age
          count 299.000000 299.000000
                                                     299.000000
                                                                299.000000
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                  60.833893
           mean
                              0.431438
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                                                                                 38.083612
            std
                  11.894809
                              0.496107
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                                                                  0.494067
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                                                                                 80.000000
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 In [ ]:
           data.shape
          (299, 13)
 Out[]:
 In [4]:
           column_names = list(data.columns)
           print(column_names)
         ['age', 'anaemia', 'creatinine_phosphokinase', 'diabetes', 'ejection_fraction', 'high_blood_pressure', 'platelet
         s', 'serum_creatinine', 'serum_sodium', 'sex', 'smoking', 'time', 'DEATH_EVENT']
In [21]:
           X = data.drop(['sex', 'time', 'DEATH_EVENT'], axis=1)
In [22]:
           y = data['DEATH_EVENT']
In [23]:
           # Split the data into training and testing sets
           X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
           # Feature scaling
```

```
scaler = StandardScaler()
                                                                    X_train_scaled = scaler.fit_transform(X_train)
                                                                    X_test_scaled = scaler.transform(X_test)
In [30]:
                                                                     ## Exploratory Data Analysis (EDA)
                                                                     # the distribution of numerical features and their relationship with the target variable
                                                                     sns.pairplot(data, hue="ejection_fraction", diag_kind="kde")
                                                                     plt.show()
                                                                                                                                                                                                                                                                                                                                                                                            50 -
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                                                                0.8 -
                                                             0.6 anaemia
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```



```
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          1)
          model.compile(optimizer='adam', loss='mean_squared_error', metrics=['mae']) # MSE for regression
In [27]:
          model.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
          history = model.fit(X_train, y_train, epochs=1000, batch_size=32, validation_split=0.2, verbose=0)
          # Evaluate on the test set
          test_loss, test_mae = model.evaluate(X_test_scaled, y_test, verbose=0)
          # Print the results
          print("\n--- Evaluation Results ---")
          print(f"Naive Bayes Accuracy: {nb_accuracy:.4f}")
          print(f"Random Forest Accuracy: {rf_accuracy:.4f}")
          print(f"TensorFlow Model Test Loss (MSE): {test_loss:.4f}")
          print(f"TensorFlow Model Test Mean Absolute Error (MAE): {test_mae:.4f}")
        --- Evaluation Results ---
        Naive Bayes Accuracy: 0.6333
        Random Forest Accuracy: 0.7000
        TensorFlow Model Test Loss (MSE): 0.7277
        TensorFlow Model Test Mean Absolute Error (MAE): 0.6333
In [29]:
          # Plot training history
          plt.figure(figsize=(12, 6))
          plt.subplot(1, 2, 1)
          plt.plot(history.history['loss'], label='Training Loss')
          plt.plot(history.history['val_loss'], label='Validation Loss')
          plt.title('Training and Validation Loss')
          plt.xlabel('Epoch')
          plt.ylabel('Loss')
          plt.legend()
```

Out[29]: <matplotlib.legend.Legend at 0x7fc9e415f580>



Epoch