```
In [147]: import pandas as pd
   import matplotlib.pyplot as plt
   import numpy as np
   import seaborn as sns
   from sklearn import preprocessing
   from sklearn.ensemble import RandomForestClassifier
   from sklearn.metrics import classification_report, roc_auc_score
   from imblearn.over_sampling import SMOTE
   from sklearn.svm import SVC
   from sklearn.metrics import accuracy_score
```

Data PreprPreprocessing

: disea	disease							
	male	age	education	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	prevalentHyp
0	1	39	4.0	0	0.0	0.0	0	С
1	0	46	2.0	0	0.0	0.0	0	С
2	1	48	1.0	1	20.0	0.0	0	C
3	0	61	3.0	1	30.0	0.0	0	1
4	0	46	3.0	1	23.0	0.0	0	С
4235	0	48	2.0	1	20.0	NaN	0	С
4236	0	44	1.0	1	15.0	0.0	0	С
4237	0	52	2.0	0	0.0	0.0	0	C
4238	1	40	3.0	0	0.0	0.0	0	1
4239	0	39	3.0	1	30.0	0.0	0	С

Renaming the male column to Sex_male to know that 1 is male and 0 is female

```
In [50]: disease.rename(columns={'male' : 'Sex_male'}, inplace = True)
```

In [51]:	disease	

Out[51]:		Sex_male	age	education	currentSmoker	cigsPerDay	BPMeds	prevalentStroke	prevale
	0	1	39	4.0	0	0.0	0.0	0	
	1	0	46	2.0	0	0.0	0.0	0	
	2	1	48	1.0	1	20.0	0.0	0	
	3	0	61	3.0	1	30.0	0.0	0	
	4	0	46	3.0	1	23.0	0.0	0	
	4235	0	48	2.0	1	20.0	NaN	0	
	4236	0	44	1.0	1	15.0	0.0	0	
	4237	0	52	2.0	0	0.0	0.0	0	
	4238	1	40	3.0	0	0.0	0.0	0	
	4239	0	39	3.0	1	30.0	0.0	0	
	4240 r	ows × 16 c	olumr	าร					
	4								•

Handling the missing values

```
In [54]: disease.isnull().sum()
Out[54]: Sex_male
                                0
          age
                                0
          currentSmoker
                                0
                               29
          cigsPerDay
          BPMeds
                               53
          prevalentStroke
                               0
          prevalentHyp
                                0
          diabetes
                                0
          totChol
                               50
                                0
          sysBP
          diaBP
                               0
          BMI
                               19
         heartRate
                                1
          glucose
                              388
         TenYearCHD
                                0
         dtype: int64
In [55]: disease['cigsPerDay'].skew()
```

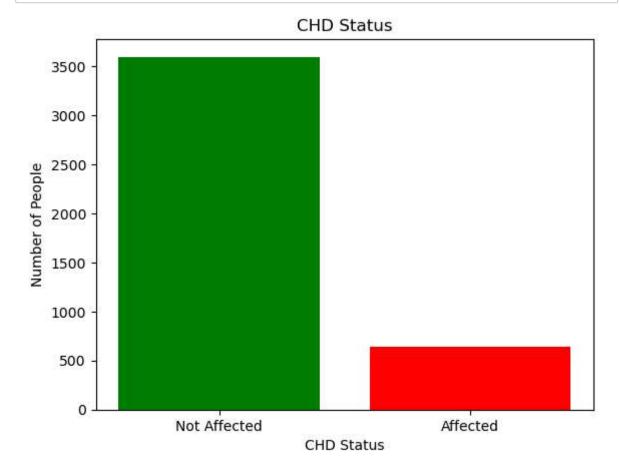
Out[55]: 1.2470523561848126

```
In [56]: #As the skew of cigsPerDay is greater than 0 so we fill the null value of t
         disease['cigsPerDay'] = disease['cigsPerDay'].fillna(disease['cigsPerDay'].
In [57]: |disease['totChol'].skew()
Out[57]: 0.8718805634765354
In [58]: #As the skew is 0.87 which is greater than 0 so we fill the null value of t
         disease['totChol']=disease['totChol'].fillna(disease['totChol'].mean())
In [59]: #As the BPMeds is in binary form so we use mode to fill the null values
         disease['BPMeds']=disease['BPMeds'].fillna(disease['BPMeds'].mode()[0])
In [60]: | disease['BMI'].skew()
Out[60]: 0.9821832986950597
In [61]: | #As the skew is 0.98 which is greater than 0 so we fill the null value of E
         disease['BMI']=disease['BMI'].fillna(disease['BMI'].median())
In [62]: |disease['glucose'].skew()
Out[62]: 6.2149483495346765
In [63]: #As the skew is 6.214 which is highly greater than 0 so we fill the null vo
         disease['glucose']=disease['glucose'].fillna(disease['glucose'].median())
In [64]: | disease.isnull().sum()
Out[64]: Sex male
                             0
                             0
         age
         currentSmoker
                             0
         cigsPerDay
                             0
         BPMeds
         prevalentStroke
                             0
         prevalentHyp
                             0
         diabetes
                             a
         totChol
                             0
         sysBP
                             0
         diaBP
                             0
         BMI
                             0
         heartRate
                             1
         glucose
                             a
         TenYearCHD
         dtype: int64
```

Making a Bar Plot to Count people affected by CHD

```
In [65]: counts = disease["TenYearCHD"].value_counts()

plt.bar(["Not Affected", "Affected"], counts, color=["green", "red"])
plt.title("CHD Status")
plt.ylabel("Number of People")
plt.xlabel("CHD Status")
plt.show()
```



Spliting the data

```
In [66]: X = np.asarray(disease[['age', 'Sex_male', 'cigsPerDay',
                                     'totChol', 'sysBP', 'glucose']])
         y = np.asarray(disease['TenYearCHD'])
         # normalization of the dataset
         X = preprocessing.StandardScaler().fit transform(X)
         # Train test split
         from sklearn.model selection import train test split
         X train,X test,y train,y test = train test split(X,y, test size=0.3, random
         print(f"Train set: {X_train.shape} {y_train.shape}")
         print(f"Test set: {X test.shape} {y test.shape}")
         Train set: (2968, 6) (2968,)
         Test set: (1272, 6) (1272,)
In [67]: # As you can see from the barplot there is a bias in data so we use smote
         # Handle class imbalance with SMOTE (Oversampling the minority class)
         smote = SMOTE(random state=42)
         X_resampled, y_resampled = smote.fit_resample(X_train, y_train)
         print(f"Train set: {X_resampled.shape} {y_resampled.shape}")
         print(f"Test set: {X_test.shape} {y_test.shape}")
         Train set: (5024, 6) (5024,)
         Test set: (1272, 6) (1272,)
```

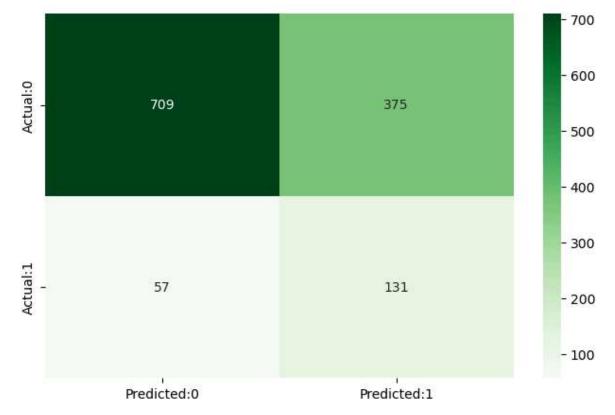
Fitting Logistic Regresssion Model for Heart Disease Prediction

```
In [111]: from sklearn.linear_model import LogisticRegression
    model = LogisticRegression()
    model.fit(X_resampled,y_resampled)
    y_pred = model.predict(X_test)
```

Checking the Accuracy of the model

```
In [114]: score_lr=round(accuracy_score(y_test,y_pred)*100,2)
    roc_lr= round(roc_auc_score(y_test, model.predict_proba(X_test)[:, 1])*100,
    print("Accuracy of the model is =",score_lr)
    print("ROC-AUC Score:",roc_lr)

Accuracy of the model is = 66.04
    ROC-AUC Score: 72.07
```



The details for confusion matrix is = precision recall f1-score support 0 0.93 0.65 0.77 1084 1 0.26 0.70 0.38 188 accuracy 0.66 1272 macro avg 0.59 0.68 0.57 1272 weighted avg 0.83 0.66 0.71 1272

Fitting Random Forest Clasifier for Heart Disease Prediction

```
In [116]: # Train a model
    model_RFC = RandomForestClassifier(class_weight='balanced', random_state=42
    model_RFC.fit(X_resampled, y_resampled)

# Evaluate
    y_pred = model_RFC.predict(X_test)

    print(classification_report(y_test, y_pred))

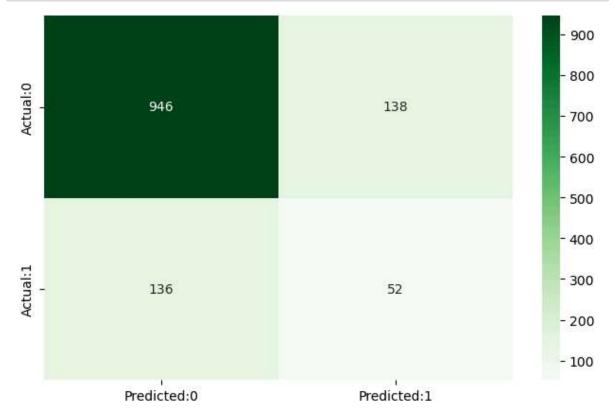
    score_rf = round(accuracy_score(y_test,y_pred)*100,2)
    roc_rf = round( roc_auc_score(y_test, model_RFC.predict_proba(X_test)[:, 1]

    print("Accuracy of the model: ",score_rf)
    print("ROC-AUC Score:",roc_rf)
```

	precision	recall	f1-score	support
0	0.87	0.87	0.87	1084
1	0.27	0.28	0.28	188
accuracy			0.78	1272
macro avg	0.57	0.57	0.57	1272
weighted avg	0.79	0.78	0.79	1272

Accuracy of the model: 78.46

ROC-AUC Score: 68.62



The details for confusion matrix is = precision recall f1-score support 0 0.87 0.87 0.87 1084 1 0.27 0.28 0.28 188 0.78 accuracy 1272 macro avg 0.57 0.57 0.57 1272 weighted avg 0.79 0.78 0.79 1272

Fitting SVC while using gaussian rbf kernel for Heart Disease Prediction

```
In [121]: # Train the SVC model with class weights
svc = SVC(kernel='rbf', class_weight='balanced', probability=True, random_s
svc.fit(X_resampled, y_resampled)

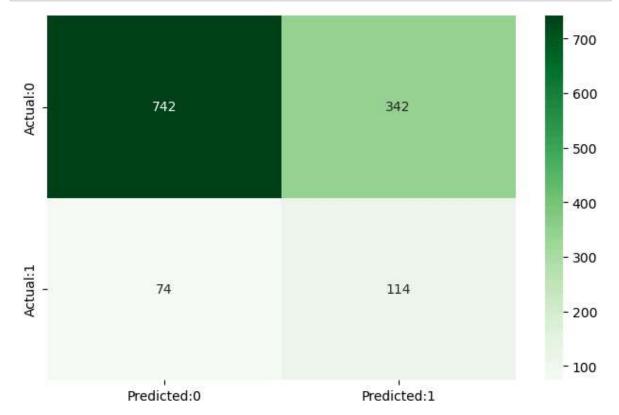
# Make predictions and evaluate the model
y_pred = svc.predict(X_test)

# Evaluate performance
roc_svc_rbf = round(roc_auc_score(y_test, svc.predict_proba(X_test)[:, 1])*
score_svc_rbf = round(accuracy_score(y_test,y_pred)*100,2)

print(classification_report(y_test, y_pred))
print("Acurracy of the model is :",score_svc_rbf)
print("ROC-AUC Score:",roc_svc_rbf)
```

	precision	recall	f1-score	support
0	0.91	0.68	0.78	1084
1	0.25	0.61	0.35	188
accuracy	0.50	0.65	0.67	1272
macro avg	0.58	0.65	0.57	1272
weighted avg	0.81	0.67	0.72	1272

Acurracy of the model is : 67.3 ROC-AUC Score: 69.62



The details for confusion matrix is = precision recall f1-score support 0 0.91 0.68 0.78 1084 1 0.25 0.61 0.35 188 0.67 accuracy 1272 macro avg 0.58 0.65 0.57 1272 weighted avg 0.81 0.67 0.72 1272

Fitting SVC while using linear kernel for Heart Disease Prediction

```
In [123]: # Train the model
linear_svc_model=SVC(kernel="linear", class_weight="balanced", probability=
linear_svc_model.fit(X_resampled,y_resampled)

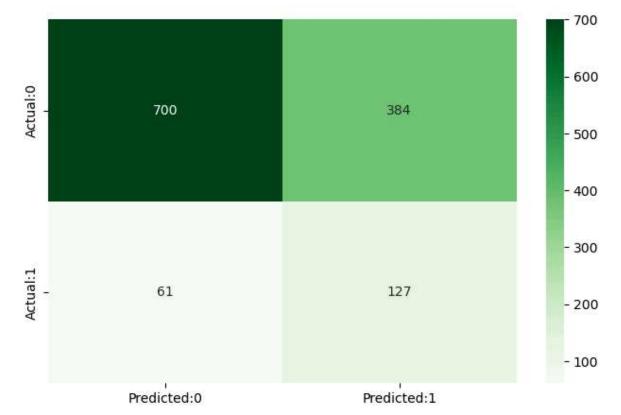
# Make predictions and evaluate the model
y_pred = linear_svc_model.predict(X_test)

# Evaluate the model
score_linearsvc = round(accuracy_score(y_test,y_pred)*100,2)
roc_linearsvc = round(roc_auc_score(y_test, linear_svc_model.predict_proba(print(classification_report(y_test, y_pred))
print("Acurracy of the model is :",score_linearsvc)
print("ROC-AUC Score:", roc_linearsvc)
```

	precision	recall	f1-score	support
0	0.92 0.25	0.65 0.68	0.76 0.36	1084 188
-	0.23	0.00	0.30	100
accuracy			0.65	1272
macro avg	0.58	0.66	0.56	1272
weighted avg	0.82	0.65	0.70	1272

Acurracy of the model is : 65.02

ROC-AUC Score: 71.87



The details for confusion matrix is = precision recall f1-score support 0.92 0 0.76 0.65 1084 1 0.25 0.68 0.36 188 0.65 accuracy 1272 macro avg 0.58 0.66 0.56 1272 weighted avg 0.82 0.65 0.70 1272

```
In [131]: # Train the model
    poly_svc_model=SVC(kernel="poly", degree=4, coef0=1, class_weight="balanced
    poly_svc_model.fit(X_resampled,y_resampled)

# Make predictions and evaluate the model
    y_train_predict =poly_svc_model.predict(X_resampled)
    y_pred = poly_svc_model.predict(X_test)

# Evaluate the model
    score_polysvc = round(accuracy_score(y_test,y_pred)*100,2)
    roc_polysvc = round(roc_auc_score(y_test,poly_svc_model.predict_proba(X_test)

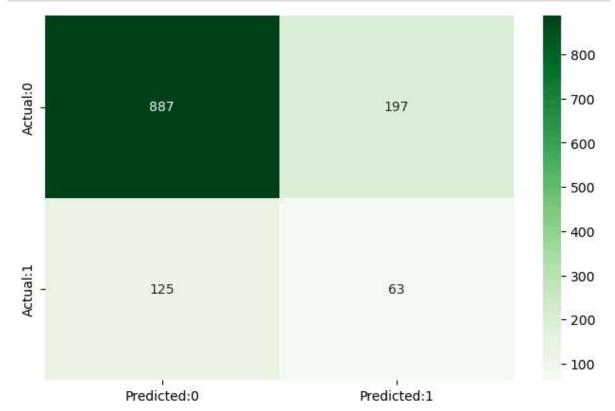
print(classification_report(y_test, y_pred))
    print("Acurracy of the model is :",score_polysvc)
    print("ROC-AUC Score:", roc_polysvc)
    print("Acurracy of the model on training is :",accuracy_score(y_resampled,y)
```

support	f1-score	recall	precision	
1084 188	0.78 0.32	0.69 0.54	0.90 0.23	0
100	0.32	0.54	0.23	1
1272	0.67			accuracy
1272	0.55	0.61	0.56	macro avg
1272	0.71	0.67	0.80	weighted avg

Acurracy of the model is : 66.9

ROC-AUC Score: 65.18

Acurracy of the model on training is: 0.7231289808917197



The details for confusion matrix is = precision recall f1-score support 0 0.88 0.82 0.85 1084 1 0.24 0.34 0.28 188 0.75 accuracy 1272 macro avg 0.56 0.58 0.56 1272 weighted avg 0.78 0.75 0.76 1272

Final Output

```
In [142]: scores= [score_lr,score_linearsvc,score_polysvc,score_rf,score_svc_rbf]
    rocs = [roc_lr,roc_linearsvc,roc_polysvc,roc_rf,roc_svc_rbf]
    algorithms = ["Logistic Regression","LinearSVC","Polynomial SVC","Random Fc

for i in range(len(algorithms)):
    print(f"The Accuracy and ROC score achieved using {algorithms[i]} is: {
```

The Accuracy and ROC score achieved using Logistic Regression is: 66.04% and 72.07%

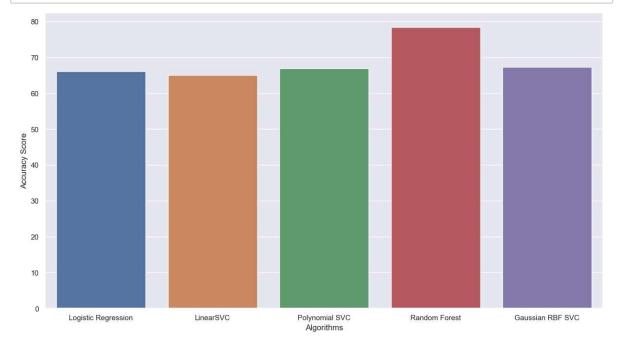
The Accuracy and ROC score achieved using LinearSVC is: 65.02% and 71.87% The Accuracy and ROC score achieved using Polynomial SVC is: 66.9% and 6 5.18%

The Accuracy and ROC score achieved using Random Forest is: 78.46% and 6 8.62%

The Accuracy and ROC score achieved using Gaussian RBF SVC is: 67.3% and 69.62%

```
In [145]: sns.set(rc={'figure.figsize': (15, 8)})
    plt.xlabel("Algorithms")
    plt.ylabel("Accuracy Score")

# Explicitly specify x and y
    sns.barplot(x=algorithms, y=scores)
    plt.show()
```



```
In [ ]:
```