Research_paper_Yogadisha_Sendhil_Kumar

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[1]:
```
import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)

# Input data files are available in the read-only "../input/" directory
# For example, running this (by clicking run or pressing Shift+Enter) will list␣
↪all files under the input directory

import os
for dirname, _, filenames in os.walk('/kaggle/input'):
    for filename in filenames:
        print(os.path.join(dirname, filename))
```

[2]:
```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
```

[3]:
```
df = pd.read_csv("Disease_symptom_and_patient_profile_dataset.csv")
```

[4]:
```
df.sample(5)
```

[4]:
```
                 Disease Fever Cough Fatigue Difficulty Breathing  Age Gender  \
332         Osteoporosis   Yes    No      No                   No   70   Male
289          Hepatitis B    No   Yes     Yes                   No   60   Male
299  Parkinson's Disease   Yes   Yes      No                   No   60   Male
197            Pneumonia   Yes   Yes     Yes                  Yes   45   Male
83         Kidney Cancer    No    No     Yes                   No   35   Male

    Blood Pressure Cholesterol Level Outcome Variable
332         Normal            Normal         Negative
289         Normal               Low         Positive
299           High            Normal         Positive
197           High              High         Positive
83            High              High         Positive
```

[5]:
```
# Checking Data Types of columns
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 349 entries, 0 to 348
Data columns (total 10 columns):
Disease                 349 non-null object
Fever                   349 non-null object
Cough                   349 non-null object
Fatigue                 349 non-null object
Difficulty Breathing    349 non-null object
Age                     349 non-null int64
Gender                  349 non-null object
Blood Pressure          349 non-null object
Cholesterol Level       349 non-null object
Outcome Variable        349 non-null object
dtypes: int64(1), object(9)
memory usage: 27.3+ KB
```

[6]:
```
#checking for null values
df.isnull().sum()
```

[6]:
```
Disease                 0
Fever                   0
Cough                   0
Fatigue                 0
Difficulty Breathing    0
Age                     0
Gender                  0
Blood Pressure          0
Cholesterol Level       0
Outcome Variable        0
dtype: int64
```

[7]:
```
# What is the size of dataset
df.shape
```

[7]:
```
(349, 10)
```

[8]:
```
df.head()
```

[8]:
```
       Disease Fever Cough Fatigue Difficulty Breathing  Age  Gender  \
0    Influenza   Yes    No     Yes                  Yes   19  Female
1  Common Cold    No   Yes     Yes                   No   25  Female
2       Eczema    No   Yes     Yes                   No   25  Female
3       Asthma   Yes   Yes      No                  Yes   25    Male
4       Asthma   Yes   Yes      No                  Yes   25    Male

  Blood Pressure Cholesterol Level Outcome Variable
0            Low            Normal         Positive
```

```
1         Normal            Normal        Negative
2         Normal            Normal        Negative
3         Normal            Normal        Positive
4         Normal            Normal        Positive
```

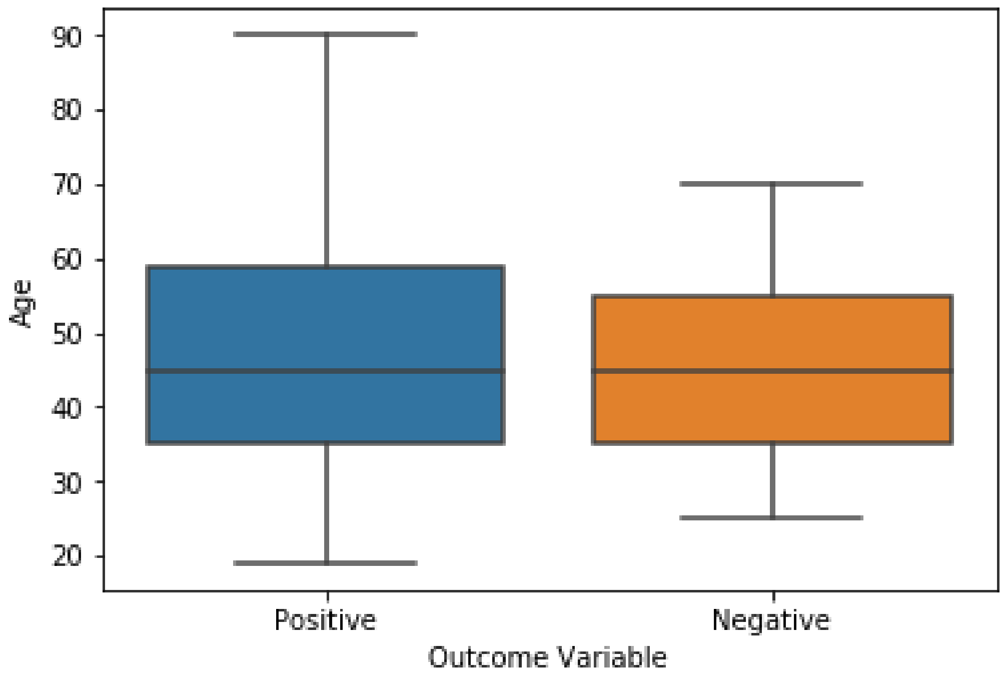
[9]:
```
#let's check for number of unique values
df.nunique()
```

[9]:
```
Disease                 116
Fever                     2
Cough                     2
Fatigue                   2
Difficulty Breathing      2
Age                      26
Gender                    2
Blood Pressure            3
Cholesterol Level         3
Outcome Variable          2
dtype: int64
```

[10]:
```
df.describe()
```

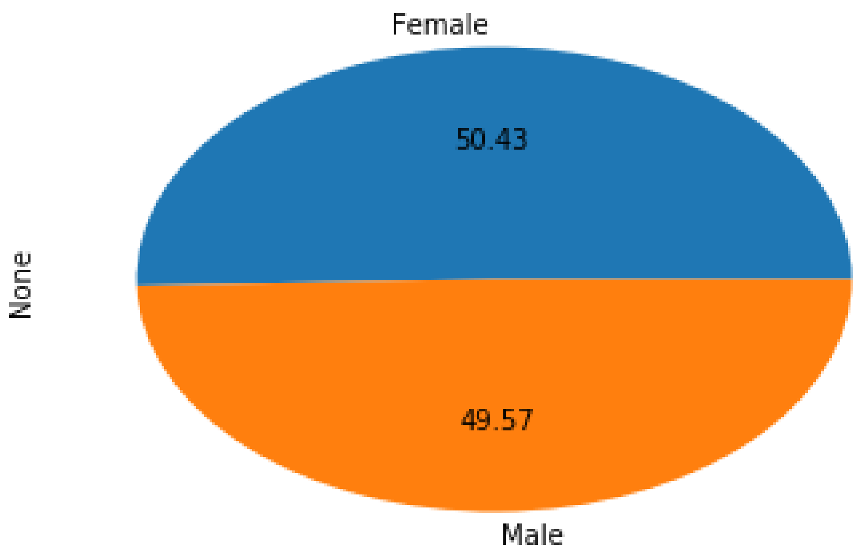
[10]:
```
              Age
count  349.000000
mean    46.323782
std     13.085090
min     19.000000
25%     35.000000
50%     45.000000
75%     55.000000
max     90.000000
```

[11]:
```
sns.boxplot(x='Outcome Variable', y='Age', data=df)
plt.show()
```

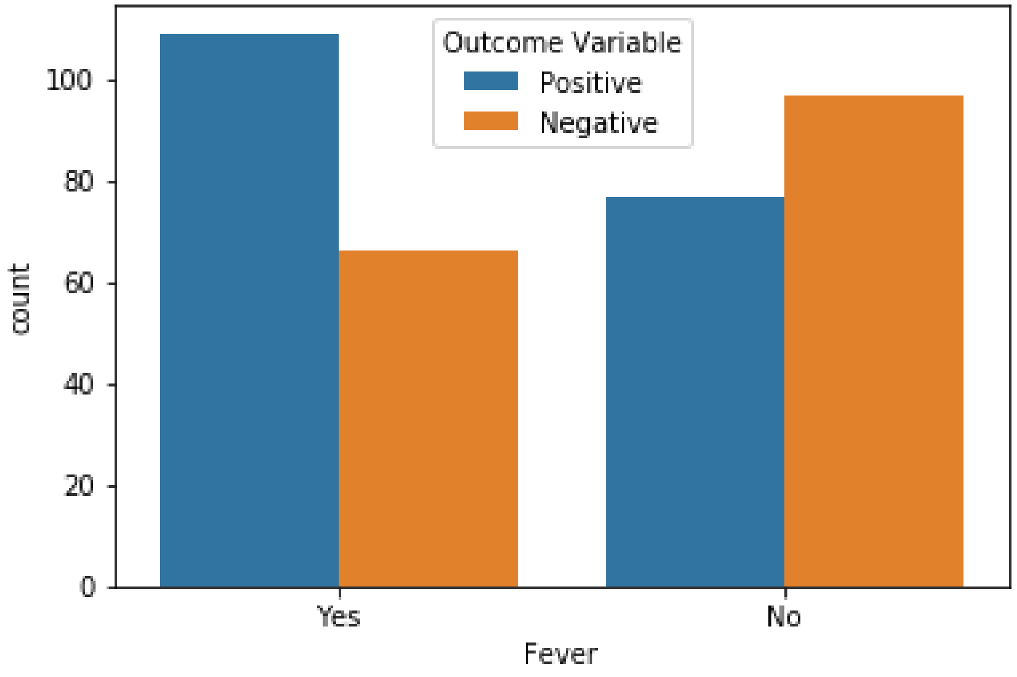


```
[12]: df.groupby('Gender').size().plot(kind='pie', autopct='%.2f')
```

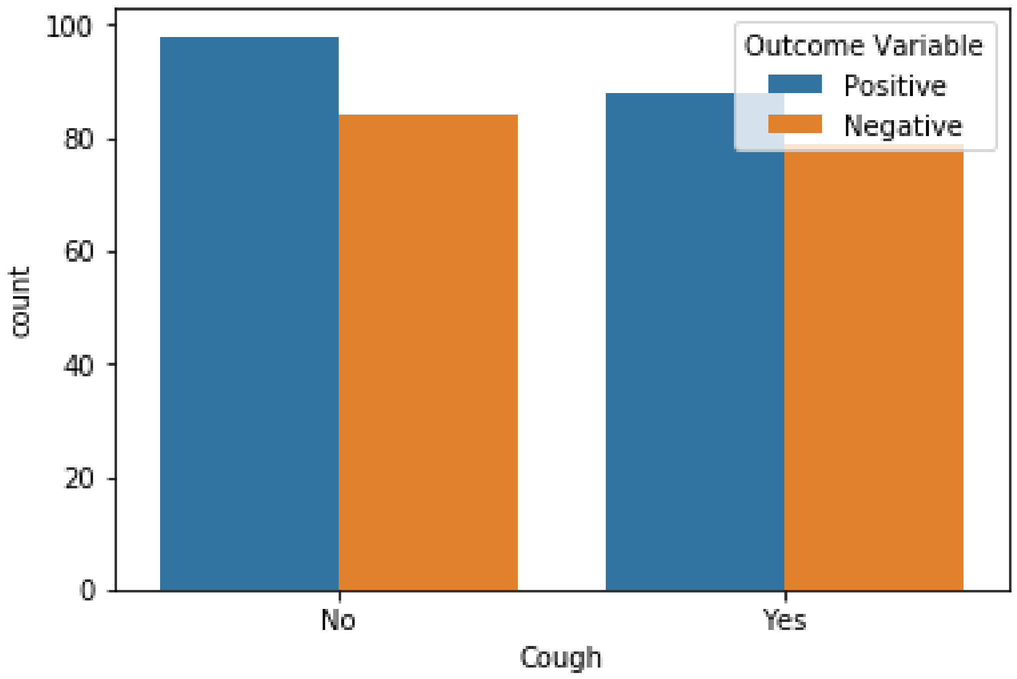
```
[12]: <matplotlib.axes._subplots.AxesSubplot at 0x2b4f8dd31828>
```



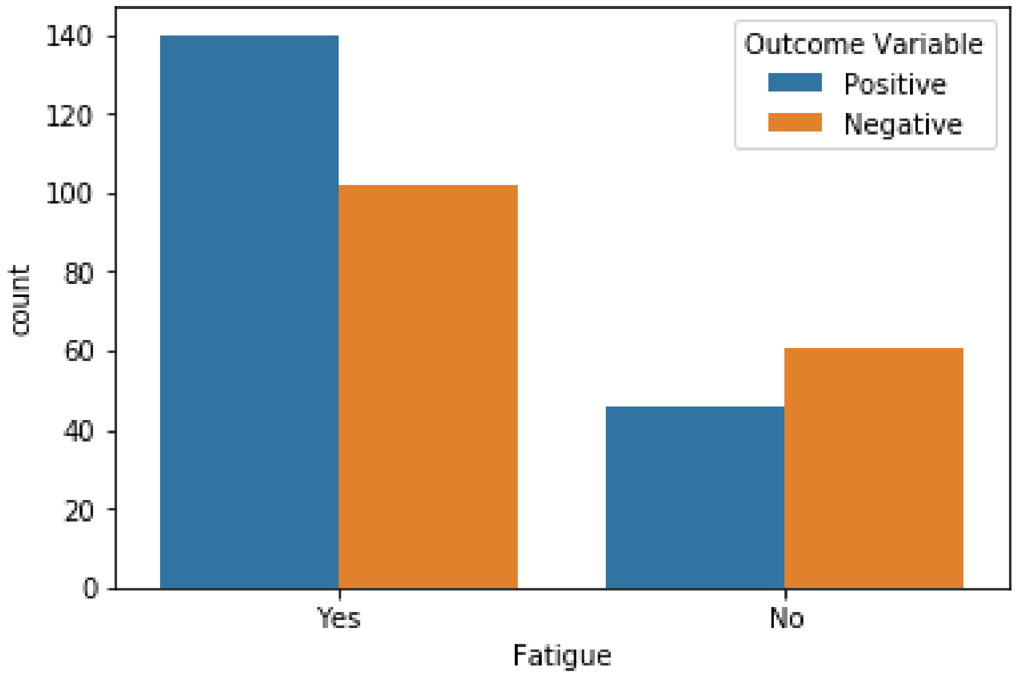
[13]:
```
sns.countplot(x='Fever', data=df, hue='Outcome Variable')
plt.show()
```



[14]:
```
sns.countplot(x='Cough', data=df, hue='Outcome Variable')
plt.show()
```

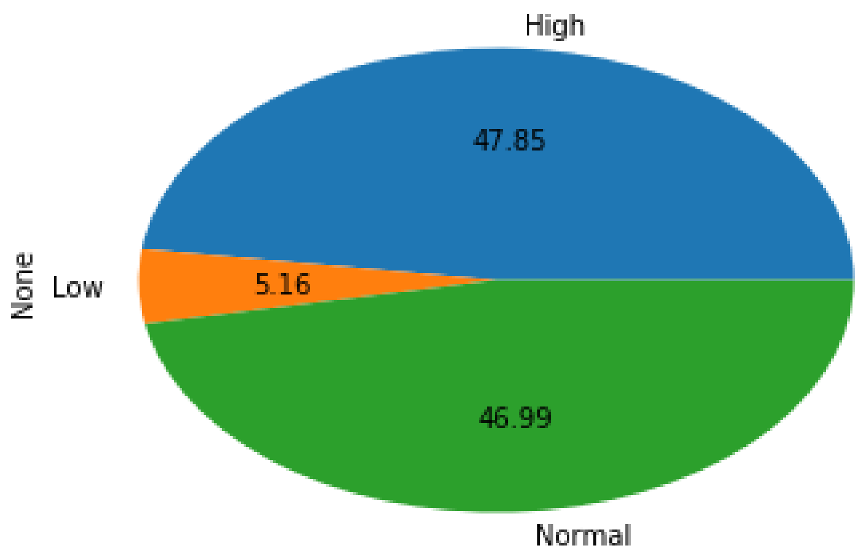


[15]:
```
sns.countplot(x='Fatigue', data=df, hue='Outcome Variable')
plt.show()
```



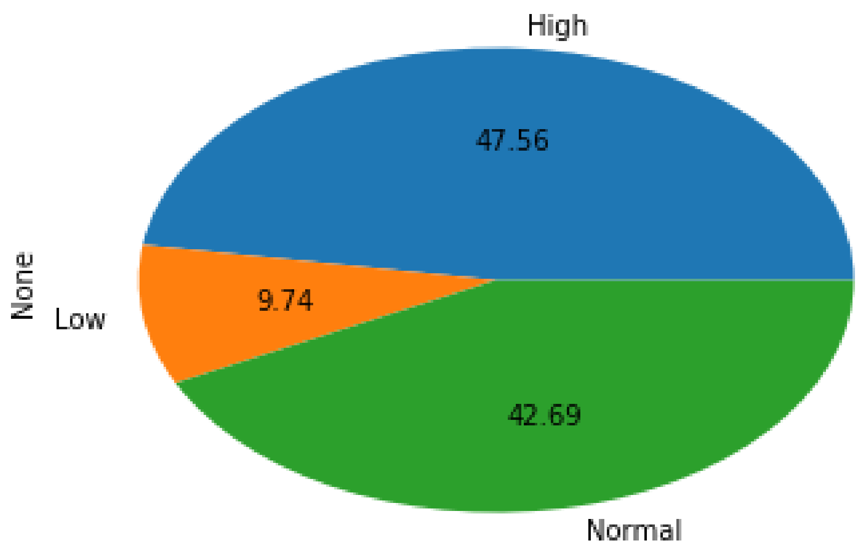
```
[16]: df.groupby('Blood Pressure').size().plot(kind='pie', autopct='%.2f')
```

```
[16]: <matplotlib.axes._subplots.AxesSubplot at 0x2b4f96f5b0b8>
```

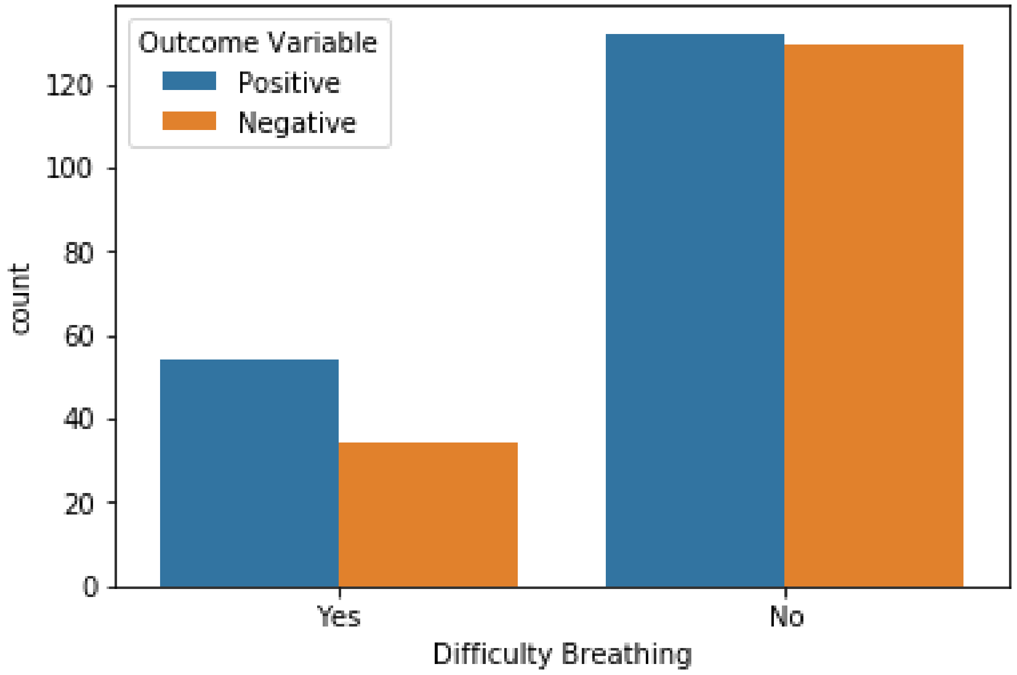


```
[17]: df.groupby('Cholesterol Level').size().plot(kind='pie', autopct='%.2f')
```

```
[17]: <matplotlib.axes._subplots.AxesSubplot at 0x2b4f96fa1c88>
```



[18]:
```
sns.countplot(x='Difficulty Breathing', data=df, hue='Outcome Variable')
plt.show()
```



[19]:
```
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LinearRegression
from sklearn.metrics import accuracy_score, classification_report
```

[20]:
```
# Convert categorical variables to dummy variables
df_ml = pd.get_dummies(df, columns=['Fever', 'Cough', 'Fatigue', 'Difficulty␣
↪Breathing', 'Gender', 'Blood Pressure', 'Cholesterol Level'],␣
↪drop_first=True)
```

[21]:
```
# Define features and target variable
X_ml = df_ml.drop(columns=['Disease', 'Outcome Variable'])
y_ml = df_ml['Outcome Variable']
```

[22]:
```
# Split data into training and testing sets
X_train_ml, X_test_ml, y_train_ml, y_test_ml = train_test_split(X_ml, y_ml,␣
↪test_size=0.2, random_state=42)
```

[23]:
```
from sklearn.preprocessing import LabelEncoder
```

[24]:
```
# Initialize LabelEncoder
label_encoder = LabelEncoder()
```

[25]:
```
# Fit and transform the target variable
y_train_ml_encoded = label_encoder.fit_transform(y_train_ml)
y_test_ml_encoded = label_encoder.transform(y_test_ml)
```

[26]:
```
# Initialize and train the MLR model
mlr_model = LinearRegression()
mlr_model.fit(X_train_ml, y_train_ml_encoded)
```

[26]:
```
LinearRegression(copy_X=True, fit_intercept=True, n_jobs=1, normalize=False)
```

[27]:
```
# Predict outcomes
y_pred_ml_encoded = mlr_model.predict(X_test_ml)
```

[28]:
```
# Convert predicted probabilities to binary predictions
y_pred_ml_encoded[y_pred_ml_encoded > 0.5] = 1
y_pred_ml_encoded[y_pred_ml_encoded <= 0.5] = 0
```

[29]:
```
# Evaluate the model
accuracy_ml_encoded = accuracy_score(y_test_ml_encoded, y_pred_ml_encoded)
print("Accuracy of MLR model with label encoding:", accuracy_ml_encoded)
print("Classification Report:")
print(classification_report(y_test_ml_encoded, y_pred_ml_encoded))
```

```
Accuracy of MLR model with label encoding: 0.5714285714285714
Classification Report:
             precision    recall  f1-score   support

          0       0.50      0.53      0.52        30
          1       0.63      0.60      0.62        40

avg / total       0.58      0.57      0.57        70
```

[30]:
```
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, classification_report
```

[31]:
```
# Define features and target variable
X_dt = df.drop(columns=['Disease', 'Outcome Variable'])
y_dt = df['Outcome Variable']
```

[32]:
```
# Convert categorical variables to dummy variables
X_dt = pd.get_dummies(X_dt, drop_first=True)
```

[33]:
```
# Split data into training and testing sets
X_train_dt, X_test_dt, y_train_dt, y_test_dt = train_test_split(X_dt, y_dt,␣
↪test_size=0.2, random_state=42)
```

[34]:
```
# Initialize and train the Decision Tree model
dt_model = DecisionTreeClassifier(random_state=42)
dt_model.fit(X_train_dt, y_train_dt)
```

[34]:
```
DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=None,
            max_features=None, max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, presort=False, random_state=42,
            splitter='best')
```

[35]:
```
# Predict outcomes
y_pred_dt = dt_model.predict(X_test_dt)
```

[36]:
```
# Evaluate the model
accuracy_dt = accuracy_score(y_test_dt, y_pred_dt)
print("Accuracy of Decision Tree model:", accuracy_dt)
print("Classification Report:")
print(classification_report(y_test_dt, y_pred_dt))
```

```
Accuracy of Decision Tree model: 0.7285714285714285
Classification Report:
             precision    recall  f1-score   support

   Negative       0.64      0.83      0.72        30
   Positive       0.84      0.65      0.73        40

avg / total       0.75      0.73      0.73        70
```