Machine Learning Security

9 Unsupervised Learning Techniques



Unsupervised Learning

- Most data is unlabeled
- Labeling usually requires human workers
- Unsupervised learning tasks:
 - Dimensionality reduction
 - Clustering
 - Anomaly detection
 - Density estimation
 - Determining the probability density function of the data

Topics

- Clustering Algorithms: k-Means and DBSCAN
- Gaussian Mixtures

Clustering Algorithms: k-Means and DBSCAN

Classification v. Clustering

- Classification on the left
 - Requires labels
- Clustering on the right
 - Can make two clusters, not three, from this data



Clustering Use Cases

- Customer segmentation
 - Grouping customers into clusters
 - Adapt products, marketing, and recommendations to them
- Data analysis
 - Group data into clusters, analyze clusters separately
- Dimensionality reduction
 - Find *k* clusters
 - Measure each instance's *affinity* with each cluster
 - Replace instance with its cluster affinities
 - This is *k*-dimensional

Clustering Use Cases

- Feature engineering
 - Cluster affinities may be useful as extra features
- Anomaly detection
 - Instances with low affinity to all clusters are anomalies
- Semi-supervised learning
 - Some data is labeled
 - Form clusters and propagate labels to all instances in the same cluster

Clustering Use Cases

- Search engines
 - Search for images similar to a reference image
 - Cluster images, return the matching cluster
- Image segmentation
 - Cluster pixels by color

k-Means

k-Means

- Proposed by Bell Labs in 1957
- This data has five Gaussian blobs



k-Means Decision Boundaries

- Minimizes distances to the centroids
- Converges to a good solution when the blobs all have the same size
- Note errors near the top left decision boundary



Hard v Soft Clustering

- Hard clustering
 - Assign each instance to a single cluster
- Soft clustering
 - Give each instance a score per cluster
 - Such as distance to the centroid

Dimensionality Reduction

- Original data was two-dimensional (x1, x2)
- Replace with 5-dimensional data, with distance from each instance to the centroids
- If original data has high dimensionality, this is a method of dimensionality reduction

>>> kmeans.transform(X_new).round(2)
array([[2.81, 0.33, 2.9 , 1.49, 2.89],
 [5.81, 2.8 , 5.85, 4.48, 5.84],
 [1.21, 3.29, 0.29, 1.69, 1.71],
 [0.73, 3.22, 0.36, 1.55, 1.22]])



k-Means Algorithm

- 1. Starts by randomly placing the centroids
- 2. Label the instances by finding the nearest centroid
- 3. Updates the centroids to the center of the instances in that class
- 4. Loop back to step 2 for the next iteration

Scores are sum of squared distances from centroids, negated

The positive score is called *inertia*



Suboptimal Solutions

- Bad luck with initial centroids
- It tries **n_init** different starting locations (default 10)



Computational Complexity

- If the data has clusters,
 - Linear in
 - Number of instances *m*
 - Number of clusters k
 - Number of dimensions *n*
 - But if the data lacks a clustered structure, the model can fail to converge and increase in complexity exponentially
 - This rarely happens; in practice, k-Means is one of the fastest clustering algorithms

Random Data Part 1

import numpy as np import matplotlib.pyplot as plt import random from sklearn.cluster import KMeans import time def plot data(X): plt.plot(X[:, 0], X[:, 1], 'k.', markersize=2) def plot centroids(centroids, weights=None, circle color='w', cross color='k'): if weights is not None: centroids = centroids[weights > weights.max() / 10] plt.scatter(centroids[:, 0], centroids[:, 1], marker='o', s=35, linewidths=8, color=circle_color, zorder=10, alpha=0.9) plt.scatter(centroids[:, 0], centroids[:, 1], marker='x', s=2, linewidths=12, color=cross_color, zorder=11, alpha=1) def plot decision boundaries(clusterer, X, resolution=1000, show centroids=True, show xlabels=True, show ylabels=True): mins = X.min(axis=0) - 0.1maxs = X.max(axis=0) + 0.1xx, yy = np.meshgrid(np.linspace(mins[0], maxs[0], resolution), np.linspace(mins[1], maxs[1], resolution)) Z = clusterer.predict(np.c_[xx.ravel(), yy.ravel()]) Z = Z.reshape(xx.shape)plt.contourf(Z, extent=(mins[0], maxs[0], mins[1], maxs[1]), cmap="Pastel2") plt.contour(Z, extent=(mins[0], maxs[0], mins[1], maxs[1]), linewidths=1, colors='k') plot data(X) if show centroids: plot centroids(clusterer.cluster centers) if show xlabels: plt.xlabel("\$x_1\$") else: plt.tick_params(labelbottom=False) if show ylabels: plt.ylabel("\$x_2\$", rotation=0) else: plt.tick_params(labelleft=False)

Random Data Part 2

```
for n in [100, 1_000, 10_000]: # Number of data points
# Make random data
 X = np.zeros(shape=(n,2))
 for i in range(n):
  X[i] = [random.uniform(0,3), random.uniform(0,3)]
 # Fit 5-way k-Means
 time_start = time.time()
 k = 5
 kmeans = KMeans(n_clusters=k, random_state=42, n_init=10)
 y_pred = kmeans.fit_predict(X)
 time_elapsed = time.time() - time_start
 print()
 print(f"n: {n:,}: ", n, "Score: ", "{:.2f}".format(kmeans.score(X)), "Time: ", "{:.2f}".format(time_elapsed))
 plt.figure(figsize=(4, 2))
 plot_decision_boundaries(kmeans, X)
 plt.show()
```





k-Means++

- An improvement proposed in 2006
- Chooses better starting centroids that are more distant from each other
- Much less likely to converge to a suboptimal solution
- The default method for the k-Means class we're using

Accelerated and Mini-Batch k-Means

- On large datasets with many clusters
- The calculation can be accelerated
- Using the triangle inequality to estimate distances using upper and lower bounds
- Doesn't always work, can make training slower

Mini-Batch k-Means

- Use only part of the data for each iteration
- Move centroids just slightly each time
- Speeds up algorithm
- Allows use of huge datasets



Choosing k

- More clusters means lower inertia
 - Even if it's overfitting the data



Silhouette Score

- Mean *silhouette coefficient* over all the instances
 - (**b a**) / max(**a**, **b**)
 - *a* is the mean distance to other instances in the same cluster
 - **b** is the mean distance to the instances in the next-closest cluster
- Varies from -1 to 1
 - +1 if an instance is well inside its own cluster and far from other clusters
 - -1 if an instance is assigned to the wrong cluster

Results for 5-Cluster Data

- 4 is the best choice
- 5 is the second-best



Limits of k-Means

- Poor behavior when the clusters have
 - varying sizes,
 - different densities, or
 - nonspherical shapes
- Gaussian mixtures are better for these elliptical clusters



Using Clusters for Image Segmentation

- Color segmentation
 - Pixels with similar colors are assigned to the same segment
 - Useful for finding forest area in a landscape
- Semantic segmentation
 - Pixels that are part of the same object are assigned to the same segment
 - All pedestrians get sorted to the pedestrian segment
- Instance segmentation
 - Pixels that are part of the same individual; are assigned to the same segment
 - Each pedestrian is a different segment

Color Segmentation with k-Means





6 colors

10 colors



4 colors

8 colors



2 colors



Figure 9-12. Image segmentation using k-means with various numbers of color clusters

Using Clustering for Semi-Supervised Learning

- Many unlabeled instances, and a few labeled instances
- This dataset has 1,797 images with labels



Fitting a Model

- Fit using all images and labels
- Over 90% accuracy

```
from sklearn.linear_model import LogisticRegression
n_labeled = 1400
log_reg = LogisticRegression(max_iter=10_000)
log_reg.fit(X_train[:n_labeled], y_train[:n_labeled])
print("{:.4f}".format(log_reg.score(X_test, y_test)))
0.9068
```

Fitting a Model to 50 Instances

• Only about 75% accurate

```
from sklearn.linear_model import LogisticRegression

n_labeled = 50
log_reg = LogisticRegression(max_iter=10_000)
log_reg.fit(X_train[:n_labeled], y_train[:n_labeled])
print("{:.4f}".format(log_reg.score(X_test, y_test)))
0.7481
```

Using a k-Means Model to form 50 Clusters

- Find representative images nearest to the centroids
- These are better images to use for training
- Label them by hand

414	34	500	7367	72885	200	249	42569	85673	91927
		y_re	presenta 1, 3, 6, 5, 4, 7, 4, 1, 3, 1, 4, 0, 4, 1, 0,	tive_dig 0, 7, 9 1, 2, 6 3, 8, 8 6, 8, 3 7, 5, 1	gits = n 9, 2, 4, 5, 1, 2, 3, 2, 5, 3, 4, 6, 1, 9, 9,	p.array(8, 9, 5, 1, 6, 9, 7, 2, 3, 7	[

Training from Representative Images

• Accuracy increases to about 85%

```
log_reg = LogisticRegression(max_iter=10_000)
log_reg.fit(X_representative_digits, y_representative_digits)
print("{:.4f}".format(log_reg.score(X_test, y_test)))
```

0.8489

Propagating Labels to All Instances

- In each of the 50 clusters
- Accuracy increases to 89%

```
y_train_propagated = np.empty(len(X_train), dtype=np.int64)
for i in range(k):
    y_train_propagated[kmeans.labels_ == i] = y_representative_digits[i]
    log_reg = LogisticRegression(max_iter=10_000)
    log_reg.fit(X_train, y_train_propagated)
    print("{:.4f}".format(log_reg.score(X_test, y_test)))
    0.8967
```

Removing Outliers

- Remove the 1% of images furthest from centroids
- Accuracy increases to over 90%

```
partially_propagated = (X_cluster_dist != -1)
X_train_partially_propagated = X_train[partially_propagated]
y_train_partially_propagated = y_train_propagated[partially_propagated]
log_reg = LogisticRegression(max_iter=10_000)
log_reg.fit(X_train_partially_propagated, y_train_partially_propagated)
print("{:.4f}".format(log_reg.score(X_test, y_test)))
0.9093
```

Summary

 Train on all data with labels 	91%
 Train on first 50 images 	75%
 Train on 50 representative images 	85%
 Propagate labels to all images 	89%
 Remove outliers 	91%

Active Learning

- A human expert interacts with the learning algorithm
- Uncertainty sampling
 - The model is trained on the instances labeled so far
 - Makes predictions on the unlabeled instances
 - Instances are given to the expert for labeling, those
 - With the most uncertainty, or
 - That would result in the largest model change, or
 - That different models disagree on
 - Iterate this process until the performance improvement stops being worth the labeling effort



Ch 9a

DBSCAN

DBSCAN

- Density-Based Spatial Clustering of Applications with Noise
- Clusters are continuous regions of high density
 - For each instance, count how many instances are near it
 - Distance <*E* (*E*-neightorhood)
 - If an instance has at least **min_samples** in its *E*-neightorhood
 - It's a *core instance* -- located in a dense region
 - All instances in the neighborhood of a core instance belong to the same cluster
 - An instance that is not a core instance and doesn't have one in its neighborhood is an anomaly

DBSCAN

- If *E* is too small, clusters are broken up, on the left below
- On the right, a correct value of *E*



Agglomerative clustering

• Connects clusters together with each iteration like bubbles

• BIRCH

- Balanced Iterative Reducing and Clustering using Hierarchies
- Designed for very large datasets
- Can be faster than batch k-Means as long as there are less than 20 features
- During training, builds a tree structure with just enough information to assign new instances to clusters

• Mean-shift

- Starts with a circle centered on each instance
- Shifts the circle to center on the mean of clusters inside
- Iterates until the circles stop moving
- Combines close circles to form clusters
- Can find clusters of any shape
- Only one hyperparameter: *bandwidth* (the circle size)

Affinity propagation

- Instances exchange messages and elect exemplars
- Each exemplar and the instances that selected it are the clusters
- Can find clusters of different sizes
- Complexity of order *m*² so not good for large datasets

Spectral clustering

- Makes a similarity matrix between clusters
- Reduces dimensionality
- Uses another clustering algorithm like k-means in this low dimensional space
- Does not scale well to large numbers of instances
- Does not handle different cluster sizes well

Gaussian Mixtures

Gaussian Mixtures

- Assume instances are a group of Gaussian distributions
- Input the number of clusters
- Estimate Gaussian parameters

from sklearn.datasets import make_blobs import numpy as np import matplotlib.pyplot as plt

X1, y1 = make_blobs(n_samples=1000, centers=((4, -4), (0, 0)), random_state=42)
X1 = X1.dot(np.array([[0.374, 0.95], [0.732, 0.598]]))
X2, y2 = make_blobs(n_samples=250, centers=1, random_state=42)
X2 = X2 + [6, -8]
X = np.r_[X1, X2]
y = np.r_[y1, y2]

plt.scatter(X[:, 0], X[:, 1], s=3)
plt.show()



Expectation-Maximization (EM)

- Initialize cluster parameters randomly
 - Assign instances to clusters (expectation)
 - Update clusters (maximization)
- A generalization of k-means
 - Allowing various cluster size, shape, and orientation
- Like k-means, it can converge to poor solutions
- Repeat n_init times (default 1, set to 10)

Gaussian Mixture Model

• Fits this simple data well



Limiting Shapes

- covariance_type hyperparameter
 - "spherical"
 - but can have different sizes
 - "diag"
 - can be ellipsoids but axes must be aligned with coordinate axes
 - "tied"
 - all ellipsoids must have the same shape, size, and orientation
 - "full"
 - no constraints

Constrained Models



Anomaly Detection

- An instance in a low-density region is an anomaly
- Choose a threshold
 - Ex: 2% of products are defective



Selecting the Number of Clusters

- Minimize Theoretical Information Criterion such as
 - Bayesian Information Criterion (BIC)
 - Akaike Information Criterion (AIC)

In these equations:

- m is the number of instances, as always.
- p is the number of parameters learned by the model.
- $\widehat{\mathscr{L}}$ is the maximized value of the *likelihood function* of the model.

BIC and AIC

• Both measures are minimized for k=3



Bayesian Gaussian Mixture Models

- Set n_components to a large value, more than the number of clusters you expect
- Algorithm will eliminate unnecessary clusters automatically
- Works for the simple 3 Gaussian cluster data
- Not so well for moons



Other Algorithms

- Fast-MCD (Minimum Covariance Determinant)
 - Useful for outlier detection, to clean up a dataset
 - Assumes that inliners are from a single Gaussian distribution
 - Classified the others as **outliers**

Other Algorithms

Isolation Forest

- Efficient for outlier detection, especially in high-dimensional datasets
- Builds a random forest, randomly picking features and thresholds at each node
- Dataset gets chopped into pieces until each instance is alone
- Anomalies get isolated in fewer steps
- Local Outlier Factor (LOF)
 - Compares density of instances around a given instance to the density around its neighbors
 - Anomalies are more isolated than the neighbors

Other Algorithms

One-class SVM

- Suited for novelty detection
- Maps instances to a high-dimensional space
- Uses a linear SVM classifier to separate the instances from the origin
- Corresponds to finding a small region that encompasses all the instances in the original space
- A new instance that is outside that region is an anomaly
- PCA and other dimensionality reduction techniques
 - Reconstruction error is larger for anomalies



Ch 9b