# MIMIC pneumonia patients data analysis and logistic regression

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## Summary



**Pneumonia** is an infection that inflames the air sacs in one or both lungs, causing cough with phlegm or pus, fever, chills, and difficulty breathing, which has been troubled human being for years already.

**The objective** of this analysis is to make data analysis on patients diagnosed with pneumonia, design a prediction algorithm using logistic regression and give the closest result. This dataset is originally from the MIMIC database. It contains data of male and female patients from age 19 to 89.



## 1.1 Data Overview and data clean

```
#import library
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
data = pd.read_csv("/content/patients with PNEUMONIA.csv")
data.head()
#data overview
data.describe()
data.info()
```

```
#data clean
#check nulls and outliers(patients
in their age over 120)
data =
data.drop(data[data['age']>120].ind
ex)
```



# 1.2 Extreme Value of pneumonia patients on Ethnicity

avg	min	max	ETHNICITY	
67.550000	43	84	ASIAN	0
78.000000	69	86	ASIAN - CHINESE	1
78.000000	70	84	BLACK/AFRICAN	2
61.247312	23	88	BLACK/AFRICAN AMERICAN	3
70.666667	55	88	BLACK/CAPE VERDEAN	4
77.500000	76	79	BLACK/HAITIAN	5
59.642857	28	87	HISPANIC OR LATINO	6
78.000000	78	78	HISPANIC/LATINO - CENTRAL AMERICAN (OTHER)	7
61.666667	52	66	HISPANIC/LATINO - PUERTO RICAN	8
79.000000	79	79	MIDDLE EASTERN	9
65.000000	65	65	MULTI RACE ETHNICITY	10
63.000000	34	82	OTHER	11
57.000000	50	63	PATIENT DECLINED TO ANSWER	12
72.500000	68	77	PORTUGUESE	13
77.666667	66	87	UNABLE TO OBTAIN	14
68.769231	19	87	UNKNOWN/NOT SPECIFIED	15
66.359877	19	89	WHITE	16
80.000000	70	87	WHITE - RUSSIAN	17



# 1.2 Extreme Value of pneumonia patients on LOS

```
# see the data overview of patients icustays table
patients icustays['LOS'] = patients icustays['LOS'].round(0)
patients icustays =
patients icustays.drop(patients icustays[patients icustays['LOS']>10].index)
patients icustays['LOS'].describe()
            2402.000000
 count
               2.943381
    mean
           2.225547
    std
    min
             0.000000
    25%
           1.000000
          2.000000
    50%
    75%
             4.000000
              10.000000
    max
    Name: LOS, dtype: float64
```

## 1.3 Top 10 common diseases occur with Pneumonia

```
# see top common disease occur with pneumonia
# extract patients' subject_id who diagnosed with Pneumonia
temp_data =
patients_admissions[patients_admissions['SUBJECT_ID'].isin(data['SUBJECT_ID'].values.tolist()
)]
df1 = temp_data.groupby(['DIAGNOSIS'],as_index=False)['DIAGNOSIS'].agg({'cnt':'count'})
df1.sort_values('cnt', inplace=True, ascending=False)
df1[1:10]
```



# 1.3 Top 10 common diseases occur with Pneumonia

	DIAGNOSIS	cnt
469	SEPSIS	59
136	CONGESTIVE HEART FAILURE	47
203	FEVER	37
65	ASTHMA;COPD EXACERBATION	33
33	ALTERED MENTAL STATUS	30
483	SHORTNESS OF BREATH	28
266	HYPOTENSION	23
182	DYSPNEA	23
425	RESPIRATORY FAILURE	20

## 1.4 Visualization-Ethnicity distribution of patients

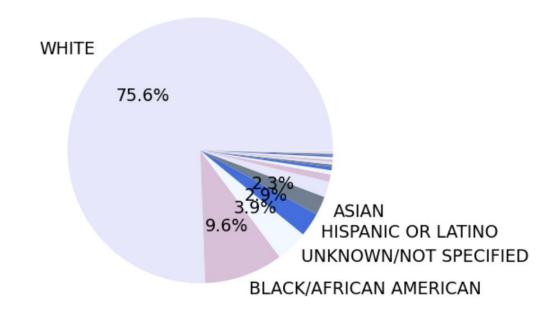
```
# demographic information of
patients--Ethnicity
# calculate number of patients by ethnicity
ethnicityGroup=data['ETHNICITY'].value_count
s()
colors=['lavender','thistle','aliceblue','ro
yalblue','slategrey']

top5Group = ethnicityGroup.index.to_list()
for i in range(5, len(top5Group)):
  top5Group[i] = ''
```

```
# Do not show the labels with small pieces of data
def my autopct(pct):
return ('%.1f%%' % pct) if pct > 2 else ''
plt.pie(x=ethnicityGroup,
       colors=colors.
       autopct=my autopct,
       labels=top5Group,
       pctdistance=0.6,
       labeldistance = 1.1,
       radius = 1.7,
       wedgeprops = {'linewidth': 2},
       textprops = {'fontsize':19 ,'color':'k'})
plt.show()
```



# 1.4 Visualization-Ethnicity distribution of patients

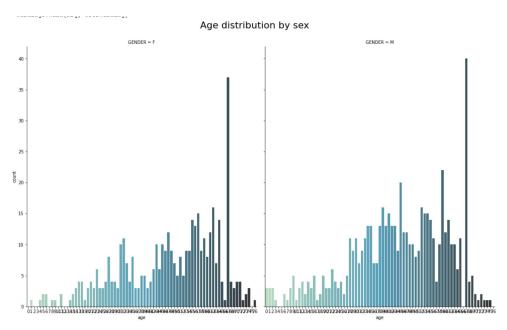


# 1.5 Visualization-Age distribution by gender

```
# age distribution by sex
agePeople=data['age'].value_counts()
g = sns.factorplot(x="age", col="GENDER",data=data, kind="count",size=10,
aspect=0.8,palette="GnBu_d");
g.set_xticklabels(np.arange(0,100));
# g.set_xticklabels(step=10);
g.fig.suptitle('Age distribution by sex',fontsize=22);
g.fig.subplots_adjust(top=.9)
```

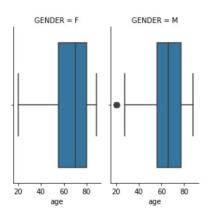


# 1.5 Visualization-Age distribution by gender



# 1.6 Visualization-Age distribution among gender

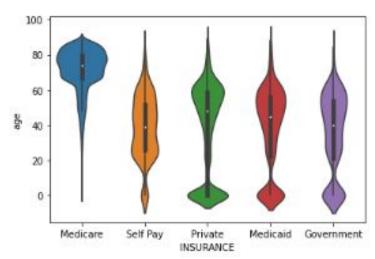
```
sns.factorplot(x='age',col='GENDER',data=data,kind='box',size=4,aspect=0.5)
```





# 1.7 Visualization-Insurance purchase by age

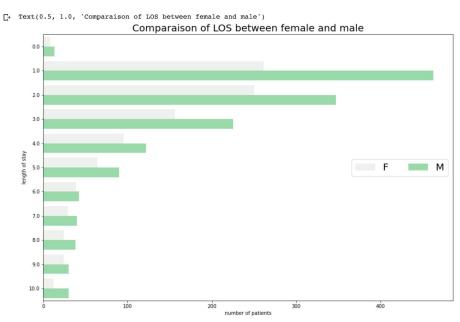
sns.violinplot(x=patients\_admissions["INSURANCE"], y=patients\_admissions["age"])
plt.show()



## 1.8 Visualization-Length of Stay staus by sex

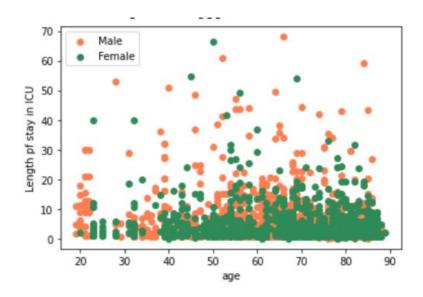
```
# LOS in ICU of patients diagnosed with pneumonia in different age groups among gender
f, ax = plt.subplots(sharex=True, figsize=(15, 10))
sns.set_color_codes("pastel")
g=sns.countplot(y='LOS', hue='GENDER', data=patients_icustays, ax=ax, color='g')
sns.set_color_codes("muted")
ax.legend(ncol=2, loc="center right", frameon=True, fontsize=20)
ax.set( ylabel="length of stay", xlabel="number of patients")
ax.set title("Comparaison of LOS between female and male", fontsize=20)
```

# 1.8 Visualization-Length of Stay staus by sex

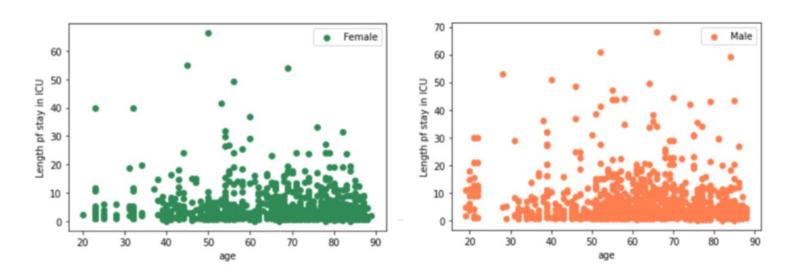


# 1.9 Visualization-Age distribition by sex on LOS

```
#Indicate each color represents what data
x_male=patients_icustays['age'].loc[patients_icustays['GENDER']=='M']
y_male=patients_icustays['LOS'].loc[patients_icustays['GENDER']=='M']
x_female=patients_icustays['age'].loc[patients_icustays['GENDER']=='F']
y_female=patients_icustays['LOS'].loc[patients_icustays['GENDER']=='F']
fig,ax=plt.subplots()
# set notes and form of graph
ax.scatter(x_male,y_male, c='coral',label='Male')
ax.scatter(x_female,y_female, c='seagreen',label='Female')
ax.set_xlabel('age')
ax.set_ylabel('Length pf stay in ICU')
ax.legend()
plt.show
```



# 1.9 Visualization-Age distribition by sex on LOS



## 2. Logistic regression

Logistic regression is a process of modeling the probability of a discrete outcome given an input variable. The most common logistic regression models a binary outcome; something that can take two values such as true/false, yes/no, and so on.

#### Classification problem

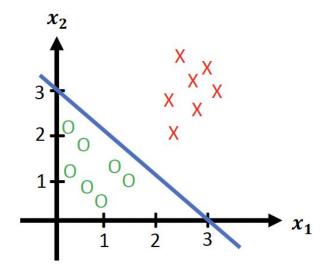
- Email: Spam/ Not Spam
- Document: Relevant/Not relevant
- Transaction: Fraudlent(Yes/No)

#### **Binary Classification Problem**

 $y \in \{0, 1\}$ 

o : Negative Class

1: Positive Class



To make predictions on y = fx, threshold classifier output condition: If  $GMTx \ge 0$ y = 1 predict Spam class

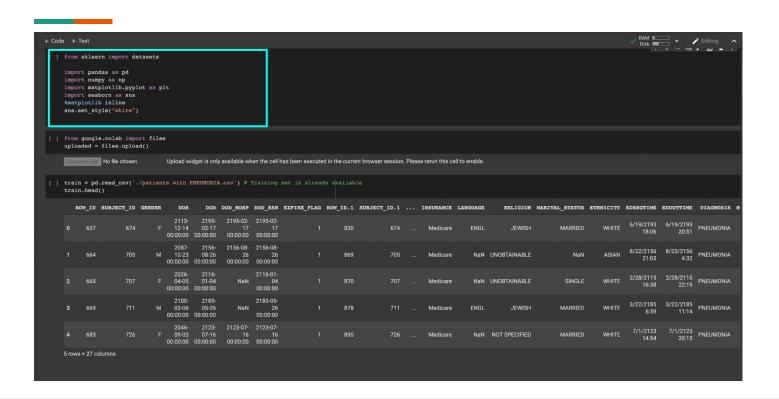


## 2.1 Import libraries and loading the dataset

The libraries we will use for this project:

- pandas: The first library that we need to import is pandas, which is a portmanteau of "panel data" and is the most popular Python library for working with tabular data.
- 2. **numpy:** we'll need to import NumPy, which is a popular library for numerical computing. Numpy is known for its NumPy array data structure as well as its useful methods reshape, arange, and append.
- 3. **%matplotlib:** we need to import matplotlib, which is Python's most popular library for data visualization.
- 4. **seaborn:** we will want to import seaborn, which is another Python data visualization library that makes it easier to create beautiful visualizations using matplotlib.



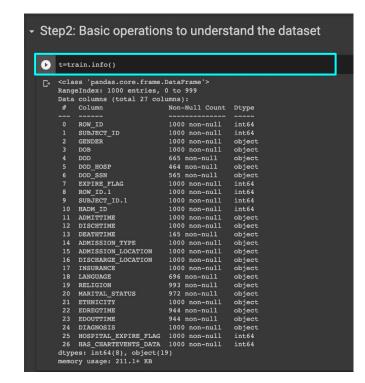




#### 2.2 Understand the dataset

The info() function is used to print a concise summary of a DataFrame. This method prints information about a DataFrame including the index dtype and column dtypes, non-null values and memory usage.

As we can see in the output, the summary includes list of all columns with their data types and the number of non-null values in each column. we also have the value of range index provided for the index axis.

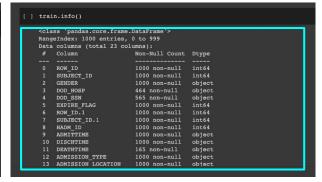




#### 2.2 Understand the dataset

The drop() function is used to drop specified labels from rows or columns. Remove rows or columns by specifying label names and corresponding axis, or by specifying directly index or column names. When using a multi-index, labels on different levels can be removed by specifying the level.

	# data overview train.describe()											
	ROW_ID	SUBJECT_ID	EXPIRE_FLAG	ROW_ID.1	SUBJECT_ID.1	HADM_ID	HOSPITAL_EXPIRE_FLAG	HAS_CHARTEVENTS_DATA				
count	1000.000000	1000.000000	1000.000000	1000.000000	1000.000000	1000.000000	1000.000000	1000.000000				
mean	19774.888000	24687.885000	0.665000	25508.516000	24687.885000	149999.458000	0.165000	0.98900				
std	11272.786471	18158.488381	0.472227	14490.284071	18158.488381	28884.903681	0.371366	0.10435				
min	61.000000	68.000000	0.000000	69.000000	68.000000	100030.000000	0.000000	0.00000				
25%	10099.750000	10672.750000	0.000000	13050.250000	10672.750000	125618.500000	0.000000	1.00000				
50%	20092.000000	21289.000000	1.000000	25987.500000	21289.000000	150052.000000	0.000000	1.00000				
75%	29512.750000	31415.750000	1.000000	38203.750000	31415.750000	174600.500000	0.000000	1.00000				
max	41904.000000	82211.000000	1.000000	53375.000000	82211.000000	199951.000000	1.000000	1.00000				



add analysis: If the probability is 0.000, the \_\_regression model is statistically valid





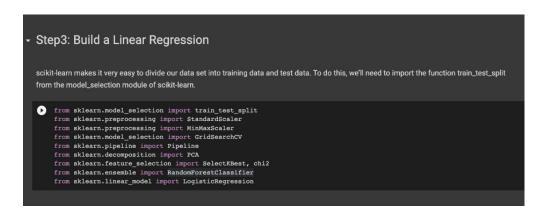
Another useful way that you can learn about this data set is by generating a pairplot. You can use the seaborn method pairplot for this, and pass in the entire DataFrame as a parameter.



## 2.3 Build a linear regression

#### **Creating Training Data and Test Data**

Next, it's time to split train\_data into training data and test data. As before, we will use built-in functionality from scikit-learn to do this. First, we need to divide our data into x values (the data we will be using to make predictions) and y values (the data we are attempting to predict).





## 2.4 Splitting data

#### **Creating Training Data and Test Data**

We can use the train\_test\_split function combined with list unpacking to generate our training data and test data:

```
def convert to binary(x):
loat
ambda
```



## 2.5 Model development

To train our model, we will first need to import the appropriate model from scikit-learn. To train the model, we need to call the fit method on the LogisticRegression object we just created and pass in our x\_training\_data and y\_training\_data variable.



#### 2.6 Prediction

Scikit-learn makes it very easy to make predictions from a machine learning model. You simply need to call the predict method on the model variable that we created earlier. The predictions variable holds the predicted values of the features stored in x\_test. Since we used the train\_test\_split method to store the real values in y\_test.

```
[ ] x= x.reshape(-1, 1)
    y= y.reshape(-1, 1)

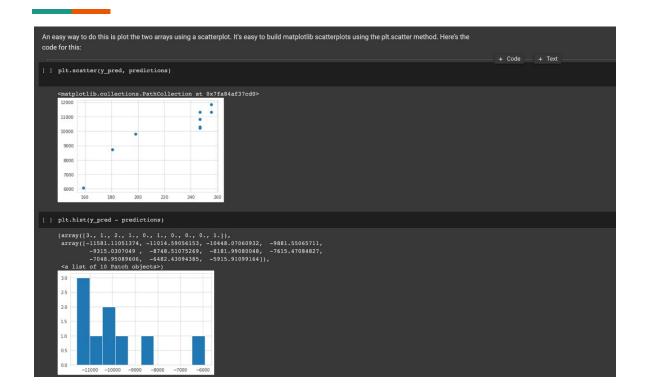
[ ] x_test=x.reshape(-1,1)

[ ] y_test=y.reshape(-1,1)

[ ] y_pred = lr.predict(x_test)

[ ] predictions=lr.predict(y_test)
```







## 2.7 Model evaulation

#### Measuring the Performance of a Logistic Regression Machine Learning Model

scikit-learn has an excellent built-in module called classification\_report that makes it easy to measure the performance of a classification machine learning model.

```
[ ] from sklearn.metrics import classification_report
[ ] y_true = [0, 1, 2, 2, 2]
   y_pred = [0, 0, 2, 2, 1]
   target names = ['class 0', 'class 1', 'class 2']
[ ] print(classification_report(y_true, y_pred, target_names=target_names))
                 precision recall f1-score support
        class 0
                     0.50
                              1.00
                                       0.67
        class 1
                     0.00
                              0.00
                                       0.00
        class 2
                     1.00
                              0.67
                                       0.80
                                       0.60
       accuracy
      macro avq
                     0.50
                              0.56
                                       0.49
    weighted avg
                              0.60
                                       0.61
```



## 2.7 Model evaulation

#### **Confusion matrix**

Compute confusion matrix to evaluate the accuracy of a classification. By definition a confusion matrix is such that is equal to the number of observations known to be in group and predicted to be in group.

```
[ ] # basic
   import pandas as pd
   import numpy as np
   import matplotlib.pyplot as plt

[ ] from sklearn.metrics import confusion_matrix
   cm = confusion_matrix(y_true, y_pred)

   df_cm = pd.DataFrame(cm)
   df_cm.rename(columns={0:'Not diagnosis'}, 1:'diagnosis'}, index={0:'Not diagnosis'}, inplace=True)

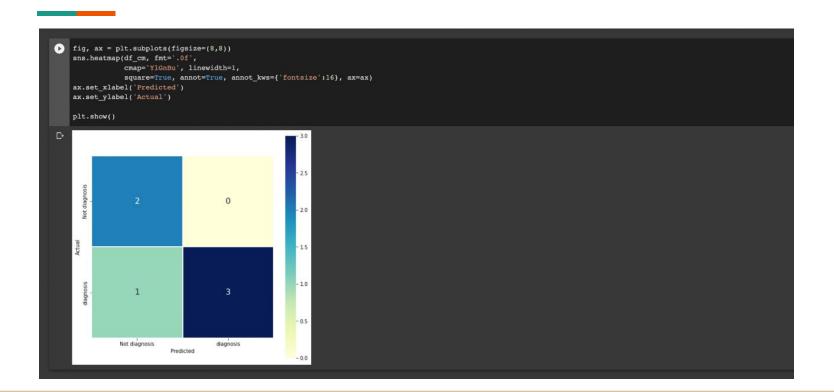
   df_cm

   Not diagnosis diagnosis

Not diagnosis 2 0

   diagnosis 1 3
```







## 2.7 Model evaulation

#### Logistic function flot

Compute confusion matrix to evaluate the accuracy of a classification. By definition a confusion matrix is such that is equal to the number of observations known to be in group and predicted to be in group.



```
3.Logistic Function Plot
                                                                                                                                                       ↑ ↓ © 目 ‡ ᡚ î :
    coef = predicted.coef_
                                             Traceback (most recent call last)
    <ipython-input-4-66c2d13729b5> in <module>()
         2 coef
    NameError: name 'predicted' is not defined
     SEARCH STACK OVERFLOW
  ] coef = coef.flatten()
  ] intercept = model.intercept_
    intercept
```



### Conclusion

#### Conclusion

Yes it can be used to predict whether a person had pneumonia or not. The accuracy and precision are above **70%.** But, it's not a good model. Especially if we look at the recall value **60%**, it's only about **61%** f1 - score. It means, this model only can catch\_\_of patients who had pneumonia..

#### **Root of Problems**

I'm not doing any data preprocessing method, such as scaling the data and balancing the target data. I use a very simple logistic regression model

#### **Future Works**

Do some data preprocessing methods and use a more complex model

