Machine Learning Task

classify fetal health to avoid the abnormalities for the child and mother while giving birth

Importing libraries

In [1]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import plotly.express as px
from sklearn.model_selection import train_test_split
from sklearn import preprocessing
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import Pipeline
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
#from sklearn.svm import LinearSVC
#from sklearn.model_selection import GridSearchCV
from sklearn.model_selection import cross_val_score
from sklearn.metrics import precision_score, recall_score, confusion_matrix, classificat
from sklearn import metrics
#from sklearn.metrics import roc_curve, auc, roc_auc_score
```

In [2]:
```
import warnings
warnings.filterwarnings("ignore")
```

Load Data

In [3]:
```
train_data = pd.read_csv("train.csv")
test_data=pd.read_csv("test.csv")
val_data=pd.read_csv("val.csv")
```

comparing test and validation data

In [4]:
```
test_data.shape
```

Out[4]:
```
(426, 21)
```

In [5]:
```
val_data.shape
```

Out[5]:
```
(426, 21)
```

In [6]:
```
com=test_data[test_data.apply(tuple,1).isin(val_data.apply(tuple,1))]
```

In [7]:
```
scv=com.to_csv("sample.csv",index=False)
```

In [8]:
```
diff=pd.read_csv("sample.csv")
```

In [9]:
```
diff.shape
```

Out[9]:
```
(426, 21)
```

As seen there is no difference between test and validataion set

Pre-processing and EDA

In [10]:
```
train_data.head()
```

Out[10]:

	baseline value	accelerations	fetal_movement	uterine_contractions	light_decelerations	severe_decelerations	prolong
0	142.0	0.000	0.000	0.007	0.000	0.0	
1	122.0	0.000	0.000	0.006	0.002	0.0	
2	129.0	0.005	0.003	0.001	0.000	0.0	
3	136.0	0.006	0.000	0.008	0.000	0.0	
4	144.0	0.000	0.000	0.006	0.000	0.0	

5 rows × 22 columns

In [11]:
```
train_data.isnull().sum()  #No null values
```

Out[11]:
```
baseline value                                            0
accelerations                                             0
fetal_movement                                            0
uterine_contractions                                      0
light_decelerations                                       0
severe_decelerations                                      0
prolongued_decelerations                                  0
abnormal_short_term_variability                           0
mean_value_of_short_term_variability                      0
percentage_of_time_with_abnormal_long_term_variability    0
mean_value_of_long_term_variability                       0
histogram_width                                           0
histogram_min                                             0
histogram_max                                             0
histogram_number_of_peaks                                 0
histogram_number_of_zeroes                                0
histogram_mode                                            0
histogram_mean                                            0
histogram_median                                          0
histogram_variance                                        0
histogram_tendency                                        0
fetal_health                                              0
dtype: int64
```

In [12]:
```
train_data.describe()
```

Out[12]:

	baseline value	accelerations	fetal_movement	uterine_contractions	light_decelerations	severe_decelerations
count	1700.000000	1700.000000	1700.000000	1700.000000	1700.000000	1700.000000
mean	133.213529	0.003212	0.010211	0.004356	0.001899	0.000004
std	9.873344	0.003888	0.050124	0.002943	0.002976	0.000059
min	106.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	126.000000	0.000000	0.000000	0.002000	0.000000	0.000000
50%	133.000000	0.002000	0.000000	0.004000	0.000000	0.000000

75%	140.000000	0.006000	0.003000	0.006000	0.003000	0.000000
max	159.000000	0.019000	0.481000	0.015000	0.015000	0.001000

8 rows × 22 columns

In [13]:
```
train_data.duplicated().sum()
```

Out[13]:
```
7
```

In [14]:
```
train_df=train_data.drop_duplicates()
```

In [15]:
```
train_df.duplicated().sum()
```

Out[15]:
```
0
```

In [16]:
```
train_df.shape
```

Out[16]:
```
(1693, 22)
```

In [17]:
```
train_df.nunique()
```

Out[17]:
```
baseline value                                             47
accelerations                                              20
fetal_movement                                             92
uterine_contractions                                       16
light_decelerations                                        16
severe_decelerations                                        2
prolongued_decelerations                                    6
abnormal_short_term_variability                            75
mean_value_of_short_term_variability                       57
percentage_of_time_with_abnormal_long_term_variability     84
mean_value_of_long_term_variability                       240
histogram_width                                           153
histogram_min                                             109
histogram_max                                              85
histogram_number_of_peaks                                  18
histogram_number_of_zeroes                                  7
histogram_mode                                             84
histogram_mean                                             99
histogram_median                                           91
histogram_variance                                        127
histogram_tendency                                          3
fetal_health                                                3
dtype: int64
```

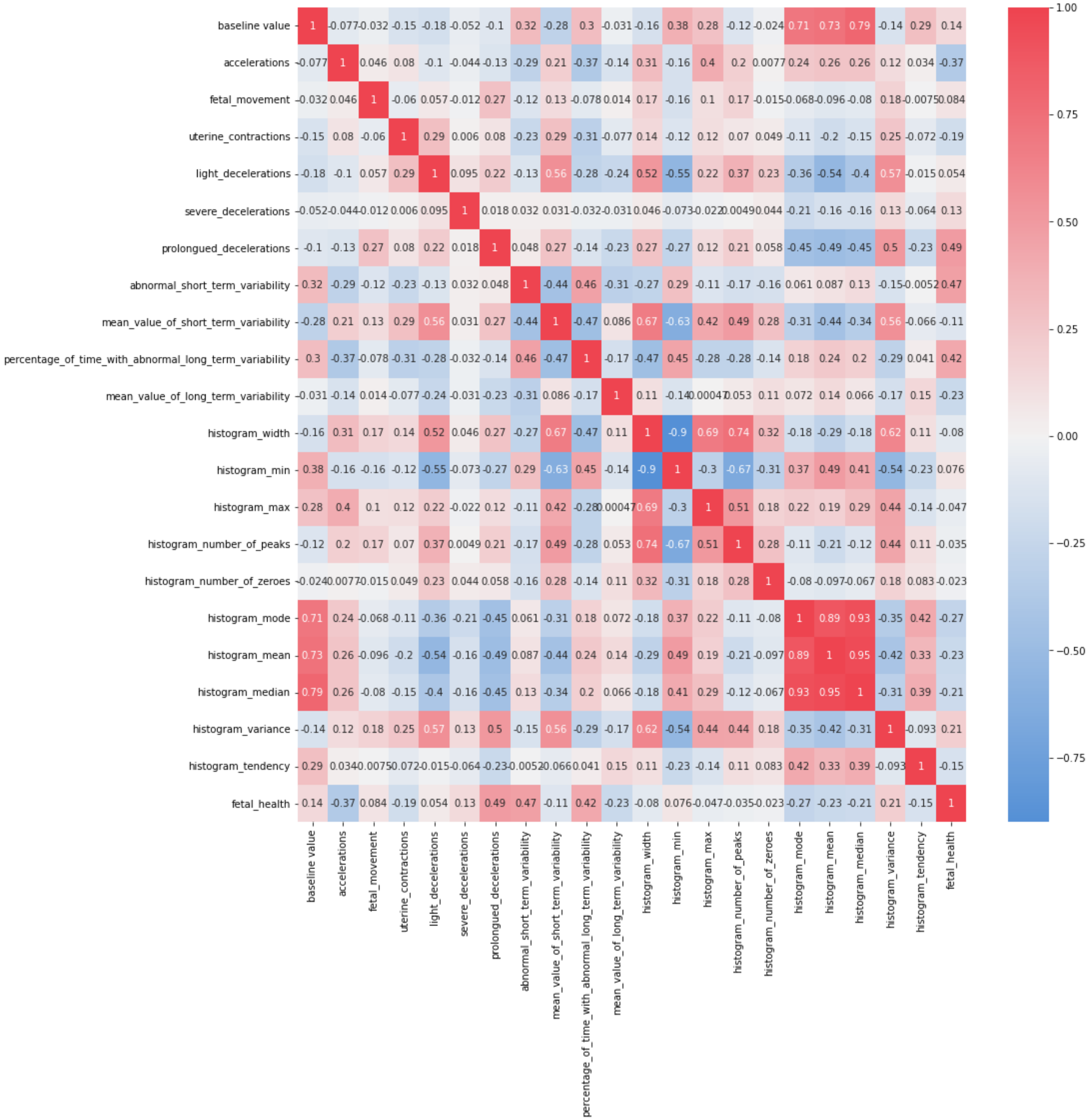
In [18]:
```
train_df['fetal_health'].unique()
```

Out[18]:
```
array([1., 3., 2.])
```

In [19]:
```
train_df['fetal_health'].value_counts()
```

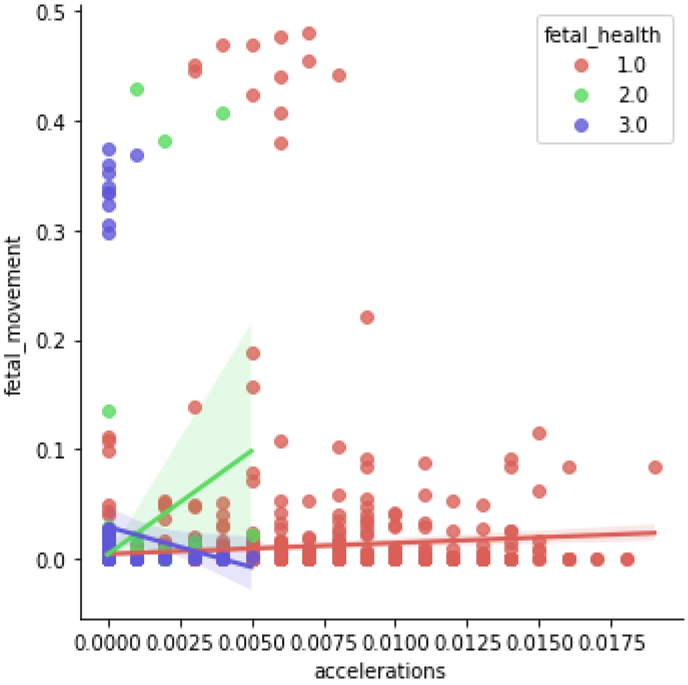
Out[19]:
```
1.0    1317
2.0     235
3.0     141
Name: fetal_health, dtype: int64
```

In [20]:
```
plt.figure(figsize=(15,15))
cmap = sns.diverging_palette(250,10, s=80, l=55, n=9, as_cmap=True)
sns.heatmap(train_df.corr(),annot=True,cmap = cmap, center=0)
plt.show()
```

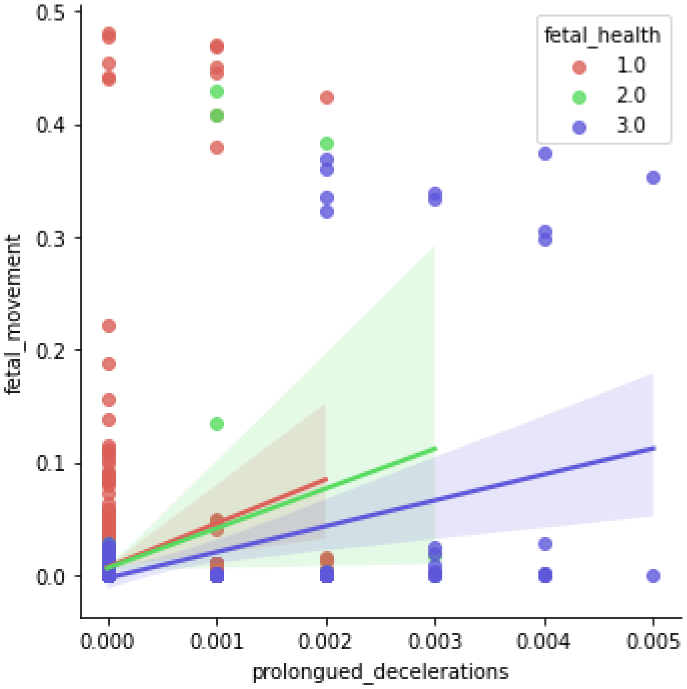


In [21]:

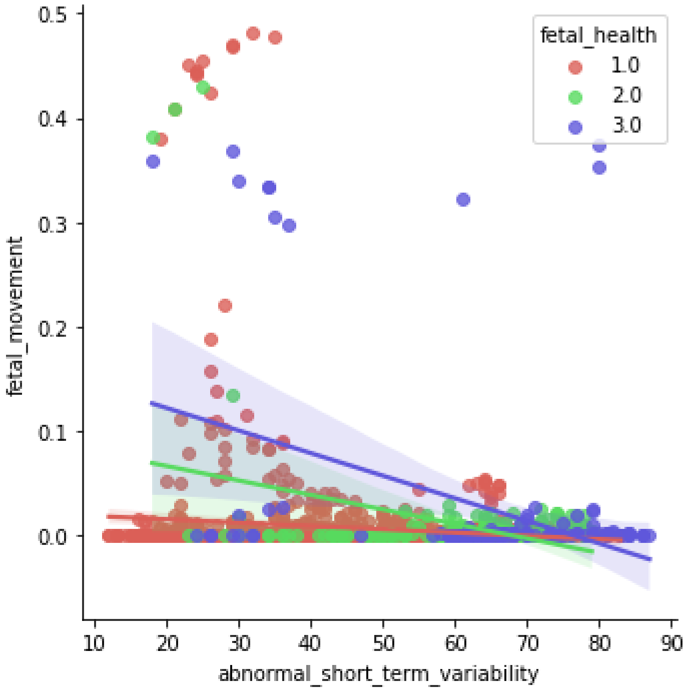
```
sns.lmplot(data = train_df, x = "accelerations", y = "fetal_movement", palette = 'hls',
plt.show()
```



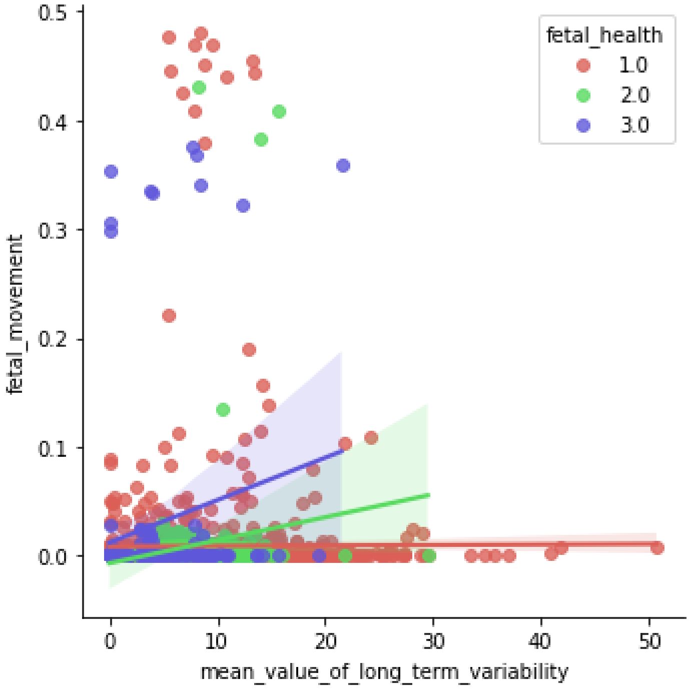
In [22]:
```
sns.lmplot(data = train_df, x = "prolongued_decelerations", y = "fetal_movement", palett
plt.show()
```



In [23]:
```
sns.lmplot(data = train_df, x = "abnormal_short_term_variability", y = "fetal_movement",
plt.show()
```



In [24]:
```
sns.lmplot(data = train_df, x = "mean_value_of_long_term_variability", y = "fetal_moveme
plt.show()
```



Model building

In [25]:
```
x = train_df.drop(['fetal_health'],axis=1)
y = train_df['fetal_health']
```

In [26]:
```
print(x.shape)
print(y.shape)
```

```
(1693, 21)
(1693,)
```

In [27]:
```
column_names = list(x.columns)
scaler = StandardScaler()
x_scaled = scaler.fit_transform(x)
x_df = pd.DataFrame(x_scaled, columns = column_names)
```

In [28]:

```
x_train, x_test, y_train, y_test = train_test_split(x_df, y, test_size = 0.2, random_sta
```

In [29]:

```
print(x_train.shape)
print(y_train.shape)
print(x_test.shape)
print(y_test.shape)
```

```
(1354, 21)
(1354,)
(339, 21)
(339,)
```

In [30]:

```
pipeline_lr = Pipeline([('lr_classifier', LogisticRegression(random_state= 42))])
pipeline_dt = Pipeline([('dt_classifier', DecisionTreeClassifier(random_state= 42))])
pipeline_rf = Pipeline([('rf_classifier', RandomForestClassifier())])
pipeline_svc = Pipeline([('sv_classifier', SVC())])
pipelines = [pipeline_lr, pipeline_dt, pipeline_rf, pipeline_svc]
pipe_dict = {0:'Logistic Regression', 1:'Decision Tree', 2:'Random Forest', 3:'SVC'}
```

In [31]:

```
for pipe in pipelines:
    pipe.fit(x_train, y_train)
```

Cross validation score

In [32]:

```
cv_results_accuracy = []
for i, model in enumerate(pipelines):
    cv_score = cross_val_score(model, x_train, y_train, cv = 10)
    cv_results_accuracy.append(cv_score)
    print("%s: %f " % (pipe_dict[i], cv_score.mean()))
```

```
Logistic Regression: 0.880381
Decision Tree: 0.923932
Random Forest: 0.932048
SVC: 0.892941
```

As seen above the cross validation score of random forest is high.so selecting random forest for model prediction

In [33]:

```
pred_rfc = pipeline_rf.predict(x_test)
```

In [34]:

```
print("Classification Report for classifier %s:\n%s\n" % (pipeline_rf, metrics.classific
```

```
Classification Report for classifier Pipeline(steps=[('rf_classifier', RandomForestClass
ifier())]):
              precision    recall  f1-score   support

         1.0       0.93      0.99      0.96       263
         2.0       0.93      0.58      0.72        48
         3.0       0.89      0.86      0.87        28

    accuracy                           0.92       339
   macro avg       0.92      0.81      0.85       339
weighted avg       0.92      0.92      0.92       339
```

confusion matrix and accuracy

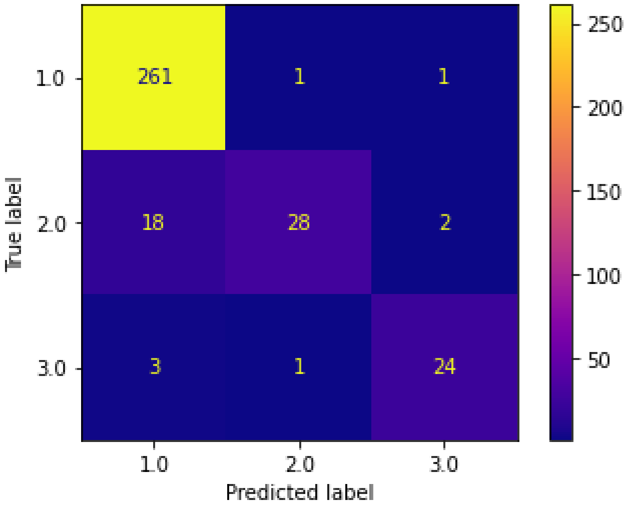
In [35]:

```
matrix = confusion_matrix(y_test, pred_rfc)
print('Confusion Matrix : \n', matrix)
```

```
Confusion Matrix :
 [[261   1   1]
 [ 18  28   2]
 [  3   1  24]]
```

In [36]:

```
from sklearn.metrics import plot_confusion_matrix
plot_confusion_matrix(pipeline_rf, x_test, y_test,cmap="plasma")
plt.show()
```



In [37]:

```
print("Accuracy"+str(accuracy_score(y_test,pred_rfc)))
```

```
Accuracy0.9233038348082596
```

Saving Model prediction

In [38]:

```
pred_rfc
```

Out[38]:

```
array([1., 1., 1., 2., 1., 1., 1., 1., 1., 1., 1., 2., 1., 1., 1., 1., 1.,
       1., 3., 1., 1., 1., 2., 1., 1., 3., 1., 1., 1., 2., 1., 1., 1., 1.,
       1., 1., 1., 1., 3., 1., 1., 1., 1., 2., 1., 3., 1., 1., 1., 1., 1.,
       1., 1., 1., 1., 3., 1., 1., 2., 1., 1., 1., 1., 1., 2., 3., 3., 1.,
       1., 1., 1., 1., 1., 1., 1., 1., 2., 1., 1., 1., 1., 1., 1., 1., 1.,
       3., 1., 1., 1., 1., 1., 1., 1., 3., 1., 1., 1., 1., 2., 1., 2., 1.,
       1., 2., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 2., 1., 1., 1., 1.,
       1., 1., 1., 2., 1., 1., 1., 1., 1., 1., 1., 1., 2., 1., 1., 1., 1.,
       1., 1., 1., 1., 1., 2., 1., 1., 3., 1., 1., 1., 1., 1., 1., 1., 1.,
       1., 1., 1., 1., 1., 1., 2., 1., 1., 1., 1., 1., 1., 2., 1., 2., 1.,
       1., 1., 1., 1., 1., 1., 1., 2., 1., 3., 1., 1., 1., 3., 1., 3., 3.,
       1., 2., 1., 1., 3., 1., 1., 1., 1., 1., 2., 1., 1., 1., 1., 1., 2.,
       1., 1., 1., 3., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1.,
       1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 3., 1.,
       1., 1., 2., 1., 1., 1., 1., 3., 2., 1., 1., 1., 1., 1., 1., 1., 1.,
       1., 1., 1., 2., 1., 3., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1., 3.,
       1., 1., 1., 1., 3., 1., 3., 1., 1., 1., 1., 1., 1., 1., 1., 1., 1.,
       1., 1., 1., 3., 1., 1., 2., 1., 1., 1., 2., 1., 1., 1., 1., 1., 3.,
       1., 1., 1., 3., 1., 1., 1., 1., 1., 1., 1., 2., 1., 1., 3., 1., 1.,
       1., 1., 1., 1., 1., 1., 1., 2., 1., 1., 2., 1., 1., 3., 1., 1.])
```

In [39]:

```
df = pd.DataFrame(pred_rfc,columns =['fetal_health'])
```

In [40]:

```
df.head()
```

Out[40]:

	fetal_health
0	1.0
1	1.0

2	1.0
3	2.0
4	1.0

In [41]:

```
df.to_csv('output.csv',header=df.columns,index=False)
```

In [42]:

```
dfg=pd.read_csv("output.csv")
dfg.head()
```

Out[42]:

	fetal_health
0	1.0
1	1.0
2	1.0
3	2.0
4	1.0

In [43]:

```
dfg.shape
```

Out[43]:

```
(339, 1)
```