

INFOSYS SPRINGBOARD INTERNSHIP

MileStone 3

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```
In [1]: import pandas as pd
import matplotlib.pyplot as plt
import warnings
warnings.filterwarnings('ignore')

data = pd.read_csv("/Users/rudranighosh/Downloads/Healthcare Providers.csv")
data.head()
```

Out [1]:

	index	National Provider Identifier	Name/Organization Name of the Provider	Last First Name of the Provider	Middle Initial of the Provider	Credentials of the Provider	Gender of the Provider	Entity Type of the Provider	Street Address 1 of the Provider	Street Address 2 of the Provider	...	HCPCS Code	HC Descrip
0	8774979	1891106191	UPADHYAYULA	SATYASREE	NaN	M.D.	F	I	1402 S GRAND BLVD	FDT 14TH FLOOR	...	99223	Initial hos inpatient typically
1	3354385	1346202256	JONES	WENDY	P	M.D.	F	I	2950 VILLAGE DR	NaN	...	G0202	Scree mammogr: bilater: view stu
2	3001884	1306820956	DUROCHER	RICHARD	W	DPM	M	I	20 WASHINGTON AVE	STE 212	...	99348	Establi patient f visit, typ 25
3	7594822	1770523540	FULLARD	JASPER	NaN	MD	M	I	5746 N BROADWAY ST	NaN	...	81002	Urina manua
4	746159	1073627758	PERROTTI	ANTHONY	E	DO	M	I	875 MILITARY TRL	SUITE 200	...	96372	Inje beneat skin o muscle i

5 rows x 27 columns

```
In [2]: # information about the dataset
data.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 100000 entries, 0 to 99999
Data columns (total 27 columns):
#   Column                                     Non-Null Count  Dtype
---  -
0    index                                     100000 non-null  int64
1    National Provider Identifier              100000 non-null  int64
2    Last Name/Organization Name of the Provider  100000 non-null  object
3    First Name of the Provider               95745 non-null   object
4    Middle Initial of the Provider           70669 non-null   object
5    Credentials of the Provider              92791 non-null   object
6    Gender of the Provider                   95746 non-null   object
7    Entity Type of the Provider              100000 non-null   object
8    Street Address 1 of the Provider          100000 non-null   object
9    Street Address 2 of the Provider          40637 non-null   object
10   City of the Provider                     100000 non-null   object
11   Zip Code of the Provider                 100000 non-null   float64
12   State Code of the Provider               100000 non-null   object
13   Country Code of the Provider             100000 non-null   object
14   Provider Type                           100000 non-null   object
15   Medicare Participation Indicator          100000 non-null   object
16   Place of Service                        100000 non-null   object
17   HCPCS Code                             100000 non-null   object
18   HCPCS Description                       100000 non-null   object
19   HCPCS Drug Indicator                    100000 non-null   object
20   Number of Services                      100000 non-null   object
21   Number of Medicare Beneficiaries         100000 non-null   object
22   Number of Distinct Medicare Beneficiary/Per Day Services  100000 non-null   object
23   Average Medicare Allowed Amount          100000 non-null   object
24   Average Submitted Charge Amount          100000 non-null   object
25   Average Medicare Payment Amount          100000 non-null   object
26   Average Medicare Standardized Amount     100000 non-null   object
dtypes: float64(1), int64(2), object(24)
memory usage: 20.6+ MB
```

```
In [3]: irrelevant_columns=['Entity Type of the Provider',
                           'Street Address 1 of the Provider',
                           'Street Address 2 of the Provider',
                           'Zip Code of the Provider',
                           'Medicare Participation Indicator',
                           'Place of Service',
                           'HCPCS Code',
                           'HCPCS Description',
                           'HCPCS Drug Indicator',
                           'Country Code of the Provider']

data=data.drop(columns=irrelevant_columns)

Columns that have no relevance in our assignment have been dropped
```

```
In [4]: data.head()
```

Out [4]:

	index	National Provider Identifier	Name/Organization Name of the Provider	Last First Name of the Provider	Middle Initial of the Provider	Credentials of the Provider	Gender of the Provider	City of the Provider	State Code of the Provider	Provider Type	Number of Services	Numbe Medic Beneficia
0	8774979	1891106191	UPADHYAYULA	SATYASREE	NaN	M.D.	F	SAINT LOUIS	MO	Internal Medicine	27	
1	3354385	1346202256	JONES	WENDY	P	M.D.	F	FAYETTEVILLE	NC	Obstetrics & Gynecology	175	
2	3001884	1306820956	DUROCHER	RICHARD	W	DPM	M	NORTH HAVEN	CT	Podiatry	32	
3	7594822	1770523540	FULLARD	JASPER	NaN	MD	M	KANSAS CITY	MO	Internal Medicine	20	
4	746159	1073627758	PERROTTI	ANTHONY	E	DO	M	JUPITER	FL	Internal Medicine	33	

Data Preprocessing

In [5]:

```
# Merging the name columns into a single column
data['Full Name'] = data['First Name of the Provider'].fillna('') + ' ' + \
                    data['Middle Initial of the Provider'].fillna('') + ' ' + \
                    data['Last Name/Organization Name of the Provider'].fillna('')
data['Full Name'] = data['Full Name'].str.strip()

data = data.drop(columns=['Last Name/Organization Name of the Provider',
                          'First Name of the Provider',
                          'Middle Initial of the Provider'])

full_name_column = data.pop('Full Name')

data.insert(1, 'Full Name', full_name_column)

data.head()
```

Out [5]:

	index	Full Name	National Provider Identifier	Credentials of the Provider	Gender of the Provider	City of the Provider	State Code of the Provider	Provider Type	Number of Services	Number of Medicare Beneficiaries	Number of Distinct Medicare Beneficiary/Per Day Services	M
0	8774979	SATYASREE UPADHYAYULA	1891106191	M.D.	F	SAINT LOUIS	MO	Internal Medicine	27	24	27	200.5
1	3354385	WENDY P JONES	1346202256	M.D.	F	FAYETTEVILLE	NC	Obstetrics & Gynecology	175	175	175	
2	3001884	RICHARD W DUROCHER	1306820956	DPM	M	NORTH HAVEN	CT	Podiatry	32	13	32	
3	7594822	JASPER FULLARD	1770523540	MD	M	KANSAS CITY	MO	Internal Medicine	20	18	20	
4	746159	ANTHONY E PERROTTI	1073627758	DO	M	JUPITER	FL	Internal Medicine	33	24	31	

A new column "Full Name" has been created to merge first name, middle name and last name

In [6]:

```
# Uniform format of credentials
data['Credentials of the Provider'] = data['Credentials of the Provider'].str.replace(r'\.', '', regex=True).str.upper()
data.head()
```

Out [6]:

	index	Full Name	National Provider Identifier	Credentials of the Provider	Gender of the Provider	City of the Provider	State Code of the Provider	Provider Type	Number of Services	Number of Medicare Beneficiaries	Number of Distinct Medicare Beneficiary/Per Day Services	M
0	8774979	SATYASREE UPADHYAYULA	1891106191	MD	F	SAINT LOUIS	MO	Internal Medicine	27	24	27	200.5
1	3354385	WENDY P JONES	1346202256	MD	F	FAYETTEVILLE	NC	Obstetrics & Gynecology	175	175	175	
2	3001884	RICHARD W DUROCHER	1306820956	DPM	M	NORTH HAVEN	CT	Podiatry	32	13	32	
3	7594822	JASPER FULLARD	1770523540	MD	M	KANSAS CITY	MO	Internal Medicine	20	18	20	
4	746159	ANTHONY E PERROTTI	1073627758	DO	M	JUPITER	FL	Internal Medicine	33	24	31	

"Credentials of the Provider" column now follows a uniform format. Such that MD and M.D and M.D. are all treated as the same unit

Converting Object to Numeric Type

In [7]:

```
numeric_columns = [
    'Number of Services',
    'Number of Medicare Beneficiaries',
    'Number of Distinct Medicare Beneficiary/Per Day Services',
    'Average Medicare Allowed Amount',
    'Average Submitted Charge Amount',
    'Average Medicare Payment Amount',
    'Average Medicare Standardized Amount'
]

for column in numeric_columns:
```

```
data[column] = pd.to_numeric(data[column], errors='coerce')

data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 100000 entries, 0 to 99999
Data columns (total 15 columns):
#   Column                                Non-Null Count  Dtype
---  -
0   index                                100000 non-null  int64
1   Full Name                            100000 non-null  object
2   National Provider Identifier          100000 non-null  int64
3   Credentials of the Provider           92791 non-null   object
4   Gender of the Provider                 95746 non-null   object
5   City of the Provider                  100000 non-null   object
6   State Code of the Provider             100000 non-null   object
7   Provider Type                         100000 non-null   object
8   Number of Services                    97347 non-null   float64
9   Number of Medicare Beneficiaries       99595 non-null   float64
10  Number of Distinct Medicare Beneficiary/Per Day Services  98500 non-null   float64
11  Average Medicare Allowed Amount        99255 non-null   float64
12  Average Submitted Charge Amount        93277 non-null   float64
13  Average Medicare Payment Amount        99534 non-null   float64
14  Average Medicare Standardized Amount   99530 non-null   float64
dtypes: float64(7), int64(2), object(6)
memory usage: 11.4+ MB
```

Looking for Missing Values and imputing them with Mean

```
In [8]: # missing values
print(data.isnull().sum())
```

```
index                                0
Full Name                            0
National Provider Identifier          0
Credentials of the Provider           7209
Gender of the Provider                 4254
City of the Provider                  0
State Code of the Provider             0
Provider Type                         0
Number of Services                    2653
Number of Medicare Beneficiaries       405
Number of Distinct Medicare Beneficiary/Per Day Services  1500
Average Medicare Allowed Amount        745
Average Submitted Charge Amount        6723
Average Medicare Payment Amount        466
Average Medicare Standardized Amount   470
dtype: int64
```

```
In [9]: # Imputation of numeric missing values with mean
data[numeric_columns] = data[numeric_columns].fillna(data[numeric_columns].mean())

print(data.isnull().sum())
```

```
index                                0
Full Name                            0
National Provider Identifier          0
Credentials of the Provider           7209
Gender of the Provider                 4254
City of the Provider                  0
State Code of the Provider             0
Provider Type                         0
Number of Services                    0
Number of Medicare Beneficiaries       0
Number of Distinct Medicare Beneficiary/Per Day Services  0
Average Medicare Allowed Amount        0
Average Submitted Charge Amount        0
Average Medicare Payment Amount        0
Average Medicare Standardized Amount   0
dtype: int64
```

Imputation of categorical columns with mode

```
In [10]: categorical_columns = ['Credentials of the Provider',
                                'Gender of the Provider',
                                'City of the Provider',
                                'State Code of the Provider']

for column in categorical_columns:
    data[column].fillna(data[column].mode()[0], inplace=True)

print(data.isnull().sum())
```

```
index                                0
Full Name                            0
National Provider Identifier          0
Credentials of the Provider           0
Gender of the Provider                 0
City of the Provider                  0
State Code of the Provider             0
Provider Type                         0
Number of Services                    0
Number of Medicare Beneficiaries       0
Number of Distinct Medicare Beneficiary/Per Day Services  0
Average Medicare Allowed Amount        0
Average Submitted Charge Amount        0
Average Medicare Payment Amount        0
Average Medicare Standardized Amount   0
dtype: int64
```

Looking for Duplicate Values

In [11]: `# Check for duplicates`
`print(data.duplicated().sum())`

0

In [12]: `data.head()`

Out[12]:

	index	Full Name	National Provider Identifier	Credentials of the Provider	Gender of the Provider	City of the Provider	State Code of the Provider	Provider Type	Number of Services	Number of Medicare Beneficiaries	Number of Distinct Medicare Beneficiary/Per Day Services	Average Medicare Standardized Amount
0	8774979	SATYASREE UPADHYAYULA	1891106191	MD	F	SAINT LOUIS	MO	Internal Medicine	27.0	24.0	27.0	200.5
1	3354385	WENDY P JONES	1346202256	MD	F	FAYETTEVILLE	NC	Obstetrics & Gynecology	175.0	175.0	175.0	123.7
2	3001884	RICHARD W DUROCHER	1306820956	DPM	M	NORTH HAVEN	CT	Podiatry	32.0	13.0	32.0	90.6
3	7594822	JASPER FULLARD	1770523540	MD	M	KANSAS CITY	MO	Internal Medicine	20.0	18.0	20.0	3.5
4	746159	ANTHONY E PERROTTI	1073627758	DO	M	JUPITER	FL	Internal Medicine	33.0	24.0	31.0	26.5

Encoding some Categorical Columns using Frequency Encoder

In [13]: `def frequency_encode(df, columns):`
 `for column in columns:`
 `freq_encoding = df[column].value_counts() / len(df)`
 `new_column_name = column + '_Freq'`
 `df.insert(df.columns.get_loc(column) + 1, new_column_name, df[column].map(freq_encoding))`
 `return df`

 `columns_to_encode=['Credentials of the Provider',`
 `'Gender of the Provider',`
 `'Provider Type',`
 `'State Code of the Provider']`

 `data = frequency_encode(data, columns_to_encode)`

 `df=data`

 `data.head()`

Out[13]:

	index	Full Name	National Provider Identifier	Credentials of the Provider	Credentials of the Provider_Freq	Gender of the Provider	Gender of the Provider_Freq	City of the Provider	State Code of the Provider	State Code of the Provider_Freq	Provider Type
0	8774979	SATYASREE UPADHYAYULA	1891106191	MD	0.73827	F	0.29105	SAINT LOUIS	MO	0.01997	Internal Medicine
1	3354385	WENDY P JONES	1346202256	MD	0.73827	F	0.29105	FAYETTEVILLE	NC	0.03725	Obstetrics & Gynecology
2	3001884	RICHARD W DUROCHER	1306820956	DPM	0.01915	M	0.70895	NORTH HAVEN	CT	0.01403	Podiatry
3	7594822	JASPER FULLARD	1770523540	MD	0.73827	M	0.70895	KANSAS CITY	MO	0.01997	Internal Medicine
4	746159	ANTHONY E PERROTTI	1073627758	DO	0.06176	M	0.70895	JUPITER	FL	0.07263	Internal Medicine

In [14]: `df.columns`

Out[14]: Index(['index', 'Full Name', 'National Provider Identifier',
 'Credentials of the Provider', 'Credentials of the Provider_Freq',
 'Gender of the Provider', 'Gender of the Provider_Freq',
 'City of the Provider', 'State Code of the Provider',
 'State Code of the Provider_Freq', 'Provider Type',
 'Provider Type_Freq', 'Number of Services',
 'Number of Medicare Beneficiaries',
 'Number of Distinct Medicare Beneficiary/Per Day Services',
 'Average Medicare Allowed Amount', 'Average Submitted Charge Amount',
 'Average Medicare Payment Amount',
 'Average Medicare Standardized Amount'],
 dtype='object')

Performing Standardization on Numerical Columns

In [15]: `from sklearn.preprocessing import StandardScaler`

 `data_copy=data.copy()`

 `standardization_columns=['Number of Services',`
 `'Number of Medicare Beneficiaries',`
 `'Number of Distinct Medicare Beneficiary/Per Day Services',`
 `'Average Medicare Allowed Amount',`
 `'Average Submitted Charge Amount',`
 `'Average Medicare Payment Amount',`
 `'Average Medicare Standardized Amount',`
 `'Credentials of the Provider_Freq',`
 `'Gender of the Provider_Freq',`
 `'State Code of the Provider_Freq']`

 `# Standardization`
 `standard_scaler = StandardScaler()`
 `data[standardization_columns] = standard_scaler.fit_transform(data[standardization_columns])`

```
print("Standardized DataFrame:")
data.head()
```

Standardized DataFrame:

Out[15]:

	index	Full Name	National Provider Identifier	Credentials of the Provider	Credentials of the Provider_Freq	Gender of the Provider	Gender of the Provider_Freq	City of the Provider	State Code of the Provider	State Code of the Provider_Freq	Provider Type
0	8774979	SATYASREE UPADHYAYULA	1891106191	MD	0.594983	F	-1.560716	SAINT LOUIS	MO	-0.737342	Internal Medicine
1	3354385	WENDY P JONES	1346202256	MD	0.594983	F	-1.560716	FAYETTEVILLE	NC	-0.004973	Obstetrics & Gynecology
2	3001884	RICHARD W DUROCHER	1306820956	DPM	-1.684316	M	0.640731	NORTH HAVEN	CT	-0.989093	Podiatry
3	7594822	JASPER FULLARD	1770523540	MD	0.594983	M	0.640731	KANSAS CITY	MO	-0.737342	Internal Medicine
4	746159	ANTHONY E PERROTTI	1073627758	DO	-1.549260	M	0.640731	JUPITER	FL	1.494517	Internal Medicine

FINAL DATASET

In [16]:

```
anomaly_detection_columns = [
    'Number of Services',
    'Number of Medicare Beneficiaries',
    'Number of Distinct Medicare Beneficiary/Per Day Services',
    'Average Medicare Allowed Amount',
    'Average Submitted Charge Amount',
    'Average Medicare Payment Amount',
    'Average Medicare Standardized Amount',
    'Credentials of the Provider_Freq',
    'Gender of the Provider_Freq',
    'State Code of the Provider_Freq',
    'Provider Type_Freq'
]

X = data[anomaly_detection_columns]

X
```

Out[16]:

	Number of Services	Number of Medicare Beneficiaries	Number of Distinct Medicare Beneficiary/Per Day Services	Average Medicare Allowed Amount	Average Submitted Charge Amount	Average Medicare Payment Amount	Average Medicare Standardized Amount	Credentials of the Provider_Freq	Gender of the Provider_Freq	State Code of the Provider_Freq	Provider Type_Freq
0	-0.497577	-0.444753	-0.482232	1.098226	0.621012	0.972452	1.003321	0.594983	-1.560716	-0.737342	Internal Medicine
1	0.503328	1.040098	0.554599	0.352134	1.940981	0.549955	0.722789	0.594983	-1.560716	-0.004973	Obstetrics & Gynecology
2	-0.463762	-0.552921	-0.447204	0.031012	-0.192958	-0.047975	-0.096209	-1.684316	0.640731	-0.989093	Podiatry
3	-0.544917	-0.503753	-0.531272	-0.814992	-1.005784	-0.718674	-0.722804	0.594983	0.640731	-0.737342	Internal Medicine
4	-0.456999	-0.444753	-0.454210	-0.591527	-0.816125	-0.541578	-0.551510	-1.549260	0.640731	1.494517	Internal Medicine
...
99995	-0.544917	-0.484087	-0.531272	-0.020219	0.126753	-0.088807	-0.078095	-1.709831	-1.560716	0.142517	Internal Medicine
99996	0.239576	0.371423	0.281380	-0.254193	-0.252286	-0.426514	-0.354403	-1.729577	-1.560716	-1.140399	Obstetrics & Gynecology
99997	-0.605783	-0.572588	-0.594322	-0.674428	-0.439269	-0.601485	-0.600151	0.594983	0.640731	-0.737342	Internal Medicine
99998	-0.599020	-0.562754	-0.587316	-0.552503	-0.680654	-0.427351	-0.482868	0.594983	-1.560716	1.112228	Internal Medicine
99999	3.303156	0.066586	3.440912	-0.474250	-0.778910	-0.429474	-0.476378	0.594983	-1.560716	1.112228	Internal Medicine

100000 rows × 11 columns

ISOLATION FOREST

In [20]:

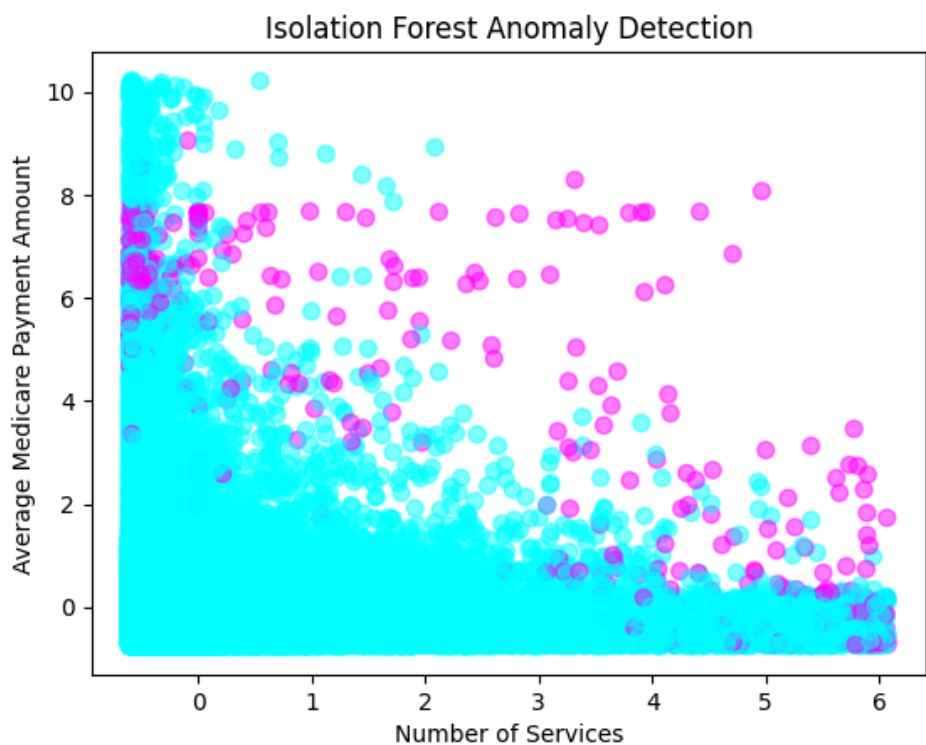
```
from sklearn.ensemble import IsolationForest

# Isolation Forest
isolation_forest = IsolationForest(contamination=0.005, random_state=0)
isolation_forest.fit(X)
data['IsolationForest'] = isolation_forest.predict(X)
data['IsolationForest'] = data['IsolationForest'].map({1: 0, -1: 1})
print("Isolation Forest anomalies detected:", data['IsolationForest'].sum())
```

Isolation Forest anomalies detected: 500

In [21]:

```
# Scatter plot between 'Number of Services' and 'Average Medicare Payment Amount'
plt.scatter(data['Number of Services'], data['Average Medicare Payment Amount'],
            c=data['IsolationForest'], cmap='cool', s=50, alpha=0.5)
plt.title('Isolation Forest Anomaly Detection')
plt.xlabel('Number of Services')
plt.ylabel('Average Medicare Payment Amount')
plt.show()
```

Using contamination as 0.005 and random_state as 0, the Isolation Forest model detected 500 anomalies

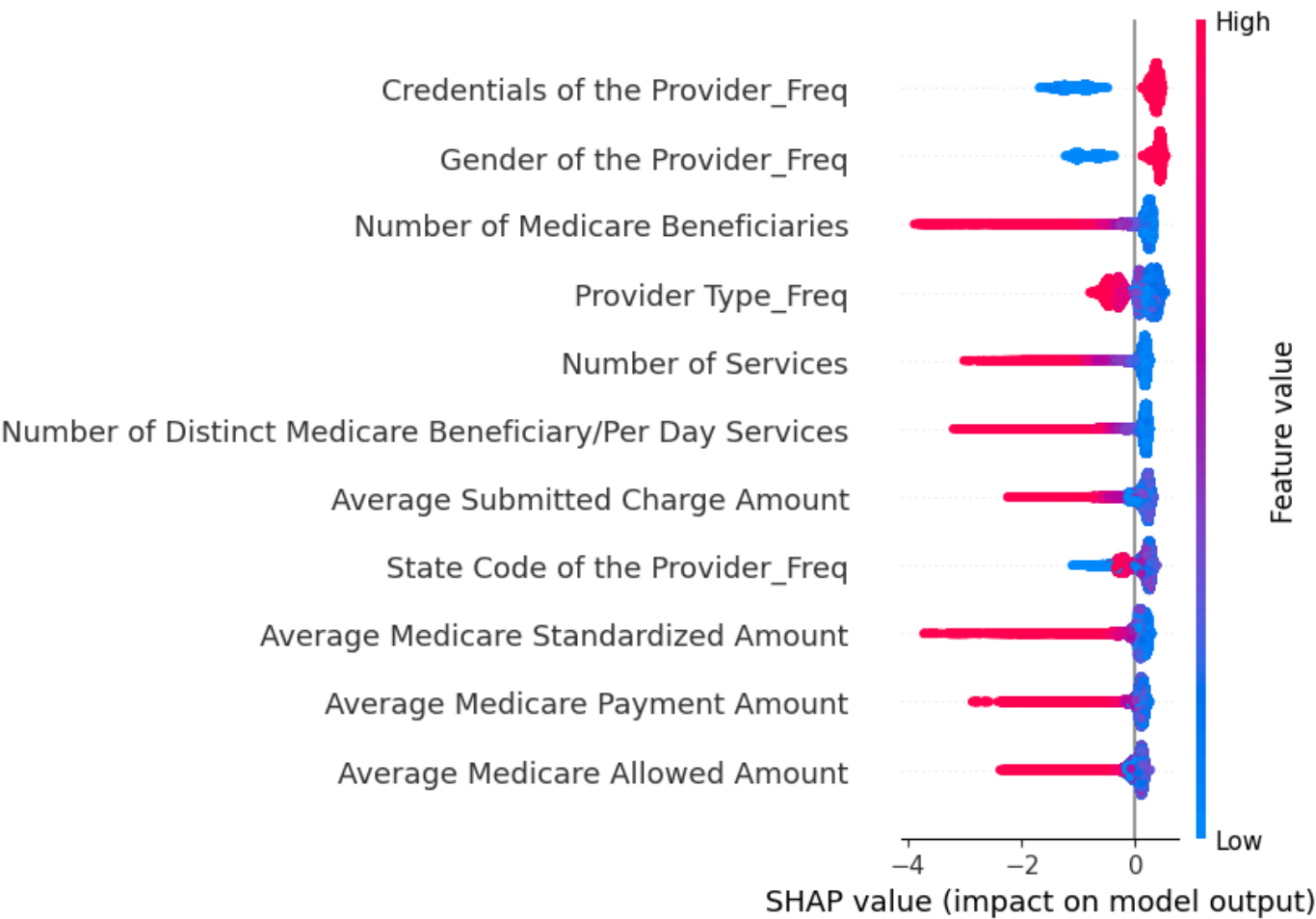
SHAP ANALYSIS OF IsolationForest Model

```
In [23]: import shap
from sklearn.ensemble import IsolationForest

# SHAP model's output
explainer = shap.Explainer(isolation_forest, X)
shap_values = explainer(X)

100%|=====| 99764/100000 [06:32<00:00]

In [24]: # SHAP summary plot
shap.summary_plot(shap_values, X, feature_names=anomaly_detection_columns)
```



INTERPRETATION

- The following columns tend to negatively affect the output:
 - 'Number of Services',
 - 'Number of Medicare Beneficiaries',
 - 'Number of Distinct Medicare Beneficiary/Per Day Services',
 - 'Average Medicare Allowed Amount',
 - 'Average Medicare Payment Amount',
 - 'Average Medicare Standardized Amount',
- this shows the tendency of fraud increases with higher values in such columns

ELLIPTIC ENVELOPE

```
In [17]: from sklearn.covariance import EllipticEnvelope

# Elliptic Envelope
elliptic_envelope = EllipticEnvelope(contamination=0.007, random_state=42)
```

Elliptic Envelope anomalies detected: 700

The scatter plot, titled "Elliptic Envelope Anomaly Detection", visualizes the relationship between the "Number of Medicare Beneficiaries" (x-axis) and the "Average Submitted Charge Amount" (y-axis). The x-axis ranges from 0 to 9, and the y-axis ranges from -1 to 4.5. The data is represented by a large number of purple circular points, which form a dense, elongated cloud. Several yellow circular points are scattered throughout the plot, representing anomalies detected by the Elliptic Envelope method. These yellow points are primarily located in the lower-left and lower-right regions of the main data cloud, indicating areas where the charge amount deviates significantly from the expected pattern for a given number of beneficiaries.

SHAP ANALYSIS OF EllipticEnvelope in combination with IsolationForest

```
100%|██████████| 100000/100000 [1:22:16<00:00, 20.26it/s]
```



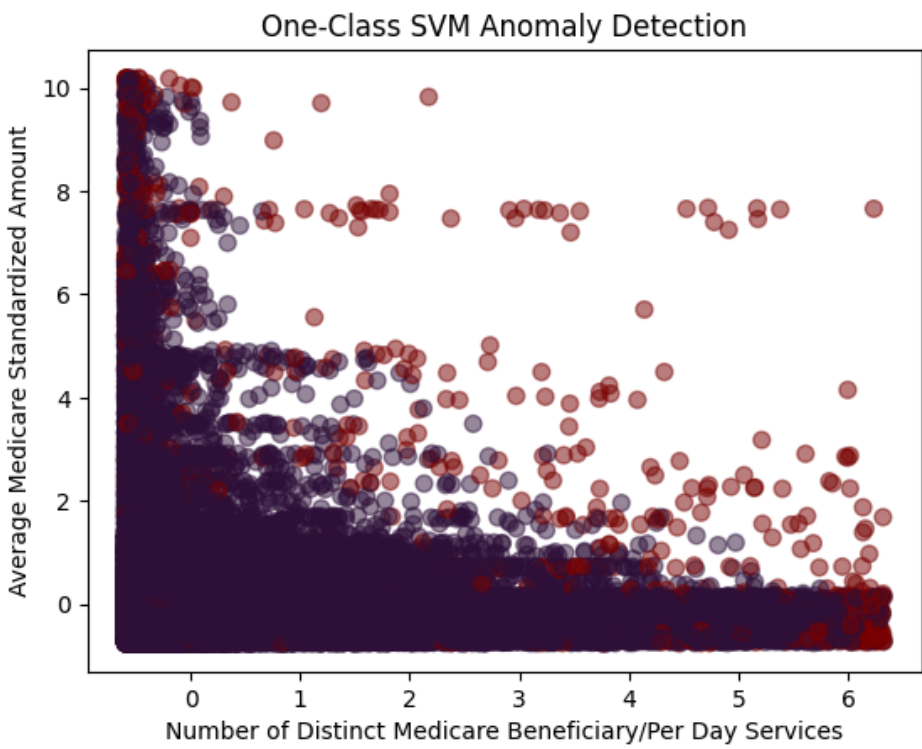
ONE CLASS SVM

```
In [17]: from sklearn.svm import OneClassSVM

# One-Class SVM
one_class_svm = OneClassSVM(gamma='auto', nu=0.01)
one_class_svm.fit(X)
data['OneClassSVM'] = one_class_svm.predict(X)
data['OneClassSVM'] = data['OneClassSVM'].map({1: 0, -1: 1})
print("One-Class SVM anomalies detected:", data['OneClassSVM'].sum())
```

One-Class SVM anomalies detected: 1012

```
In [18]: plt.scatter(data['Number of Distinct Medicare Beneficiary/Per Day Services'], data['Average Medicare Standardized Amount'],
                    c=data['OneClassSVM'], cmap='turbo', s=50, alpha=0.5)
plt.title('One-Class SVM Anomaly Detection')
plt.xlabel('Number of Distinct Medicare Beneficiary/Per Day Services')
plt.ylabel('Average Medicare Standardized Amount')
plt.show()
```



Using One-Class SVM model and setting gamma as 'auto' and nu as 0.01, 1012 anomalies have been detected

SHAP ANALYSIS OF OneClassSVM in combination with IsolationForest

```
In [19]: import shap
from sklearn.ensemble import IsolationForest

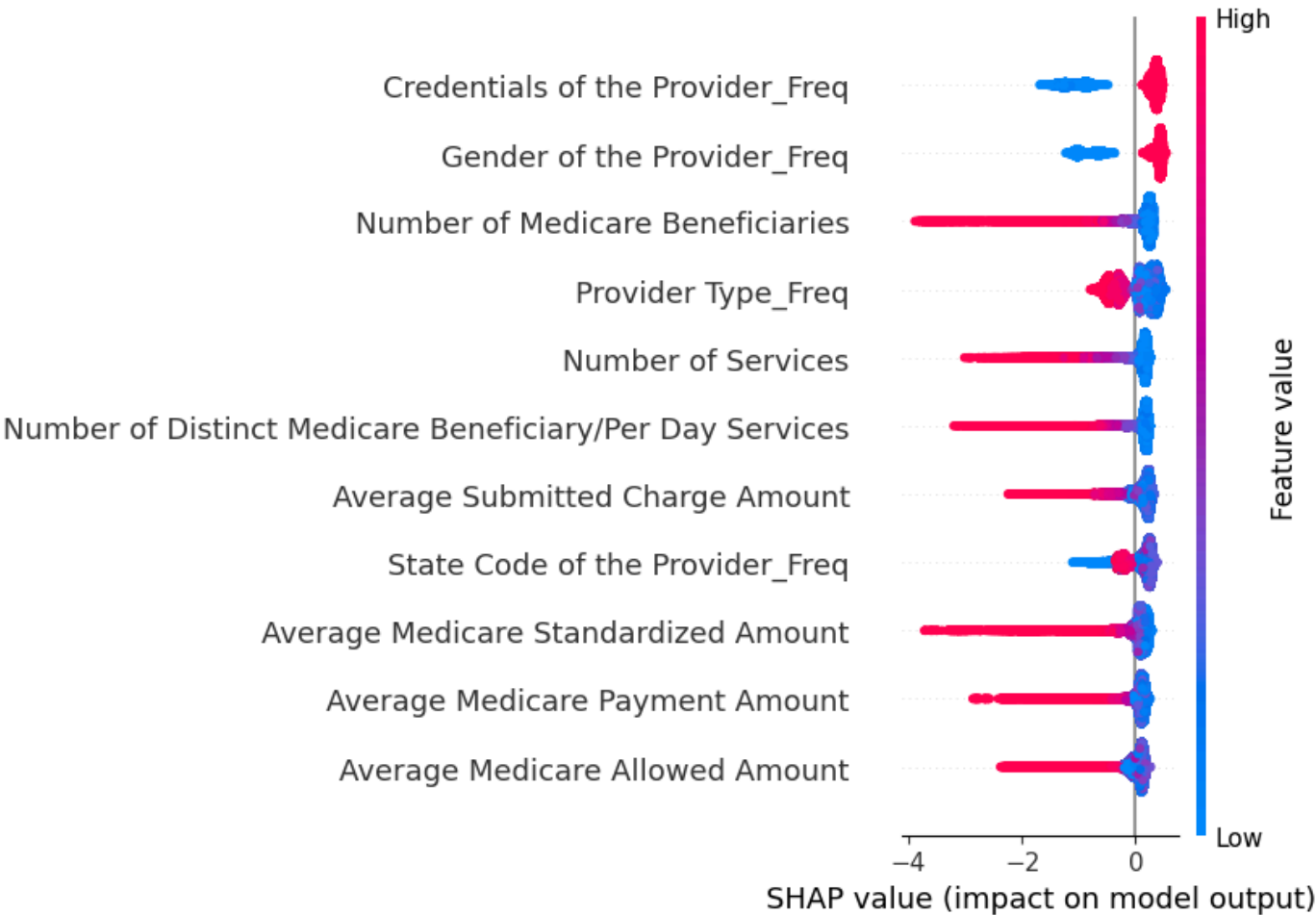
# Convert predictions to binary labels
data['OneClassSVM'] = data['OneClassSVM'].apply(lambda x: 1 if x == -1 else 0)

# Fit the Isolation Forest model
isolation_forest = IsolationForest(contamination=0.005, random_state=0)
isolation_forest.fit(X)

# Perform SHAP analysis on the Isolation Forest model
explainer = shap.Explainer(isolation_forest, X)
shap_values = explainer(X)

# Plot the SHAP summary plot
shap.summary_plot(shap_values, X, feature_names=anomaly_detection_columns)
```

100%|=====| 99922/100000 [06:42<00:00]



INTERPRETATION

- The following columns tend to negatively affect the output:
 - 'Number of Services',
 - 'Number of Medicare Beneficiaries',
 - 'Number of Distinct Medicare Beneficiary/Per Day Services',
 - 'Average Medicare Allowed Amount',
 - 'Average Medicare Payment Amount',
 - 'Average Medicare Standardized Amount',
- this shows the tendency of fraud increases with higher values in such columns

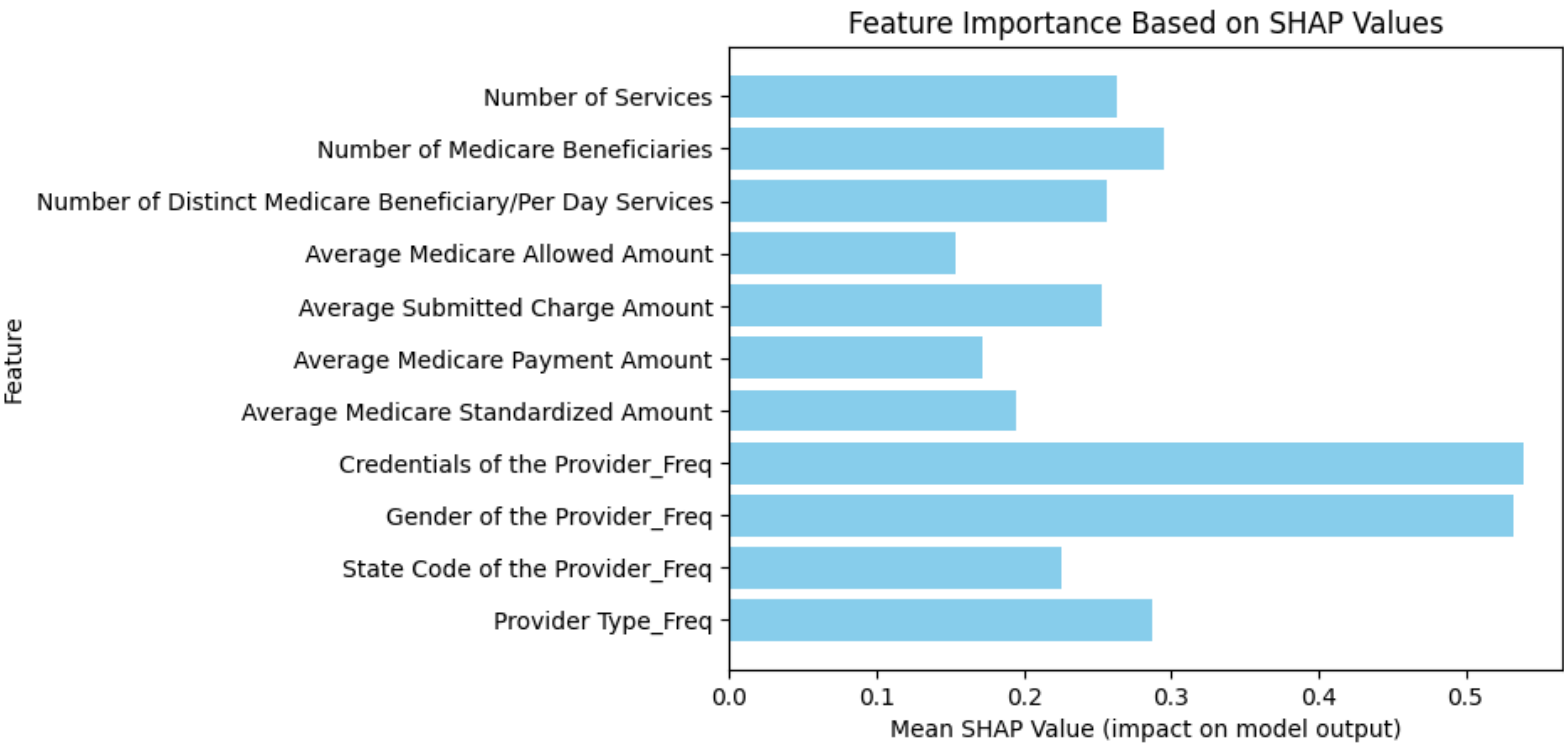
FURTHER INTERPRETATION :

The following bargraph shows the dependence on every feature in making prediction

```
In [34]: import numpy as np

# Converting SHAP values to numpy array
shap_values_array = np.array(shap_values.values)
shap_values_summary = np.abs(shap_values_array).mean(axis=0)

# Plot of the summarized SHAP values as a stacked bar plot
plt.barh(anomaly_detection_columns, shap_values_summary, color='skyblue')
plt.xlabel('Mean SHAP Value (impact on model output)')
plt.ylabel('Feature')
plt.title('Feature Importance Based on SHAP Values')
plt.gca().invert_yaxis()
plt.show()
```



From the above graph, we can see that 'Credentials of the Provider_Freq', and 'Gender of the Provider_Freq' have the highest impact in the model output.

Visualization of Anamolies in the 'Credentials of the Provider_Freq' and 'Gender of the Provider_Freq' columns using stacked bar graphs

```
In [36]: import matplotlib.pyplot as plt
import seaborn as sns

# Ensure One-Class SVM Anomaly Labels are Correctly Applied
one_class_svm = OneClassSVM(gamma='auto', nu=0.05)
one_class_svm.fit(X)
data['OneClassSVM'] = one_class_svm.predict(X)
data['OneClassSVM'] = data['OneClassSVM'].map({1: 0, -1: 1})
print("One-Class SVM anomalies detected:", data['OneClassSVM'].sum())

# Group the data by 'Credentials of the Provider_Freq' and 'OneClassSVM'
credentials_grouped = data.groupby(['Credentials of the Provider_Freq', 'OneClassSVM']).size().unstack().fillna(0)
credentials_grouped.columns = ['Normal', 'Anomaly'] if credentials_grouped.shape[1] == 2 else (['Normal'] if 0 in credentials_grouped.columns else ['Anomaly'])
credentials_grouped = credentials_grouped.reset_index()

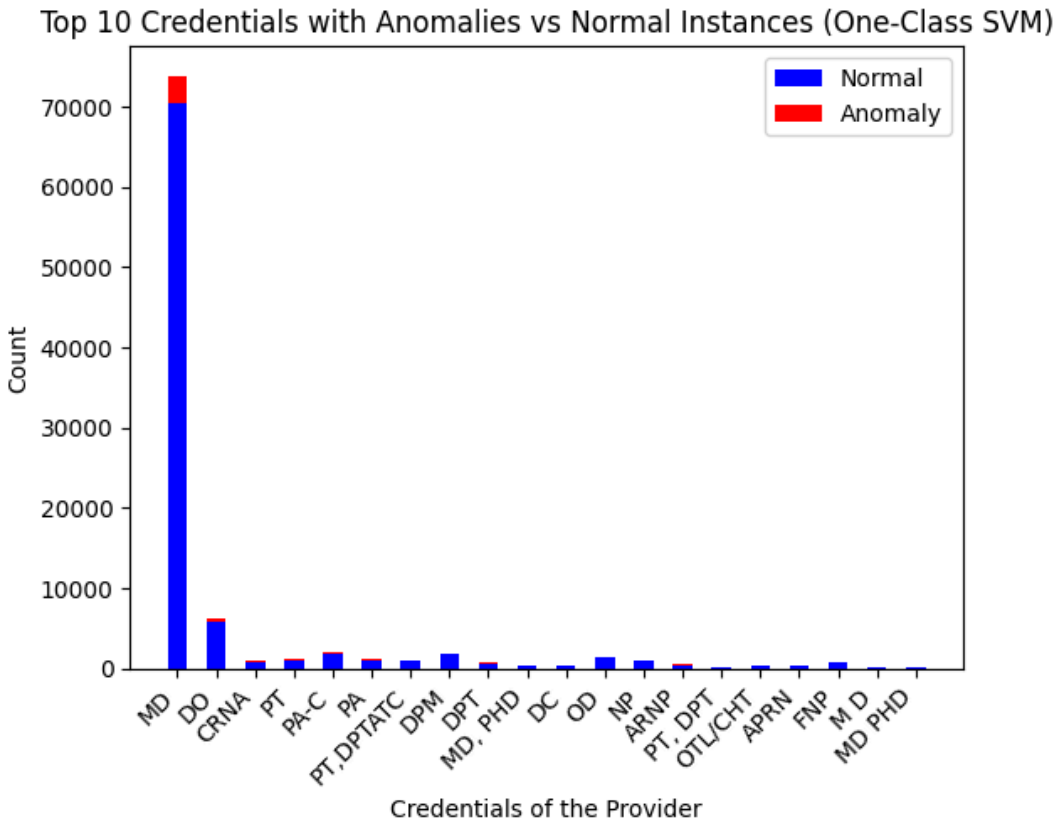
#top 10 credentials with most anomalies
top_credentials = credentials_grouped.sort_values(by='Anomaly', ascending=False).head(20)

credentials_mapping = data[['Credentials of the Provider', 'Credentials of the Provider_Freq']].drop_duplicates()
credentials_mapping_dict = credentials_mapping.set_index('Credentials of the Provider_Freq')['Credentials of the Provider'].to_dict()

# Mapping the frequency-encoded values back to the original values for labels
top_credentials['Credentials of the Provider'] = top_credentials['Credentials of the Provider_Freq'].map(credentials_mapping_dict)

# stacked bar plot for 'Credentials of the Provider'
bar_width = 0.5
bars1 = plt.bar(top_credentials['Credentials of the Provider'], top_credentials['Normal'], color='blue', label='Normal', width=bar_width)
bars2 = plt.bar(top_credentials['Credentials of the Provider'], top_credentials['Anomaly'], bottom=top_credentials['Normal'], color='red')
plt.xlabel('Credentials of the Provider')
plt.ylabel('Count')
plt.title('Top 10 Credentials with Anomalies vs Normal Instances (One-Class SVM)')
plt.xticks(rotation=45, ha='right')
plt.legend()
plt.show()
```

One-Class SVM anomalies detected: 5000



We can see that most anomalies are present with Credential 'MD'

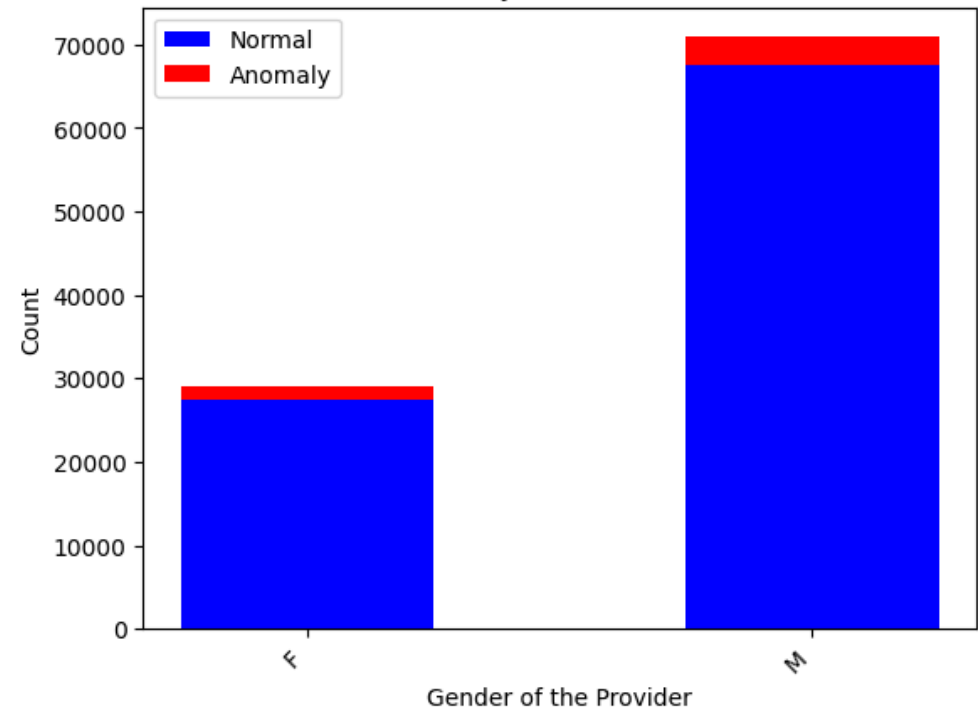
```
In [38]: # Grouping the data by 'Gender of the Provider_Freq' and 'OneClassSVM'
gender_grouped = data.groupby(['Gender of the Provider_Freq', 'OneClassSVM']).size().unstack().fillna(0)
gender_grouped.columns = ['Normal', 'Anomaly'] if gender_grouped.shape[1] == 2 else (['Normal'] if 0 in gender_grouped.columns else ['Anomaly'])
gender_grouped = gender_grouped.reset_index()

gender_mapping = data[['Gender of the Provider', 'Gender of the Provider_Freq']].drop_duplicates()
gender_mapping_dict = gender_mapping.set_index('Gender of the Provider_Freq')['Gender of the Provider'].to_dict()

# Mapping the frequency-encoded values back to the original values for labels
gender_grouped['Gender of the Provider'] = gender_grouped['Gender of the Provider_Freq'].map(gender_mapping_dict)

#stacked bar plot for 'Gender of the Provider'
bar_width = 0.5
bars1 = plt.bar(gender_grouped['Gender of the Provider'], gender_grouped['Normal'], color='blue', label='Normal', width=bar_width)
bars2 = plt.bar(gender_grouped['Gender of the Provider'], gender_grouped['Anomaly'], bottom=gender_grouped['Normal'], color='red')
plt.xlabel('Gender of the Provider')
plt.ylabel('Count')
plt.title('Anomalies vs Normal Instances by Gender of the Provider (One-Class SVM)')
plt.xticks(rotation=45, ha='right')
plt.legend()
plt.show()
```

Anomalies vs Normal Instances by Gender of the Provider (One-Class SVM)



We can see that more anomalies are present when Gender is Male

In []: