Breast Cancer Analysis

```
!pip install dataprep
```

```
Requirement already satisfied: entrypoints>=0.2.2 in /usr/local/lib/python3.7/dist
Requirement already satisfied: defusedxml in /usr/local/lib/python3.7/dist-package
Requirement already satisfied: bleach in /usr/local/lib/python3.7/dist-packages (f
Requirement already satisfied: testpath in /usr/local/lib/python3.7/dist-packages
Requirement already satisfied: pandocfilters>=1.4.1 in /usr/local/lib/python3.7/di
Requirement already satisfied: mistune<2,>=0.8.1 in /usr/local/lib/python3.7/dist-
Requirement already satisfied: webencodings in /usr/local/lib/python3.7/dist-packa
Building wheels for collected packages: metaphone, pystache, python-Levenshtein
  Building wheel for metaphone (setup.py) ... done
  Created wheel for metaphone: filename=Metaphone-0.6-py3-none-any.whl size=13918
  Stored in directory: /root/.cache/pip/wheels/1d/a8/cb/6f8902aa5457bd71344e00665c
  Building wheel for pystache (PEP 517) ... done
  Created wheel for pystache: filename=pystache-0.6.0-py3-none-any.whl size=83635
  Stored in directory: /root/.cache/pip/wheels/78/87/45/383bd15701a08a94c735e9eaf3
  Building wheel for python-Levenshtein (setup.py) ... done
  Created wheel for python-Levenshtein: filename=python_Levenshtein-0.12.2-cp37-cp
  Stored in directory: /root/.cache/pip/wheels/05/5f/ca/7c4367734892581bb5ff896f15
Successfully built metaphone pystache python-Levenshtein
Installing collected packages: jinja2, locket, Werkzeug, partd, multidict, itsdang
  Attempting uninstall: jinja2
    Found existing installation: Jinja2 2.11.3
    Uninstalling Jinja2-2.11.3:
      Successfully uninstalled Jinja2-2.11.3
  Attempting uninstall: Werkzeug
    Found existing installation: Werkzeug 1.0.1
    Uninstalling Werkzeug-1.0.1:
      Successfully uninstalled Werkzeug-1.0.1
  Attempting uninstall: itsdangerous
    Found existing installation: itsdangerous 1.1.0
    Uninstalling itsdangerous-1.1.0:
      Successfully uninstalled itsdangerous-1.1.0
  Attempting uninstall: click
    Found existing installation: click 7.1.2
    Uninstalling click-7.1.2:
      Successfully uninstalled click-7.1.2
  Attempting uninstall: regex
    Found existing installation: regex 2019.12.20
    Uninstalling regex-2019.12.20:
      Successfully uninstalled regex-2019.12.20
  Attempting uninstall: flask
    Found existing installation: Flask 1.1.4
    Uninstalling Flask-1.1.4:
      Successfully uninstalled Flask-1.1.4
  Attempting uninstall: dask
    Found existing installation: dask 2.12.0
    Uninstalling dask-2.12.0:
      Successfully uninstalled dask-2.12.0
  Attempting uninstall: wordcloud
    Found existing installation: wordcloud 1.5.0
    Uninstalling wordcloud-1.5.0:
      Successfully uninstalled wordcloud-1.5.0
  Attempting uninstall: nltk
```

```
    Found existing installation: nltk 3.2.5
    Uninstalling nltk-3.2.5:
      Successfully uninstalled nltk-3.2.5
ERROR: pip's dependency resolver does not currently take into account all the pack
datascience 0.10.6 requires folium==0.2.1, but you have folium 0.8.3 which is inco
```

```
import numpy as np
import pandas as pd

import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.decomposition import PCA

from dataprep.eda import create_report
from dataprep.eda import plot_missing
from dataprep.eda import plot_correlation
from dataprep.eda import plot

from sklearn.model_selection import train_test_split

from sklearn.metrics import f1_score, accuracy_score, confusion_matrix, classification_rep
from sklearn.model_selection import learning_curve, cross_val_score, GridSearchCV
from sklearn.model_selection import train_test_split

from sklearn.ensemble import RandomForestClassifier, AdaBoostClassifier
from sklearn.svm import SVC
from sklearn.pipeline import make_pipeline
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import RobustScaler,StandardScaler,MinMaxScaler

import warnings
warnings.filterwarnings('ignore')
```

```
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import pandas as pd

import matplotlib.pyplot as plt
import seaborn as sns
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from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import RobustScaler,StandardScaler,MinMaxScaler

import warnings
warnings.filterwarnings('ignore')
```

Dataset Analysis

```
data = pd.read_csv('BRCA.csv')
df = data.copy()
pd.set_option('display.max_row',df.shape[0])
pd.set_option('display.max_column',df.shape[1])
df.head()
```

	Patient_ID	Age	Gender	Protein1	Protein2	Protein3	Protein4	Tumour_Stage
0	TCGA-D8-A1XD	36	FEMALE	0.080353	0.42638	0.54715	0.273680	III
1	TCGA-EW-A1OX	43	FEMALE	-0.420320	0.57807	0.61447	-0.031505	II
2	TCGA-A8-A079	69	FEMALE	0.213980	1.31140	-0.32747	-0.234260	III
3	TCGA-D8-A1XR	56	FEMALE	0.345090	-0.21147	-0.19304	0.124270	II
4	TCGA-BH-A0BF	56	FEMALE	0.221550	1.90680	0.52045	-0.311990	II

```
(df.isna().sum()/df.shape[0]*100).sort_values(ascending=False)
```

```
Date_of_Last_Visit    5.089820
Patient_Status        3.892216
Patient_ID            0.000000
Age                   0.000000
Gender                0.000000
Protein1              0.000000
Protein2              0.000000
Protein3              0.000000
Protein4              0.000000
```

```
    Tumour_Stage         0.000000
    Histology            0.000000
    ER status            0.000000
    PR status            0.000000
    HER2 status          0.000000
    Surgery_type         0.000000
    Date_of_Surgery      0.000000
    dtype: float64
```

```
plot_missing(df)
```

Stats Bar Chart Spectrum Heat Map Dendrogram

Missing Statistics

Missing Cells	30
Missing Cells (%)	0.6%
Missing Columns	2
Missing Rows	17
Avg Missing Cells per Column	1.88
Avg Missing Cells per Row	0.09

```
plt.figure(figsize=(10,8))
sns.heatmap(df.isna(),cbar=False)
plt.show()
```

```
print('There is' , df.shape[0] , 'rows')
print('There is' , df.shape[1] , 'columns')
```

```
There is 334 rows
There is 16 columns
```

Checking for duplicates

```
df.duplicated().sum()
```

```
0
```

```
df.loc[df.duplicated(keep=False),:]
```

Patient_ID	Age	Gender	Protein1	Protein2	Protein3	Protein4	Tumour_Stage	H

```
df.drop_duplicates(keep='first',inplace=True)
df.shape
```

```
(334, 16)
```

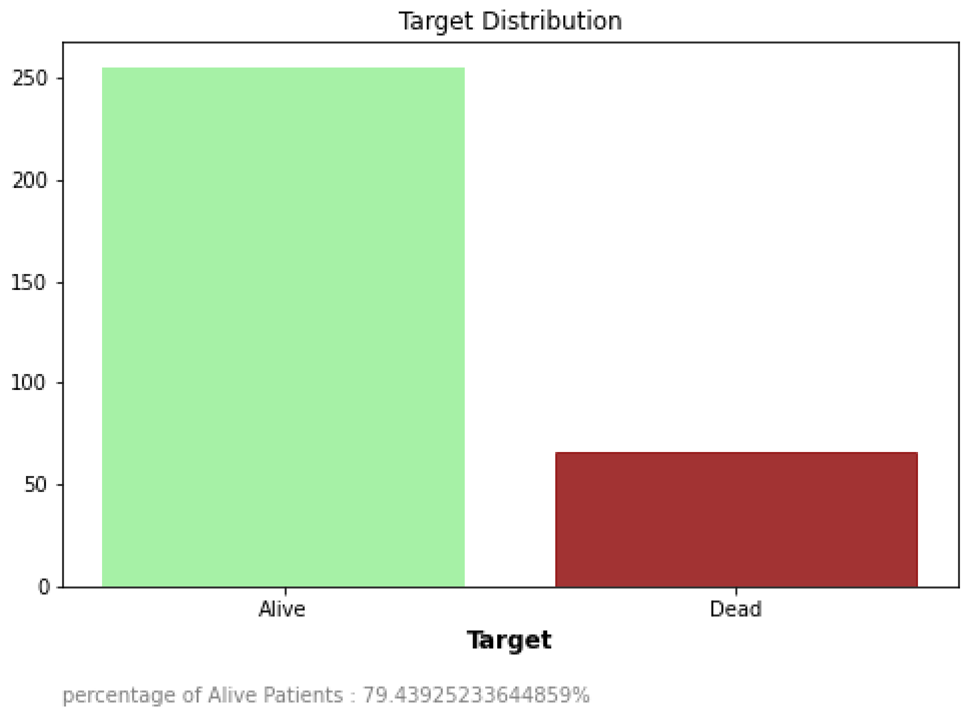
Target Distribution

```
df = data.copy()
df = df.drop(['Patient_ID','Date_of_Surgery','Date_of_Last_Visit'],axis=1)
df['Patient_Status'].value_counts(normalize=True) #Classes déséquilibrées
```

```
Alive    0.794393
Dead     0.205607
Name: Patient_Status, dtype: float64
```

```
target_dist = df['Patient_Status'].value_counts()

fig, ax = plt.subplots(1, 1, figsize=(8,5))

barplot = plt.bar(target_dist.index, target_dist, color = 'lightgreen', alpha = 0.8)
barplot[1].set_color('darkred')

ax.set_title('Target Distribution')
percentage = df['Patient_Status'].value_counts(normalize=True)[0]*100
```

```
ax.annotate("percentage of Alive Patients : {}%".format(percentage),
             xy=(0, 0),xycoords='axes fraction',
             xytext=(0,-50), textcoords='offset points',
             va="top", ha="left", color='grey',
             bbox=dict(boxstyle='round', fc="w", ec='w'))

plt.xlabel('Target', fontsize = 12, weight = 'bold')
plt.show()
```

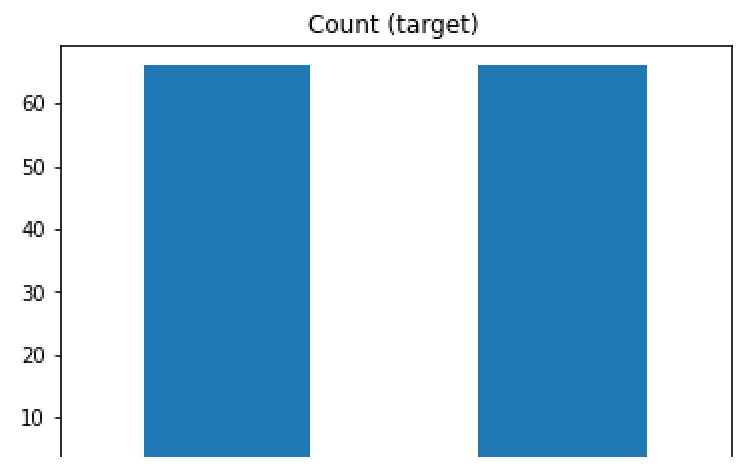


```
# Class count
count_class_0, count_class_1 = df['Patient_Status'].value_counts()

# Divide by class
df_class_0 = df[df['Patient_Status'] == 'Alive']
df_class_1 = df[df['Patient_Status'] == 'Dead']

print(count_class_0)
print(count_class_1)
```

```
255
66
```

```
df_class_0_under = df_class_0.sample(count_class_1,random_state=42)
df_under = pd.concat([df_class_0_under, df_class_1], axis=0)

print('Random under-sampling:')
print(df_under['Patient_Status'].value_counts())

df_under['Patient_Status'].value_counts().plot(kind='bar', title='Count (target)');
```

```
Random under-sampling:
Alive     66
Dead      66
Name: Patient_Status, dtype: int64
```

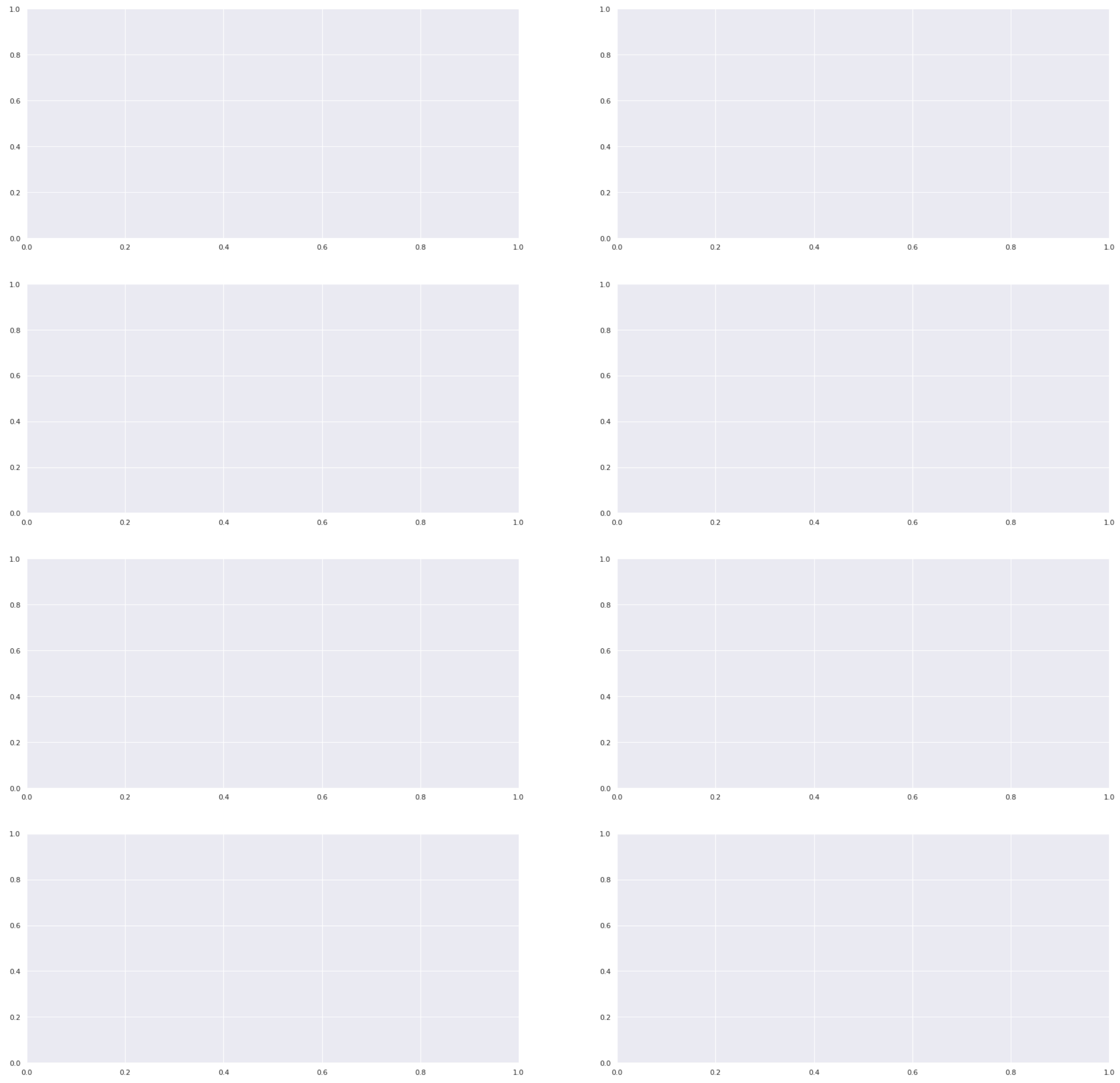


Categorical Features

```
for col in df.select_dtypes("object"):
    print(f'{col :-<50} {df[col].unique()}')
```

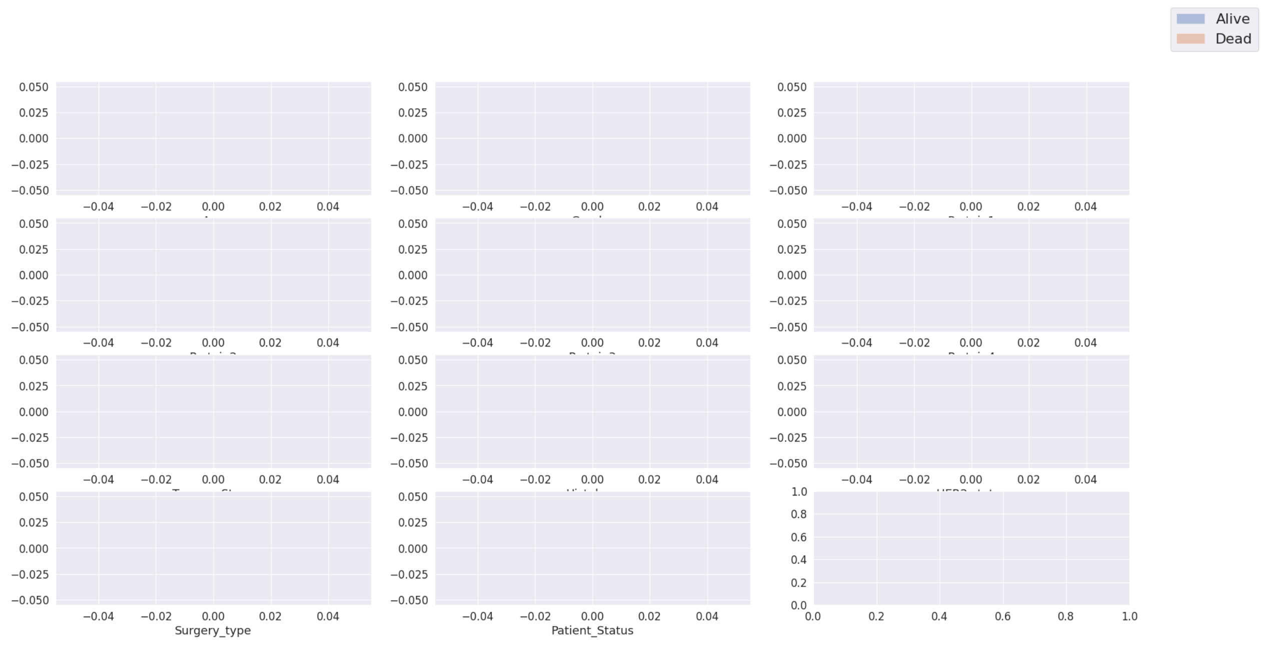
```
Gender-------------------------------------------- ['FEMALE' 'MALE']
Tumour_Stage-------------------------------------- ['III' 'II' 'I']
Histology----------------------------------------- ['Infiltrating Ductal Carcinoma'
 'Infiltrating Lobular Carcinoma']
ER status----------------------------------------- ['Positive']
PR status----------------------------------------- ['Positive']
HER2 status--------------------------------------- ['Negative' 'Positive']
Surgery_type-------------------------------------- ['Modified Radical Mastectomy' 'Lu
Patient_Status------------------------------------ ['Alive' 'Dead' nan]
```

```
fig, ax = plt.subplots(4,2, figsize=(30, 30))
i=0
sns.set(font_scale = 1.5)
for col in df.select_dtypes('object'):
    sns.countplot(df_under[col], hue=df_under['Patient_Status'], ax=ax[i//2][i%2])
    i=i+1
plt.show()

import warnings
warnings.filterwarnings('ignore')
```



Continuous Features

```
Alive_df = df[df['Patient_Status']=="Alive"]
Dead_df = df[df['Patient_Status']=="Dead"]
sns.set(font_scale = 1.5)
fig, ax = plt.subplots(4,3, figsize=(30, 15))
i=0
for col in df.select_dtypes(include=['float64','int64']):
    sns.distplot(Alive_df[col],label='Alive',ax=ax[i//3][i%3])
    sns.distplot(Dead_df[col],label='Dead',ax=ax[i//3][i%3])
    i=i+1
fig.legend(labels=['Alive','Dead'],fontsize='22')
fig.show()
```

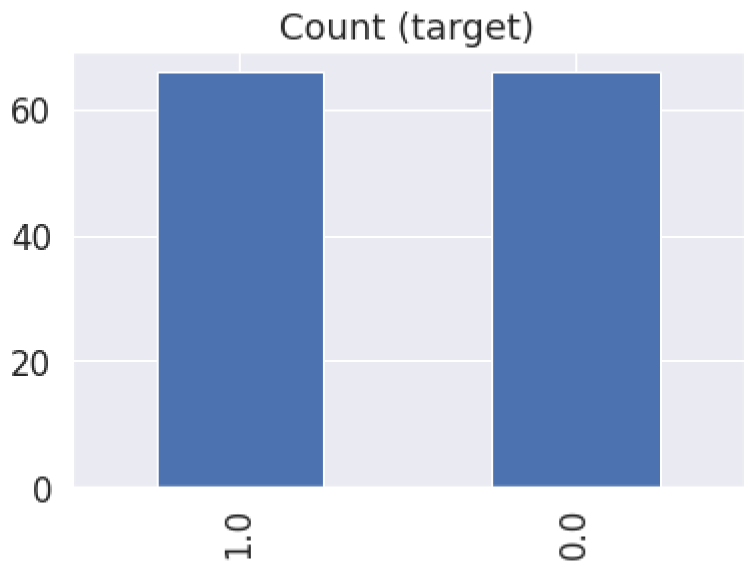


A bit od Data Engineering

```
def encoding(df):                                         #We can now analyze categorical
    code = {'FEMALE':0,
            'MALE':1,
            'III':3,
            'II':2,
            'I':1,
            'Infiltrating Ductal Carcinoma':0,
            'Mucinous Carcinoma':1,
            'Infiltrating Lobular Carcinoma':2,
            'Negative':0,
            'Positive':1,
            'Modified Radical Mastectomy':0,
            'Lumpectomy':1,
            'Simple Mastectomy':2,
            'Other':3,
            'Alive':1,
            'Dead':0
           }
    for col in df.select_dtypes('object'):
        df.loc[:,col]=df[col].map(code)
    return df

def imputation(df):
    df = df.fillna(df.median())
    df = df.dropna()
    return df

def feature_engineering(df):
    useless_columns = ['Patient_ID','Date_of_Surgery','Date_of_Last_Visit','ER status','PR
    df = df.drop(useless_columns,axis=1)
    return df

def preprocessing(df):
    df = encoding(df)
    df = feature_engineering(df)
    df = imputation(df)

    X = df.drop('Patient_Status',axis=1)
    y = df['Patient_Status']

    return df,X,y



df = data.copy()
df,X,y=preprocessing(df)


# Class count
count_class_0, count_class_1 = df['Patient_Status'].value_counts()

# Divide by class
df_class_0 = df[df['Patient_Status'] == 1]
df_class_1 = df[df['Patient_Status'] == 0]
```

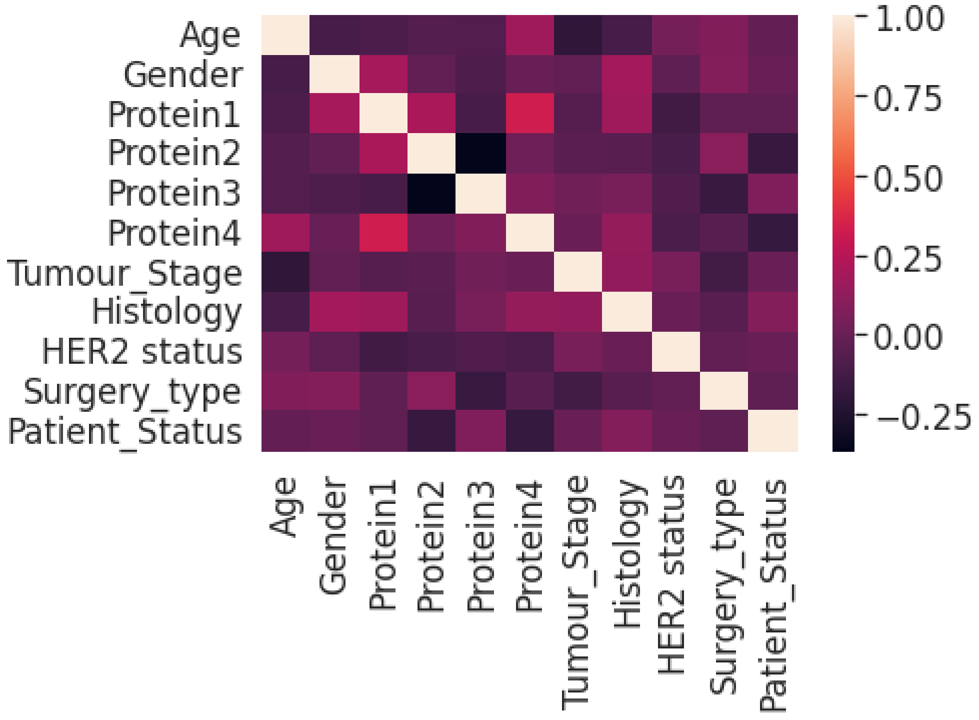
```
df_class_0_under = df_class_0.sample(count_class_1,random_state=42)
df_under = pd.concat([df_class_0_under, df_class_1], axis=0)

print('Random under-sampling:')
print(df_under['Patient_Status'].value_counts())

# Resampling
df_under['Patient_Status'].value_counts().plot(kind='bar', title='Count (target)');
```

```
Random under-sampling:
1.0    66
0.0    66
Name: Patient_Status, dtype: int64
```



```
sns.heatmap(df_under.corr())
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f890fa94350>
```



```
sns.pairplot(df, height=2)
```

```
<seaborn.axisgrid.PairGrid at 0x7f890f9aaa50>
```

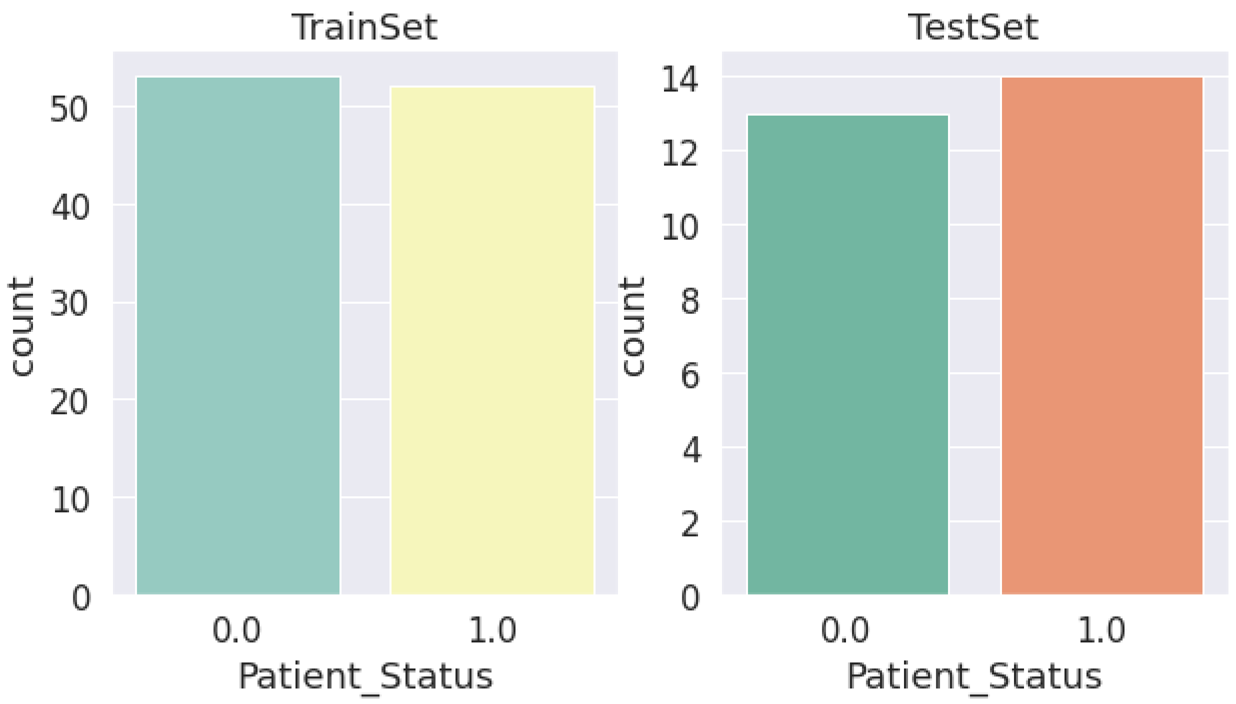
Age
75
50
Gender
1.0
0.5
0.0
Protein1
0
−2
in2
2

Modelling

```
from sklearn.model_selection import train_test_split

from sklearn.metrics import f1_score, accuracy_score, confusion_matrix, classification_rep
from sklearn.model_selection import learning_curve, cross_val_score, GridSearchCV
from sklearn.model_selection import train_test_split
```

```
trainset, testset = train_test_split(df_under, test_size=0.2, random_state=0)
fig, ax = plt.subplots(1,2, figsize=(10, 5))
sns.countplot(x = trainset['Patient_Status'] , data = trainset['Patient_Status'],ax=ax[0],
sns.countplot(x = testset['Patient_Status'] , data = testset['Patient_Status'],ax=ax[1],pa
```

```
Text(0.5, 1.0, 'TestSet')
```



```
from sklearn.ensemble import RandomForestClassifier, AdaBoostClassifier
from sklearn.svm import SVC
from sklearn.pipeline import make_pipeline
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.preprocessing import RobustScaler,StandardScaler,MinMaxScaler
```

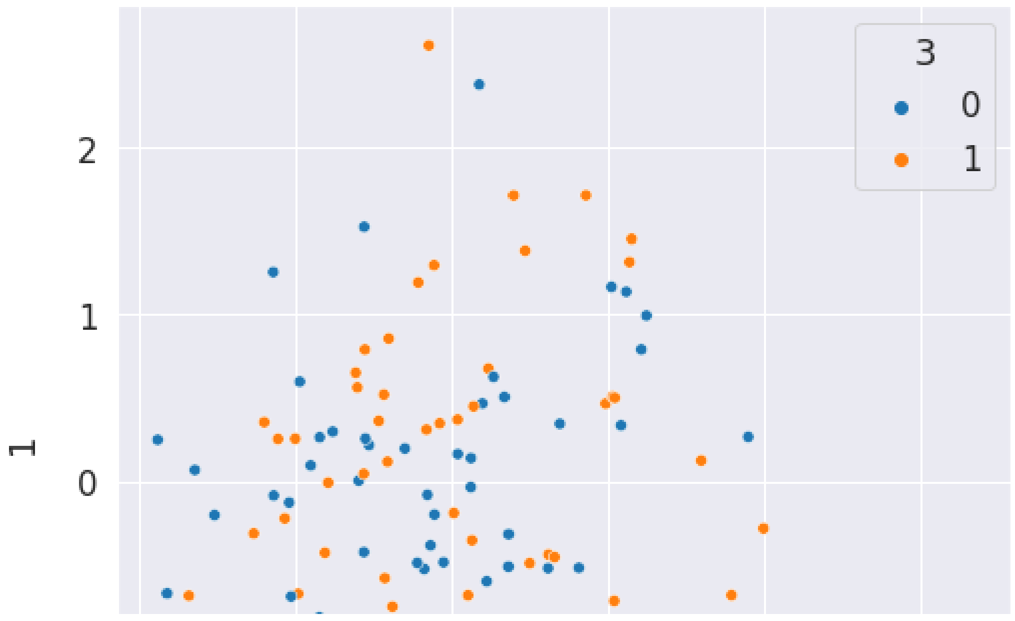
```
X_train = trainset.drop(['Patient_Status'],axis=1)
y_train = trainset['Patient_Status']
X_test = testset.drop(['Patient_Status'],axis=1)
y_test = testset['Patient_Status']


preprocessor = make_pipeline(RobustScaler())

PCAPipeline = make_pipeline(preprocessor, PCA(n_components=3,random_state=42))

RandomPipeline = make_pipeline(preprocessor,RandomForestClassifier(random_state=42))
AdaPipeline = make_pipeline(preprocessor,AdaBoostClassifier(random_state=42))
SVMPipeline = make_pipeline(preprocessor,SVC(random_state=42,probability=True))
KNNPipeline = make_pipeline(preprocessor,KNeighborsClassifier())
LRPipeline = make_pipeline(preprocessor,LogisticRegression(solver='sag',random_state=42))
```

PCA Analysis

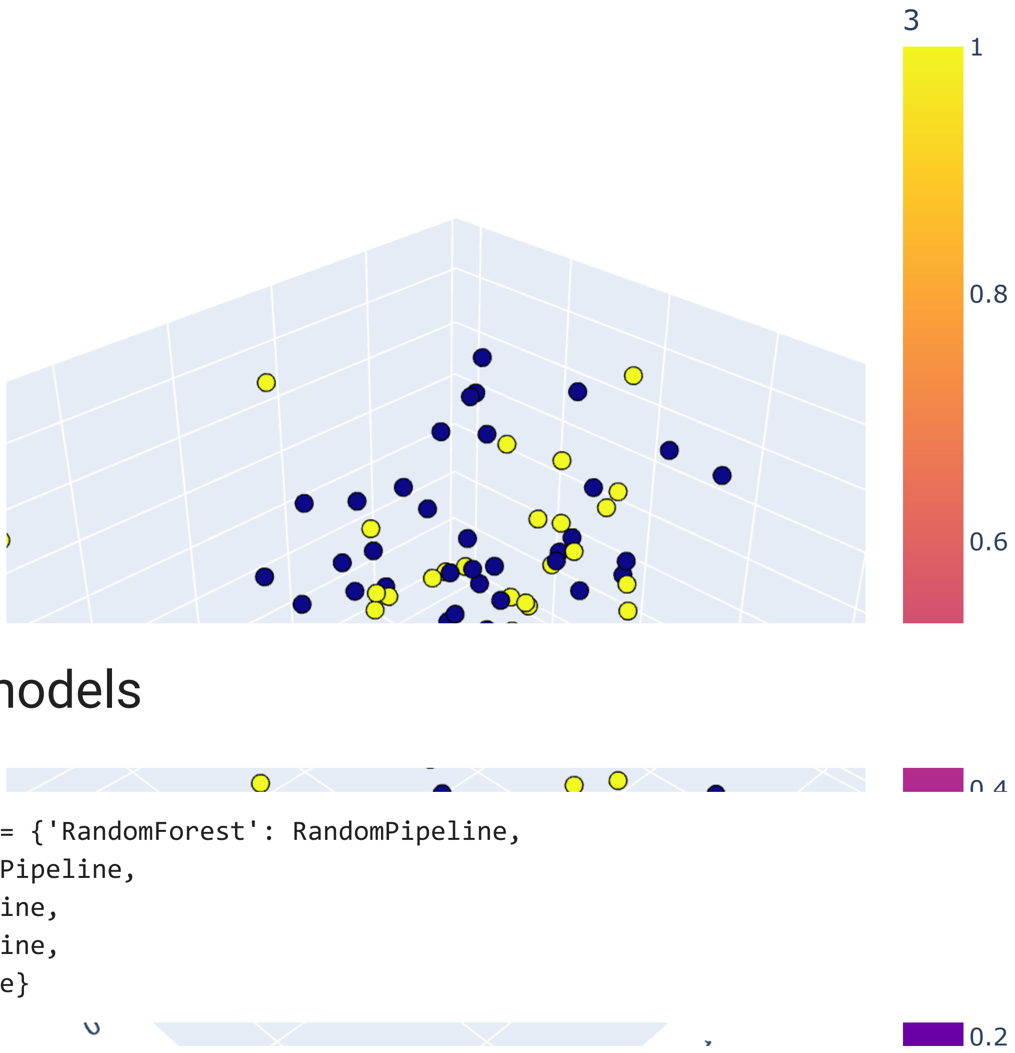
```
PCA_df = pd.DataFrame(PCAPipeline.fit_transform(X_train))
y_train = y_train.astype(int)
y_train.reset_index(drop=True, inplace=True)
PCA_df = pd.concat([PCA_df, y_train], axis=1, ignore_index=True )
PCA_df.head()
```

	0	1	2	3
0	-0.792496	-0.009582	-0.707232	1
1	-0.561121	1.524745	-0.453318	0
2	-0.072062	-1.668854	-0.343776	0
3	0.236570	0.675897	-0.401078	1
4	-0.275412	-0.856502	0.431383	0

```
plt.figure(figsize=(8,8))
sns.scatterplot(PCA_df[0],PCA_df[1],hue=PCA_df[3],palette=sns.color_palette("tab10", 2))
plt.show()
```



```
import plotly.express as px
figure1 = px.scatter_3d(PCA_df,
        x=0,
        y=1,
        z=2,
        color = 3,
                       width=600, height=800)
figure1.update_traces(marker=dict(size=5,
                              line=dict(width=0.2,
                                        color='DarkSlateGrey')),
                  selector=dict(mode='markers'))

figure1.show()
```

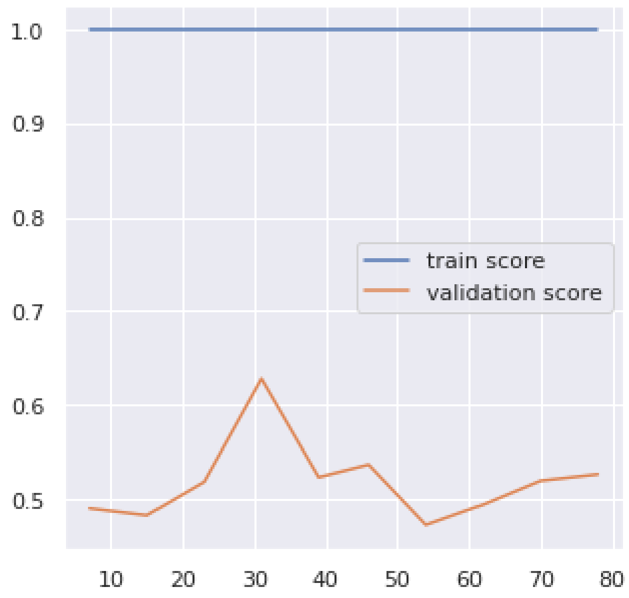


Training models

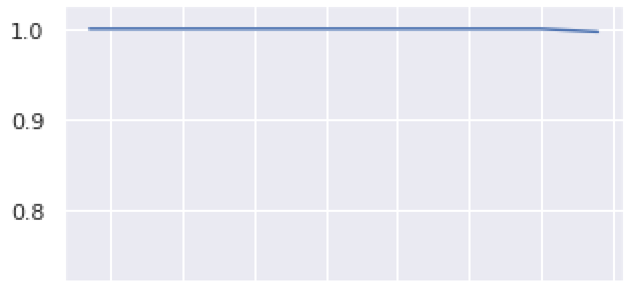
```
dict_of_models = {'RandomForest': RandomPipeline,
'AdaBoost': AdaPipeline,
'SVM': SVMPipeline,
'KNN': KNNPipeline,
'LR': LRPipeline}

def evaluation(model):
    # calculating the probabilities
    y_pred_proba = model.predict_proba(X_test)

    # finding the predicted valued
    y_pred = np.argmax(y_pred_proba,axis=1)
    print('Accuracy = ', accuracy_score(y_test, y_pred))
    print('-')
    print(confusion_matrix(y_test,y_pred))
    print('-')
    print(classification_report(y_test,y_pred))
    print('-')

    N, train_score, test_score = learning_curve(model, X_train, y_train,
                                                 cv=4, scoring='f1',
                                                 train_sizes=np.linspace(0.1,1,10))
    plt.figure(figsize=(5,5))
    plt.plot(N, train_score.mean(axis=1), label='train score')
    plt.plot(N, test_score.mean(axis=1), label='validation score')
    plt.legend()
    plt.show()
```

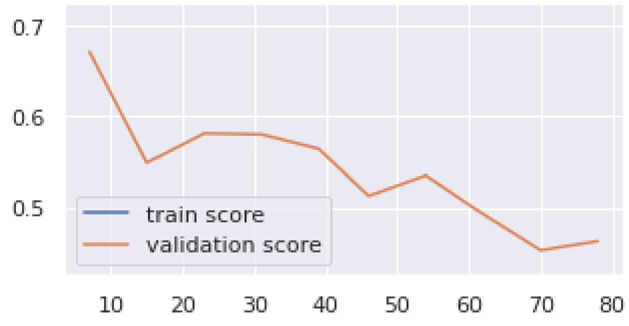
```
sns.set(font_scale = 1)
for name, model in dict_of_models.items():
    print('--------------------------------')
    print(name)
    model.fit(X_train,y_train)
    evaluation(model)
```

```
---------------------------------
RandomForest
Accuracy =  0.48148148148148145
-
[[8 5]
 [9 5]]
-
              precision    recall  f1-score   support

         0.0       0.47      0.62      0.53        13
         1.0       0.50      0.36      0.42        14

    accuracy                           0.48        27
   macro avg       0.49      0.49      0.47        27
weighted avg       0.49      0.48      0.47        27

-
```

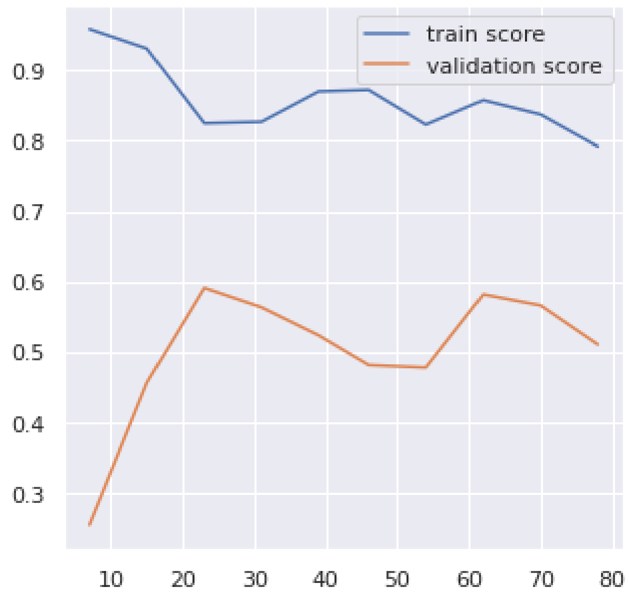


```
---------------------------------
AdaBoost
Accuracy =  0.48148148148148145
-
[[6 7]
 [7 7]]
-
              precision    recall  f1-score   support

         0.0       0.46      0.46      0.46        13
         1.0       0.50      0.50      0.50        14

    accuracy                           0.48        27
   macro avg       0.48      0.48      0.48        27
weighted avg       0.48      0.48      0.48        27

-
```





```
---------------------------------
SVM
Accuracy =  0.48148148148148145
-
[[10  3]
 [11  3]]
-
              precision    recall  f1-score   support

         0.0       0.48      0.77      0.59        13
         1.0       0.50      0.21      0.30        14

    accuracy                           0.48        27
   macro avg       0.49      0.49      0.44        27
weighted avg       0.49      0.48      0.44        27

-
```



```
---------------------------------
KNN
Accuracy =  0.3333333333333333
-
[[4 9]
 [9 5]]
-
              precision    recall  f1-score   support

         0.0       0.31      0.31      0.31        13
         1.0       0.36      0.36      0.36        14

    accuracy                           0.33        27
   macro avg       0.33      0.33      0.33        27
weighted avg       0.33      0.33      0.33        27
```

-

Tuning threshold

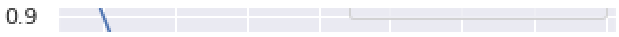
```
best_classifier = KNNPipeline

thresholds = [0.3,0.4,0.5,0.6,0.7,0.8]
best_t = 0.3
best_acc = 0
for t in thresholds:
    y_pred = (best_classifier.predict_proba(X_test)[:,1] >= t).astype(int)
    acc = accuracy_score(y_test, y_pred)
    if acc > best_acc:
        best_acc=acc
        best_t=t
     LR

print('Accuracy on test set :',round(best_acc*100),"%")
print('Best threshold :',best_t)
```

```
Accuracy on test set : 44 %
Best threshold : 0.7
```

Training Artificial Neural Network

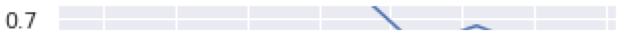
```
        macro avg       0.44      0.44      0.44        27
```

```
# Importing the Keras libraries and packages
import tensorflow as tf
from keras.models import Sequential
from keras.layers import Dense, Dropout
```



```
X_train.shape
```

```
(105, 10)
```



```
# Initialising the ANN
classifier = Sequential()

# Adding the input layer and the first hidden layer
classifier.add(Dense(units = 16, kernel_initializer = 'uniform', activation = 'relu', inpu
classifier.add(Dropout(0.2))
# Adding the second hidden layer
classifier.add(Dense(units = 32, kernel_initializer = 'uniform', activation = 'relu'))
classifier.add(Dropout(0.2))
# Adding the third hidden layer
classifier.add(Dense(units = 8, kernel_initializer = 'uniform', activation = 'relu'))
classifier.add(Dropout(0.2))
# Adding the output layer
classifier.add(Dense(units = 1, kernel_initializer = 'uniform', activation = 'sigmoid'))
classifier.add(Dropout(0.2))
```

```
# Compiling the ANN
classifier.compile(optimizer = 'adam', loss = 'binary_crossentropy', metrics = ['accuracy'
callback = tf.keras.callbacks.EarlyStopping(monitor='accuracy', patience=80)
history =classifier.fit(X_train, y_train, batch_size = 10, epochs = 100, callbacks=callbac
```

```
11/11 [==============================] - 0s 2ms/step - loss: 1.4336 - accuracy: 0.
Epoch 72/100
11/11 [==============================] - 0s 2ms/step - loss: 2.4132 - accuracy: 0.
Epoch 73/100
11/11 [==============================] - 0s 2ms/step - loss: 2.2750 - accuracy: 0.
Epoch 74/100
11/11 [==============================] - 0s 2ms/step - loss: 1.7191 - accuracy: 0.
Epoch 75/100
11/11 [==============================] - 0s 2ms/step - loss: 2.2849 - accuracy: 0.
Epoch 76/100
11/11 [==============================] - 0s 2ms/step - loss: 1.7727 - accuracy: 0.
Epoch 77/100
11/11 [==============================] - 0s 2ms/step - loss: 2.0054 - accuracy: 0.
Epoch 78/100
11/11 [==============================] - 0s 2ms/step - loss: 2.0040 - accuracy: 0.
Epoch 79/100
11/11 [==============================] - 0s 2ms/step - loss: 2.0000 - accuracy: 0.
Epoch 80/100
11/11 [==============================] - 0s 2ms/step - loss: 1.8518 - accuracy: 0.
Epoch 81/100
11/11 [==============================] - 0s 2ms/step - loss: 1.5920 - accuracy: 0.
Epoch 82/100
11/11 [==============================] - 0s 2ms/step - loss: 2.7609 - accuracy: 0.
Epoch 83/100
11/11 [==============================] - 0s 2ms/step - loss: 1.7562 - accuracy: 0.
Epoch 84/100
11/11 [==============================] - 0s 2ms/step - loss: 1.8306 - accuracy: 0.
Epoch 85/100
11/11 [==============================] - 0s 2ms/step - loss: 2.0108 - accuracy: 0.
Epoch 86/100
11/11 [==============================] - 0s 2ms/step - loss: 1.3253 - accuracy: 0.
Epoch 87/100
11/11 [==============================] - 0s 2ms/step - loss: 1.5698 - accuracy: 0.
Epoch 88/100
11/11 [==============================] - 0s 2ms/step - loss: 2.2903 - accuracy: 0.
Epoch 89/100
11/11 [==============================] - 0s 2ms/step - loss: 2.5561 - accuracy: 0.
Epoch 90/100
11/11 [==============================] - 0s 2ms/step - loss: 2.4442 - accuracy: 0.
Epoch 91/100
11/11 [==============================] - 0s 2ms/step - loss: 1.8833 - accuracy: 0.
Epoch 92/100
11/11 [==============================] - 0s 3ms/step - loss: 2.2885 - accuracy: 0.
Epoch 93/100
11/11 [==============================] - 0s 3ms/step - loss: 2.5388 - accuracy: 0.
Epoch 94/100
11/11 [==============================] - 0s 3ms/step - loss: 1.8753 - accuracy: 0.
Epoch 95/100
11/11 [==============================] - 0s 2ms/step - loss: 2.1522 - accuracy: 0.
Epoch 96/100
11/11 [==============================] - 0s 2ms/step - loss: 3.2595 - accuracy: 0.
Epoch 97/100
11/11 [==============================] - 0s 2ms/step - loss: 2.2788 - accuracy: 0.
Epoch 98/100
11/11 [==============================] - 0s 2ms/step - loss: 2.5718 - accuracy: 0.
```

```
Epoch 99/100
11/11 [==============================] - 0s 2ms/step - loss: 2.1429 - accuracy: 0.
```

Conclusion

According to the results shown above, these models (RF, AdaBoost, KNN, SVM, XGBoost, LR, ANN) can't make the classification between Dead and Alive patients. Best we can do is getting a 1/2 chance of guessing right...

Hypothesis

The features have no impact on the target There isn't enough rows in the dataset (need more people) The dataset isn't representative of the population As we undersampled the dataset, we only have 66*2 rows in the end. I could have tried to oversample instead

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