In [1]:

```
import warnings
warnings.filterwarnings('ignore')
import numpy as np
import pandas as pd
import random
import matplotlib.pyplot
%matplotlib inline

#model validation
from sklearn.metrics import classification_report,confusion_matrix,precision_score,f1_score
from sklearn import metrics

# cross validation
from sklearn.model_selection import StratifiedKFold
from sklearn.svm import SVC
```

In [2]:

```
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score
from sklearn import metrics
```

In [3]:

```
#import the heart disease dataset
df = pd.read_csv("heart_statlog.csv")
df
```

Out[3]:

	age	sex	chest	resting_blood_pressure	serum_cholestoral	fasting_blood_sugar	resting_6
0	70	1	4	130	322	0	
1	67	0	3	115	564	0	
2	57	1	2	124	261	0	
3	64	1	4	128	263	0	
4	74	0	2	120	269	0	
265	52	1	3	172	199	1	
266	44	1	2	120	263	0	
267	56	0	2	140	294	0	
268	57	1	4	140	192	0	
269	67	1	4	160	286	0	

270 rows × 14 columns

In [4]:

```
from sklearn import preprocessing
le = preprocessing.LabelEncoder()
df['class'] = le.fit_transform(df["class"])
df
```

Out[4]:

		age	sex	chest	resting_blood_pressure	serum_cholestoral	fasting_blood_sugar	resting_6
	0	70	1	4	130	322	0	
	1	67	0	3	115	564	0	
	2	57	1	2	124	261	0	
	3	64	1	4	128	263	0	
	4	74	0	2	120	269	0	
26	5	52	1	3	172	199	1	
26	6	44	1	2	120	263	0	
26	7	56	0	2	140	294	0	
26	8	57	1	4	140	192	0	
26	9	67	1	4	160	286	0	

270 rows × 14 columns

←

In [5]:

```
# segregating dataset into features i.e., X and target variables i.e., y
X = df.drop(['class'],axis=1)
y = df['class']
```

In [6]:

```
#splitting the model into training and testing set
X_train, X_test, y_train, y_test = train_test_split(X, y, stratify=y, test_size=0.2,shuffle
```

In [7]:

```
from sklearn.preprocessing import MinMaxScaler
scaler = MinMaxScaler()
X_train[['age','resting_blood_pressure','serum_cholestoral','maximum_heart_rate_achieved','
X_train.head()
```

Out[7]:

	age	sex	chest	resting_blood_pressure	serum_cholestoral	fasting_blood_sugar re	Si
197	0.465116	0	3	0.10	0.302405	0	_
174	0.000000	1	1	0.18	0.192440	0	
173	0.790698	0	3	0.20	0.292096	0	
249	0.604651	1	4	0.45	0.536082	0	
207	0.558140	1	3	0.05	0.391753	0	

→

In [8]:

```
from sklearn.preprocessing import MinMaxScaler
scaler = MinMaxScaler()
X_test[['age','resting_blood_pressure','serum_cholestoral','maximum_heart_rate_achieved','o
X_test.head()
```

Out[8]:

	age	sex	chest	resting_blood_pressure	serum_cholestoral	fasting_blood_sugar	res
260	0.617021	0	3	0.309524	0.460241	0	
194	0.404255	1	3	0.357143	0.255422	1	
112	0.659574	0	4	0.761905	0.375904	0	
14	0.595745	0	4	0.404762	0.371084	0	
206	0.659574	0	3	0.095238	0.407229	0	
4							•

In [9]:

```
from sklearn import model selection
from sklearn.model_selection import cross_val_score
# function initializing baseline machine learning models
def GetBasedModel():
   basedModels = []
   basedModels.append(('SVM Linear' , SVC(kernel='linear',gamma='auto',probability=True))
   return basedModels
# function for performing 10-fold cross validation of all the baseline models
def BasedLine2(X_train, y_train,models):
   # Test options and evaluation metric
   num_folds = 10
   scoring = 'accuracy'
   seed = 7
   results = []
   names = []
   for name, model in models:
        kfold = model_selection.KFold(n_splits=10, random_state=None)
        cv_results = model_selection.cross_val_score(model, X_train, y_train, cv=kfold, sco
        results.append(cv_results)
        names.append(name)
        msg = "%s: %f (%f)" % (name, cv_results.mean(), cv_results.std())
        print(msg)
   return results, msg
```

In [10]:

```
models = GetBasedModel()
names,results = BasedLine2(X_train, y_train,models)
```

SVM Linear: 0.813203 (0.128437)

In [11]:

```
svc = SVC(kernel='linear',gamma='auto',probability=True)
svc.fit(X_train,y_train)
y_pred_svc = svc.predict(X_test)
```

In [12]:

Out[12]:

	Model	Accuracy	Precision	Recall	f1 score	Sensitivity	Specificity
0	SVM	0.851852	0.807692	0.875	0.84	0.875	0.833333