Step 0

The goal of this analysis is to use various patient data at time of hospitalization to identify at-risk patients who are more likely to not survive in the hospital. Medical negligence is a big problem in the modern world, with a Johns Hopkins study claiming that nearly 250,000 people die from medical accidents each year [1] . My main aim is to predict all possible causes of in-hospital mortality so that risks can be identified and worked on.

Step 1.1

The selected dataset is a patient surivival prediction dataset from kaggle. (link to dataset). This dataset is one that can be constantly updated, since multiple people are admitted in various hospitals daily.

Requirements

1. There is a possibility of finding versions of the data: Different hospitals will have different measurement metrics. These can be evaluated to refine the data.
2. Possibility of change in the data: As newer medical devices and measurement techniques are adopted, data will change drastically.
3. Possibility of update in data: People are hospitalized daily, so there is a constant stream of new data to work with.
4. Have at least two protected features: This dataset has varios protected features: including age, bmi, surgery type, and ethnicity

Step 1.2

Since this is a classification problem, the ML metrics used to evaluate it will be accuracy, ROC curve and recall. Precision will be considered, but recall is more important in this case since it is important to identify all at risk patients. Some false positives are bearable. The accuracy will simply be the percentage of correctly estimated values in the test set.

The ROC curve will estimate the benefit of this model over random guesses

The recall will provide the True Positive Rate (TPR), and give us the ratio of correctly identified positive instances.

Precision is the accuracy of positive predictions

Step 1.3

Business metrics to evaluate this model can include:

1. Training time
2. Performance and investment
3. Time to market
4. Hardware cost
5. Cost of gathering data
6. Financial benefit of model

Step 1.4

Software metrics to evaluate this model:

1. Number of code smells
2. Throughput
3. Turnaround time for predictions
4. Scalability
5. Modularity of code

Step 2.1

The objective of the dataset is to predict whether patients will survive or not based on various patient-related factors.

This dataset was picked because of its good number of rows, and its inclusion of BMI, surgery type, condition details, and ICU location features. Each of these features provide a great deal of detail and consider most of the critical features needed for the objective of this analysis.

Important features in this dataset include:

1. Patient age
2. Patient BMI
3. Patient surgery type (elective or not)
4. Number of days spent in ICU
5. Heart rate
6. Respiratory rate

7. Presence of various medical conditions including: Cirrhosis, Lymphoma, etc.

Step 2.1: Dataset quality radar

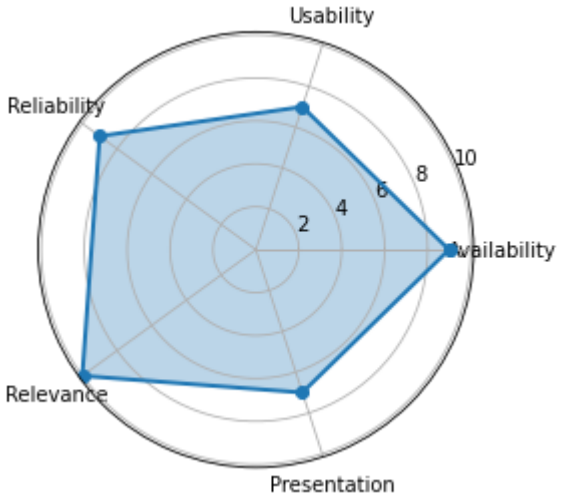
The following metrics were used to create a radar chart to estimate the quality of this dataset

1. Availability: This dataset is **accessible**, since hospitals record and upload data daily, will arrive at required **timelines**, since there is not much of an extra effort in gathering and moving the data, and it will be regularly updated. For **authorization**, this dataset will need to be released with permission by hospital authorities. Hospitals already have the right to use this data given by patients, but extra authorization can be obtained as necessary.
2. Usability: The **documentation** of this dataset is not very detailed, but it provides sufficient information to work with. This dataset is **credible**, since it is gathered through MIT's GOSSIS (Global Open Source Severity of Illness Score). The **metadata** for this dataset is sufficient, but could be better.
3. Reliability: The **accuracy, credibility, consistency and integrity** of this data can be relied on because it is gathered through an MIT program. The completeness of this dataset seems good, especially with the number of features it covers. However, more features can be added over time after exploratory analyses. This data will also have high **auditability**, since it is open source.
4. Relevance: This data is highly relevant to the problem this analysis intends to solve. It provides data to predict patient survival based on various patient conditions
5. Presentation: The **readability** of this dataset is sufficient, however, some colum descriptions could be more detailed. The **structure** seems good too, all columns are organized properly, and categorical variables are seperated sufficiently.

The radar chart below visualizes the score given to each of these metrics out of a maximum score of 10.

```
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
labels=np.array(['Availability', 'Usability', 'Reliability', 'Relevance', 'Presentati
stats=np.array([9, 7, 9, 10, 7])
angles=np.linspace(0, 2*np.pi, len(labels), endpoint=False)
# close the plot
stats=np.concatenate((stats,[stats[0]]))
angles=np.concatenate((angles,[angles[0]]))
```

```
fig=plt.figure()
ax = fig.add_subplot(111, polar=True)
ax.plot(angles, stats, 'o-', linewidth=2)
ax.fill(angles, stats, alpha=0.3)
ax.set_thetagrids(angles * 180/np.pi, labels)
ax.grid(True)
```



Step 3

The features of the dataset are:

1. encounter_id: Patienty case ID
2. patient_id: Patient ID
3. hospital_id: Hospital ID
4. age: The age of the patient in admission
5. bmi: The body mass index of the person on unit admission
6. elective_surgery: Whether the patient was admitted to the hospital for an elective surgic
7. ethnicity: The common national or cultural tradition which the person belongs to
8. gender: Sex of the patient
9. height: The height of the person on unit admission
10. icu_admit_source: The location of the patient prior to being admitted to the unit
11. icu_id: A unique identifier for the unit to which the patient was admitted
12. icu_stay_type: Whether person was transferred into ICU or was staying there
13. icu_type: A classification which indicates the type of care the unit is capable of provi
14. pre_icu_los_days: The length of stay of the patient between hospital admission and unit
15. weight: The weight (body mass) of the person on unit admission
16. apache_2_diagnosis: The APACHE II diagnosis for the ICU admission. Apache (acronym for A
17. apache_3j_diagnosis: The APACHE III-J sub-diagnosis code which best describes the reasor
18. apache_post_operative: The APACHE operative status; 1 for post-operative, 0 for non-oper
19. arf_apache: Whether the patient had acute renal failure during the first 24 hours of the
20. gcs_eyes_apache: The eye opening component of the Glasgow Coma Scale measured during the

21. gcs_motor_apache: The motor component of the Glasgow Coma Scale measured during the firs
22. gcs_unable_apache: Whether the Glasgow Coma Scale was unable to be assessed due to patie
23. gcs_verbal_apache: The verbal component of the Glasgow Coma Scale measured during the fi
24. heart_rate_apache: The heart rate measured during the first 24 hours
25. intubated_apache: Whether the patient was intubated at the time of the highest scoring a
26. map_apache: The mean arterial pressure measured during the first 24 hours
27. resprate_apache: The respiratory rate measured during the first 24 hours
28. temp_apache: The temperature measured during the first 24 hours
29. ventilated_apache: Whether the patient was invasively ventilated at the time of the high
30. d1_diasbp_max: The patient's highest diastolic blood pressure during the first 24 hours
31. d1_diasbp_min: The patient's lower diastolic blood pressure during the first 24 hours of
32. d1_diasbp_noninvasive_max: BP measured noninvasively
33. d1_diasbp_noninvasive_min: BP measured noninvasively
34. d1_heartrate_max: The patient's highest heart rate during the first 24 hours of their un
35. d1_heartrate_min: The patient's lowest heart rate during the first 24 hours of their uni
36. d1_mbp_max: The patient's highest mean blood pressure during the first 24 hours of their
37. d1_mbp_min: The patient's lowest mean blood pressure during the first 24 hours of their
38. d1_mbp_noninvasive_max: The patient's highest mean blood pressure during the first 24 ho
39. d1_mbp_nonvasive_min: The patient's lowest mean blood pressure during the first 24 hours
40. d1_resprate_max: The patient's highest respiratory rate during the first 24 hours of the
41. d1_resprate_min: The patient's lowest respiratory rate during the first 24 hours of thei
42. d1_spo2_max: The patient's highest peripheral oxygen saturation during the first 24 hour
43. d1_spo2_min: The patient's lowest peripheral oxygen saturation during the first 24 hours
44. d1_sysbp_max: The patient's highest systolic blood pressure during the first 24 hours of
45. d1_sysbp_min: The patient's lower systolic blood pressure during the first 24 hours of t
46. d1_sysbp_noninvasive_max: The patient's highest systolic blood pressure during the first
47. d1_sysbp_noninvasive_min: The patient's lower systolic blood pressure during the first 2
48. d1_temp_max: The patient's highest core temperature during the first 24 hours of their u
49. d1_temp_min: The patient's lower core temperature during the first 24 hours of their uni
50. h1_diasbp_max: The patient's highest diastolic blood pressure during the first hour of t
51. h1_diasbp_min: The patient's lowest diastolic blood pressure during the first hour of th
52. h1_diasbp_noninvasive_max: The patient's highest diastolic blood pressure during the fir
53. h1_diasbp_noninvasive_min: The patient's lowest diastolic blood pressure during the firs
54. h1_heartrate_max: The patient's highest heart rate during the first hour of their unit s
55. h1_heartrate_min: The patient's lowest heart rate during the first hour of their unit st
56. h1_mbp_max: The patient's highest mean blood pressure during the first hour of their uni
57. h1_mbp_min: The patient's lowest mean blood pressure during the first hour of their unit
58. and 59. Above two stats measure noninvasively
60. h1_resprate_max: The patient's highest respiratory rate during the first hour of their u
61. h1_resprate_min: The patient's lowest respiratory rate during the first hour of their un
62. h1_spo2_max: The patient's highest peripheral oxygen saturation during the first hour of
63. h1_spo2_min: The patient's lowest peripheral oxygen saturation during the first hour of
64. h1_sysbp_max: The patient's highest systolic blood pressure during the first hour of the

65. h1_sysbp_min: The patient's lowest systolic blood pressure during the first hour of thei
66. and 67. Above to metrics measured noninvasively
68. d1_glucose_max: The highest glucose concentration of the patient in their serum or plasm
69. d1_glucose_min: The lowest glucose concentration of the patient in their serum or plasma
70. d1_potassium_max: The highest potassium concentration of the patient in their serum or p
71. d1_potassium_min: The lowest potassium concentration of the patient in their serum or pl
72. apache_4a_hospital_death_prob: The APACHE IVa probabilistic prediction of in-hospital mo
73. apache_4a_icu_death_prob: The APACHE IVa probabilistic prediction of in ICU mortality fo
74. aids: Whether the patient has a definitive diagnosis of acquired immune deficiency syndr
75. cirrhosis: Whether the patient has a history of heavy alcohol use with portal hypertensi
76. diabetes_mellitus: Whether the patient has been diagnosed with diabetes, either juvenile
77. hepatic_failure: Whether the patient has cirrhosis and additional complications includir
78. immunosuppression: Whether the patient has their immune system suppressed within six mor
79. leukemia: Whether the patient has been diagnosed with acute or chronic myelogenous leuke
80. lymphoma: Whether the patient has been diagnosed with non-Hodgkin lymphoma.
81. solid_tumor_with_metastasis: Whether the patient has been diagnosed with any solid tumor
82. apache_3j_bodysystem: Admission diagnosis group for APACHE III
83. apache_2_bodysystem: Admission diagnosis group for APACHE II
84. **hospital_death**: Whether the patient died during this hospitalization. **This is the

```
# The features in the dataset are as follows

import pandas as pd

dataset = pd.read_csv('survival.csv')

dataset.columns
```

```
Index(['encounter_id', 'patient_id', 'hospital_id', 'age', 'bmi',
       'elective_surgery', 'ethnicity', 'gender', 'height', 'icu_admit_source',
       'icu_id', 'icu_stay_type', 'icu_type', 'pre_icu_los_days', 'weight',
       'apache_2_diagnosis', 'apache_3j_diagnosis', 'apache_post_operative',
       'arf_apache', 'gcs_eyes_apache', 'gcs_motor_apache',
       'gcs_unable_apache', 'gcs_verbal_apache', 'heart_rate_apache',
       'intubated_apache', 'map_apache', 'resprate_apache', 'temp_apache',
       'ventilated_apache', 'd1_diasbp_max', 'd1_diasbp_min',
       'd1_diasbp_noninvasive_max', 'd1_diasbp_noninvasive_min',
       'd1_heartrate_max', 'd1_heartrate_min', 'd1_mbp_max', 'd1_mbp_min',
       'd1_mbp_noninvasive_max', 'd1_mbp_noninvasive_min', 'd1_resprate_max',
       'd1_resprate_min', 'd1_spo2_max', 'd1_spo2_min', 'd1_sysbp_max',
       'd1_sysbp_min', 'd1_sysbp_noninvasive_max', 'd1_sysbp_noninvasive_min',
       'd1_temp_max', 'd1_temp_min', 'h1_diasbp_max', 'h1_diasbp_min',
       'h1_diasbp_noninvasive_max', 'h1_diasbp_noninvasive_min',
       'h1_heartrate_max', 'h1_heartrate_min', 'h1_mbp_max', 'h1_mbp_min',
       'h1_mbp_noninvasive_max', 'h1_mbp_noninvasive_min', 'h1_resprate_max',
       'h1_resprate_min', 'h1_spo2_max', 'h1_spo2_min', 'h1_sysbp_max',
       'h1_sysbp_min', 'h1_sysbp_noninvasive_max', 'h1_sysbp_noninvasive_min',
```

```
       'd1_glucose_max', 'd1_glucose_min', 'd1_potassium_max',
       'd1_potassium_min', 'apache_4a_hospital_death_prob',
       'apache_4a_icu_death_prob', 'aids', 'cirrhosis', 'diabetes_mellitus',
       'hepatic_failure', 'immunosuppression', 'leukemia', 'lymphoma',
       'solid_tumor_with_metastasis', 'apache_3j_bodysystem',
       'apache_2_bodysystem', 'Unnamed: 83', 'hospital_death'],
      dtype='object')
```

Step 4

Step 5

Protected features in this dataset are:

1. Age
2. BMI
3. Choice of elective surgery
4. All the apache report values
5. Various diagnoses, including cirrhosis and leukemia
6. Ethnicity

Step 6

```
dataset = dataset.drop(["Unnamed: 83"], axis=1)
```

```
dataset.head()
```

	encounter_id	patient_id	hospital_id	age	bmi	elective_surgery	ethnicity
0	66154	25312	118	68.0	22.73	0	Caucasian

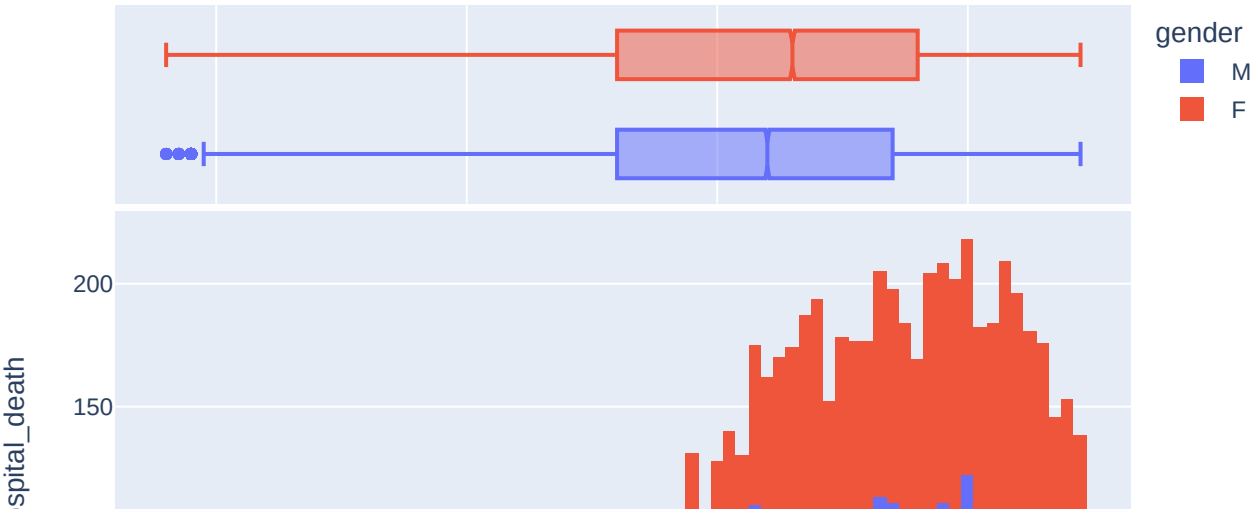
```
dataset.describe()
```

	encounter_id	patient_id	hospital_id	age	bmi	ele
count	91713.000000	91713.000000	91713.000000	87485.000000	88284.000000	
mean	65606.079280	65537.131464	105.669262	62.309516	29.185818	
std	37795.088538	37811.252183	62.854406	16.775119	8.275142	
min	1.000000	1.000000	2.000000	16.000000	14.844926	
25%	32852.000000	32830.000000	47.000000	52.000000	23.641975	
50%	65665.000000	65413.000000	109.000000	65.000000	27.654655	
75%	98342.000000	98298.000000	161.000000	75.000000	32.930206	
max	131051.000000	131051.000000	204.000000	89.000000	67.814990	

8 rows × 77 columns

```
import plotly.express as px
import plotly.offline as py
import plotly.graph_objs as go
import plotly.tools as tls
from plotly.subplots import make_subplots
import plotly.figure_factory as ff


fig = px.histogram(dataset[['age', 'gender', 'hospital_death', 'bmi']].dropna(), x= '
                   marginal = 'box', hover_data = dataset[['age', 'gender', 'hospital_
fig.show()
```




```
dataset.isnull().sum(axis=0).sort_values(ascending=False)
```

```
d1_potassium_max            9053
d1_potassium_min            9053
h1_mbp_noninvasive_min      8455
h1_mbp_noninvasive_max      8455
apache_4a_icu_death_prob    7594
                            ...
icu_stay_type                  0
height                         0
elective_surgery               0
bmi                            0
hospital_death                 0
Length: 80, dtype: int64
```

```
large_missing = dataset.isnull().sum(axis=0).sort_values(ascending=False)[dataset.isr

print("\nTotal features with more than", 25000, "missing values:", len(large_missing)

dataset.drop(large_missing.index.tolist() + ['encounter_id', 'icu_admit_source', 'icu
             axis=1,
            inplace = True)
dataset
```

```
Total features with more than 25000 missing values: 0
```

	age	bmi	elective_surgery	ethnicity	gender	height	icu_type	pre_
0	68.0	22.730000	0	Caucasian	M	180.3	CTICU	
1	77.0	27.420000	0	Caucasian	F	160.0	Med-Surg ICU	
2	25.0	31.950000	0	Caucasian	F	172.7	Med-Surg ICU	
3	81.0	22.640000	1	Caucasian	F	165.1	CTICU	
4	19.0	NaN	0	Caucasian	M	188.0	Med-Surg ICU	
...	...	...	...	...	...	...	...	
91708	75.0	23.060250	0	Caucasian	M	177.8	Cardiac ICU	
91709	56.0	47.179671	0	Caucasian	F	183.0	Med-Surg ICU	
91710	48.0	27.236914	0	Caucasian	M	170.2	Med-Surg ICU	

```
dataset = dataset[dataset[['bmi', 'weight', 'height']].isna().sum(axis=1) == 0]
dataset
```

	age	bmi	elective_surgery	ethnicity	gender	height	icu_type	pre_
0	68.0	22.730000	0	Caucasian	M	180.3	CTICU	
1	77.0	27.420000	0	Caucasian	F	160.0	Med-Surg ICU	
2	25.0	31.950000	0	Caucasian	F	172.7	Med-Surg ICU	

```
numerical = [
 'elective_surgery',
 'apache_post_operative',
 'arf_apache',
 'gcs_unable_apache',
 'intubated_apache',
 'ventilated_apache',
 'aids',
 'cirrhosis',
 'diabetes_mellitus',
 'hepatic_failure',
 'immunosuppression',
 'leukemia',
 'lymphoma',
 'solid_tumor_with_metastasis']

categorical = ['ethnicity',
 'gender',
 'icu_type',
 'apache_3j_bodysystem',
 'apache_2_bodysystem']


not_numeric = dataset[numerical + categorical + ['hospital_death']].columns.tolist()
numeric_only = dataset.drop(not_numeric,axis=1).columns.tolist()
numeric_only
```

```
['age',
 'bmi',
 'height',
 'pre_icu_los_days',
 'weight',
 'apache_2_diagnosis',
 'apache_3j_diagnosis',
 'gcs_eyes_apache',
 'gcs_motor_apache',
 'gcs_verbal_apache',
 'heart_rate_apache',
 'map_apache',
 'resprate_apache',
 'temp_apache',
 'd1_diasbp_max',
 'd1_diasbp_min',
```

```
        'd1_diasbp_noninvasive_max',
        'd1_diasbp_noninvasive_min',
        'd1_heartrate_max',
        'd1_heartrate_min',
        'd1_mbp_max',
        'd1_mbp_min',
        'd1_mbp_noninvasive_max',
        'd1_mbp_noninvasive_min',
        'd1_resprate_max',
        'd1_resprate_min',
        'd1_spo2_max',
        'd1_spo2_min',
        'd1_sysbp_max',
        'd1_sysbp_min',
        'd1_sysbp_noninvasive_max',
        'd1_sysbp_noninvasive_min',
        'd1_temp_max',
        'd1_temp_min',
        'h1_diasbp_max',
        'h1_diasbp_min',
        'h1_diasbp_noninvasive_max',
        'h1_diasbp_noninvasive_min',
        'h1_heartrate_max',
        'h1_heartrate_min',
        'h1_mbp_max',
        'h1_mbp_min',
        'h1_mbp_noninvasive_max',
        'h1_mbp_noninvasive_min',
        'h1_resprate_max',
        'h1_resprate_min',
        'h1_spo2_max',
        'h1_spo2_min',
        'h1_sysbp_max',
        'h1_sysbp_min',
        'h1_sysbp_noninvasive_max',
        'h1_sysbp_noninvasive_min',
        'd1_glucose_max',
        'd1_glucose_min',
        'd1_potassium_max',
        'd1_potassium_min',
        'apache_4a_hospital_death_prob',
        'apache 4a icu death prob']

for col in numerical:
    dataset[col] = dataset[col].astype('Int64')

for col in numerical:
    dataset[col] = dataset[col].fillna(dataset[col].mode()[0])


dataset[numeric_only].isna().sum(axis=0).sort_values(ascending=False)

     d1_potassium_max                9053
     h1_mbp_noninvasive_min          8455

     h1_mbp_noninvasive_max          8455
     apache_4a_icu_death_prob        7594
```

```
apache_4a_icu_death_prob          7594
apache_4a_hospital_death_prob     7594
h1_diasbp_noninvasive_max         6982
h1_diasbp_noninvasive_min         6982
h1_sysbp_noninvasive_min          6972
h1_sysbp_noninvasive_max          6972
d1_glucose_min                    5458
d1_glucose_max                    5458
h1_mbp_min                        4287
h1_mbp_max                        4287
h1_resprate_min                   4062
h1_resprate_max                   4062
age                               4055
h1_spo2_min                       3925
h1_spo2_max                       3925
temp_apache                       3884
h1_diasbp_min                     3388
h1_diasbp_max                     3388
h1_sysbp_max                      3379
h1_sysbp_min                      3379
h1_heartrate_min                  2621
h1_heartrate_max                  2621
d1_temp_min                       2205
d1_temp_max                       2205
gcs_motor_apache                  1794
gcs_verbal_apache                 1794
gcs_eyes_apache                   1794
apache_2_diagnosis                1566
d1_mbp_noninvasive_min            1333
d1_mbp_noninvasive_max            1333
resprate_apache                   1131
apache_3j_diagnosis               1026
d1_diasbp_noninvasive_max          959
d1_diasbp_noninvasive_min          959
d1_sysbp_noninvasive_min           946
d1_sysbp_noninvasive_max           946
map_apache                         913
heart_rate_apache                  809
d1_resprate_max                    332
d1_resprate_min                    332
d1_spo2_max                        280
d1_spo2_min                        280
d1_mbp_min                         173
d1_mbp_max                         173
d1_diasbp_min                      124
d1_diasbp_max                      124
d1_sysbp_max                       118
d1_sysbp_min                       118
d1_heartrate_max                   108
d1_heartrate_min                   108
bmi                                  0
weight                               0
pre_icu_los_days                     0
height                               0
dtype: int64
```

```
no_na = dataset.dropna(axis=0)

no_na[categorical].nunique()
```

```
ethnicity               6
gender                  2
icu_type                8
apache_3j_bodysystem   11
apache_2_bodysystem    10
dtype: int64
```

```
processed_df = pd.get_dummies(no_na, prefix='cat-', prefix_sep='_', columns=categoric
processed_df.reset_index(drop = True, inplace = True)
processed_df
```

	age	bmi	elective_surgery	height	pre_icu_los_days	weight	apache_
0	68.0	22.730000	0	180.3	0.541667	73.9	
1	77.0	27.420000	0	160.0	0.927778	70.2	
2	67.0	27.560000	0	190.5	0.000694	100.0	
3	72.0	28.257052	1	154.9	0.004861	67.8	
4	46.0	25.845717	0	167.6	0.000000	72.6	
...	...	...	...	...	...	...	
56981	47.0	51.439842	1	195.0	0.033333	186.0	
56982	54.0	19.770448	0	177.8	0.025694	62.5	
56983	75.0	23.060250	0	177.8	0.298611	72.9	
56984	56.0	47.179671	0	183.0	0.120139	158.0	
56985	82.0	22.031250	1	160.0	0.018056	56.4	

56986 rows × 110 columns

```
processed_df.columns = [x.lower() for x in processed_df.columns.tolist()]
processed_df = processed_df.loc[:,~processed_df.columns.duplicated()]
```

```
t = processed_df['arf_apache'].dtype
for col in processed_df.columns.tolist():
    if processed_df[col].values.dtype == 'uint8' or t == processed_df[col].values.dty
        processed_df[col] = processed_df[col].astype(int)
```

```
age                          float64
bmi                          float64
elective_surgery               int64
height                       float64
pre_icu_los_days             float64
                              ...
cat-_trauma                    int64
cat-_haematologic              int64
cat-_neurologic                int64
cat-_renal/genitourinary       int64
cat-_undefined diagnoses       int64
Length: 104, dtype: object
```

```
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.metrics import (accuracy_score,
                             classification_report,
                             roc_auc_score, roc_curve, auc, precision_recall_curve,
                             confusion_matrix)

# from xgboost import XGBClassifier
from sklearn.ensemble import ExtraTreesClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import StratifiedKFold, KFold
import xgboost as xgb
from xgboost import XGBClassifier


X = processed_df.drop(['hospital_death'], axis=1)
y = processed_df['hospital_death']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.30,
                                                    stratify = y)


import keras
from keras.models import Sequential
from keras.layers import Dense


# Neural network
model = Sequential()
model.add(Dense(103, input_dim=103, activation='relu'))
model.add(Dense(3, activation='relu'))
# model.add(Dense(30, activation='relu'))
model.add(Dense(1,activation='sigmoid'))


import tensorflow as tf
opt = tf.keras.optimizers.SGD(learning_rate=0.00001)
```

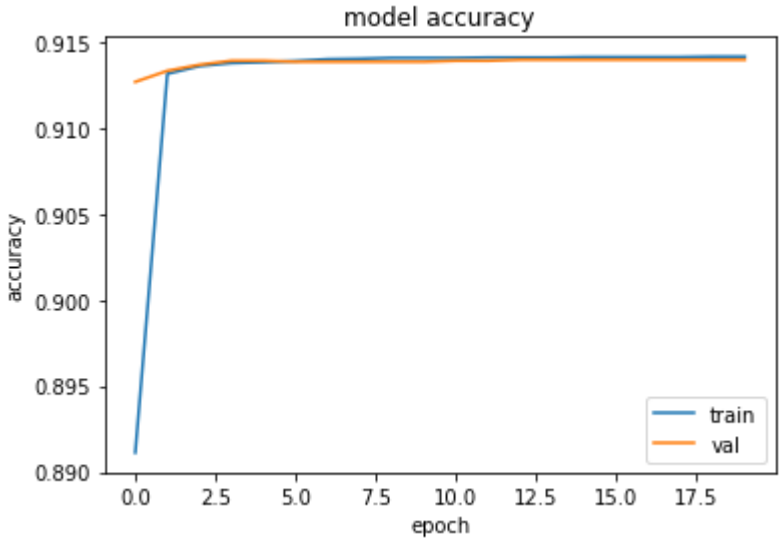
```
model.compile(loss='binary_crossentropy', optimizer=opt, metrics=['accuracy'])


history = model.fit(X_train, y_train,validation_data=(X_test,y_test), epochs=20, batc
```

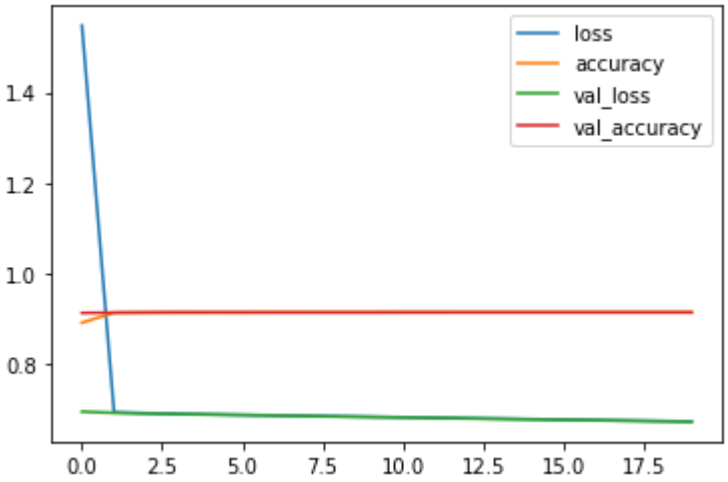
```
Epoch 1/20
624/624 [==============================] - 2s 3ms/step - loss: 1.5476 - accuracy
Epoch 2/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6931 - accuracy
Epoch 3/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6913 - accuracy
Epoch 4/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6899 - accuracy
Epoch 5/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6886 - accuracy
Epoch 6/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6875 - accuracy
Epoch 7/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6864 - accuracy
Epoch 8/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6853 - accuracy
Epoch 9/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6842 - accuracy
Epoch 10/20
624/624 [==============================] - 3s 5ms/step - loss: 0.6832 - accuracy
Epoch 11/20
624/624 [==============================] - 4s 6ms/step - loss: 0.6821 - accuracy
Epoch 12/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6811 - accuracy
Epoch 13/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6800 - accuracy
Epoch 14/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6790 - accuracy
Epoch 15/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6780 - accuracy
Epoch 16/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6769 - accuracy
Epoch 17/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6759 - accuracy
Epoch 18/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6749 - accuracy
Epoch 19/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6739 - accuracy
Epoch 20/20
624/624 [==============================] - 2s 3ms/step - loss: 0.6729 - accuracy
```

```
from tensorflow import keras
import matplotlib.pyplot as plt
plt.plot(history.history['accuracy'])
plt.plot(history.history['val_accuracy'])
plt.title('model accuracy')
plt.ylabel('accuracy')
plt.xlabel('epoch')
```

```
    plt.legend(['train', 'val'])
    plt.show()
```




```
    pd.DataFrame(history.history).plot()
    plt.show()
```




```
    gkf = KFold(n_splits=3, shuffle=True, random_state=42).split(X=X_train, y=y_train)

    fit_params_of_xgb = {
        "early_stopping_rounds":100,
        "eval_metric" : 'auc',
        "eval_set" : [(X_test, y_test)],
        'verbose': 100,
    }


    # A parameter grid for XGBoost
    params = {
        'booster': ["gbtree"],
        'learning_rate': [0.1],
```

```
        'n_estimators': range(100, 500, 100),
        'min_child_weight': [1],
        'gamma': [0],
        'subsample': [0.8],
        'colsample_bytree': [0.8],
        'max_depth': [5],
        "scale_pos_weight": [1]
    }

    xgb_estimator = XGBClassifier(
        objective='binary:logistic',
        # silent=True,
    )

    gsearch = GridSearchCV(
        estimator=xgb_estimator,
        param_grid=params,
        scoring='roc_auc',
        n_jobs=-1,
        cv=gkf
    )

    xgb_model = gsearch.fit(X=X_train, y=y_train, **fit_params_of_xgb)
    (gsearch.best_params_, gsearch.best_score_)

         [0]     validation_0-auc:0.848269
         Will train until validation_0-auc hasn't improved in 100 rounds.
         [99]    validation_0-auc:0.879961
         ({'booster': 'gbtree',
           'colsample_bytree': 0.8,
           'gamma': 0,
           'learning_rate': 0.1,
           'max_depth': 5,
           'min_child_weight': 1,
           'n_estimators': 100,
           'scale_pos_weight': 1,
           'subsample': 0.8},
          0.8811049523410902)

    def model_performance(model, y_test, y_hat) :
        conf_matrix = confusion_matrix(y_test, y_hat)

        #Show metrics
        tp = conf_matrix[1,1]
        fn = conf_matrix[1,0]
        fp = conf_matrix[0,1]
        tn = conf_matrix[0,0]
        accuracy  =  ((tp+tn)/(tp+tn+fp+fn))
        precision =  (tp/(tp+fp))
        recall    =  (tp/(tp+fn))
        f1_score  =  (2*(((tp/(tp+fp))*(tp/(tp+fn)))/((tp/(tp+fp))+(tp/(tp+fn)))))

        print(f"Accuracy: {accuracy}")
```

```
        print(f"Accuracy: {accuracy}")
        print(f"Recall: {recall}")
        print(f"Precision: {precision}")
        print(f"F1 score: {f1_score}")

        #Roc curve
        model_roc_auc = round(roc_auc_score(y_test, y_hat) , 3)
        fpr, tpr, t = roc_curve(y_test, y_hat)
        trace3 = go.Scatter(x = fpr,y = tpr,
                            name = "Roc : " + str(model_roc_auc),
                            line = dict(color = ('rgb(22, 96, 167)'),width = 2), fill='to
        trace4 = go.Scatter(x = [0,1],y = [0,1],
                            line = dict(color = ('black'),width = 1.5,
                            dash = 'dot'))

        # Precision-recall curve
        precision, recall, thresholds = precision_recall_curve(y_test, y_hat)
        trace5 = go.Scatter(x = recall, y = precision,
                            name = "Precision" + str(precision),
                            line = dict(color = ('lightcoral'),width = 2), fill='tozeroy'


        #plots
        model = model

        #Subplots
        fig = tls.make_subplots(rows=2, cols=2, print_grid=False,
                              specs=[
                                     [{}, {}],
                                     [{}, {}],
                                    ],
                              subplot_titles=(
                                           'ROC curve'+" "+ '('+ str(model_roc_auc)+')',
                                           'Precision - Recall curve',
                                           ))

        fig.append_trace(trace3,1,1)
        fig.append_trace(trace4,1,1)
        fig.append_trace(trace5,1,2)

        fig['layout'].update(showlegend = False, title = '<b>Model performance report</b>
                            autosize = False, height = 1500,width = 830,
                            plot_bgcolor = 'rgba(240,240,240, 0.95)',
                            paper_bgcolor = 'rgba(240,240,240, 0.95)',
                            margin = dict(b = 195))
        fig.layout.titlefont.size = 14

        py.iplot(fig)


    xgb_tuned = XGBClassifier(n_estimators=3000,
        objective='binary:logistic',
```

```
        booster="gbtree",
        learning_rate=0.01,
        scale_pos_weight=1,
        max_depth=4,
        min_child_weight=6,
        gamma=0,
        subsample=0.4,
        colsample_bytree=0.8,
        reg_alpha=0.08,
        n_jobs=-1)

    xgb_tuned.fit(X_train._get_numeric_data(), np.ravel(y_train, order='C'))
    y__hat = xgb_tuned.predict(X_test._get_numeric_data())
```

Step 7

XGBoostClassifier was used to solve this problem. It was selected since XGB performs well with multiple variables, and it was able to circumvent the problems faced by the neural network (too low precision).

Step 8

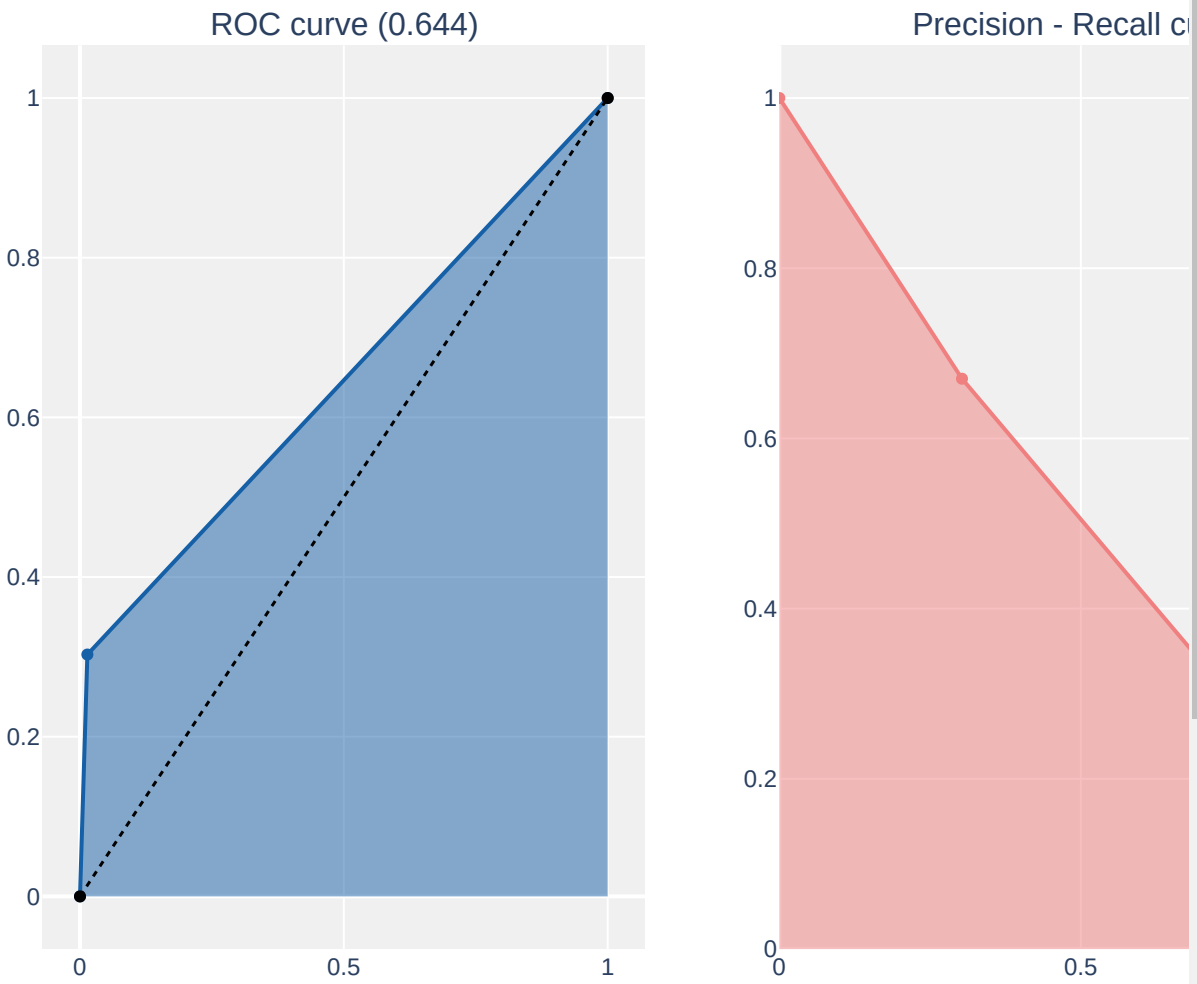
```
model_performance(xgb_tuned,y_test, y__hat)
```

```
Accuracy: 0.9272929340196537
Recall: 0.30292716133424097
Precision: 0.6701807228915663
F1 score: 0.41725269573370843
/usr/local/lib/python3.7/dist-packages/plotly/tools.py:465: DeprecationWarning

plotly.tools.make_subplots is deprecated, please use plotly.subplots.make_subp
```

Model performance report

XGBClassifier(colsample_bytree=0.8, learning_rate=0.01, max_depth=4, min_child_weigh



Step 9

```
wrong_yhat = y__hat[y__hat != y_test]
```

```
pd.Series(wrong_yhat).value_counts()
```

```
0    1024
1     219
dtype: int64
```

```
# A lot of false negatives are present
wrong_indices = []

for i,x in enumerate(y__hat):
  if x != y_test.iloc[i] and x == 0:
    wrong_indices.append(i)
```

```
X_test.iloc[wrong_indices].describe()
```

	age	bmi	elective_surgery	height	pre_icu_los_days	
count	1024.000000	1024.000000	1024.000000	1024.000000	1024.000000	102
mean	68.405273	28.720128	0.079102	168.927744	1.371888	8
std	14.486614	9.048690	0.270029	10.908383	3.677337	2
min	18.000000	14.844926	0.000000	137.200000	-0.215278	3

```
X_test.describe()
```

st_operative	arf_apache	...	cat- _metabolic	cat- _musculoskeletal/skin	cat- _neurological
17096.000000	17096.000000	...	17096.000000	17096.000000	17096.000000
0.184546	0.029890	...	0.088968	0.011816	0.128978
0.387940	0.170289	...	0.284706	0.108059	0.335185
0.000000	0.000000	...	0.000000	0.000000	0.000000
0.000000	0.000000	...	0.000000	0.000000	0.000000
0.000000	0.000000	...	0.000000	0.000000	0.000000
0.000000	0.000000	...	0.000000	0.000000	0.000000
1.000000	1.000000	...	1.000000	1.000000	1.000000

From above tables, we can see that elective surgery, sepsis and musculo-skeletal issues cause are predominant in the wrong predictions. These features should be given more weight for improving the model

Step 10

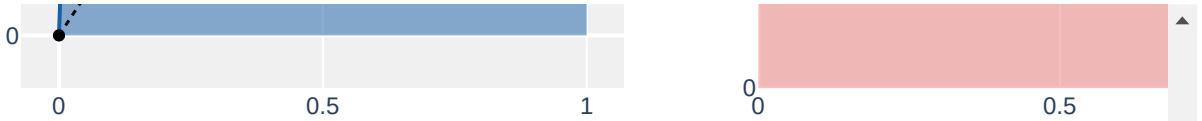
```
['age',
 'bmi',
 'elective_surgery',
```

```
        'height',
        'pre_icu_los_days',
        'weight',
        'apache_2_diagnosis',
        'apache_3j_diagnosis',
        'apache_post_operative',
        'arf_apache',
        'gcs_eyes_apache',
        'gcs_motor_apache',
        'gcs_unable_apache',
        'gcs_verbal_apache',
        'heart_rate_apache',
        'intubated_apache',
        'map_apache',
        'resprate_apache',
        'temp_apache',
        'ventilated_apache',
        'd1_diasbp_max',
        'd1_diasbp_min',
        'd1_diasbp_noninvasive_max',
        'd1_diasbp_noninvasive_min',
        'd1_heartrate_max',
        'd1_heartrate_min',
        'd1_mbp_max',
        'd1_mbp_min',
        'd1_mbp_noninvasive_max',
        'd1_mbp_noninvasive_min',
        'd1_resprate_max',
        'd1_resprate_min',
        'd1_spo2_max',
        'd1_spo2_min',
        'd1_sysbp_max',
        'd1_sysbp_min',
        'd1_sysbp_noninvasive_max',
        'd1_sysbp_noninvasive_min',
        'd1_temp_max',
        'd1_temp_min',
        'h1_diasbp_max',
        'h1_diasbp_min',
        'h1_diasbp_noninvasive_max',
        'h1_diasbp_noninvasive_min',
        'h1_heartrate_max',
        'h1_heartrate_min',
        'h1_mbp_max',
        'h1_mbp_min',
        'h1_mbp_noninvasive_max',
        'h1_mbp_noninvasive_min',
        'h1_resprate_max',
        'h1_resprate_min',
        'h1_spo2_max',
        'h1_spo2_min',
        'h1_sysbp_max',
        'h1_sysbp_min',
        'h1_sysbp_noninvasive_max',
        'h1_sysbp_noninvasive_min',
```

```
females = X_test[X_test['cat-_f'] == 1]
males = X_test[X_test['cat-_m'] == 1]


yf = y_test[X_test['cat-_f'] == 1]
ym = y_test[X_test['cat-_m'] == 1]


yhf = xgb_tuned.predict(females._get_numeric_data())
model_performance(xgb_tuned,yf, yhf)
```



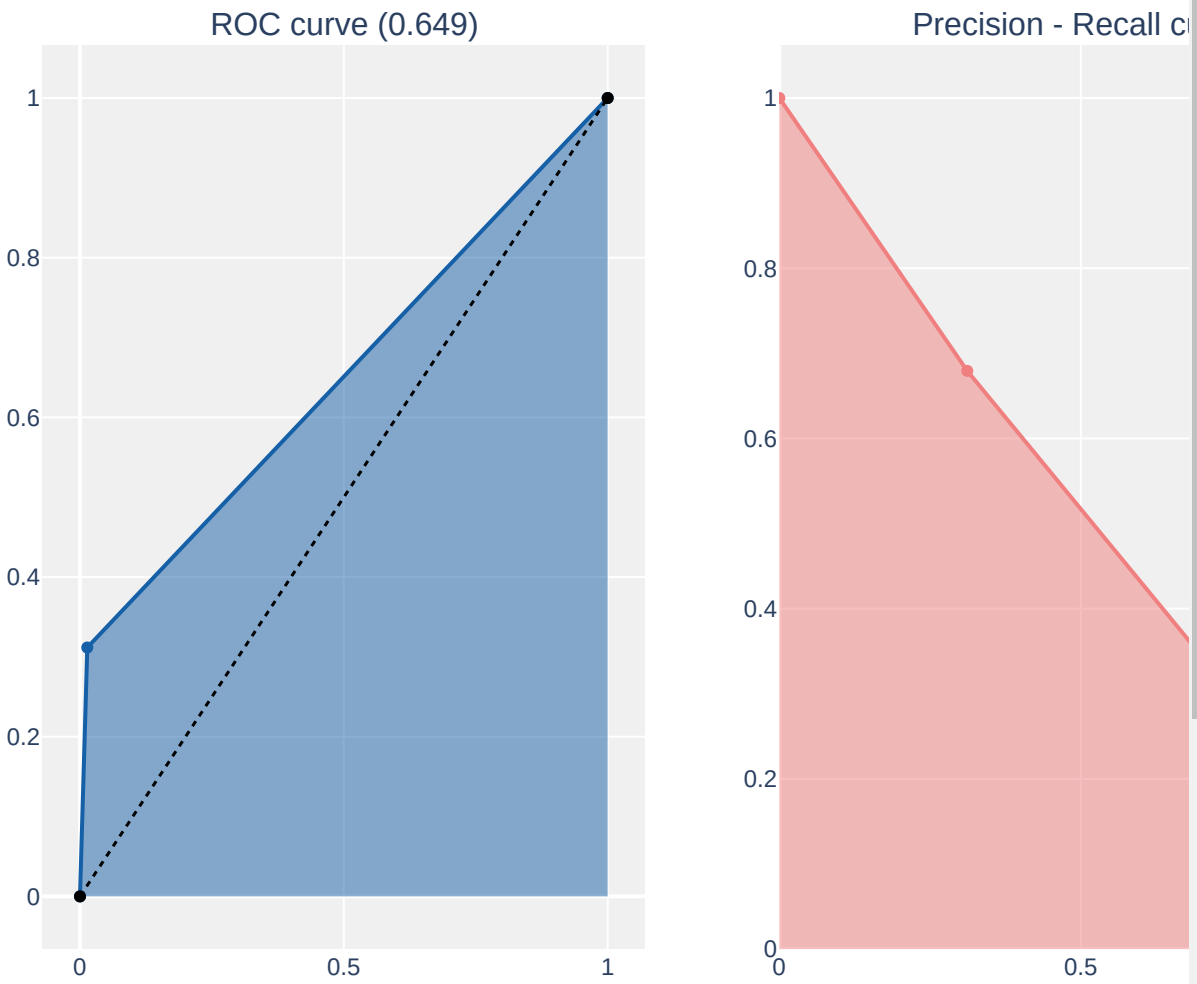

```
yhm = xgb_tuned.predict(males._get_numeric_data())
model_performance(xgb_tuned,ym, yhm)
```

```
Accuracy: 0.9281115879828327
Recall: 0.3117206982543641
Precision: 0.6793478260869565
F1 score: 0.4273504273504274
/usr/local/lib/python3.7/dist-packages/plotly/tools.py:465: DeprecationWarning

plotly.tools.make_subplots is deprecated, please use plotly.subplots.make_subp
```

Model performance report

XGBClassifier(colsample_bytree=0.8, learning_rate=0.01, max_depth=4, min_child_weigh



Above cells show that model performs fairly for both genders

Step 11

```
try:
  import colab
  !pip install --upgrade pip
except:
  pass
!pip install tfx
```

```
        Uninstalling prompt-toolkit-1.0.18:
          Successfully uninstalled prompt-toolkit-1.0.18
      Attempting uninstall: packaging
        Found existing installation: packaging 21.3
```

```
    Uninstalling packaging-21.3:
      Successfully uninstalled packaging-21.3
  Attempting uninstall: dill
    Found existing installation: dill 0.3.5.1
    Uninstalling dill-0.3.5.1:
      Successfully uninstalled dill-0.3.5.1
  Attempting uninstall: cloudpickle
    Found existing installation: cloudpickle 1.3.0
    Uninstalling cloudpickle-1.3.0:
      Successfully uninstalled cloudpickle-1.3.0
  Attempting uninstall: attrs
    Found existing installation: attrs 21.4.0
    Uninstalling attrs-21.4.0:
      Successfully uninstalled attrs-21.4.0
  Attempting uninstall: ipython
    Found existing installation: ipython 5.5.0
    Uninstalling ipython-5.5.0:
      Successfully uninstalled ipython-5.5.0
  Attempting uninstall: google-resumable-media
    Found existing installation: google-resumable-media 0.4.1
    Uninstalling google-resumable-media-0.4.1:
      Successfully uninstalled google-resumable-media-0.4.1
  Attempting uninstall: google-auth-httplib2
    Found existing installation: google-auth-httplib2 0.0.4
    Uninstalling google-auth-httplib2-0.0.4:
      Successfully uninstalled google-auth-httplib2-0.0.4
  Attempting uninstall: google-cloud-core
    Found existing installation: google-cloud-core 1.0.3
    Uninstalling google-cloud-core-1.0.3:
      Successfully uninstalled google-cloud-core-1.0.3
  Attempting uninstall: google-cloud-storage
    Found existing installation: google-cloud-storage 1.18.1
    Uninstalling google-cloud-storage-1.18.1:
      Successfully uninstalled google-cloud-storage-1.18.1
  Attempting uninstall: google-cloud-language
    Found existing installation: google-cloud-language 1.2.0
    Uninstalling google-cloud-language-1.2.0:
      Successfully uninstalled google-cloud-language-1.2.0
  Attempting uninstall: google-cloud-bigquery-storage
    Found existing installation: google-cloud-bigquery-storage 1.1.1
    Uninstalling google-cloud-bigquery-storage-1.1.1:
      Successfully uninstalled google-cloud-bigquery-storage-1.1.1
  Attempting uninstall: google-cloud-bigquery
    Found existing installation: google-cloud-bigquery 1.21.0
    Uninstalling google-cloud-bigquery-1.21.0:
      Successfully uninstalled google-cloud-bigquery-1.21.0
ERROR: pip's dependency resolver does not currently take into account all the
pandas-gbq 0.13.3 requires google-cloud-bigquery[bqstorage,pandas]<2.0.0dev,>=
multiprocess 0.70.13 requires dill>=0.3.5.1, but you have dill 0.3.1.1 which i
jupyter-console 5.2.0 requires prompt-toolkit<2.0.0,>=1.0.0, but you have prom
gym 0.17.3 requires cloudpickle<1.7.0,>=1.2.0, but you have cloudpickle 2.1.0
google-colab 1.0.0 requires ipython~=5.5.0, but you have ipython 7.34.0 which
google-colab 1.0.0 requires requests~=2.23.0, but you have requests 2.28.0 whi
datascience 0.10.6 requires folium==0.2.1, but you have folium 0.8.3 which is
```

```
import os
from absl import logging
import urllib.request
import tempfile
import pandas as pd
logging.set_verbosity(logging.INFO)  # Set default logging level.

import tensorflow as tf
print('TensorFlow version: {}'.format(tf.__version__))
from tfx import v1 as tfx
print('TFX version: {}'.format(tfx.__version__))
```

```
TensorFlow version: 2.8.2
```

```
# Define the following variables:
# PIPELINE_NAME to give a name to your pipeline
# 2 => CODE HERE #
PIPELINE_NAME = "pipeline"

# PIPELINE_ROOT for output directory to store artifacts generated from the pipeline.
# 3 => CODE HERE #
PIPELINE_ROOT = os.path.join('pipelines', PIPELINE_NAME)

# METADATA_PATH for storing meta data
# 4 => CODE HERE #
METADATA_PATH = os.path.join('metadata', PIPELINE_NAME, 'metadata.db')

# SERVING_MODEL_DIR to deploy your model
# 5 => CODE HERE #
SERVING_MODEL_DIR = os.path.join('serving_model', PIPELINE_NAME)


DATA_ROOT = tempfile.mkdtemp(prefix='tfx-data')  # Create a temporary directory.
_data_filepath = os.path.join(DATA_ROOT, "survival.csv")


_trainer_module_file = 'trainer.py'


%%writefile {_trainer_module_file}

from typing import List
from absl import logging
import tensorflow as tf
from tensorflow import keras
from tensorflow_transform.tf_metadata import schema_utils

from tfx import v1 as tfx
from tfx_bsl.public import tfxio
from tensorflow_metadata.proto.v0 import schema_pb2
```

```
# define the list of features in _FEATURE_KEYS variable
# 8 => CODE HERE #
_FEATURE_KEYS = list(X_train.columns)

# define your target variable _LABEL_KEY
# 9 => CODE HERE #
_LABEL_KEY = 'hospital_death'

_TRAIN_BATCH_SIZE = 20
_EVAL_BATCH_SIZE = 10

# Since we're not generating or creating a schema, we will instead create
# a feature spec.  Since there are a fairly small number of features this is
# manageable for this dataset.
_FEATURE_SPEC = {
    **{
        feature: tf.io.FixedLenFeature(shape=[1], dtype=tf.float32)
           for feature in _FEATURE_KEYS
       },
    _LABEL_KEY: tf.io.FixedLenFeature(shape=[1], dtype=tf.int64)
}


def _input_fn(file_pattern: List[str],
              data_accessor: tfx.components.DataAccessor,
              schema: schema_pb2.Schema,
              batch_size: int = 200) -> tf.data.Dataset:
  """Generates features and label for training.

  Args:
    file_pattern: List of paths or patterns of input tfrecord files.
    data_accessor: DataAccessor for converting input to RecordBatch.
    schema: schema of the input data.
    batch_size: representing the number of consecutive elements of returned
      dataset to combine in a single batch

  Returns:
    A dataset that contains (features, indices) tuple where features is a
      dictionary of Tensors, and indices is a single Tensor of label indices.
  """
  return data_accessor.tf_dataset_factory(
      file_pattern,
      tfxio.TensorFlowDatasetOptions(
          batch_size=batch_size, label_key=_LABEL_KEY),
      schema=schema).repeat()


def _build_keras_model() -> tf.keras.Model:
  """Creates a DNN Keras model for classifying penguin data.

  Returns:
```

```
      A Keras Model.
    """
    # The model below is built with Functional API, please refer to
    # https://www.tensorflow.org/guide/keras/overview for all API options.
    inputs = [keras.layers.Input(shape=(1,), name=f) for f in _FEATURE_KEYS]
    d = keras.layers.concatenate(inputs)
    # compelete your model architecture here
    # 10 => CODE HERE #
    d = keras.layers.Dense(8, activation='relu')(d)
    d = keras.layers.Dense(8, activation='relu')(d)
    d = keras.layers.Dense(8, activation='relu')(d)

    outputs = keras.layers.Dense(3)(d)

    model = keras.Model(inputs=inputs, outputs=outputs)
    model.compile(
        optimizer=keras.optimizers.Adam(1e-2),
        loss=tf.keras.losses.SparseCategoricalCrossentropy(from_logits=True),
        metrics=[keras.metrics.SparseCategoricalAccuracy()])

    model.summary(print_fn=logging.info)
    return model


# TFX Trainer will call this function.
def run_fn(fn_args: tfx.components.FnArgs):
    """Train the model based on given args.

    Args:
      fn_args: Holds args used to train the model as name/value pairs.
    """

    # This schema is usually either an output of SchemaGen or a manually-curated
    # version provided by pipeline author. A schema can also derived from TFT
    # graph if a Transform component is used. In the case when either is missing,
    # `schema_from_feature_spec` could be used to generate schema from very simple
    # feature_spec, but the schema returned would be very primitive.
    schema = schema_utils.schema_from_feature_spec(_FEATURE_SPEC)

    train_dataset = _input_fn(
        fn_args.train_files,
        fn_args.data_accessor,
        schema,
        batch_size=_TRAIN_BATCH_SIZE)
    eval_dataset = _input_fn(
        fn_args.eval_files,
        fn_args.data_accessor,
        schema,
        batch_size=_EVAL_BATCH_SIZE)

    model = _build_keras_model()
```

```
    model.fit(
        train_dataset,
        steps_per_epoch=fn_args.train_steps,
        validation_data=eval_dataset,
        validation_steps=fn_args.eval_steps)

    # The result of the training should be saved in `fn_args.serving_model_dir`
    # directory.
    model.save(fn_args.serving_model_dir, save_format='tf')



def _create_pipeline(pipeline_name: str, pipeline_root: str, data_root: str,
                     module_file: str, serving_model_dir: str,
                     metadata_path: str) -> tfx.dsl.Pipeline:
    """Creates a three component penguin pipeline with TFX."""
    # Brings data into the pipeline.
    example_gen = tfx.components.CsvExampleGen(input_base=data_root)

    # Uses user-provided Python function that trains a model.
    trainer = tfx.components.Trainer(
        module_file=module_file,
        examples=example_gen.outputs['examples'],
        train_args=tfx.proto.TrainArgs(num_steps=100),
        eval_args=tfx.proto.EvalArgs(num_steps=5))

    # Pushes the model to a filesystem destination.
    pusher = tfx.components.Pusher(
        model=trainer.outputs['model'],
        push_destination=tfx.proto.PushDestination(
            filesystem=tfx.proto.PushDestination.Filesystem(
                base_directory=serving_model_dir)))

    # Following three components will be included in the pipeline.
    components = [
        example_gen,
        trainer,
        pusher,
    ]

    return tfx.dsl.Pipeline(
        pipeline_name=pipeline_name,
        pipeline_root=pipeline_root,
        metadata_connection_config=tfx.orchestration.metadata
        .sqlite_metadata_connection_config(metadata_path),
        components=components)


tfx.orchestration.LocalDagRunner().run(
    _create_pipeline(
        pipeline_name=PIPELINE_NAME,
        pipeline_root=PIPELINE_ROOT,
```