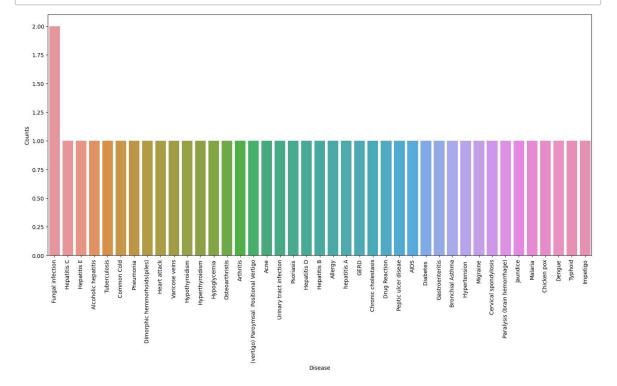
```
In [1]: # Importing libraries
   import numpy as np
   import pandas as pd
   from scipy.stats import mode
   import matplotlib.pyplot as plt
   import seaborn as sns
   from sklearn.preprocessing import LabelEncoder
   from sklearn.model_selection import train_test_split, cross_val_score
   from sklearn.svm import SVC
   from sklearn.naive_bayes import GaussianNB
   from sklearn.ensemble import RandomForestClassifier
   from sklearn.metrics import accuracy_score, confusion_matrix
   %matplotlib inline
```

```
In [3]: # Reading the train.csv by removing the
    # Last column since it's an empty column
DATA_PATH = "Testing.csv"
    data = pd.read_csv(DATA_PATH).dropna(axis = 1)

# Checking whether the dataset is balanced or not
disease_counts = data["prognosis"].value_counts()
temp_df = pd.DataFrame({
        "Disease": disease_counts.index,
        "Counts": disease_counts.values
})

plt.figure(figsize = (18,8))
sns.barplot(x = "Disease", y = "Counts", data = temp_df)
plt.xticks(rotation=90)
plt.show()
```



```
In [4]: # Encoding the target value into numerical
# value using LabelEncoder
encoder = LabelEncoder()
data["prognosis"] = encoder.fit_transform(data["prognosis"])
```

```
In [5]: X = data.iloc[:,:-1]
y = data.iloc[:, -1]
X_train, X_test, y_train, y_test =train_test_split(
X, y, test_size = 0.2, random_state = 24)

print(f"Train: {X_train.shape}, {y_train.shape}")
print(f"Test: {X_test.shape}, {y_test.shape}")
```

Train: (33, 132), (33,) Test: (9, 132), (9,)

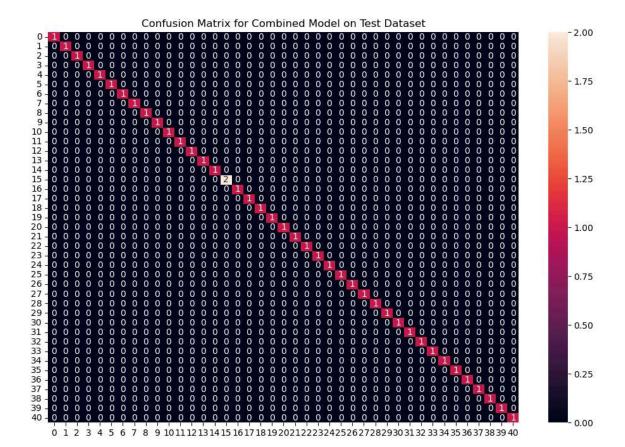
```
In [7]: # Training and testing SVM Classifier
        svm_model = SVC()
        svm model.fit(X train, y train)
        preds = svm model.predict(X test)
        print(f"Accuracy on train data by SVM Classifier\
        : {accuracy_score(y_train, svm_model.predict(X_train))*100}")
        print(f"Accuracy on test data by SVM Classifier\
        : {accuracy score(y test, preds)*100}")
        cf_matrix = confusion_matrix(y_test, preds)
        plt.figure(figsize=(12,8))
        sns.heatmap(cf_matrix, annot=True)
        plt.title("Confusion Matrix for SVM Classifier on Test Data")
        plt.show()
        # Training and testing Naive Bayes Classifier
        nb model = GaussianNB()
        nb_model.fit(X_train, y_train)
        preds = nb_model.predict(X_test)
        print(f"Accuracy on train data by Naive Bayes Classifier\
        : {accuracy_score(y_train, nb_model.predict(X_train))*100}")
        print(f"Accuracy on test data by Naive Bayes Classifier\
        : {accuracy_score(y_test, preds)*100}")
        cf_matrix = confusion_matrix(y_test, preds)
        plt.figure(figsize=(12,8))
        sns.heatmap(cf matrix, annot=True)
        plt.title("Confusion Matrix for Naive Bayes Classifier on Test Data")
        plt.show()
        # Training and testing Random Forest Classifier
        rf_model = RandomForestClassifier(random_state=18)
        rf model.fit(X train, y train)
        preds = rf model.predict(X test)
        print(f"Accuracy on train data by Random Forest Classifier\
        : {accuracy_score(y_train, rf_model.predict(X_train))*100}")
        print(f"Accuracy on test data by Random Forest Classifier\
        : {accuracy score(y test, preds)*100}")
        cf_matrix = confusion_matrix(y_test, preds)
        plt.figure(figsize=(12,8))
        sns.heatmap(cf_matrix, annot=True)
        plt.title("Confusion Matrix for Random Forest Classifier on Test Data")
        plt.show()
```

```
In [9]:
        # Training the models on whole data
        final_svm_model = SVC()
        final nb model = GaussianNB()
        final rf model = RandomForestClassifier(random state=18)
        final svm model.fit(X, y)
        final nb model.fit(X, y)
        final_rf_model.fit(X, y)
        # Reading the test data
        test data = pd.read csv("Testing.csv").dropna(axis=1)
        test X = test data.iloc[:, :-1]
        test_Y = encoder.transform(test_data.iloc[:, -1])
        # Making prediction by take mode of predictions
        # made by all the classifiers
        svm_preds = final_svm_model.predict(test_X)
        nb preds = final nb model.predict(test X)
        rf_preds = final_rf_model.predict(test_X)
        final_preds = [mode([i,j,k])[0][0] for i,j,
                    k in zip(svm_preds, nb_preds, rf_preds)]
        print(f"Accuracy on Test dataset by the combined model\
        : {accuracy score(test Y, final preds)*100}")
        cf_matrix = confusion_matrix(test_Y, final_preds)
        plt.figure(figsize=(12,8))
        sns.heatmap(cf matrix, annot = True)
        plt.title("Confusion Matrix for Combined Model on Test Dataset")
        plt.show()
```

C:\Users\anith\AppData\Local\Temp\ipykernel_2040\2510567820.py:21: FutureW arning: Unlike other reduction functions (e.g. `skew`, `kurtosis`), the de fault behavior of `mode` typically preserves the axis it acts along. In Sc iPy 1.11.0, this behavior will change: the default value of `keepdims` wil l become False, the `axis` over which the statistic is taken will be elimi nated, and the value None will no longer be accepted. Set `keepdims` to Tr ue or False to avoid this warning.

final_preds = [mode([i,j,k])[0][0] for i,j,

Accuracy on Test dataset by the combined model: 100.0



```
In [10]:
         symptoms = X.columns.values
         # Creating a symptom index dictionary to encode the
         # input symptoms into numerical form
         symptom index = {}
         for index, value in enumerate(symptoms):
             symptom = " ".join([i.capitalize() for i in value.split("_")])
             symptom_index[symptom] = index
         data dict = {
             "symptom_index":symptom_index,
             "predictions_classes":encoder.classes_
         }
         # Defining the Function
         # Input: string containing symptoms separated by commas
         # Output: Generated predictions by models
         def predictDisease(symptoms):
             symptoms = symptoms.split(",")
             # creating input data for the models
             input_data = [0] * len(data_dict["symptom_index"])
             for symptom in symptoms:
                 index = data_dict["symptom_index"][symptom]
                 input data[index] = 1
             # reshaping the input data and converting it
             # into suitable format for model predictions
             input data = np.array(input data).reshape(1,-1)
             # generating individual outputs
             rf_prediction = data_dict["predictions_classes"][final_rf_model.predict
             nb_prediction = data_dict["predictions_classes"][final_nb_model.predict
             svm prediction = data dict["predictions classes"][final svm model.predictions
             # making final prediction by taking mode of all predictions
             final_prediction = mode([rf_prediction, nb_prediction, svm_prediction])
             predictions = {
                 "rf_model_prediction": rf_prediction,
                 "naive_bayes_prediction": nb_prediction,
                 "svm model prediction": svm prediction,
                 "final_prediction":final_prediction
             }
             return predictions
         # Testing the function
         print(predictDisease("Itching, Skin Rash, Nodal Skin Eruptions"))
```

{'rf_model_prediction': 'Fungal infection', 'naive_bayes_prediction': 'Fungal infection', 'svm_model_prediction': 'Fungal infection', 'final_prediction': 'Fungal infection'}

C:\Users\anith\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarnin
g: X does not have valid feature names, but RandomForestClassifier was fit
ted with feature names

warnings.warn(

C:\Users\anith\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarnin
g: X does not have valid feature names, but GaussianNB was fitted with fea
ture names

warnings.warn(

C:\Users\anith\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarnin
g: X does not have valid feature names, but SVC was fitted with feature na
mes

warnings.warn(

C:\Users\anith\AppData\Local\Temp\ipykernel_2040\95506011.py:37: FutureWar ning: Unlike other reduction functions (e.g. `skew`, `kurtosis`), the default behavior of `mode` typically preserves the axis it acts along. In SciP y 1.11.0, this behavior will change: the default value of `keepdims` will become False, the `axis` over which the statistic is taken will be eliminated, and the value None will no longer be accepted. Set `keepdims` to True or False to avoid this warning.

final_prediction = mode([rf_prediction, nb_prediction, svm_prediction])
[0][0]

C:\Users\anith\anaconda3\lib\site-packages\scipy\stats_stats_py.py:110: R untimeWarning: The input array could not be properly checked for nan value s. nan values will be ignored.

warnings.warn("The input array could not be properly "

C:\Users\anith\AppData\Local\Temp\ipykernel_2040\95506011.py:37: Deprecati onWarning: Support for non-numeric arrays has been deprecated as of SciPy 1.9.0 and will be removed in 1.11.0. `pandas.DataFrame.mode` can be used i nstead, see https://pandas.pydata.org/docs/reference/api/pandas.DataFrame.mode.html. (https://pandas.pydata.org/docs/reference/api/pandas.DataFrame.mode.html.)

final_prediction = mode([rf_prediction, nb_prediction, svm_prediction])
[0][0]

In []:	in []:	
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