Breast_Cancer_Survival_Prediction

About Dataset Breast cancer is a type of cancer that develops in the cells of the breast. It occurs when the cells in the breast grow and divide uncontrollably, forming a mass or lump. Breast cancer can spread to other parts of the body if not detected and treated early.

The dataset contains information on breast cancer patients, including their Patient_ID, Age, Gender, and expression levels of four proteins (Protein1, Protein2, Protein3, Protein4). The dataset also includes the Breast cancer stage of the patient (Tumor_Stage), Histology (type of cancer), ER, PR, and HER2 status, Surgery_type, Date of Surgery, Date of Last Visit, and Patient Status (Alive/Dead).

This information can be used to analyze the relationship between protein expression levels, cancer stage, and patient outcomes. It can also be used to understand the impact of different types of surgeries on patient survival and to identify potential risk factors for breast cancer progression.

```
In [2]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import plotly.express as px
import warnings
warnings.filterwarnings('ignore')
In [3]: df=pd.read_csv('downloads/breast_cancer_survival.csv')
df.head()
```

Out[3]:		Age	Gender	Protein1	Protein2	Protein3	Protein4	Tumour_Stage	Histology	ER status	PR status	HER2 status	Surgery_type	Date_c
	0	42	FEMALE	0.95256	2.15000	0.007972	-0.048340	II	Infiltrating Ductal Carcinoma	Positive	Positive	Negative	Other	;
	1	54	FEMALE	0.00000	1.38020	-0.498030	-0.507320	II	Infiltrating Ductal Carcinoma	Positive	Positive	Negative	Other	
	2	63	FEMALE	-0.52303	1.76400	-0.370190	0.010815	II	Infiltrating Ductal Carcinoma	Positive	Positive	Negative	Lumpectomy	
	3	78	FEMALE	-0.87618	0.12943	-0.370380	0.132190	I	Infiltrating Ductal Carcinoma	Positive	Positive	Negative	Other	
	4	42	FEMALE	0.22611	1.74910	-0.543970	-0.390210	11	Infiltrating Ductal Carcinoma	Positive	Positive	Positive	Lumpectomy	
														•

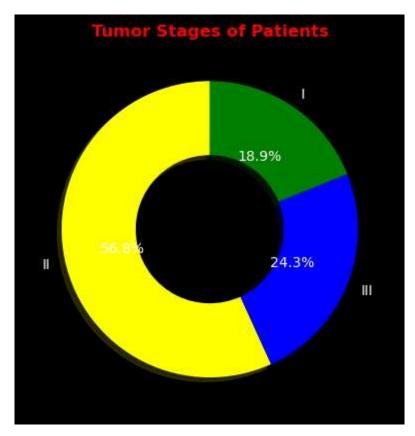
In [4]: df.info()

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 334 entries, 0 to 333
Data columns (total 15 columns):
     Column
                        Non-Null Count Dtype
 0
    Age
                        334 non-null
                                        int64
 1
    Gender
                         334 non-null
                                        object
     Protein1
                         334 non-null
                                        float64
                                        float64
    Protein2
                        334 non-null
                                        float64
    Protein3
                        334 non-null
 5
    Protein4
                         334 non-null
                                        float64
    Tumour Stage
                         334 non-null
                                        object
                                        object
     Histology
                        334 non-null
    ER status
                        334 non-null
                                        object
    PR status
                         334 non-null
                                        object
10 HER2 status
                         334 non-null
                                        object
11 Surgery type
                        334 non-null
                                        object
12 Date_of_Surgery
                        334 non-null
                                        object
13 Date of Last Visit 317 non-null
                                        object
                         321 non-null
14 Patient Status
                                         object
dtypes: float64(4), int64(1), object(10)
memory usage: 39.3+ KB
```

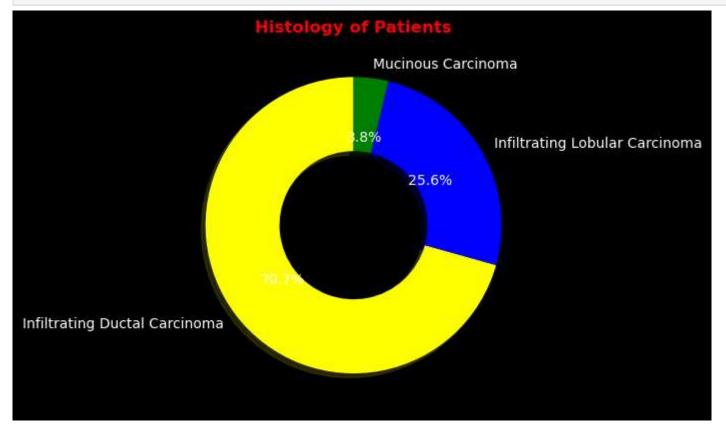
```
In [5]: df.describe()
```

Out[5]:		Age	Protein1	Protein2	Protein3	Protein4
,	count	334.000000	334.000000	334.000000	334.000000	334.000000
	mean	58.886228	-0.029991	0.946896	-0.090204	0.009819
	std	12.961212	0.563588	0.911637	0.585175	0.629055
	min	29.000000	-2.340900	-0.978730	-1.627400	-2.025500
	25%	49.000000	-0.358888	0.362173	-0.513748	-0.377090
	50%	58.000000	0.006129	0.992805	-0.173180	0.041768
	75%	68.000000	0.343598	1.627900	0.278353	0.425630
	max	90.000000	1.593600	3.402200	2.193400	1.629900
In [6]:	df.isı	null().sum(()			
Out[6]:	Age Gender Protein1 Protein2 Protein3 Protein4 Tumour_Stage Histology ER status PR status HER2 status Surgery_type Date_of_Surgery Date_of_Last_Visit Patient_Status dtype: int64		0 0 0 0 0 0 0 0 0 0 sit 17 13			
In [7]:	df=df.dropna()					

```
In [8]: df.isnull().sum()
                               0
         Age
Out[8]:
         Gender
         Protein1
         Protein2
         Protein3
         Protein4
         Tumour_Stage
         Histology
         ER status
         PR status
         HER2 status
         Surgery type
         Date of Surgery
                                0
         Date of Last Visit
         Patient Status
                                0
         dtype: int64
In [9]: df.Gender.value_counts()
         FEMALE
                   313
Out[9]:
         MALE
                     4
         Name: Gender, dtype: int64
         plt.style.use('dark background')
In [10]:
         stage=df['Tumour Stage'].value counts()
         transactions=stage.index
         quantity=stage.values
         plt.pie(quantity,labels=transactions, autopct='%1.1f%%', shadow=True,
                 startangle=90, wedgeprops={'width':0.5},colors=['yellow','blue','green'])
         plt.title('Tumor Stages of Patients', weight='bold',color='red')
         plt.show()
```



plt.show()



```
In [12]: # ER Status

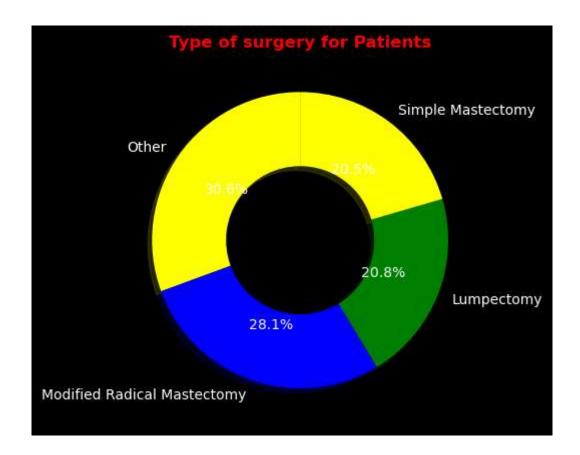
print(df['ER status'].value_counts())

#PR Status

print(df['PR status'].value_counts())

#HER2 Status
```

```
print(df['HER2 status'].value_counts())
         Positive
                     317
         Name: ER status, dtype: int64
         Positive
                     317
         Name: PR status, dtype: int64
         Negative
                     288
         Positive
                      29
         Name: HER2 status, dtype: int64
In [13]: plt.style.use('dark background')
         surgery type=df['Surgery type'].value counts()
         transactions=surgery type.index
         quantity=surgery type.values
         plt.pie(quantity,labels=transactions, autopct='%1.1f%', shadow=True,
                startangle=90, wedgeprops={'width':0.5},colors=['yellow','blue','green'])
         plt.title('Type of surgery for Patients', weight='bold',color='red')
         plt.show()
```



Data Encoding

In [28]: df.isnull().sum()

```
0
         Age
Out[28]:
                                0
         Gender
         Protein1
                                0
         Protein2
         Protein3
         Protein4
         Tumour Stage
         Histology
         ER status
         PR status
         HER2 status
         Surgery type
         Date of Surgery
                                0
         Date of Last Visit
                                0
         Patient Status
         dtype: int64
         df=df.dropna()
In [27]:
In [14]: df['Tumour Stage']=df['Tumour Stage'].map({'I':1,'II':2,'III':3})
         df['Histology']=df['Histology'].map({'Infiltrating Ductal Carcinoma':1, 'Infiltrating Lobular Carcinoma':2,
                                               'Mucinous Carcinoma':3})
         df['ER status']=df['ER status'].map({'Positive':1})
         df['PR status']=df['PR status'].map({'Positive':1})
         df['HER2 status']=df['HER2 status'].map({'Positive':1,'Negative':2})
         df['Gender']=df['Gender'].map({'MALE':0,'FEMALE':1})
         df['Surgery type']=df['Surgery type'].map({'Other':1, 'Modified RadicalMastectomy':2,
                                                    'Lumpectomy':3,'Mastectomy':4})
         print(df.head())
```

```
Gender Protein1 Protein2 Protein3 Protein4 Tumour Stage \
   Age
                0.95256
   42
                          2.15000 0.007972 -0.048340
                                                                  2
   54
                0.00000
                          1.38020 -0.498030 -0.507320
                                                                  2
1
   63
            1 -0.52303
                          1.76400 -0.370190 0.010815
                                                                  2
   78
            1 -0.87618
                        0.12943 -0.370380 0.132190
   42
                0.22611
                         1.74910 -0.543970 -0.390210
             ER status PR status HER2 status Surgery type Date of Surgery \
  Histology
0
          1
                     1
                                1
                                                         1.0
                                                                   20-May-18
          1
                     1
                                1
                                             2
                                                         1.0
                                                                   26-Apr-18
1
                     1
                                1
                                                         3.0
                                                                   24-Aug-18
3
          1
                                1
                                                                   16-Nov-18
                     1
                                                         1.0
                                                                   12-Dec-18
          1
                     1
                                1
                                                         3.0
 Date of Last Visit Patient Status
          26-Aug-18
0
                             Alive
          25-Jan-19
1
                              Dead
                             Alive
          08-Apr-20
          28-Jul-20
                             Alive
          05-Jan-19
                             Alive
```

Model Training

```
Out[35]: array([['Alive'],
                 ['Dead'],
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                                                                      ['Alive'],
                                                                      ['Alive'],
                                                                      ['Alive']], dtype=object)
                                       from sklearn.model_selection import train_test_split
In [36]:
                                         from sklearn.svm import SVC
                                       X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.10,random_state=42)
In [41]:
                                        model=SVC()
In [38]:
                                        model.fit(X train,y train)
In [39]:
Out[39]: ▼ SVC
                                       SVC()
In [42]: y pred=model.predict(X test)
                                       y pred
                                       array(['Alive', 'Alive', 
Out[42]:
                                                                       'Alive', 'Alive', 'Alive', 'Alive', 'Alive', 'Alive',
                                                                      'Alive', 'Alive', 'Alive'], dtype=object)
```

Model Accuracy

```
from sklearn.metrics import confusion_matrix
In [46]:
         cm=confusion_matrix(y_test,y_pred)
         array([[15, 0],
Out[46]:
                [ 2, 0]], dtype=int64)
In [47]:
         tp=cm[0][0]
         fp=cm[0][1]
         fn=cm[1][0]
         tn=cm[1][1]
In [48]: acc=(tp+tn)/(tp+fp+fn+tn)
         acc
         0.8823529411764706
Out[48]:
         precision=tp/(tp+fp)
In [49]:
         precision
Out[49]:
         recall=tp/(tp+fn)
In [50]:
         recall
         0.8823529411764706
Out[50]:
         f1score=2*(recall*precision)/(recall+precision)
In [51]:
         f1score
         0.9375
Out[51]:
```