Anomaly detection - Part 4

One should look for what is and not what he thinks should be. -Albert Einstein

Module completion checklist

Objective	Complete
Implement LOF to detect anomalies	
Describe the isolation forest algorithm	
Implement isolation forest	
Implement isolation forest to detect anomalies	

Loading packages

Let's load the packages we will be using:

```
import os
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import pickle

from sklearn import metrics
from sklearn.model_selection import train_test_split
from sklearn.metrics import confusion_matrix, roc_auc_score
from sklearn.neighbors import LocalOutlierFactor
from sklearn.svm import OneClassSVM
from sklearn.ensemble import IsolationForest
```

Directory settings

- In order to maximize the efficiency of your workflow, you should encode your directory structure into `variables`
- We will use the `pathlib` library
- Let the `main_dir` be the variable corresponding to your course materials folder
- `data_dir` be the variable corresponding to your `data` folder

```
# Set 'main_dir' to location of the project folder
from pathlib import Path
home_dir = Path(".").resolve()
main_dir = home_dir.parent.parent
print(main_dir)
```

```
data_dir = str(main_dir) + "/data"
print(data_dir)
```

Load pickled data from previous module

```
non_fraud = pickle.load(open((data_dir + "/non_fraud.sav"),"rb"))
test = pickle.load(open((data_dir + "/test.sav"),"rb"))
actual_test = pickle.load(open((data_dir + "/actual_test.sav"),"rb"))
performance_df = pickle.load(open((data_dir + "/performance_anomalies.sav"),"rb"))
```

Data: load energy consumption

- Load the `PJME.csv` dataset and print the head

```
pjm_energy = pd.read_csv(str(data_dir)+"/PJME_hourly.csv")
pjm_energy.head()
```

```
                 Datetime  PJME_MW
0  2002-12-31 01:00:00  26498.0
1  2002-12-31 02:00:00  25147.0
2  2002-12-31 03:00:00  24574.0
3  2002-12-31 04:00:00  24393.0
4  2002-12-31 05:00:00  24860.0
```

Data: preprocessing

- Let's convert the `Datatime` variable from type **object** to **datetime**

```
pjm_energy['Datetime'] = pd.to_datetime(pjm_energy['Datetime'])
pjm_energy.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 145366 entries, 0 to 145365
Data columns (total 2 columns):
 #   Column    Non-Null Count   Dtype         
---  ------    --------------   -----         
 0   Datetime  145366 non-null  datetime64[ns]
 1   PJME_MW   145366 non-null  float64       
dtypes: datetime64[ns](1), float64(1)
memory usage: 2.2 MB
```

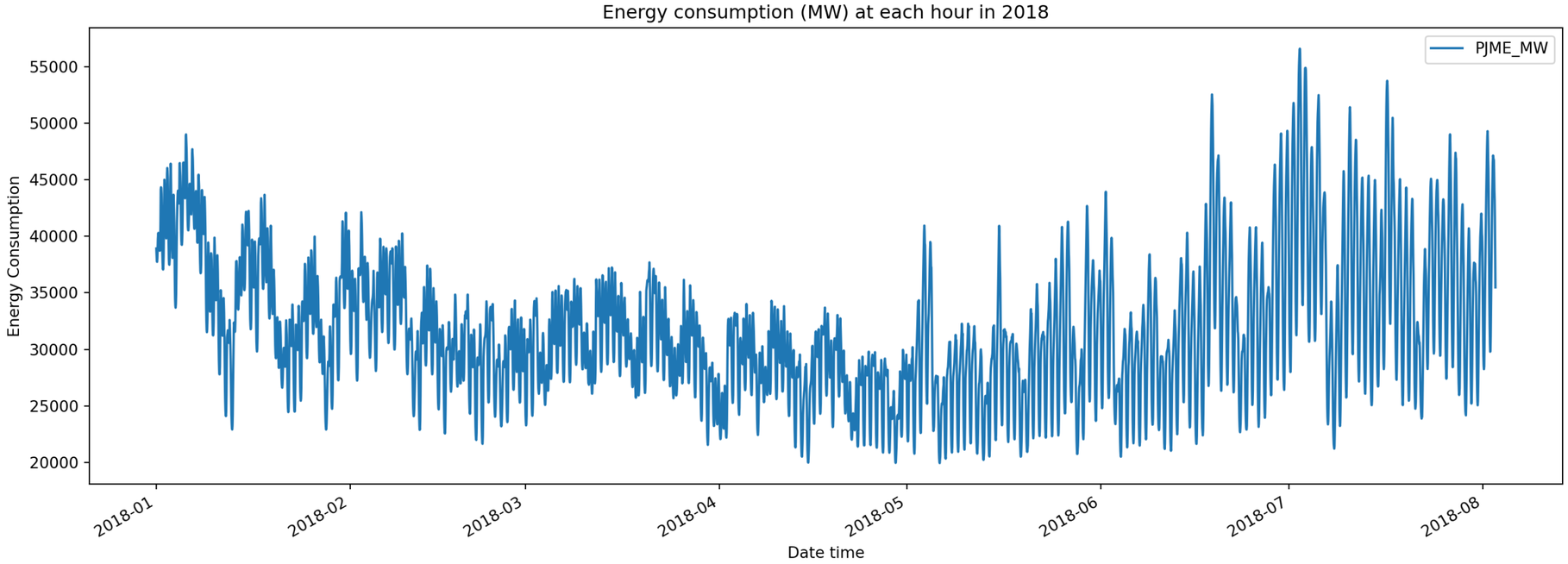
- We will filter the data to contain values for the year 2018

```
pjm_energy = pjm_energy[pjm_energy['Datetime'] > '2018-01-01 00:00:00']
pjm_energy.shape
```

```
(5135, 2)
```

Visualize the data: line plot

```
pjm_energy.plot(x='Datetime', y='PJME_MW', figsize=(17,6))
plt.xlabel('Date time')
plt.ylabel('Energy Consumption')
plt.title('Energy consumption (MW) at each hour in 2018')
plt.show()
```



LOF model: energy consumption

- Since we don't have a target variable to evaluate the LOF model, we will fit the model on the entire data. This will enable the model to understand the underlying data distribution
- Once we have the model trained, we predict the anomalies on the same dataset
- The predicted values would be +1 for inliers and -1 for outliers
- We will implement the LOF model with `n_neighbors` set to **50** and `contamination` set to **0.01**

Note: *As we have no evaluation metric, these values were picked based on experimenting with different parameters values and finalized with the one that showed good anomaly detection*

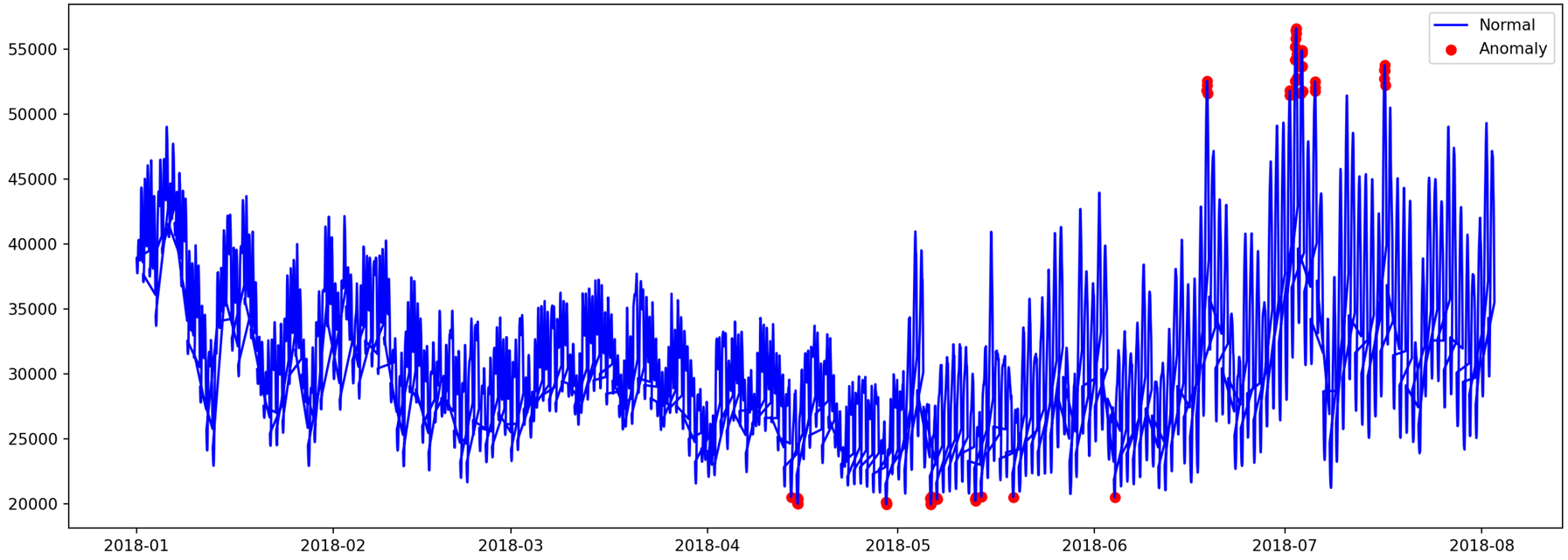
Create and fit LOF model: energy consumption

- We now will instantiate our LOF model with `n_neighbors` set to **50**

```
lof_energy_model = LocalOutlierFactor(n_neighbors = 50,
                                      metric = "manhattan",
                                      contamination = 0.01,
                                      novelty = False)

pjm_energy['anomaly'] = lof_energy_model.fit_predict(pd.DataFrame(pjm_energy['PJME_MW']))
```

LOF - visualize anomalies

```
# visualization
fig, ax = plt.subplots(figsize=(17,6))

a = pjm_energy.loc[pjm_energy['anomaly'] == -1, ['Datetime', 'PJME_MW']] #anomaly

ax.plot(pjm_energy['Datetime'], pjm_energy['PJME_MW'], color='blue', label = 'Normal')
ax.scatter(a['Datetime'],a['PJME_MW'], color='red', label = 'Anomaly')
plt.legend()
plt.show();
```



LOF - visualize anomalies

- Identify the lower and the upper range of anomalies detected

```
lower_threshold = pjm_energy['PJME_MW'].quantile(0.25)
upper_threshold = pjm_energy['PJME_MW'].quantile(0.75)
lof_anomalies = pjm_energy[pjm_energy['anomaly'] == -1]
```

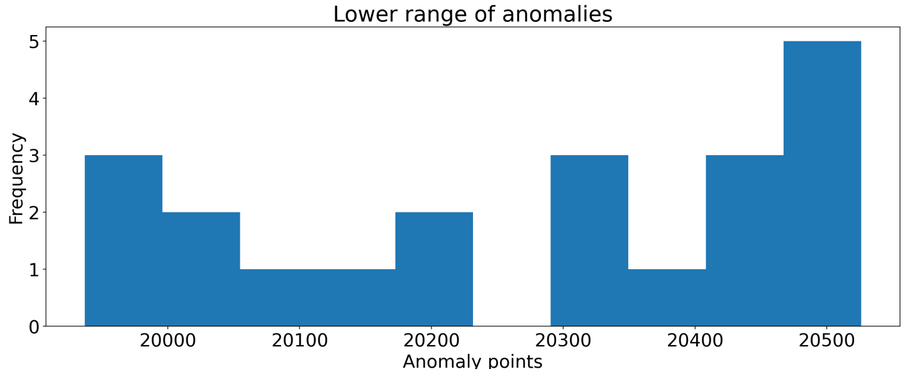
```
# Upper range of anomalies
lof_upper_anomalies = lof_anomalies[lof_anomalies['PJME_MW'] > upper_threshold]['PJME_MW']

# Lower range of anomalies
lof_lower_anomalies = lof_anomalies[lof_anomalies['PJME_MW'] < lower_threshold]['PJME_MW']
```

LOF - visualize anomalies

- Lower range of anomalies

```
plt.rcParams.update({'font.size': 20})
plt.hist(lof_lower_anomalies)
```

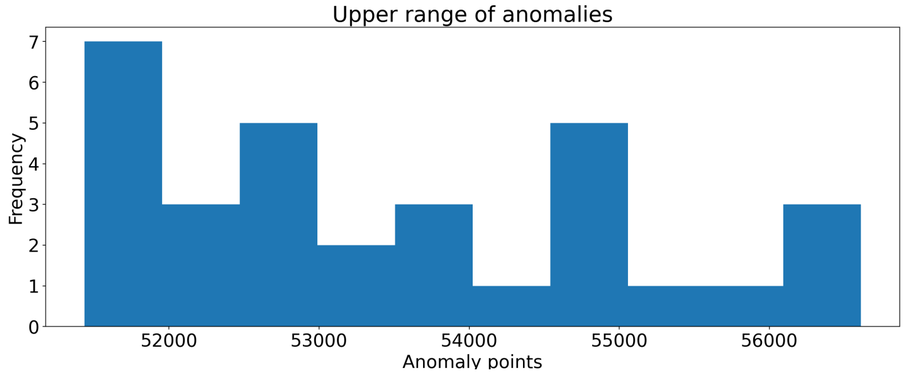
```
plt.xlabel("Anomaly points")
plt.ylabel("Frequency")
plt.title("Lower range of anomalies")
plt.show()
```



- Upper range of anomalies

```
plt.hist(lof_upper_anomalies)
```

```
plt.xlabel("Anomaly points")
plt.ylabel("Frequency")
plt.title("Upper range of anomalies")
plt.show()
```



Exercise 3

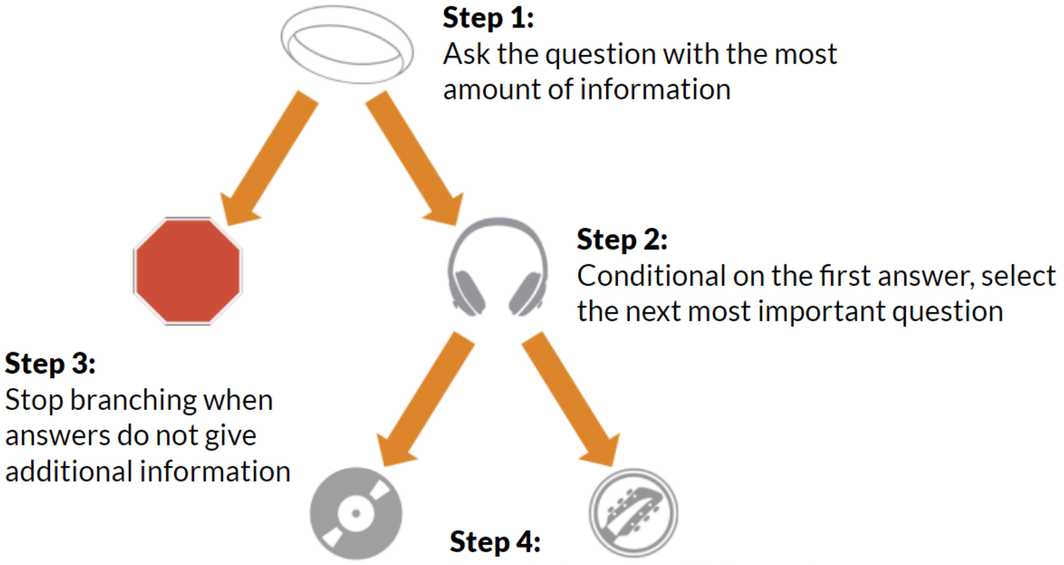
Module completion checklist

Objective	Complete
Implement LOF to detect anomalies	✔
Describe the isolation forest algorithm	
Implement isolation forest	
Implement isolation forest to detect anomalies	

Decision trees: recap

- Isolation forests are built on the basis of decision trees
- In decision trees, partitions are created by first randomly selecting a feature and then selecting a random split value between the minimum and maximum value of the selected feature

Growing decision trees steps



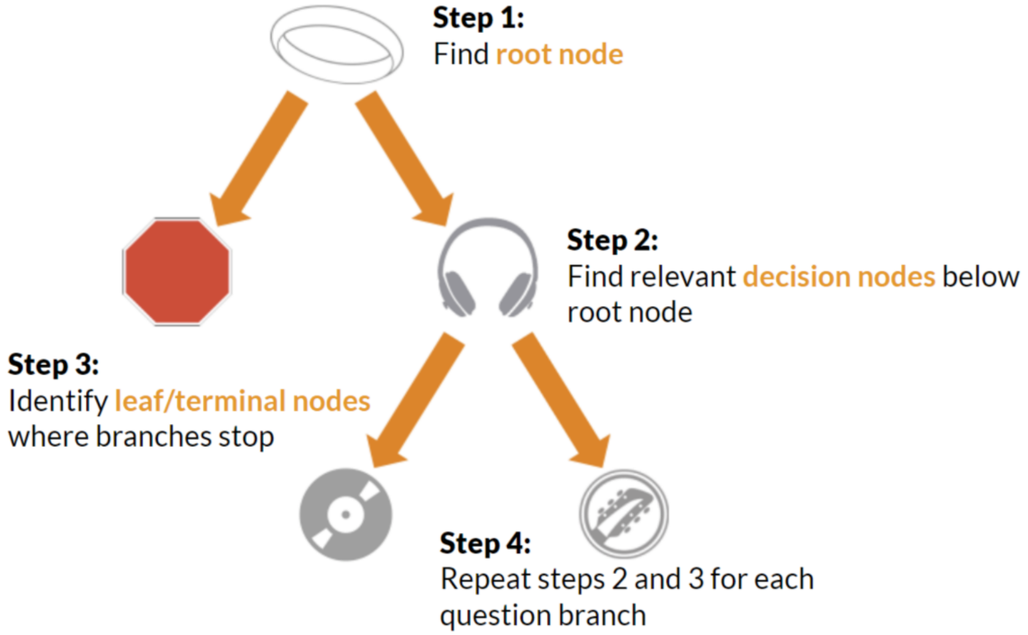
Step 1:
Ask the question with the most amount of information

Step 2:
Conditional on the first answer, select the next most important question

Step 3:
Stop branching when answers do not give additional information

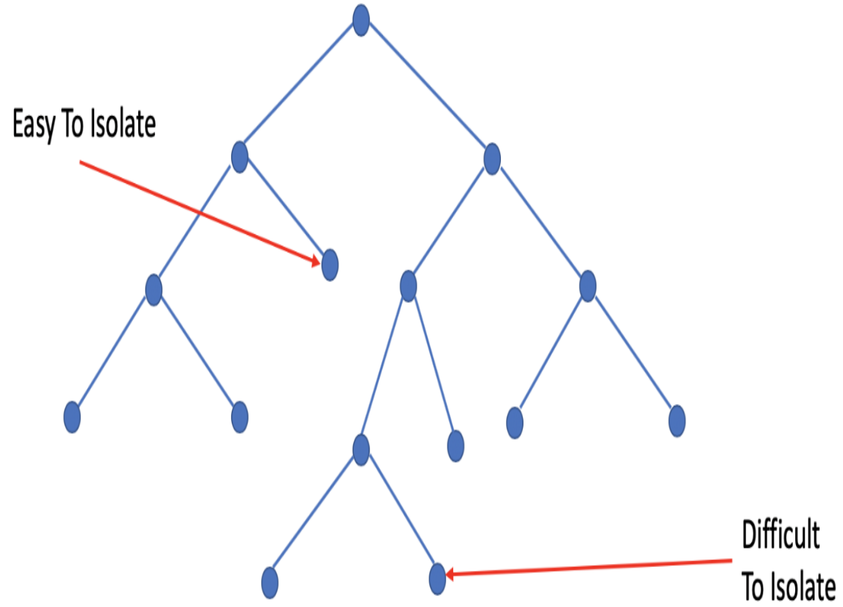
Step 4:
Repeat steps 2 and 3 for each question branch

Growing decision trees with vocabulary



Isolation forest

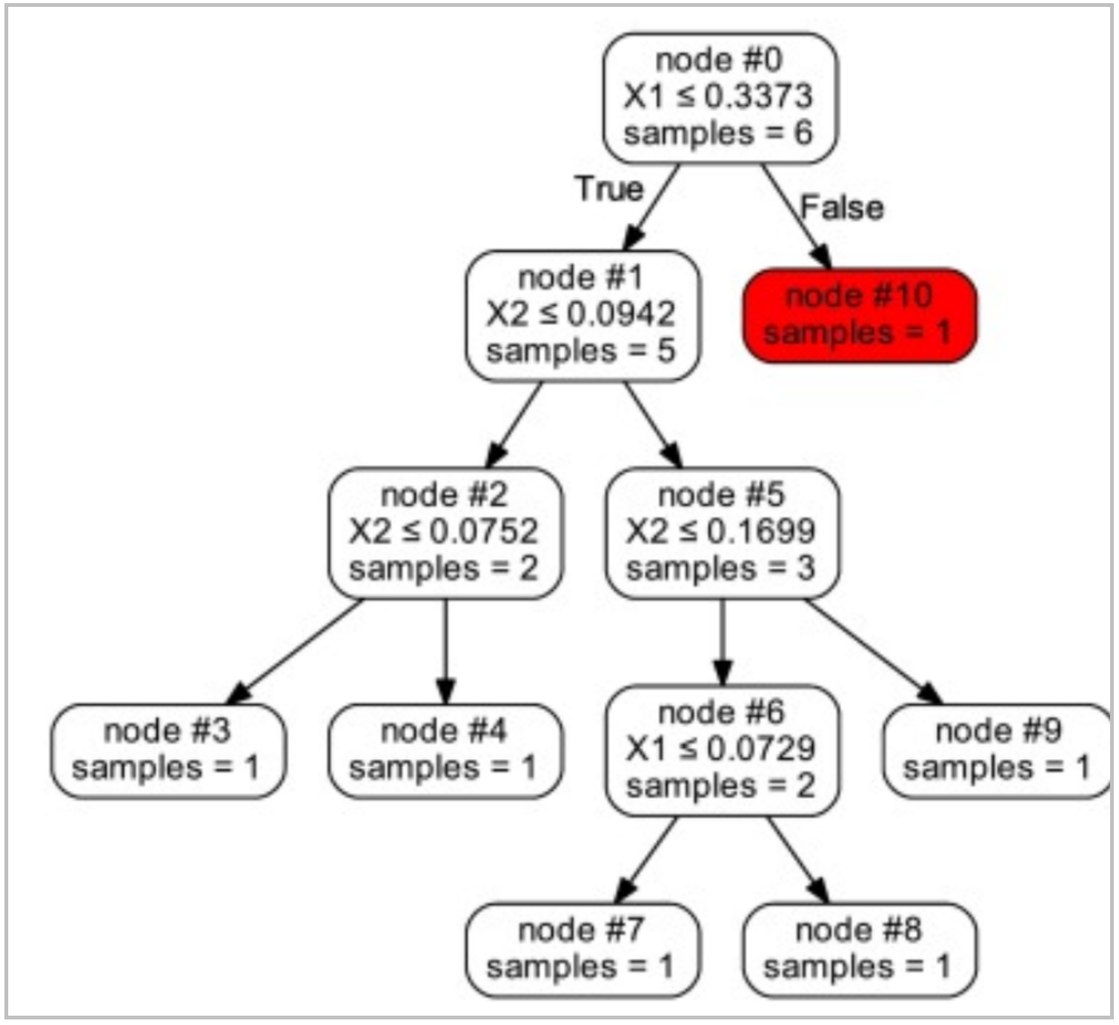
- We know that outliers are less frequent and differ from regular observations
- This means they will also be identified faster and closer to the root during the partitioning at each feature node
- An isolation forest algorithm calculates an anomaly score for each test observation which we want to classify based on the path length
- Path length is the number of nodes the observation travels down the decision tree
- Based on the anomaly score, it is classified either as an inlier (1) or outlier (-1)



Working of isolation forest

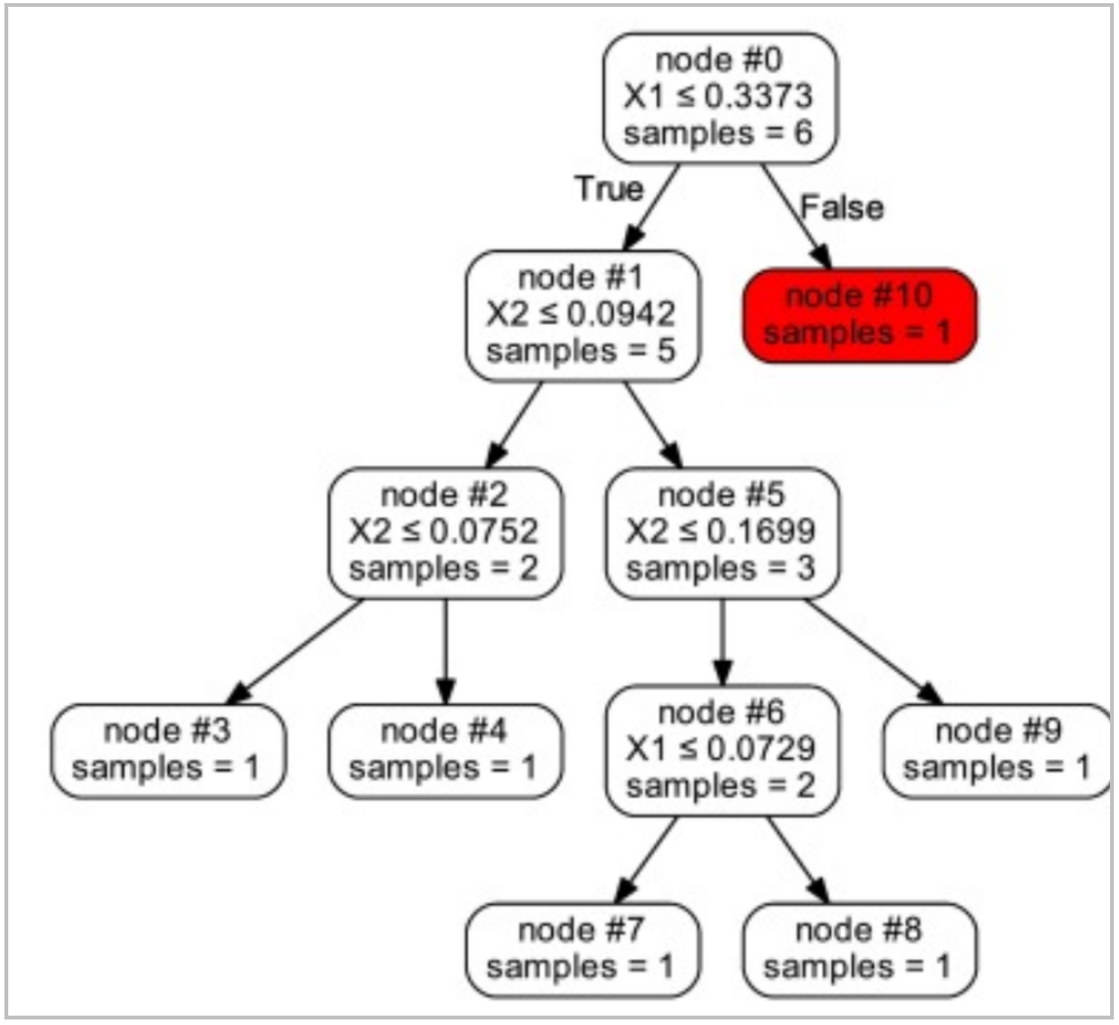
- In the isolation forest, the model is built only on regular observations
- When we get a new test data point, it travels through each node and gets classified as either
  - inlier or normal observation (+1)
  - outlier or anomaly (-1)
- Like random forest, isolation forest has multiple decision trees where the results are aggregated
- Let's say we have a new observation `a`, which is an outlier
- As the new observation travels down the tree, we note that none of its features have the same range as the regular observation
- The features of the new observation are very different from the tree model
- Hence, the new observation is classified as an anomaly and assigned label `-1`

Working of isolation forest with example 1



- Let’s say we built our tree model with regular observation as shown
- We have a new observation which has a variable(X1) value greater than a threshold (0.3373), then it gets classified as an anomaly because all the observations in the tree model has X1 <= threshold (0.3373)

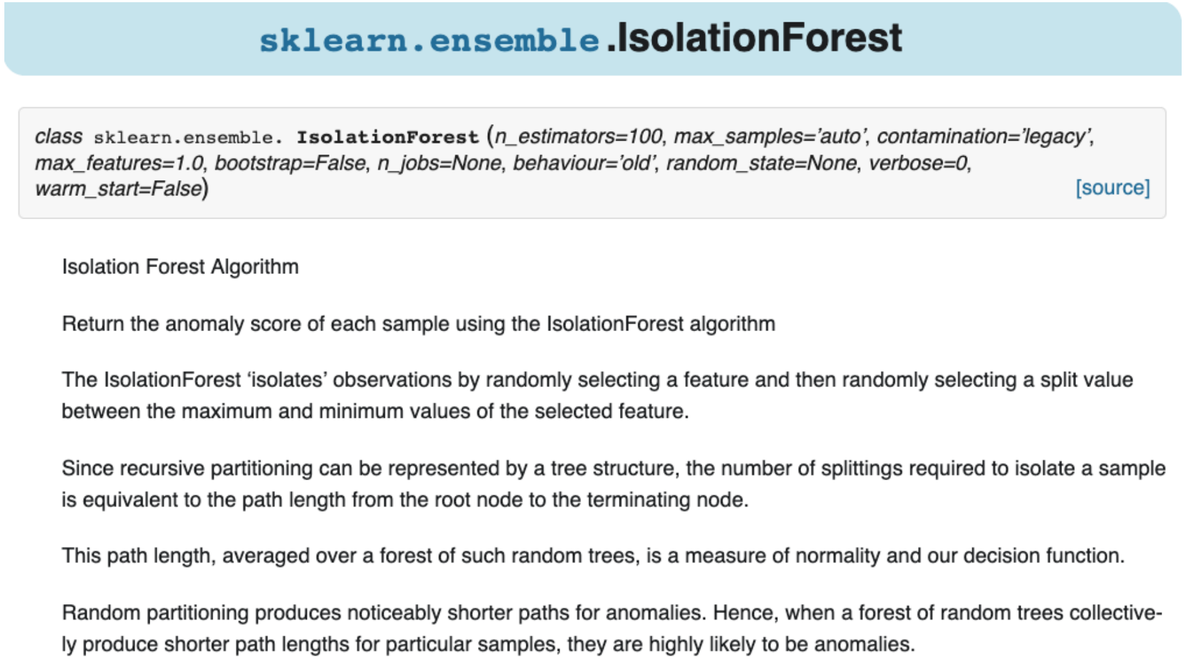
Working of isolation forest with example 2



- Let's say we have another new observation which is also an anomaly but its X1 <= threshold (0.3373)
- But its other variable (X2) is greater than threshold2 (0.0942)
- That observation gets classified as outlier at the second node (node #1) because all the observations within the tree model data have values with X2 <= threshold2 (0.0942)

Isolation forest in Python

- Our SciKit library has a package for isolation forest
- Read more on it ***here***



sklearn.ensemble.IsolationForest

class sklearn.ensemble. **IsolationForest** (*n_estimators=100, max_samples='auto', contamination='legacy', max_features=1.0, bootstrap=False, n_jobs=None, behaviour='old', random_state=None, verbose=0, warm_start=False*) [source]

Isolation Forest Algorithm

Return the anomaly score of each sample using the IsolationForest algorithm

The IsolationForest 'isolates' observations by randomly selecting a feature and then randomly selecting a split value between the maximum and minimum values of the selected feature.

Since recursive partitioning can be represented by a tree structure, the number of splittings required to isolate a sample is equivalent to the path length from the root node to the terminating node.

This path length, averaged over a forest of such random trees, is a measure of normality and our decision function.

Random partitioning produces noticeably shorter paths for anomalies. Hence, when a forest of random trees collectively produce shorter path lengths for particular samples, they are highly likely to be anomalies.

Module completion checklist

Objective	Complete
Implement LOF to detect anomalies	✔
Describe the isolation forest algorithm	✔
Implement isolation forest	
Implement isolation forest to detect anomalies	

Create and fit isolation forest model

- We now will instantiate our isolation forest model and run it on non_fraud data
- At first, we will simply run the model on our training data and predict on test
- We set default parameter for **n_estimators = 100** and contamination as **0.1**

```
iforest = IsolationForest(n_estimators=100, contamination = 0.1)

# model fitting
iforest.fit(non_fraud)
```

```
IsolationForest(contamination=0.1)
```

Test predictions

- Predict on the test data using the trained isolation forest

```
fraud_pred = iforest.predict(test.iloc[:,:-1])
fraud_pred
```

```
array([1, 1, 1, ..., 1, 1, 1])
```

- We know that an isolation forest classifies data points as -1 and +1 instead of 1 and 0
- Let's replace these values into 0 and 1 as we have in our Paysim dataset

```
fraud_pred[fraud_pred == 1] = 0
fraud_pred[fraud_pred == -1] = 1
```

Find TPR and TNR

- Let’s evaluate the isolation forest model

```
tn, fp, fn, tp = confusion_matrix(actual_test, fraud_pred).ravel()
non_fraud_eval = tn / (tn + fp)
print(non_fraud_eval)
```

```
0.9033872851660271
```

```
fraud_eval = tp / (tp + fn)
print(fraud_eval)
```

```
0.3
```

Load performance_df dataframe

- Append the scores of the isolation forest to the `performance_df` dataframe

```
s = pd.Series(['Isolation Forest', fraud_eval, non_fraud_eval],
              index=['model_name', 'TPR', 'TNR'])
performance_df = performance_df.append(s, ignore_index = True)
performance_df
```

	model_name	TPR	TNR
0	Decision_tree_baseline	0.671642	0.999667
1	SMOTE	0.865672	0.991332
2	LOF	0.772727	0.890927
3	LOF	0.759091	0.903280
4	LOF	0.750000	0.894868
5	LOF	0.745455	0.900367
6	LOF	0.754545	0.892982
7	LOF	0.722727	0.893376
8	Isolation Forest	0.300000	0.903387

Isolation model: hyperparameter tuning

- The hyperparameters that can be tuned for optimizing the isolation forest model are shown below
  - **n_estimators**: the number of base estimators in the ensemble
  - **contamination**: the amount of contamination of the data set, i.e., the proportion of outliers in the data set
  - **max_features**: the number of features to draw from X to train each base estimator
  - **max_samples**: the number of samples to draw from X to train each base estimator
- We wouldn't be tuning the hyperparameters for isolation model here, as the model results showed no significant improvement on this dataset

Knowledge check 3

Exercise 4

Module completion checklist

Objective	Complete
Implement LOF to detect anomalies	✔
Describe the isolation forest algorithm	✔
Implement isolation forest	✔
Implement isolation forest to detect anomalies	

Isolation forest on time series data

- We now will instantiate our isolation forest model and run it on time series data
- We set default parameter for **n_estimators = 100** and contamination as **0.01**

```
isolation_energy = IsolationForest(n_estimators=100, contamination = 0.01)

# model fitting
isolation_energy.fit(pd.DataFrame(pjm_energy['PJME_MW']))
```

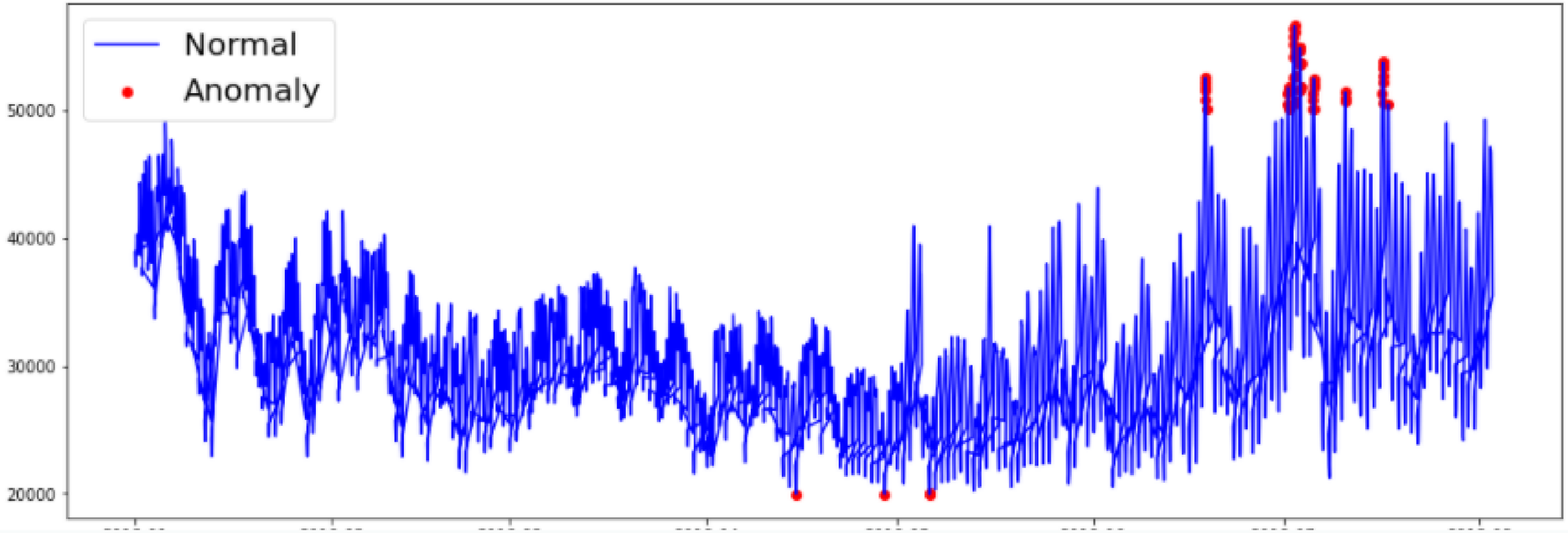
```
IsolationForest(contamination=0.01)
```

```
pjm_energy['anomaly'] = isolation_energy.predict(pd.DataFrame(pjm_energy['PJME_MW']))
```

Isolation forest - visualize anomalies

- We will now visualize the anomalies detected by isolation forest

```
# visualization
fig, ax = plt.subplots(figsize=(15,5))

a = pjm_energy.loc[pjm_energy['anomaly'] == -1, ['Datetime', 'PJME_MW']] #anomaly

ax.plot(pjm_energy['Datetime'], pjm_energy['PJME_MW'], color='blue', label = 'Normal')
ax.scatter(a['Datetime'],a['PJME_MW'], color='red', label = 'Anomaly')
plt.legend()
plt.show()
```



Isolation forest - visualize anomalies

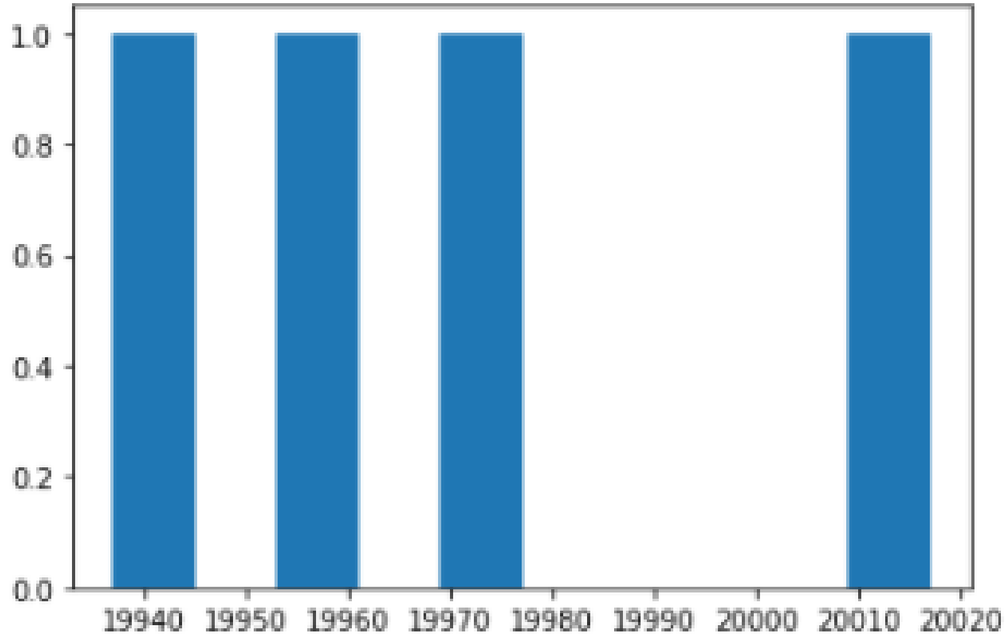
- Identify the lower and the upper range of anomalies detected

```
# visualization
lower_threshold = pjm_energy['PJME_MW'].quantile(0.25)
upper_threshold = pjm_energy['PJME_MW'].quantile(0.75)
if_anomalies = pjm_energy[pjm_energy['anomaly'] == -1]

if_upper_anomalies = if_anomalies[if_anomalies['PJME_MW'] > upper_threshold]['PJME_MW']
if_lower_anomalies = if_anomalies[if_anomalies['PJME_MW'] < lower_threshold]['PJME_MW']
```

Isolation forest - visualize anomalies

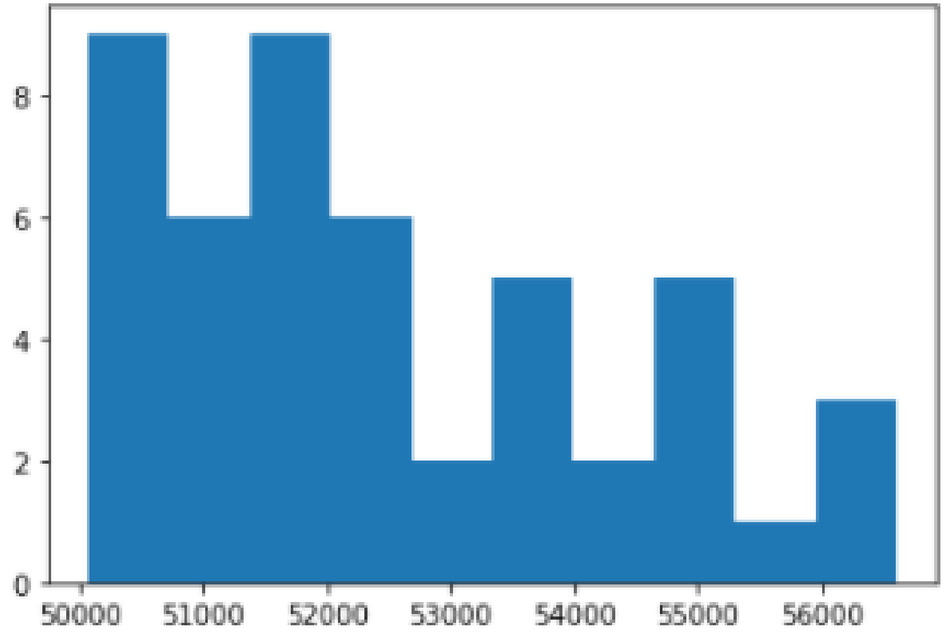
- Lower range of anomalies

```
plt.hist(if_lower_anomalies)
plt.xlabel("Anomaly points")
plt.ylabel("Frequency")
plt.title("Lower range of anomalies")
plt.show()
```



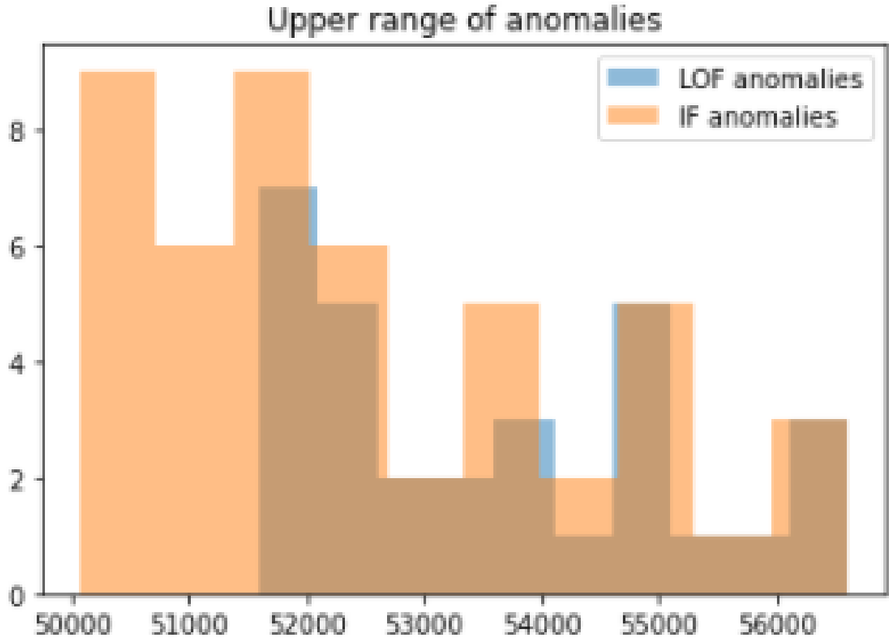
- Upper range of anomalies

```
plt.hist(if_upper_anomalies)
plt.xlabel("Anomaly points")
plt.ylabel("Frequency")
plt.title("Upper range of anomalies")
plt.show()
```

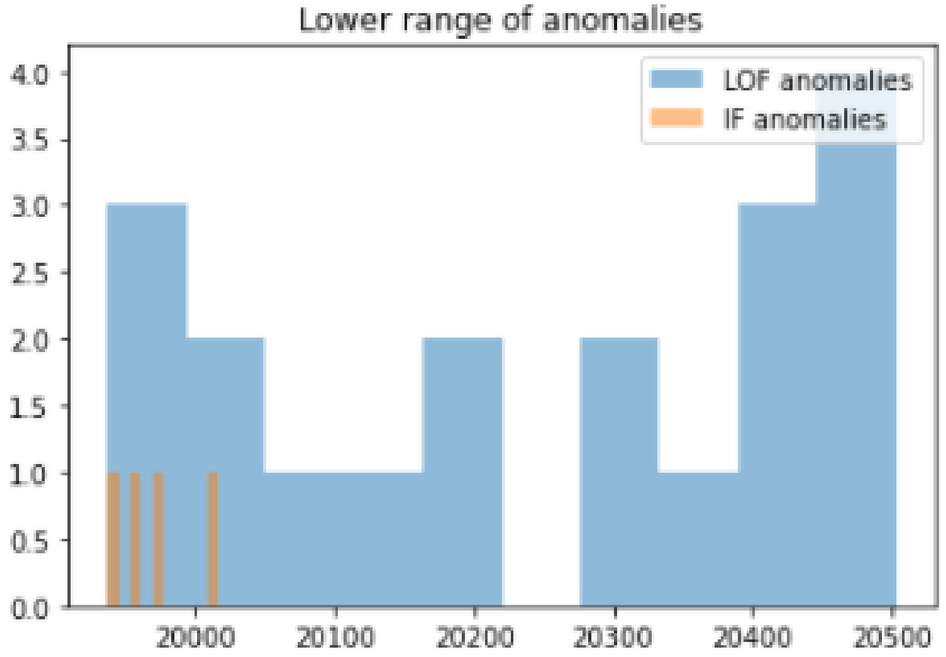


Compare anomalies

```
plt.hist(lof_upper_anomalies,alpha =
0.5,label='LOF anomalies')
plt.hist(if_upper_anomalies,alpha = 0.5,label='IF
anomalies')
plt.title('Upper range of anomalies')
plt.legend(loc='upper right')
plt.show()
```




```
plt.hist(lof_lower_anomalies,alpha =
0.5,label='LOF anomalies')
plt.hist(if_lower_anomalies,alpha = 0.5,label='IF
anomalies')
plt.title('Lower range of anomalies')
plt.legend(loc='upper right')
plt.show()
```



Exercise 5

Module completion checklist

Objective	Complete
Implement LOF to detect anomalies	✔
Describe the isolation forest algorithm	✔
Implement isolation forest	✔
Implement isolation forest to detect anomalies	✔

What’s next?

- In this module we’ve learned about two anomaly detection techniques - LOF and isolation forest
- We implemented these techniques to detect fraud and anomalies in energy consumption
- In the next module we will learn:
  - concepts of time series modeling and its implementation
  - how ARIMA model can be used for anomaly detection

Congratulations on completing this module!