workshop_05_tasks_GColab_Version

March 28, 2021

1 Anomaly Detection

- ### 1.1 Demo for anomaly detection with LOF and iForest
- ### 1.2 Task 2.1 Tuning the performance with respect to k (number of neighbors) for LOF
- ### 1.3 Task 2.2 Turning the performance with respect to sample size for iForest
- ### 1.4 Task 2.3 (optional) Perform anomaly detection with One-Class SVM

[1]:
```
from google.colab import drive

# click on the link, copy and paste the 'authorization code' in the prompt. and␣
 ↪press enter button.
drive.mount('/content/drive')
```

```
Mounted at /content/drive
```

[3]:
```
!pip install -U -q PyDrive
from pydrive.auth import GoogleAuth
from pydrive.drive import GoogleDrive
from google.colab import auth
from oauth2client.client import GoogleCredentials
# Authenticate and create the PyDrive client.
auth.authenticate_user()
gauth = GoogleAuth()
gauth.credentials = GoogleCredentials.get_application_default()
# click on the link, copy and paste the 'authorization code' in the prompt. and␣
 ↪press enter button.
```

```
drive = GoogleDrive(gauth)
```

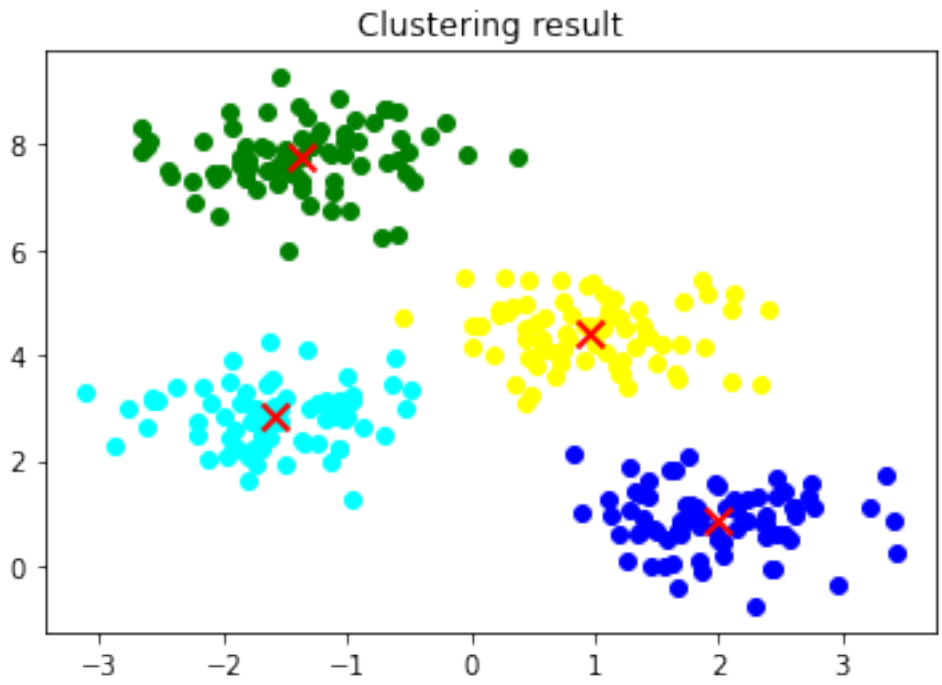
[6]:
```
import numpy as np

import pandas as pd

link = 'https://drive.google.com/file/d/1Hx9JY8iAz3Nvy0etD72pxAqf43o2MboM/view?
↪usp=sharing'

#fluff, id = link.split('=')
#print (id) # Verify that you have everything after '='

id = '1Hx9JY8iAz3Nvy0etD72pxAqf43o2MboM'
downloaded = drive.CreateFile({'id':id})
downloaded.GetContentFile('kdd99-0.01.csv')
data = pd.read_csv('kdd99-0.01.csv')
```

[7]:
```
import pandas as pd
import numpy as np
import math
from matplotlib import pyplot as plt

# Pre-processing
from sklearn import preprocessing

# Anomaly Detection
from sklearn.neighbors import LocalOutlierFactor
from sklearn.ensemble import IsolationForest
from sklearn.metrics import roc_auc_score
```

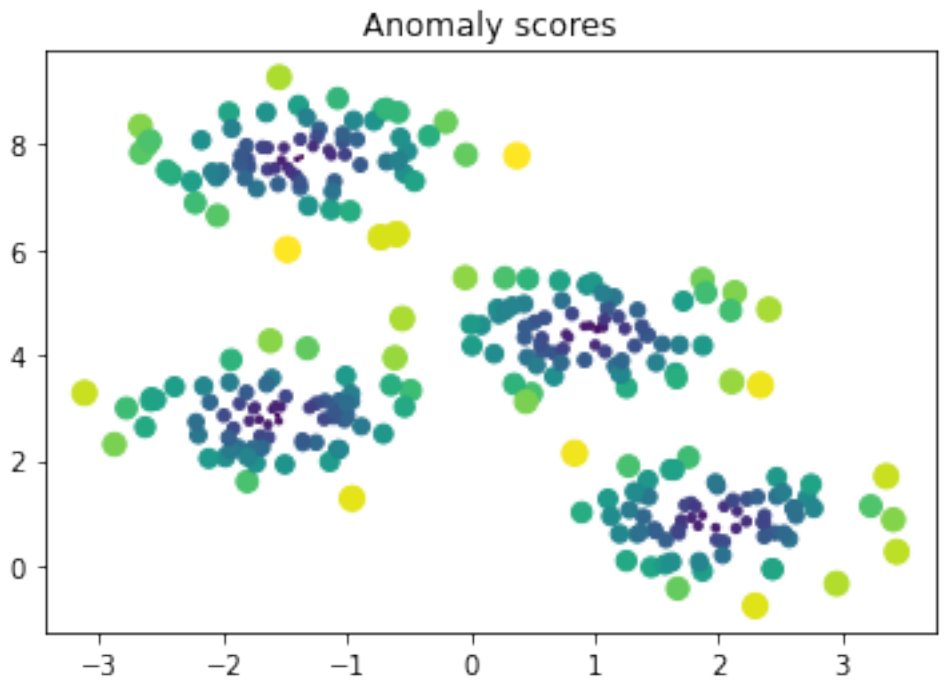
[8]:
```
# We first show how clustering method KMeans introduced before can be used for␣
↪anomaly detection with minor modification

from sklearn.datasets.samples_generator import make_blobs

from sklearn.cluster import KMeans

# Generate an exmaple 2-dimensional datasets containing 4 clusters for a demo

X, y = make_blobs(n_samples=300, centers=4, cluster_std=0.60, random_state=0)

# Create a K-means clustering model with k=4, and k-means++ as the␣
↪intialization strategy

kmeans = KMeans(n_clusters=4, init='k-means++', max_iter=300, random_state=0)
```

```
# Perform clustering by fitting the model with the data

kmeans.fit(X)

# Predict the cluster for each data instance. This step can be combined with␣
 ↪the last one by using kmeans.fit_predict(X)

y_pred = kmeans.predict(X)

# Visualize the cluster centers to explore how the clustering result looks like

colors = ['blue', 'yellow', 'green', 'cyan']

for i, color in enumerate(colors):

    plt.scatter(X[y_pred == i, 0], X[y_pred == i, 1], c=color)

plt.scatter(kmeans.cluster_centers_[:, 0], kmeans.cluster_centers_[:, 1],␣
 ↪marker='x', lw=2, c='red', s=100)

plt.title('Clustering result')

plt.show()

print('\n Cluter center: \n', kmeans.cluster_centers_)

# Transform X to a cluster-distance space. In the new space, each dimension is␣
 ↪the distance to the cluster centers.

# In this way, we could derive the anomaly scores from clustering

X_new=kmeans.transform(X)

scores=X_new.min(axis=1)

plt.scatter(X[:, 0], X[:, 1], marker="o", c=scores, s=50*scores)

plt.title('Anomaly scores')

plt.show()
```

```
/usr/local/lib/python3.7/dist-packages/sklearn/utils/deprecation.py:144:
FutureWarning: The sklearn.datasets.samples_generator module is  deprecated in
version 0.22 and will be removed in version 0.24. The corresponding classes /
functions should instead be imported from sklearn.datasets. Anything that cannot
be imported from sklearn.datasets is now part of the private API.
  warnings.warn(message, FutureWarning)
```




```
Cluter center:
[[ 1.98258281  0.86771314]
 [ 0.94973532  4.41906906]
 [-1.37324398  7.75368871]
 [-1.58438467  2.83081263]]
```



[28]:
```
# Load the data. Orignal data set has been processed (downsampled) to␣
↪facilitate your data analysis. Anomaly label has been given. Only numerical␣
↪attributes are used in this data set
#raw_data = pd.read_csv("data/kdd99-0.01.csv")
raw_data = data
print('\n data size: (%d, %d)\n' % raw_data.shape)

raw_data.head(10)
```

```
 data size: (14081, 39)
```

[28]:

	Feature 1	Feature 2	Feature 3	…	Feature 37	Feature 38	Label
0	0	256	1169	…	0.0	0.0	1
1	0	248	2129	…	0.0	0.0	1
2	0	212	1309	…	0.0	0.0	1
3	0	217	18434	…	0.0	0.0	1
4	0	290	460	…	0.0	0.0	1
5	0	300	42747	…	0.0	0.0	1
6	0	309	1030	…	0.0	0.0	1
7	0	239	304	…	0.0	0.0	1
8	0	297	2000	…	0.0	0.0	1
9	0	329	1735	…	0.0	0.0	1

```
[10 rows x 39 columns]
```

[32]:
```
raw_data.shape
```

[32]:
```
(14081, 39)
```

[37]:
```
# Question 1: How can we drop a specific column in the data from processing?

# Specifying features and target attribute
X = raw_data.drop(['Label'], axis='columns') # Drop specified labels from rows
 ↪or columns.

#X.head()
X.shape
```

[37]:
```
(14081, 38)
```

[38]:
```
# Question 2: How can we scale the numbers to given range for Anomly detection?

# Transform features by scaling each feature to a given range.
#This estimator scales and translates each feature individually such that it is
 ↪in the given range on the training set, e.g. between zero and one.

scaler = preprocessing.MinMaxScaler()
X_data = X.values

X_scaled = scaler.fit_transform(X_data)
X = X_scaled

y = raw_data['Label'].values
```

[41]:
```
X[0]
```

[41]:
```
array([0.00000000e+00, 4.98473619e-05, 2.26955477e-04, 0.00000000e+00,
       0.00000000e+00, 0.00000000e+00, 0.00000000e+00, 0.00000000e+00,
       1.00000000e+00, 0.00000000e+00, 0.00000000e+00, 0.00000000e+00,
       0.00000000e+00, 0.00000000e+00, 0.00000000e+00, 0.00000000e+00,
       0.00000000e+00, 0.00000000e+00, 0.00000000e+00, 5.88235294e-03,
       5.88235294e-03, 0.00000000e+00, 0.00000000e+00, 0.00000000e+00,
       0.00000000e+00, 1.00000000e+00, 0.00000000e+00, 0.00000000e+00,
       1.18110236e-02, 5.43307087e-01, 1.00000000e+00, 0.00000000e+00,
       2.50000000e-01, 4.00000000e-02, 0.00000000e+00, 0.00000000e+00,
       0.00000000e+00, 0.00000000e+00])
```

[34]:
```
max(X['Feature 20']), min(X['Feature 20'])
```

[34]:
```
(511, 1)
```

[35]:
```
max(X['Feature 31']), min(X['Feature 31'])
```

[35]: (1.0, 0.0)

[43]:
```
max(X[11]), min(X[11])
```

[43]: (1.0, 0.0)

[46]:
```
# Question 3: What is Anomly rate? What does it tell us?

# Anomaly rate. Assuming that the target attribute has '1' for normal␣
 ↪instances, and '-1' for anomalies
print('\n Anomaly rate: %f \n' % (100*-1.0*(y-1).sum()/2.0/X.shape[0]))
print('\n The number of Anomalous data-points: %f \n' % (raw_data.shape[0]*-1.
 ↪0*(y-1).sum()/2.0/X.shape[0]))
```

```
 Anomaly rate: 3.884667


 The number of Anomalous data-points: 547.000000
```

[48]:
```
# Question 4: How can we measure the local deviation of density of a given␣
 ↪sample with respect to its neighbors?

# Unsupervised Outlier Detection using Local Outlier Factor (LOF)

# The anomaly score of each sample is called Local Outlier Factor.

# Create the local outlier factor (LOF). Note here we need to set 'novelty'␣
 ↪parameter as 'True' to get LOF scores
detector_lof = LocalOutlierFactor(n_neighbors=10, novelty=True)

# Train the model (Compute the LOF scores)
detector_lof.fit(X)

# Obtain anomaly score (Note that this is not the yes/no prediction as we don't␣
 ↪know the threshold)
y_score = detector_lof.decision_function(X)
print(y_score)
```

```
[0.19076799 0.50956163 0.5099336  … 0.40971203 0.33866019 0.53182027]
```

[54]:
```
# Question 5: What is Area Under Curve (AUC) and what information it conveys?

# Evaluate using AUC, the higher, the better
```

```
# AUC ranges in value from 0 to 1. A model whose predictions are 100% wrong has␣
 ↪an AUC of 0.0; one whose predictions are 100% correct has an AUC of 1.0.
# Reference: https://developers.google.com/machine-learning/crash-course/
 ↪classification/roc-and-auc

auc = roc_auc_score(y, y_score)
print('\n AUC score: %f\n' % (auc * 100.0))

# Is AUC high enough? What does the lower value of AUC conveys?
```

```
AUC score: 62.488596
```

[55]:
```
# Predict the Yes/No label. The algorithm set a default threshold. But note␣
 ↪that this is really data-dependent
y_pred = detector_lof.predict(X)
auc = roc_auc_score(y, y_pred)
print('\n AUC score: %f\n' % (auc * 100.0))
```

```
AUC score: 57.829405
```

[58]:
```
# Create the iForest model
'''
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.
'''
detector_if = IsolationForest()
```

[59]:
```
# Train the model
detector_if.fit(X)

# Obtain anomaly score (Note that this is not the yes/no prediction as we don't␣
 ↪know the threshold)
y_score = detector_if.decision_function(X)
print(y_score)
```

```
[0.13362792 0.14608338 0.15428699 … 0.11734885 0.11981837 0.13770096]
```

[60]:
```
# Evaluate using AUC (Area Under Curve)
auc = roc_auc_score(y, y_score)
print('\n AUC score: %f\n' % (auc * 100.0))
```

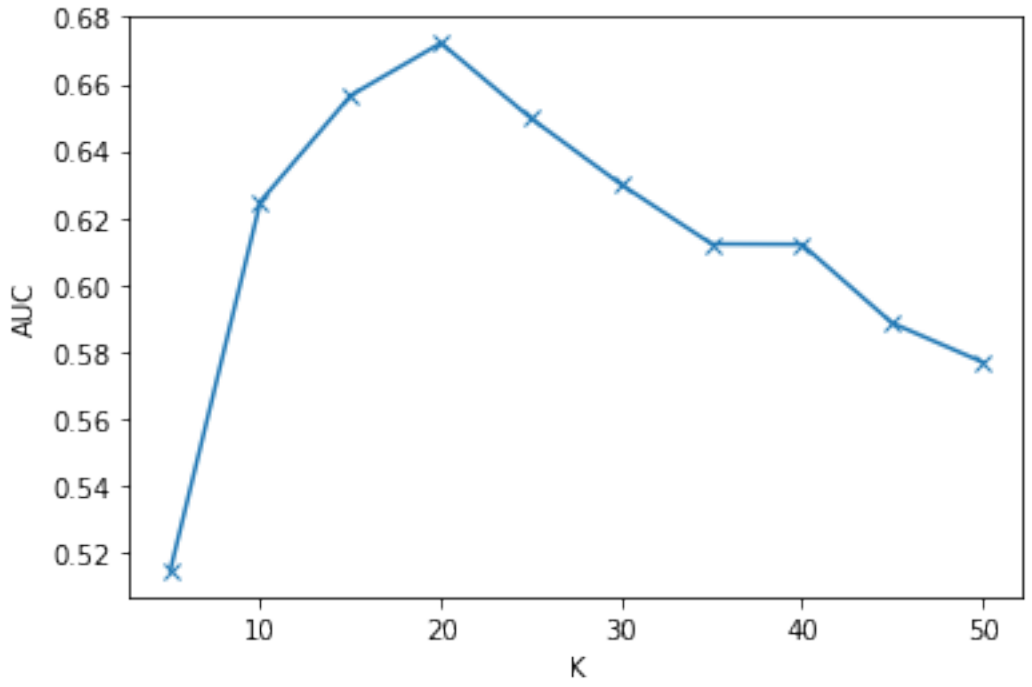
```
 AUC score: 93.492670
```

[61]:
```
# Predict the Yes/No label. The algorithm set a default threshold. But note␣
 ↪that this is really data-dependent
y_pred = detector_if.predict(X)
print('\n AUC score: %f\n' % roc_auc_score(y, y_pred))
```

```
 AUC score: 0.795015
```

[62]:
```
# Task 2.1. Try different values of k ('n_neighbors' parameter) for LOF to␣
 ↪identify a good one.
# Plot the relationship for k changing from 5 to 50 with 5 as the step.

# Please refer to https://scikit-learn.org/stable/modules/generated/sklearn.
 ↪neighbors.LocalOutlierFactor.html

# Computer the auc values for different k
auc_scores = []
for i in range (5, 51, 5):
  detector_lof = LocalOutlierFactor(n_neighbors=i, novelty=True)
  detector_lof.fit(X)
  y_score= detector_lof.decision_function(X)
  auc= roc_auc_score(y, y_score)
  auc_scores.append(auc)

# Plot the relationship between auc and k
plt.plot(range(5,51,5), auc_scores, marker='x')
plt.xlabel('K')
plt.ylabel('AUC')
```

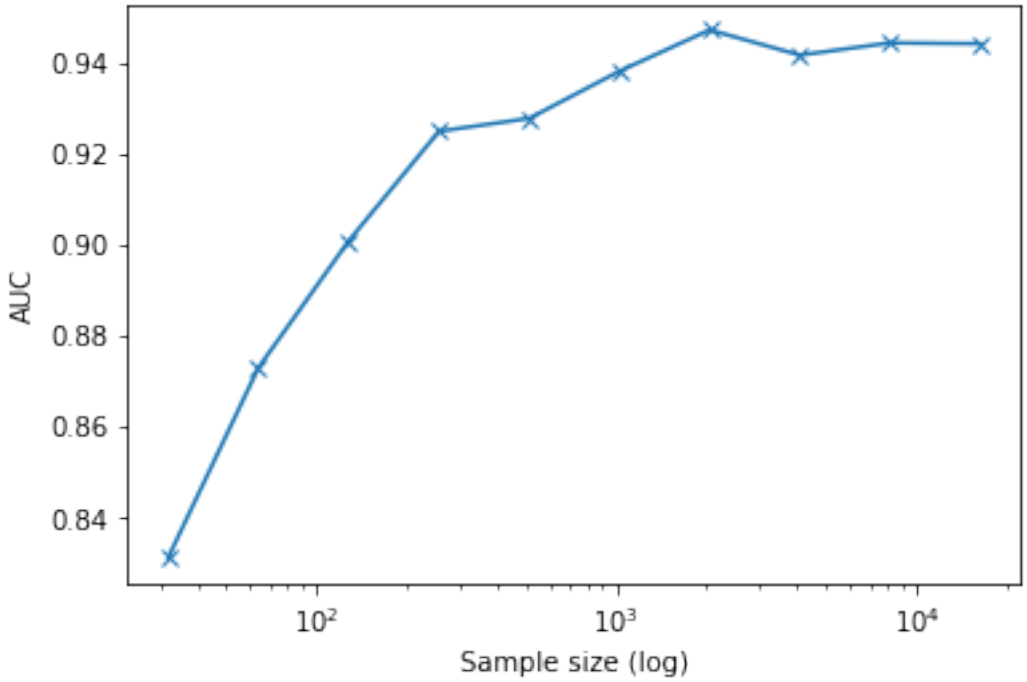
```
plt.show()
```



[63]:
```
# Task 2.2 Try different sample size ('max_samples' parameter) for iforest to␣
 ↪identify a good one.
# Plot the relationship for the size from 2**5 to 2**14 with an exponential␣
 ↪step 2**i.

# Computer the auc values for different sample size
auc_scores = []
sample_sizes = []
for i in range(5,15):
  sample_sizes.append(2**i)
  detector_if = IsolationForest(max_samples=2**i)
  detector_if.fit(X)
  y_score = detector_if.decision_function(X)
  auc = roc_auc_score(y, y_score)
  auc_scores.append(auc)


# Plot the relationship between auc and sample size
plt.plot(sample_sizes, auc_scores, marker='x')
plt.xscale('log')
plt.xlabel('Sample size (log)')
plt.ylabel('AUC')
```

```
plt.show()
```

```
/usr/local/lib/python3.7/dist-packages/sklearn/ensemble/_iforest.py:281:
UserWarning: max_samples (16384) is greater than the total number of samples
(14081). max_samples will be set to n_samples for estimation.
  % (self.max_samples, n_samples))
```



[22]:
```
# Optional task: Perform anomaly detection with One-Class SVM (https://
 ↪scikit-learn.org/stable/modules/generated/sklearn.svm.OneClassSVM.html)
```

[23]:
```
# Putting All-together, Comparing anomaly detection algorithms for outlier␣
 ↪detection on toy datasets
# Reference: https://scikit-learn.org/stable/auto_examples/miscellaneous/
 ↪plot_anomaly_comparison.
 ↪html#sphx-glr-auto-examples-miscellaneous-plot-anomaly-comparison-py
import time

import numpy as np
import matplotlib
import matplotlib.pyplot as plt

from sklearn import svm
from sklearn.datasets import make_moons, make_blobs
from sklearn.covariance import EllipticEnvelope
```

```
from sklearn.ensemble import IsolationForest
from sklearn.neighbors import LocalOutlierFactor

print(__doc__)

matplotlib.rcParams['contour.negative_linestyle'] = 'solid'

# Example settings
n_samples = 300
outliers_fraction = 0.15
n_outliers = int(outliers_fraction * n_samples)
n_inliers = n_samples - n_outliers

# define outlier/anomaly detection methods to be compared
anomaly_algorithms = [
    ("Robust covariance", EllipticEnvelope(contamination=outliers_fraction)),
    ("One-Class SVM", svm.OneClassSVM(nu=outliers_fraction, kernel="rbf",
                                      gamma=0.1)),
    ("Isolation Forest", IsolationForest(contamination=outliers_fraction,
                                         random_state=42)),
    ("Local Outlier Factor", LocalOutlierFactor(
        n_neighbors=35, contamination=outliers_fraction))]

# Define datasets
blobs_params = dict(random_state=0, n_samples=n_inliers, n_features=2)
datasets = [
    make_blobs(centers=[[0, 0], [0, 0]], cluster_std=0.5,
               **blobs_params)[0],
    make_blobs(centers=[[2, 2], [-2, -2]], cluster_std=[0.5, 0.5],
               **blobs_params)[0],
    make_blobs(centers=[[2, 2], [-2, -2]], cluster_std=[1.5, .3],
               **blobs_params)[0],
    4. * (make_moons(n_samples=n_samples, noise=.05, random_state=0)[0] -
          np.array([0.5, 0.25])),
    14. * (np.random.RandomState(42).rand(n_samples, 2) - 0.5)]

# Compare given classifiers under given settings
xx, yy = np.meshgrid(np.linspace(-7, 7, 150),
                     np.linspace(-7, 7, 150))

plt.figure(figsize=(len(anomaly_algorithms) * 2 + 3, 12.5))
plt.subplots_adjust(left=.02, right=.98, bottom=.001, top=.96, wspace=.05,
                    hspace=.01)

plot_num = 1
rng = np.random.RandomState(42)
```

```
for i_dataset, X in enumerate(datasets):
    # Add outliers
    X = np.concatenate([X, rng.uniform(low=-6, high=6,
                       size=(n_outliers, 2))], axis=0)

    for name, algorithm in anomaly_algorithms:
        t0 = time.time()
        algorithm.fit(X)
        t1 = time.time()
        plt.subplot(len(datasets), len(anomaly_algorithms), plot_num)
        if i_dataset == 0:
            plt.title(name, size=18)

        # fit the data and tag outliers
        if name == "Local Outlier Factor":
            y_pred = algorithm.fit_predict(X)
        else:
            y_pred = algorithm.fit(X).predict(X)

        # plot the levels lines and the points
        if name != "Local Outlier Factor":  # LOF does not implement predict
            Z = algorithm.predict(np.c_[xx.ravel(), yy.ravel()])
            Z = Z.reshape(xx.shape)
            plt.contour(xx, yy, Z, levels=[0], linewidths=2, colors='black')

        colors = np.array(['#377eb8', '#ff7f00'])
        plt.scatter(X[:, 0], X[:, 1], s=10, color=colors[(y_pred + 1) // 2])

        plt.xlim(-7, 7)
        plt.ylim(-7, 7)
        plt.xticks(())
        plt.yticks(())
        plt.text(.99, .01, ('%.2fs' % (t1 - t0)).lstrip('0'),
                 transform=plt.gca().transAxes, size=15,
                 horizontalalignment='right')
        plot_num += 1

plt.show()
```

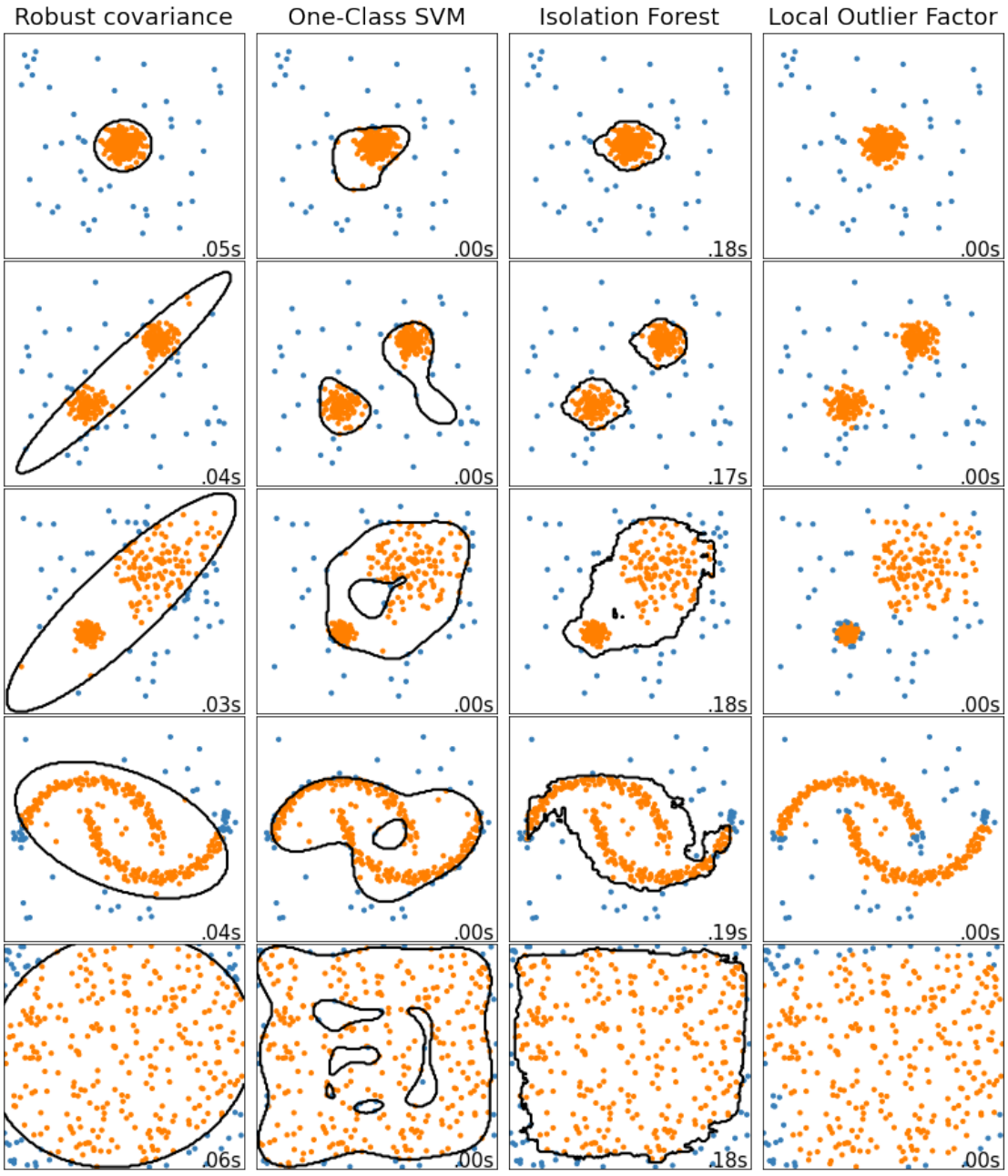
Return the anomaly score of each sample using the IsolationForest algorithm

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.



[24]:
```
'''
This example shows characteristics of different anomaly detection algorithms on␣
 ↪2D datasets.
Datasets contain one or two modes (regions of high density) to illustrate the␣
 ↪ability of algorithms
to cope with multimodal data.
```

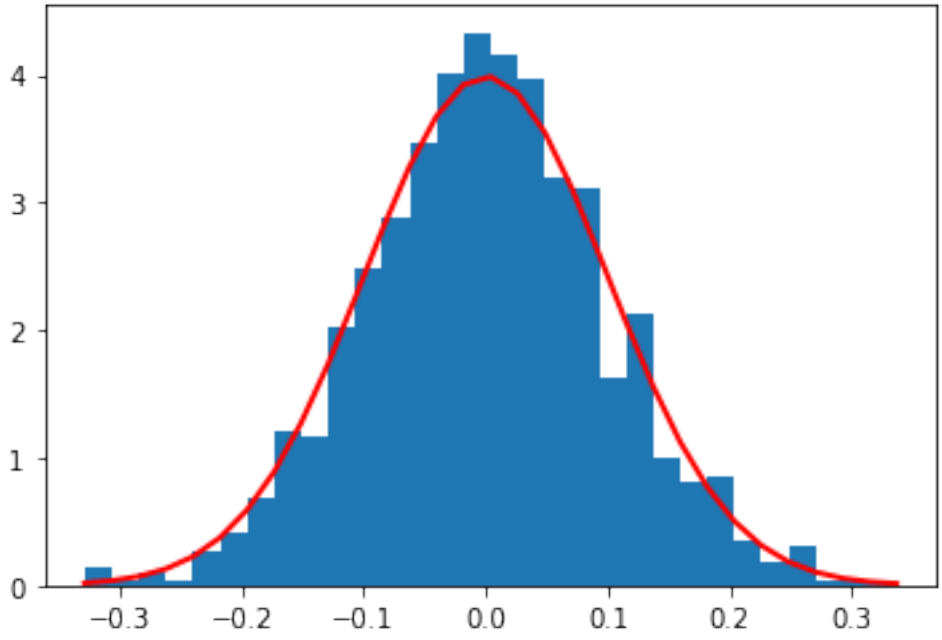
```
For each dataset, 15% of samples are generated as random uniform noise. This␣
 ↪proportion is the value
given to the nu parameter of the OneClassSVM and the contamination parameter of␣
 ↪the other outlier
detection algorithms. Decision boundaries between inliers and outliers are␣
 ↪displayed in black except
for Local Outlier Factor (LOF) as it has no predict method to be applied on new␣
 ↪data when it is used
for outlier detection.

The OneClassSVM is known to be sensitive to outliers and thus does not perform␣
 ↪very well for outlier
detection. This estimator is best suited for novelty detection when the␣
 ↪training set is not contaminated
by outliers. That said, outlier detection in high-dimension, or without any␣
 ↪assumptions on the distribution
of the inlying data is very challenging, and a One-class SVM might give useful␣
 ↪results in these situations
depending on the value of its hyperparameters.

EllipticEnvelope (i.e., Robust covariance) assumes the data is Normal or␣
 ↪Gaussian (see https://www.itl.nist.gov/div898/handbook/pmc/section5/pmc51.
 ↪htm)
and learns an ellipse. It thus degrades when the data is not unimodal. Notice␣
 ↪however that this estimator is robust to outliers.

IsolationForest and LocalOutlierFactor seem to perform reasonably well for␣
 ↪multi-modal data sets.
The advantage of LocalOutlierFactor over the other estimators is shown for the␣
 ↪third data set, where
the two modes have different densities. This advantage is explained by the␣
 ↪local aspect of LOF, meaning
that it only compares the score of abnormality of one sample with the scores of␣
 ↪its neighbors.

Finally, for the last data set, it is hard to say that one sample is more␣
 ↪abnormal than another
sample as they are uniformly distributed in a hypercube. Except for the␣
 ↪OneClassSVM which overfits
a little, all estimators present decent solutions for this situation. In such a␣
 ↪case, it would be
wise to look more closely at the scores of abnormality of the samples as a good␣
 ↪estimator should
assign similar scores to all the samples.
```

```
While these examples give some intuition about the algorithms, this intuition␣
 ↪might not apply to
very high dimensional data.

Finally, note that parameters of the models have been here handpicked but that␣
 ↪in practice they
need to be adjusted. In the absence of labelled data, the problem is completely␣
 ↪unsupervised so
model selection can be a challenge.
'''
```

[24]: '\nThis example shows characteristics of different anomaly detection algorithms on 2D datasets. \nDatasets contain one or two modes (regions of high density) to illustrate the ability of algorithms \nto cope with multimodal data.\n\nFor each dataset, 15% of samples are generated as random uniform noise. This proportion is the value \ngiven to the nu parameter of the OneClassSVM and the contamination parameter of the other outlier \ndetection algorithms. Decision boundaries between inliers and outliers are displayed in black except \nfor Local Outlier Factor (LOF) as it has no predict method to be applied on new data when it is used \nfor outlier detection.\n\nThe OneClassSVM is known to be sensitive to outliers and thus does not perform very well for outlier \ndetection. This estimator is best suited for novelty detection when the training set is not contaminated \nby outliers. That said, outlier detection in high-dimension, or without any assumptions on the distribution \nof the inlying data is very challenging, and a One-class SVM might give useful results in these situations \ndepending on the value of its hyperparameters.\n\nEllipticEnvelope (i.e., Robust covariance) assumes the data is Normal or Gaussian (see https://www.itl.nist.gov/div898/handbook/pmc/section5/pmc51.htm) \nand learns an ellipse. It thus degrades when the data is not unimodal. Notice however that this estimator is robust to outliers.\n\nIsolationForest and LocalOutlierFactor seem to perform reasonably well for multi-modal data sets. \nThe advantage of LocalOutlierFactor over the other estimators is shown for the third data set, where \nthe two modes have different densities. This advantage is explained by the local aspect of LOF, meaning \nthat it only compares the score of abnormality of one sample with the scores of its neighbors.\n\nFinally, for the last data set, it is hard to say that one sample is more abnormal than another \nsample as they are uniformly distributed in a hypercube. Except for the OneClassSVM which overfits \na little, all estimators present decent solutions for this situation. In such a case, it would be \nwise to look more closely at the scores of abnormality of the samples as a good estimator should \nassign similar scores to all the samples.\n\nWhile these examples give some intuition about the algorithms, this intuition might not apply to \nvery high dimensional data.\n\nFinally, note that parameters of the models have been here handpicked but that in practice they \nneed to be adjusted. In the absence of labelled data, the problem is completely unsupervised so \nmodel selection can be a challenge.\n'

[25]:
```
import matplotlib.pyplot as plt
mu, sigma = 0, 0.1 # mean and standard deviation
s = np.random.normal(mu, sigma, 1000)

absolute = abs(mu - np.mean(s))
print("abs(mu - np.mean(s) :: " + str(absolute))

count, bins, ignored = plt.hist(s, 30, density=True)
plt.plot(bins, 1/(sigma * np.sqrt(2 * np.pi)) *
               np.exp( - (bins - mu)**2 / (2 * sigma**2) ),
         linewidth=2, color='r')
plt.show()
```

```
abs(mu - np.mean(s) :: 0.0009984089142363864
```



[ ]: