Intrusion Detection: Techniques

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Introduction

Introduction

Definition of an anomaly:

"An observation that deviates so much from other observations as to arouse suspicions that it was generated by a different mechanism"

The anomaly detection literature is fragmented in various domains

- Works on **intrusion detection** tries to detect attacks, typically in a computer system or network. The goal is to produce alerts that warn a security expert.
- Works on **outlier detection** try to detect **uncommon data patterns** in a dataset. The goal is to either analyze them further due to their importance or to discard them in order to clean the dataset.
- **Anomaly detection** is a catch-all term that includes both intrusion and outlier detection

We will use the terms intrusion, outlier and anomaly interchangeably

Introduction

Various intrusion detection algorithms have been developed depending on:

- the data distribution and prior knowledge
- the data dimensionality i.e. the number of features in a datapoint
- the number of expected anomalies
- the various anomaly types
- computational efficiency
- algorithm robustness
- failures of existing algorithms

Introduction

Note that we can train and test the IDS using various configurations:

- **Supervised IDS.** Train the IDS for both the normal behavior and the anomaly (2 classes)
- **Threshold IDS.** Train the IDS for both the normal behavior only and use a threshold to detect anomalies (single class)
- **Untainted dataset.** Train the normal behavior of the IDS using datapoints that originated from the normal behavior only
- **Tainted dataset.** Train the normal behavior of the IDS using datapoints that may include anomalies. This could happen because we are not able to label all anomalies.

Box Plot

Box Plot

- We can use Tukey's box plot to detect outliers
- This technique sets the threshold *th* on its own

Box plot outlier detection procedure:

1. Assume the following dataset $\mathcal{D}$

$$\mathcal{D} = \begin{bmatrix} 0.08 & 0.07 & 0.10 & 0.05 & -0.03 & 0.04 & 0.45 & -0.02 & -0.11 \end{bmatrix}$$

2. Sort the dataset $\mathcal{D}$

$$\mathcal{D}_{sorted} = \begin{bmatrix} -0.11 & -0.03 & -0.02 & 0.04 & 0.05 & 0.07 & 0.08 & 0.10 & 0.45 \end{bmatrix}$$

3. Compute the 1st quartile Q_1 i.e. 25% of the data is below this datapoint. MATLAB provides the `quantile` function.

$$Q_1 = \texttt{quantile}(\mathcal{D}_{sorted}\texttt{,0.25) = -0.0225}$$

Box Plot

4. Compute the 2nd quartile Q_2 i.e. 50% of the data is below this datapoint (a.k.a. the median)

$$Q_2 = \texttt{quantile}(\mathcal{D}_{sorted}, \texttt{0.5}) \texttt{ = 0.05}$$

5. Compute the 3rd quartile Q_3 i.e. 75% of the data is below this datapoint

$$Q_3 = \texttt{quantile}(\mathcal{D}_{sorted}, \texttt{0.75}) \texttt{ = 0.085}$$

6. Compute the lower and upper thresholds th_{lo} and th_{up}

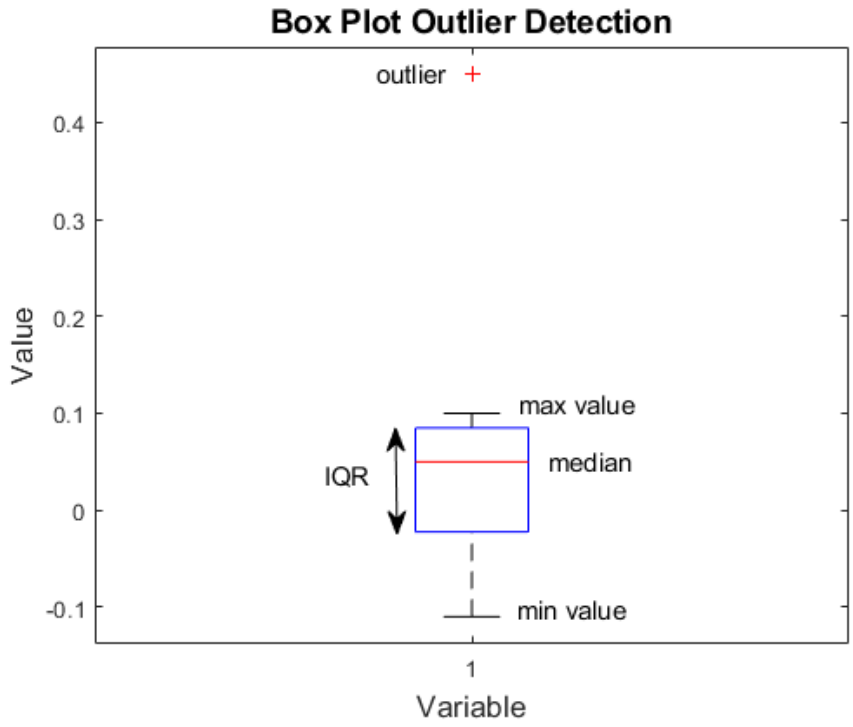
$$th_{lo} = Q_1 - 1.5 * (Q_3 - Q_1), \quad th_{up} = Q_3 + 1.5 * (Q_3 - Q_1)$$

$$th_{lo} = -0.1837, \quad th_{up} = 0.2462$$

The value $(Q_3 - Q_1)$ is known as the interquartile range IQR

Box Plot

- Any datapoint o that is lower than th_{lo} or greater than th_{up} is considered an outlier. Thus the datapoint $o = 0.45 > 0.2462$ is an outlier.
- Below we visualise the box plot of dataset $\mathcal{D}$ with instruction `boxplot`



Multivariate Normal Distribution

MVN

Multi-dimensional IDS idea

- Most datasets have multiple dimensions
- Often anomalies can be detected using a single feature

- However looking at a higher-dimensional space can reveal additional anomalies or increase our confidence about existing ones

  e.g. the `http` KDDCUP99 dataset has 3 features: `duration`, `src_bytes`, `dst_bytes` of an http connection

  Analyzing them in a joint manner can improve the accuracy of the IDS

MVN

- We will use the **multivariate normal distribution** to model the normal system behavior
- The multivariate normal distribution is a generalization of the univariate normal distribution with $d > 1$ dimensions

- Assume dataset $\mathcal{D} = \{\mathbf{x}_0, \mathbf{x}_1, \ldots, \mathbf{x}_{n-1}\}$ that contains n datapoints
- Every datapoint contains d features i.e. $\mathbf{x}_i = [x^0 \; x^1 \; \ldots \; x^{d-1}]^\intercal$

- We used the univariate normal probability density function (pdf)

$$f(x) = \frac{1}{\sigma\sqrt{2\pi}} exp\left(-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2\right)$$

- Now we will use the multivariate normal probability density function (pdf)

$$f(\mathbf{x}) = f([x^0 \; x^1 \; \ldots \; x^{d-1}]^\intercal) = \frac{1}{\sqrt{(2\pi)^d det(\mathbf{\Sigma})}} exp\left(-\frac{1}{2}(\mathbf{x}-\boldsymbol{\mu})^\intercal \mathbf{\Sigma}^{-1}(\mathbf{x}-\boldsymbol{\mu})\right)$$

MVN

$$f(\mathbf{x}) = f([x^0\ x^1\ \ldots\ x^{d-1}]^\intercal) = \frac{1}{\sqrt{(2\pi)^d det(\mathbf{\Sigma})}} exp\left(-\frac{1}{2}(\mathbf{x}-\boldsymbol{\mu})^\intercal \mathbf{\Sigma}^{-1}(\mathbf{x}-\boldsymbol{\mu})\right)$$

- We denote the d-dimensional datapoint using a random vector $\mathbf{X}$
- The expression $\mathbf{X} \sim \mathcal{N}(\boldsymbol{\mu}, \mathbf{\Sigma})$ states that the datapoint follows a multivariate normal distribution

- The distribution has 2 parameters that we need to specify
  - mean vector $\boldsymbol{\mu}$
  - covariance matrix $\mathbf{\Sigma}$

MVN

Training the multivariate normal distribution

- To train the IDS we must estimate the mean vector $\boldsymbol{\mu}$ and the covariance matrix $\boldsymbol{\Sigma}$ from our trainset $\mathcal{D}$

$$\mathcal{D} = \begin{bmatrix} \mathbf{x}_0^\mathsf{T} \\ \mathbf{x}_1^\mathsf{T} \\ \vdots \\ \mathbf{x}_{n-1}^\mathsf{T} \end{bmatrix} = \begin{bmatrix} x_0^0 & x_0^1 & \dots & x_0^{d-1} \\ x_1^0 & x_1^1 & \dots & x_1^{d-1} \\ \vdots & \vdots & \ddots & \vdots \\ x_{n-1}^0 & x_{n-1}^1 & \dots & x_{n-1}^{d-1} \end{bmatrix}$$

- The mean vector is estimated using the mean of every column of $\mathcal{D}$

$$\boldsymbol{\mu} = \begin{bmatrix} \frac{1}{n}\sum_{i=0}^{n-1} x_i^0 & \frac{1}{n}\sum_{i=0}^{n-1} x_i^1 & \dots & \frac{1}{n}\sum_{i=0}^{n-1} x_i^{d-1} \end{bmatrix}^\mathsf{T}$$

- Apply the `mean` function on the trainset

MVN

- The covariance matrix $\mathbf{\Sigma}$ is a $d \times d$ matrix
- Every matrix element s_{ij} of $\mathbf{\Sigma}$ is computed as follows

$$s_{ij} = \frac{1}{n-1} \sum_{t=0}^{n-1} (x_t^i - \overline{x}^i)(x_t^j - \overline{x}^j)$$

- Apply the `cov` function on the trainset

MVN

Testing the multivariate normal distribution

- As in the univariate case, we will use the pdf
- The outlier score of datapoint $\mathbf{o}$ is:

$$score(\mathbf{o}) = f(\mathbf{o}) = \frac{1}{\sqrt{(2\pi)^d det(\mathbf{\Sigma})}} exp\left(-\frac{1}{2}(\mathbf{o}-\boldsymbol{\mu})^\intercal \mathbf{\Sigma}^{-1}(\mathbf{o}-\boldsymbol{\mu})\right)$$

- Higher score implies higher likelihood that the datapoint $\mathbf{o}$ has normal behavior
- MATLAB can use the `mvnpdf(o, mean_vector, covariance_matrix)` function
- We can use $score(\mathbf{o})$ in conjunction with a threshold (threshold IDS) or we could also train a multivariate normal distribution with the anomalies (supervised IDS)

MVN

Input: testset $\mathcal{T}_l = \{\mathbf{o}_0, \mathbf{o}_1, \ldots \mathbf{o}_{q-1}\}$
Input: distribution $\mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Sigma})$, threshold th
Output: TP, FN rates

$TPcount = 0$; $FNcount = 0$
// iterate over the elements of the testset
for i=1 *until* q **do**
  // compute likelihood score
  $score = mvnpdf(\mathbf{o}_i, \boldsymbol{\mu}, \boldsymbol{\Sigma})$
  // count match/mismatch
  if $score < th$ **then**
    $TPcount = TPcount + 1$
  else
    $FNcount = FNcount + 1$
  end
end
// compute the rates
$TP = TPcount/q$; $FN = FNcount/q$

- The process is repeated for the normal behavior testset $\mathcal{T}_{\neg l}$ and results in TN, FP rates

MVN

Curse of dimensionality

- Increasing the number of features in every datapoint (dimension d) can cause several computational problems

- Computing the scores using the density function `mvnpdf` has significant computational cost and results in very small values that could underflow

  e.g. `mvnpdf(zeros(1, 20), zeros(1,20), eye(20)) = 1.0428e-08`

- Estimating well the mean vector $\boldsymbol{\mu}$ and covariance matrix $\boldsymbol{\Sigma}$ parameters requires a very large dataset for high dimension d

  e.g. if your dataset has only a small number of datapoints, would you train a univariate or a multivariate model? Undertraining may imply large estimation errors on the model parameters.

MVN

Using the exponent as score. Taking the log function of the p.d.f. we reach:

$$log(f(\mathbf{o})) = log\left(\frac{1}{\sqrt{(2\pi)^d det(\mathbf{\Sigma})}} exp\left(-\frac{1}{2}(\mathbf{o}-\boldsymbol{\mu})^\intercal \mathbf{\Sigma}^{-1}(\mathbf{o}-\boldsymbol{\mu})\right)\right) =$$

$$log\left(\frac{1}{\sqrt{(2\pi)^d det(\mathbf{\Sigma})}}\right) + \log\left(exp(-\frac{1}{2}(\mathbf{o}-\boldsymbol{\mu})^\intercal \mathbf{\Sigma}^{-1}(\mathbf{o}-\boldsymbol{\mu}))\right) =$$

$$\text{constant} - \frac{1}{2}(\mathbf{o}-\boldsymbol{\mu})^\intercal \mathbf{\Sigma}^{-1}(\mathbf{o}-\boldsymbol{\mu})$$

- Thus instead of $score(\mathbf{o}) = f(\mathbf{o})$ we can use the following alternative score

$$score(\mathbf{o}) = (\mathbf{o}-\boldsymbol{\mu})^\intercal \mathbf{\Sigma}^{-1}(\mathbf{o}-\boldsymbol{\mu})$$

MVN

Identity covariance matrix. If we assume the data to be homoscedastic we can avoid the covariance matrix estimation and inversion.

- This assumption implies an identity covariance matrix:

$$\mathbf{\Sigma} = \begin{bmatrix} 1 & 0 & \dots & 0 \\ 0 & 1 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & 1 \end{bmatrix}$$

- Then the score can be reduced to:

$$score(\mathbf{o}) = (\mathbf{o} - \boldsymbol{\mu})^\intercal \mathbf{\Sigma}^{-1} (\mathbf{o} - \boldsymbol{\mu}) = (\mathbf{o} - \boldsymbol{\mu})^\intercal (\mathbf{o} - \boldsymbol{\mu})$$

- Thus instead of a score that uses matrix multiplication, we can simply compute an inner product, which is much faster
- Naturally, this assumption must be checked

MVN

Dimensionality reduction. Not all features of a dataset are crucial to anomaly detection. It is possible to either **ignore** certain features or **compress** them in order to reduce the dimension d.

Subsequently the multivariate normal distribution becomes easier to train and more efficient computationally.

- mean/variance statistic, correlation-based techniques
- principal component analysis, linear discriminant analysis
- classifiers that automatically perform dimensionality reduction such as neural networks

Distance Based Outliers

DBO

DBO idea

- Assuming that the normal behavior follows a certain probability distribution is often restrictive
- In addition, distribution-based techniques can often be computationally hard to train, especially with high-dimensional data

- We will simplify the anomaly detection problem and define anomaly scores for the datapoints on the basis of the **nearest neighbour problem**

DBO

- **Distance-based outlier.** A datapoint $\mathbf{o} \in \mathcal{D}$ is a $DB(p, d)$ outlier if at least fraction p of the datapoints in $\mathcal{D}$ lie in distance greater than d from $\mathbf{o}$

  1. Construct the following set $\mathcal{S}$

     $$\mathcal{S} = \{\mathbf{x} \in \mathcal{D} \text{ s.t. } dist(\mathbf{o}, \mathbf{x}) \leq d\}$$

     where $dist(\mathbf{o}, \mathbf{x})$ denotes the Euclidean distance between datapoints $\mathbf{o}$ and $\mathbf{x}$
  2. Compute the set cardinality $|\mathcal{S}|$
  3. If $|\mathcal{S}| \leq (1 - p)|\mathcal{D}|$ then the datapoint $\mathbf{o}$ is an outlier
  4. If $|\mathcal{S}| > (1 - p)|\mathcal{D}|$ then the datapoint $\mathbf{o}$ is normal behavior

DBO

Example 1

- Assume the univariate dataset $\mathcal{D}$

$$\mathcal{D} = \begin{bmatrix} 0.11 & 0.13 & 0.09 & 0.63 & 0.07 & 0.12 \end{bmatrix}$$

- Is the datapoint $\mathbf{o} = 0.63$ a $DB(0.6, 0.2)$-outlier?

  1. Construct the set $\mathcal{S}$

$$\mathcal{S} = \{\mathbf{x} \in \mathcal{D} \text{ s.t. } dist(0.63, \mathbf{x}) \leq 0.2\} = \{0.63\}$$

  2. $|\mathcal{S}| = 1$
  3. We compute $(1 - p)|\mathcal{D}| = (1 - 0.6) * 6 = 2.4$

     It holds that $|\mathcal{S}| = 1 \leq 2.4$

Thus the datapoint $\mathbf{o} = 0.63$ is a $DB(0.6, 0.2)$-outlier

i.e at least 60% of the datapoints in dataset $\mathcal{D}$ have distance from 0.63 that is greater than 0.2

DBO

Example 2

- Assume the univariate dataset $\mathcal{D}$

$$\mathcal{D} = \begin{bmatrix} 0.11 & 0.13 & 0.09 & 0.63 & 0.07 & 0.12 \end{bmatrix}$$

- Is the datapoint $\mathbf{o} = 0.11$ a $DB(0.7, 0.02)$-outlier?

  1. Construct the set $\mathcal{S}$

$$\mathcal{S} = \{\mathbf{x} \in \mathcal{D} \text{ s.t. } dist(0.11, \mathbf{x}) \leq 0.02\} = \{0.13, 0.09, 0.12\}$$

  2. $|\mathcal{S}| = 3$
  3. We compute $(1 - p)|\mathcal{D}| = (1 - 0.7) * 6 = 1.8$

     It holds that $|\mathcal{S}| = 3 > 1.8$

Thus the datapoint $\mathbf{o} = 0.11$ is not a $DB(0.7, 0.02)$-outlier

DBO

DBO detection algorithm

- The detection process takes as input n datapoints (from dataset $\mathcal{D}$) and must decide if a certain datapoint $\mathbf{o}$ is a $DB(p, d)$-outlier or not

```
1  DBO({x_0, x_1, ..., x_{n-1}}, o, p, d)
2  count = 0
3  max_points = (1 − p) ∗ n
4  for i=0 until n-1 do
5  |   if dist(x_i, o) ≤ d then
6  |   |   count = count +1
7  |   end
8  |   if count > max_points then
9  |   |   outlier = False
10 |   |   return outlier
11 |   end
12 end
13 outlier = True
14 return outlier
```

- Solving the $DB(p, d)$-outlier problem is equivalent to answering the **nearest-neighbour** problem
- We search in radius d around $\mathbf{o}$ and if we find more than *max_points*, then $\mathbf{o}$ is not an outlier

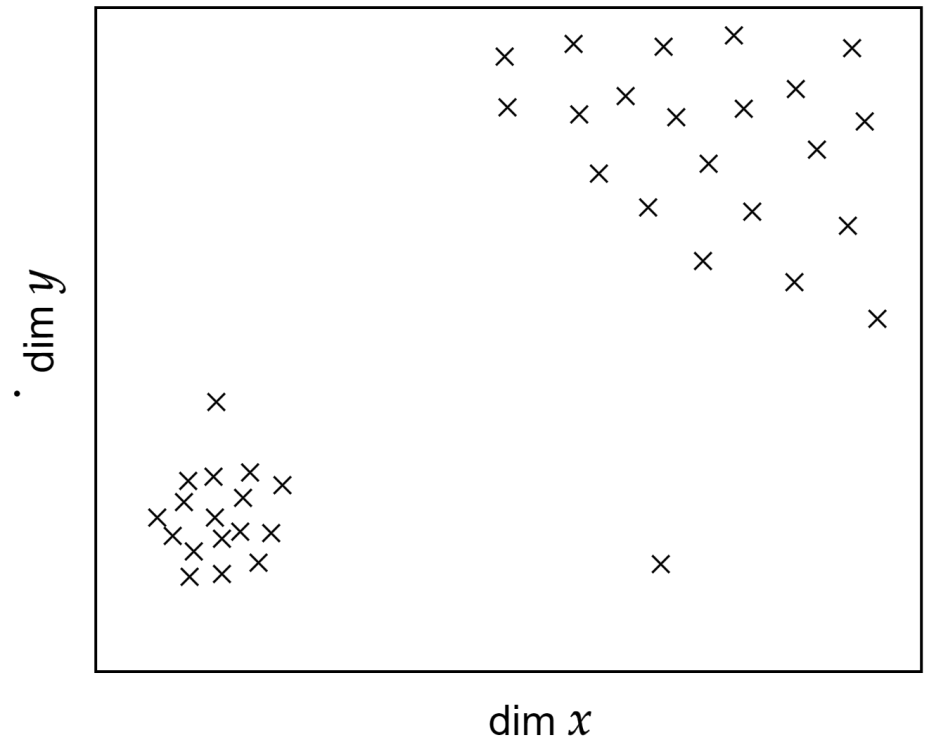
DBO

Final notes on DBO:

- DBO uses a generic distance-based definition of outliers, making it flexible and model-free
- Since it does not use probabilistic models it avoids slow computations like the pdf of a univariate/multivariate distribution
- The distance metric used reduces multi-dimensional datapoints to a single scalar, thus the technique can cope with a large number of dimensions

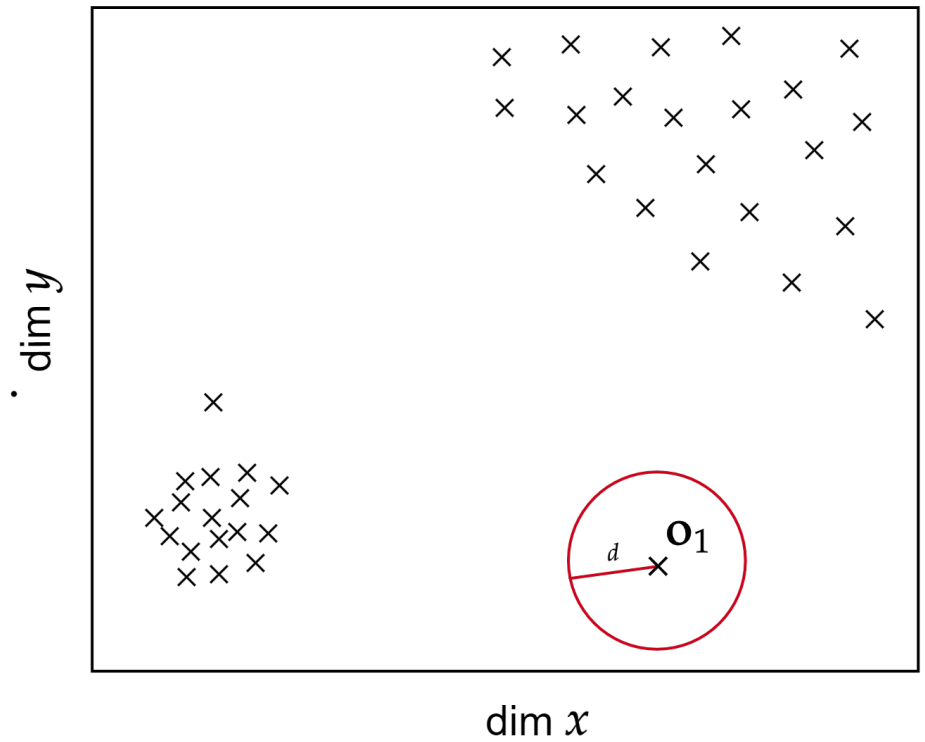
Local Outlier Factor

LOF



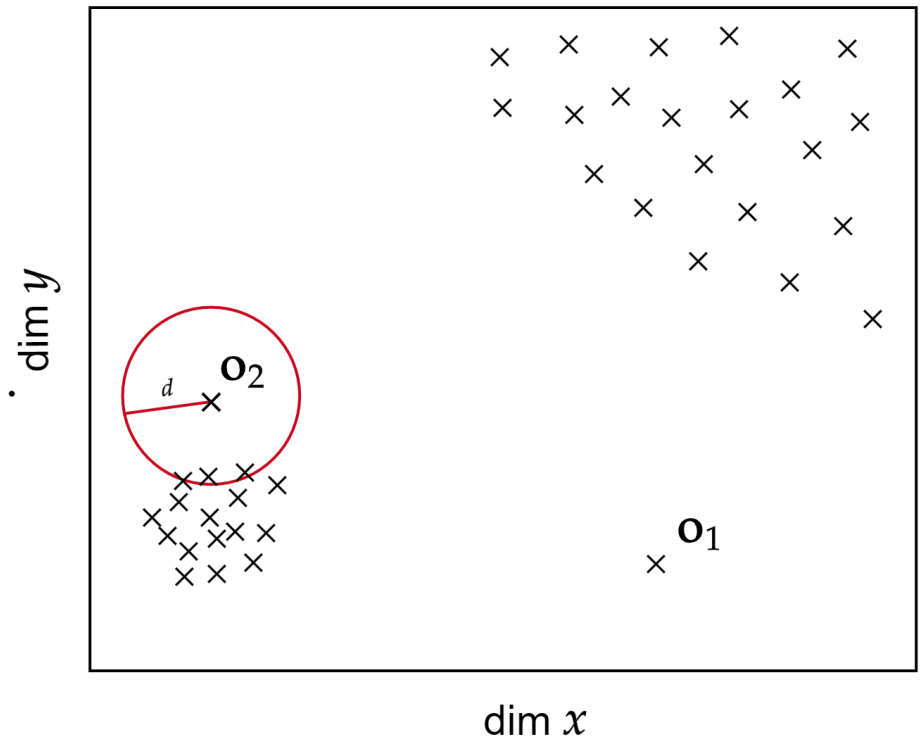
- To introduce LOF we will consider a special dataset as example
- The 2-dimensional dataset $\mathcal{D}$ has two main clusters

LOF



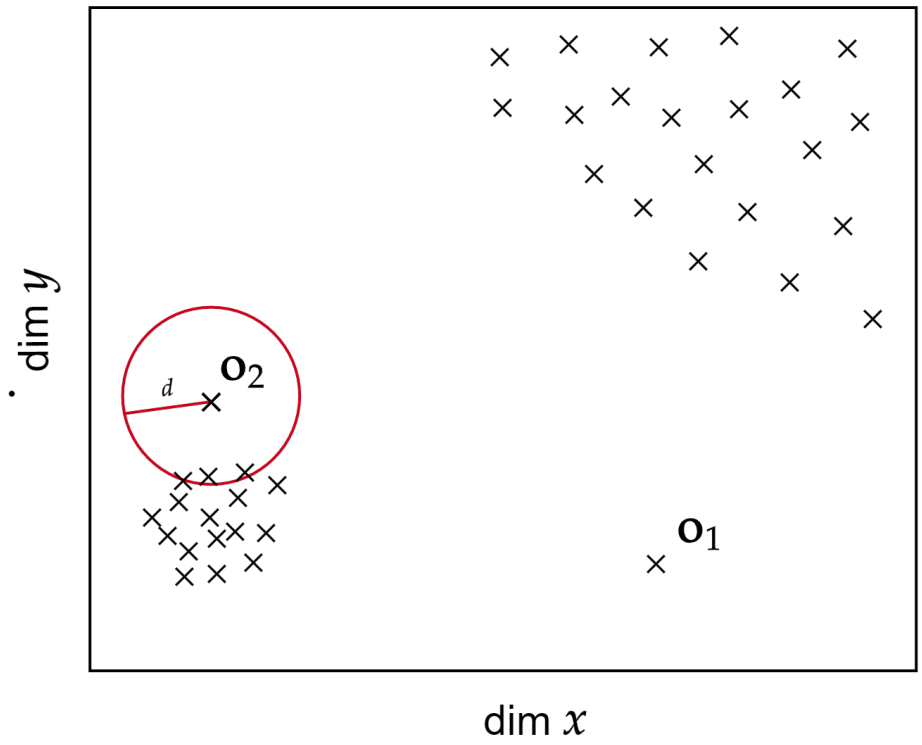
- If we search in radius d around $\mathbf{o}_1$ then we will find no other datapoints
- Thus DBO will easily mark $\mathbf{o}_1$ as an outlier

LOF



- What about datapoint $\mathbf{o}_2$ though?
- If we search in radius d around $\mathbf{o}_2$ we will find datapoints from cluster 2
- Thus, unless we pick a very small radius, DBO will not mark $\mathbf{o}_2$ as an outlier

LOF

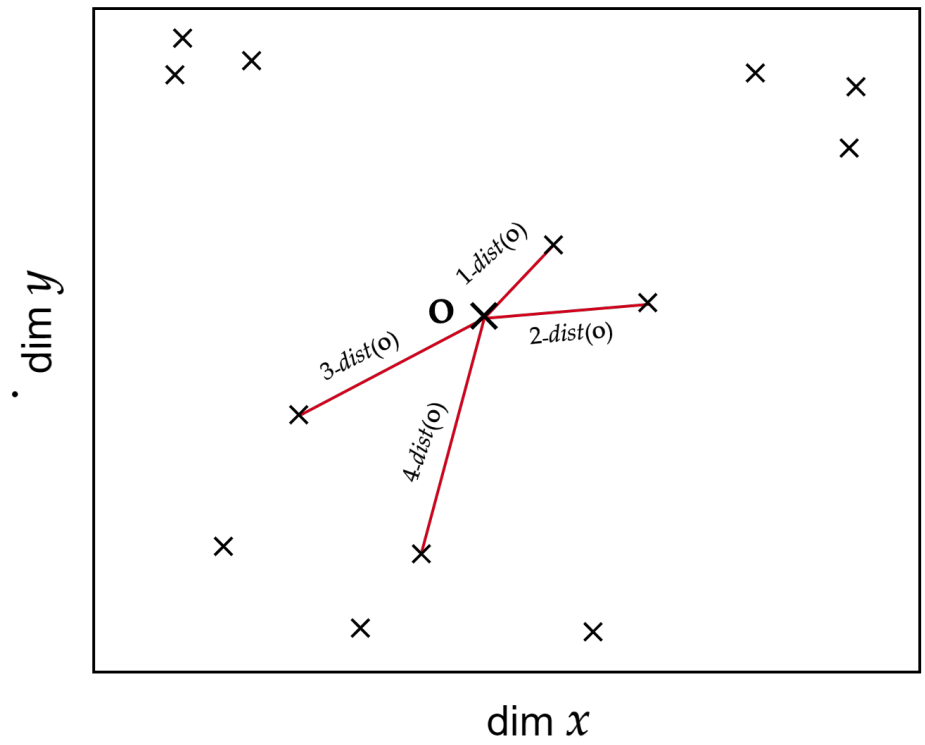


- For DBO o_1 is a **global outlier**
- But o_2 is not a global outlier
- Still, it is an outlier **relative to the local neighbourhood**

LOF

- When clusters of different densities exist, outliers can be merged to a cluster
- This results to undetected outliers and is known as **masking**
- The **Local Outlier Factor (LOF)** is a technique that can deal with such cases

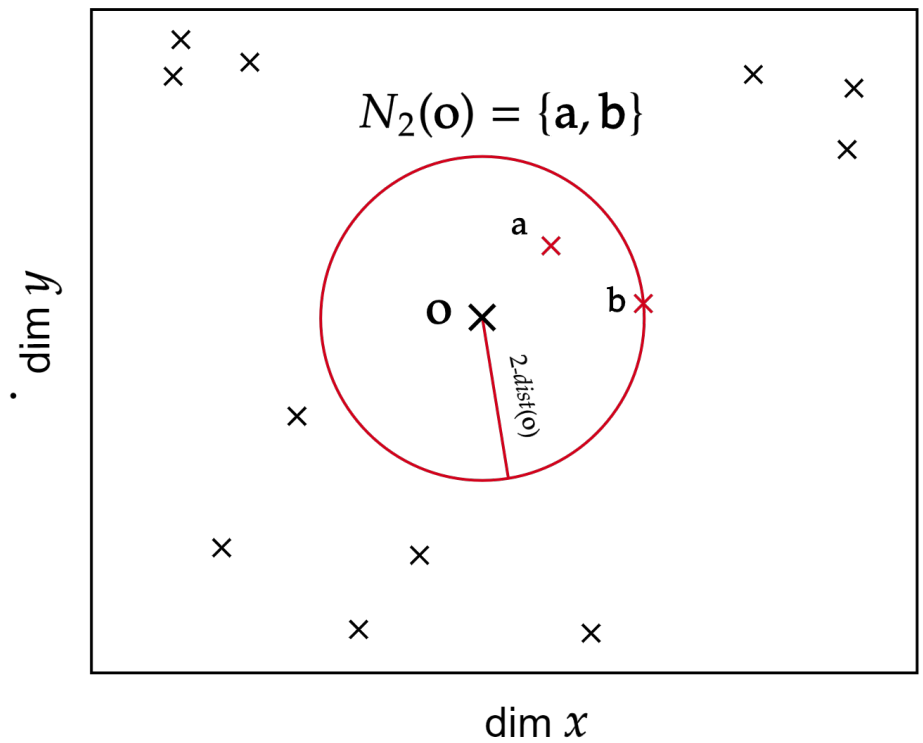
k-**distance.** For any integer $k > 0$, we define the the *k*-distance of datapoint **o** as the distance of **o** to its *k*-th nearest neighbour. We refer to this distance as *k*-*dist*(**o**)



LOF

***k*-neighbourhood.** We define the k-neighbourhood of datapoint $\mathbf{o}$ as the set of all datapoints $\mathbf{x}$ in dataset $\mathcal{D}$ (except $\mathbf{o}$) whose distance from $\mathbf{o}$ is not greater than the k-distance of $\mathbf{o}$. We refer to this set as $N_k(\mathbf{o})$.

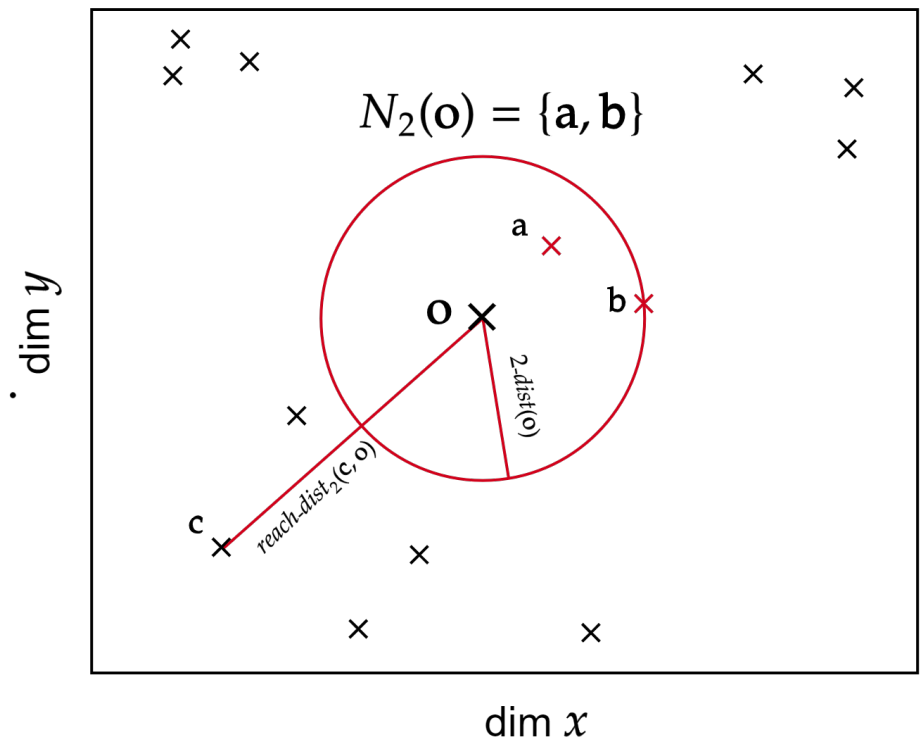
$$N_k(\mathbf{o}) = \{\mathbf{x} \in \mathcal{D} / \{\mathbf{o}\} \text{ s.t. } dist(\mathbf{x}, \mathbf{o}) \leq k\text{-}dist(\mathbf{o})\}$$



LOF

Reachability distance. We define the reachability distance of datapoint **x** w.r.t. datapoint **o** as:

$$reach\text{-}dist_k(\mathbf{x}, \mathbf{o}) = max\{k\text{-}dist(\mathbf{o}), dist(\mathbf{x}, \mathbf{o})\}$$



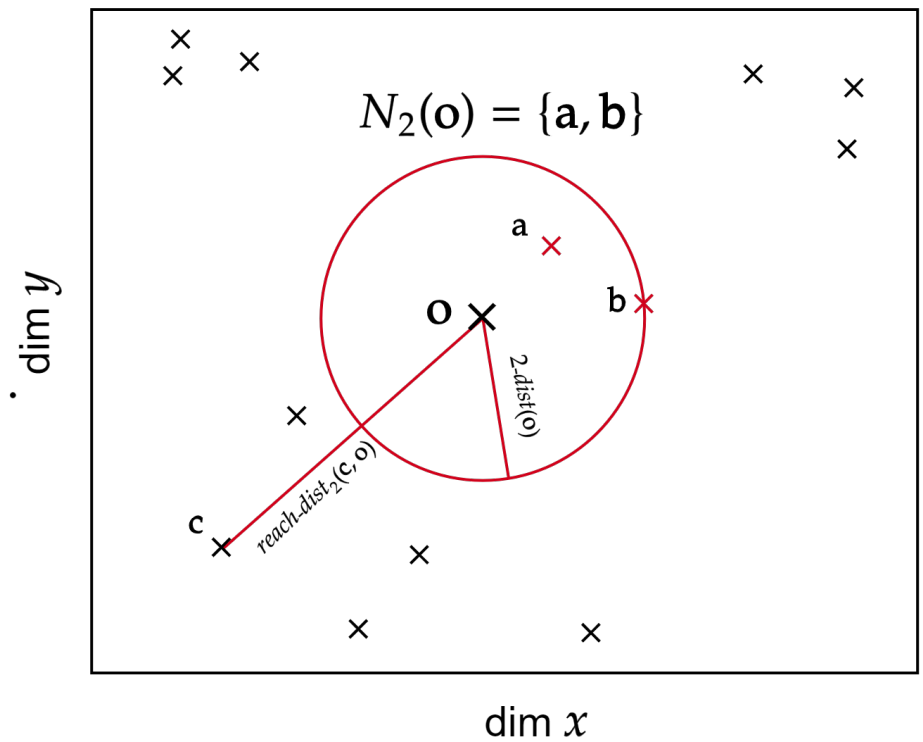
- If datapoint **x** is far away from datapoint **o** then their reachability distance is their actual distance between them

  e.g. $reach\text{-}dist_2(\mathbf{c}) = dist(\mathbf{c}, \mathbf{o})$

LOF

Reachability distance. We define the reachability distance of datapoint **x** w.r.t. datapoint **o** as:

$$reach\text{-}dist_k(\mathbf{x}, \mathbf{o}) = max\{k\text{-}dist(\mathbf{o}), dist(\mathbf{x}, \mathbf{o})\}$$



- However if the datapoints are sufficiently close then the reachability distance is the k-distance of **o**.

  e.g. $reach\text{-}dist_2(\mathbf{a}) = 2\text{-}dist(\mathbf{o})$

LOF

Note that k is a hyper-parameter of LOF i.e. we need to fine-tune the algorithm by trying various values of k

Local reachability density. We define the lrd_k of datapoint $\mathbf{o}$ as the inverse of the average reachability distances for a certain k-neighbourhood.

$$lrd_k(\mathbf{o}) = \left(\frac{\sum_{\mathbf{x} \in N_k(\mathbf{o})} reach\text{-}dist(\mathbf{x}, \mathbf{o})}{|N_k(\mathbf{o})|} \right)^{-1}$$

- $lrd_k(\mathbf{o})$ quantifies the density of datapoints in the neighbourhood of $\mathbf{o}$

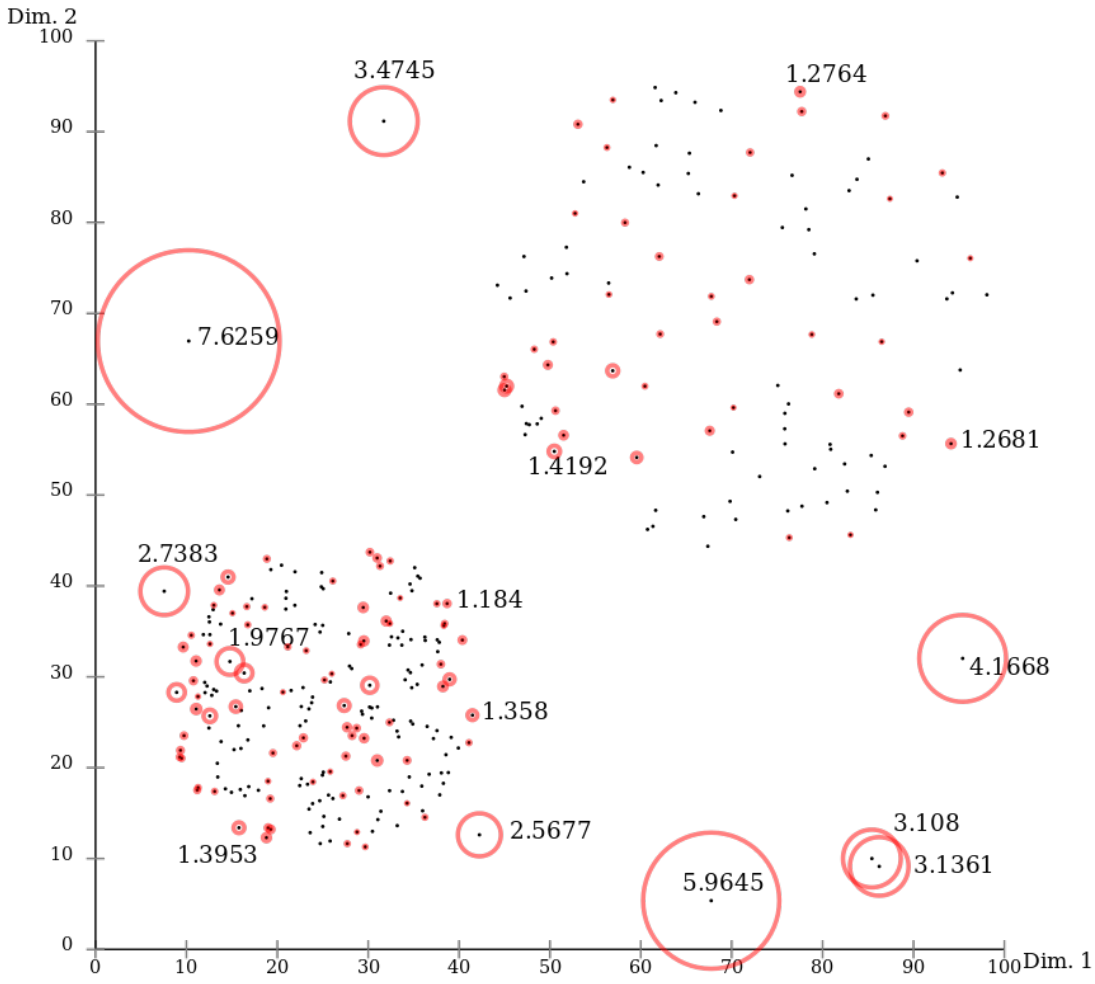
LOF

Local Outlier Factor (LOF). We define the LOF_k as the average ratio of local reachabilities of $\mathbf{o}$ and the local reachabilities of the k-neighbourhood of $\mathbf{o}$.

$$LOF_k(\mathbf{o}) = \frac{\sum_{x \in N_k(\mathbf{o})} \frac{lrd_k(\mathbf{x})}{lrd_k(\mathbf{o})}}{|N_k(\mathbf{x})|}$$

- The LOF captures the degree to which the datapoint $\mathbf{o}$ is an outlier

LOF



- $LOF \approx 1$ means similar density as neighbours
- $LOF < 1$ means higher density than neighbours
- $LOF > 1$ means lower density than neighbours i.e. potential outlier

Isolation Forest

iForest

- Most IDSs profile the normal behavior of a system and then identify outliers
- The isolation forest algorithm (iForest) works by isolating anomalies instead of profiling the normal behavior
- iForest takes advantage of the following two properties of anomalies:
  1. Anomalies are few compared to the number of normal instances
  2. The features of an anomaly are very different from the features of normal instances
- Since anomalies are "few and different" they are more susceptible to **isolation**, compared to normal instances

iForest

Constructing an isolation Tree (iTree)

Assume that we have the following training dataset with:

- 6 datapoints stored in vectors $\{\mathbf{x_0}, \mathbf{x_1}, \mathbf{x_2}, \mathbf{x_3}, \mathbf{x_4}, \mathbf{x_5}\}$
- 5 features $[x^0, x^1, x^2, x^3, x^4]$ for each datapoint $\mathbf{x_i}$

$$\mathcal{D} = \begin{bmatrix} \mathbf{x_0}^\mathsf{T} \\ \mathbf{x_1}^\mathsf{T} \\ \mathbf{x_2}^\mathsf{T} \\ \mathbf{x_3}^\mathsf{T} \\ \mathbf{x_4}^\mathsf{T} \\ \mathbf{x_5}^\mathsf{T} \end{bmatrix} = \begin{bmatrix} 4.74 & 0.71 & -0.26 & 2.79 & 5.11 \\ 4.71 & 0.75 & -0.30 & 2.50 & 5.58 \\ 4.72 & 0.82 & -0.28 & 2.61 & 5.26 \\ 4.66 & 0.72 & -0.31 & 2.62 & 5.30 \\ 4.80 & 0.71 & -0.27 & 2.71 & 5.33 \\ 4.81 & 0.77 & -0.29 & 2.72 & 5.40 \end{bmatrix}$$

iForest

1. Randomly select a feature q from $\{x^0, x^1, x^2, x^3, x^4\}$

   e.g. we select feature $q = x^2$

2. Randomly select a split point p between the maximum and the minimum values of the selected feature q

   e.g. $max(x^2) = -0.26$ and $min(x^2) = -0.31$

   we select randomly $p \in \{-0.31, -0.26\}$ and we pick $p = -0.28$

$$\mathcal{D} = \begin{bmatrix} 4.74 & 0.71 & \mathbf{-0.26} & 2.79 & 5.11 \\ 4.71 & 0.75 & -0.30 & 2.50 & 5.58 \\ 4.72 & 0.82 & -0.28 & 2.61 & 5.26 \\ 4.66 & 0.72 & \mathbf{-0.31} & 2.62 & 5.30 \\ 4.80 & 0.71 & -0.27 & 2.71 & 5.33 \\ 4.81 & 0.77 & -0.29 & 2.72 & 5.40 \end{bmatrix}$$

iForest

3. We partition the dataset $\mathcal{D}$ to the left and right sets $\mathcal{D}_l$ and $\mathcal{D}_r$ such that:

$$\mathcal{D}_l = \{\mathbf{x} \in \mathcal{D} \text{ s.t. } q < p\} \quad \text{and} \quad \mathcal{D}_r = \{\mathbf{x} \in \mathcal{D} \text{ s.t. } q \geq p\}$$

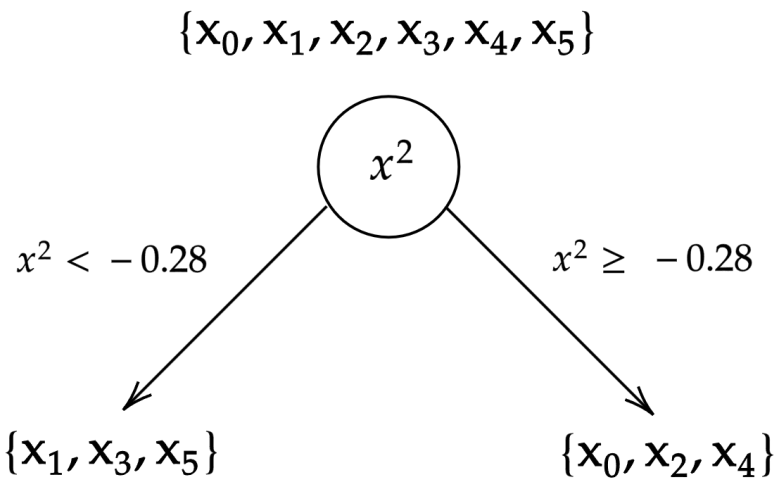
e.g. we split the dataset in the following way:

$$\mathcal{D}_l = \{\mathbf{x} \in \mathcal{D} \text{ s.t. } x^2 < -0.28\} \quad \text{and} \quad \mathcal{D}_r = \{\mathbf{x} \in \mathcal{D} \text{ s.t. } x^2 \geq -0.28\}$$

$$\mathcal{D} = \begin{bmatrix} 4.74 & 0.71 & -0.26 & 2.79 & 5.11 \\ 4.71 & 0.75 & -0.30 & 2.50 & 5.58 \\ 4.72 & 0.82 & -0.28 & 2.61 & 5.26 \\ 4.66 & 0.72 & -0.31 & 2.62 & 5.30 \\ 4.80 & 0.71 & -0.27 & 2.71 & 5.33 \\ 4.81 & 0.77 & -0.29 & 2.72 & 5.40 \end{bmatrix}$$

iForest

- We organize the partitioned sets using a binary tree structure
- We refer to this as the **isolation tree** (iTree)



selected feature q: x^2

split point p: -0.28

iForest

4. The construction of the iTree continues recursively

   - We focus on the left set $\mathcal{D}_l$

$$\mathcal{D}_l = \begin{bmatrix} 4.71 & 0.75 & -0.30 & 2.50 & 5.58 \\ 4.66 & 0.72 & -0.31 & 2.62 & 5.30 \\ 4.81 & 0.77 & -0.29 & 2.72 & 5.40 \end{bmatrix}$$

   - We select randomly feature $q = x^0$ and then select split point $p \in \{min(x^0), max(x^0)\} \iff p \in \{4.66, 4.81\}$. We pick $p = 4.80$

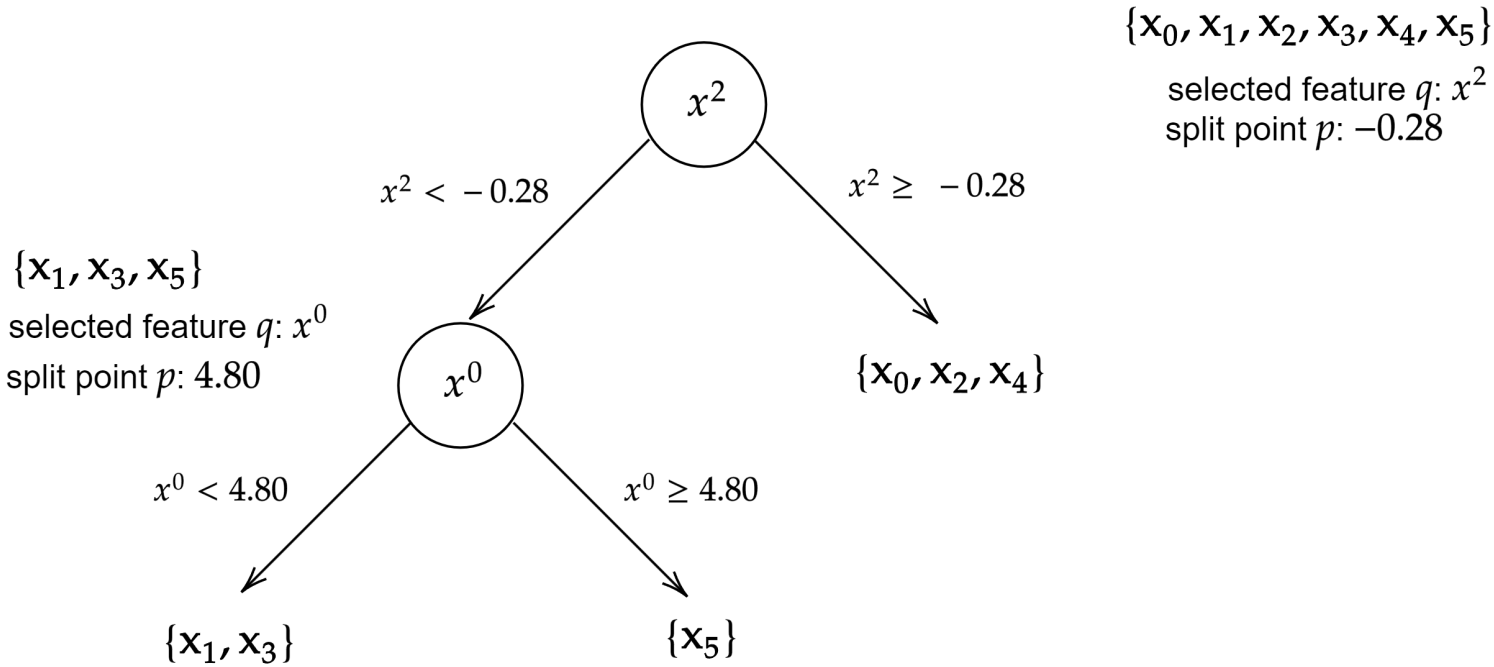
$$\mathcal{D}_l = \begin{bmatrix} 4.71 & 0.75 & -0.30 & 2.50 & 5.58 \\ \mathbf{4.66} & 0.72 & -0.31 & 2.62 & 5.30 \\ \mathbf{4.81} & 0.77 & -0.29 & 2.72 & 5.40 \end{bmatrix}$$

   - We split $\mathcal{D}_l$ to $\{\mathbf{x} \in \mathcal{D}_l \text{ s.t. } x^0 < 4.80\}$ and $\{\mathbf{x} \in \mathcal{D}_l \text{ s.t. } x^0 \geq 4.80\}$

$$\mathcal{D}_l = \begin{bmatrix} 4.71 & 0.75 & -0.30 & 2.50 & 5.58 \\ 4.66 & 0.72 & -0.31 & 2.62 & 5.30 \\ 4.81 & 0.77 & -0.29 & 2.72 & 5.40 \end{bmatrix}$$

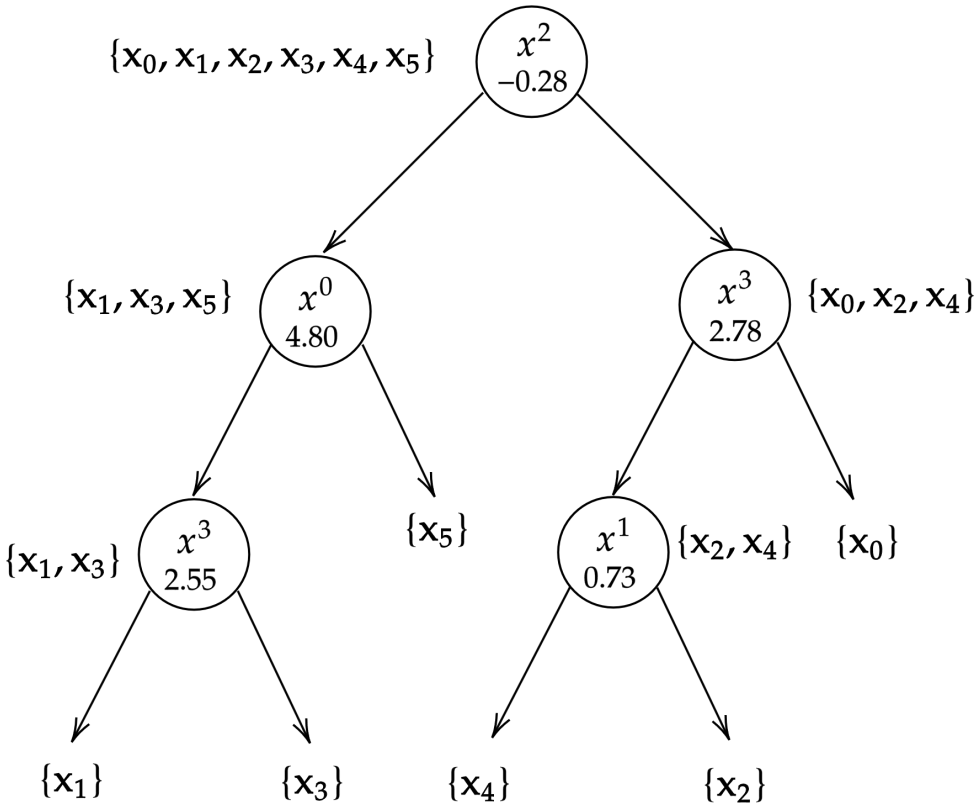
iForest

- The iTree grows as we keep splitting the dataset



iForest

- The full iTree is constructed once all nodes have set size 1 or when a predefined tree height limit is reached



iForest

- The iTree algorithm is initialized with dataset $\mathcal{D}$ and possibly and upper limit on the tree height l. The function works recursively, keeping track of the current tree height e.
- During recursion, the function should also keep track of all selected features q and all the split values p

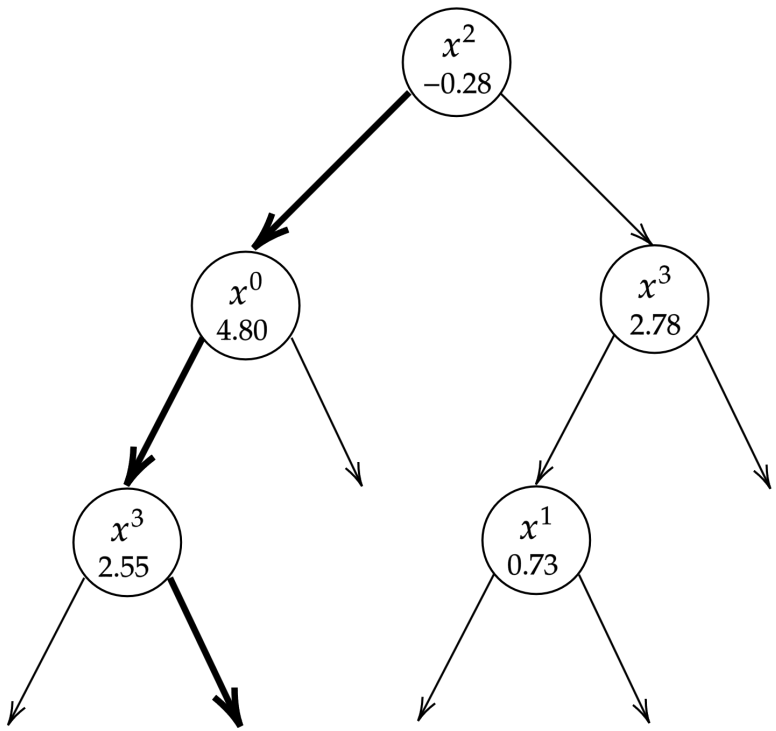
1 iTree($\mathcal{D}, e, l, q, p$)
2 **if** $e \geq l$ *or* $|\mathcal{D}| \leq 1$ **then**
3 | return $\emptyset$
4 **end**
5 select randomly feature q
6 select randomly split point $p \in [min(q), max(q)]$
7 $\mathcal{D}_l = \{\mathbf{x} \in \mathcal{D} \text{ s.t. } q < p\}$
8 $\mathcal{D}_r = \{\mathbf{x} \in \mathcal{D} \text{ s.t. } q \geq p\}$
9 return iTree($\mathcal{D}_l, e + 1, l, p, q$)
10 return iTree($\mathcal{D}_r, e + 1, l, p, q$)

iForest

Testing data on an iTree

- We have used the training dataset $\mathcal{D}$ to construct an iTree
- Let's test it with a datapoint $\mathbf{x}$ that is labeled as "normal behavior"

$$\mathbf{x} = \begin{bmatrix} 4.70 & 0.73 & -0.29 & 2.65 & 5.41 \end{bmatrix}$$

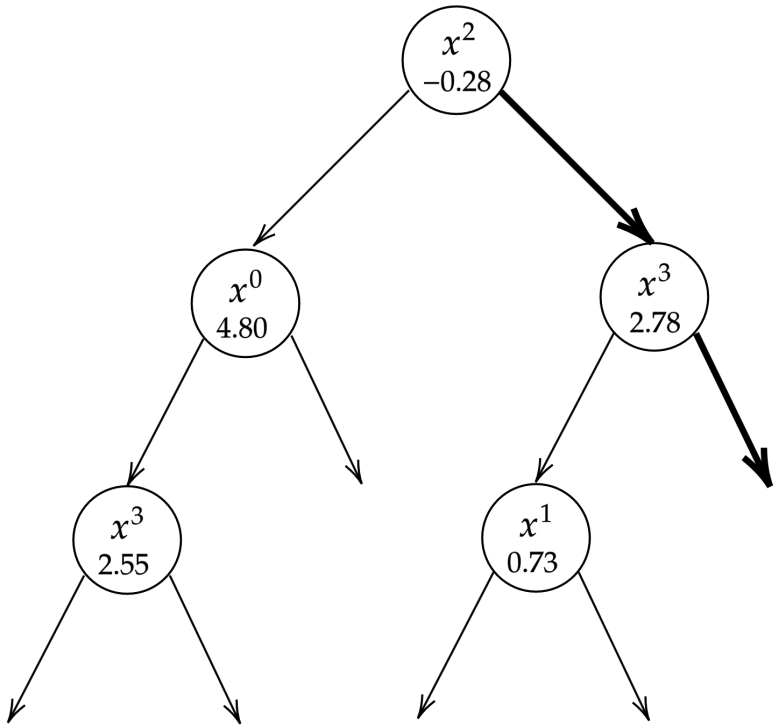


- Passing $\mathbf{x}$ through the iTree results in path length equal to 3

iForest

- Let's test it with a datapoint $\mathbf{x}'$ that is labeled as "anomaly"

$$\mathbf{x}' = \begin{bmatrix} 5.70 & 0.71 & -0.09 & 3.51 & 5.39 \end{bmatrix}$$



- Passing $\mathbf{x}'$ through the iTree results in path length equal to 2
- **iForest idea:** On average, the path length of anomalies is shorter compared to the path length of normal datapoints

iForest

Training phase

- Constructing an iTree is a probabilistic process, since we choose randomly the feature q and the split point p
- The iForest generates t iTrees (ensemble) to perform anomaly detection using the training dataset $\mathcal{D}$
- Since the goal is not to model the normal behavior, every iTree can be constructed using a sub-sample $\mathcal{D}'$ of the training dataset $\mathcal{D}$ with size $\psi < |\mathcal{D}|$

```
1 iForest(D, t, ψ)
2 forest = ∅
3 for i=1 to t do
4 |   D' ←R sample(D, ψ)
5 |   forest = forest ∪ iTree(D')
6 end
7 return forest
```

iForest

Testing phase

- Let datapoint **x** that we need to decide if it is "anomaly" or "normal"
- iForest gets the path lengths produced by **x** across all iTrees in the ensemble
- The average path length is computed and possibly normalized by factor c to produce the anomaly score

1 Score(**x**, *forest*)
2 **for** *i=1 to t* **do**
3 $\quad$ *tree* $=$ *forest*(i)
4 $\quad$ *pl*(i) $=$ PathLength(**x**, *tree*)
5 **end**
6 $\overline{pl} = \sum_{i=1}^{t} pl(i)$
7 $c = 2(log(\psi - 1) + 0.5772156649) - 2(\psi - 1)/\psi$
8 $score = 2^{-\overline{pl}/c}$
9 return score

iForest

Final notes on iForest

- Simple and efficient algorithm that matches the accuracy of more complex anomaly detection methods.
- iForest does not model the normal behavior, thus it can sub-sample the training dataset and work with partial models. This reduces the computational cost.
- iForest does not use a standard distance/density metric, reducing the computational cost.
- iForest has linear time complexity and low memory requirements, thus it can scale up to process large datasets and/or datasets with a large number of dimensions.
- Works effectively with high-dimensional datasets when several dimensions are not related to the anomalies.
- Deals well with masking effects

Lightweight Online Detector of Anomalies

LODA

- The amount and dimensionality of data to process with an IDS is increasing rapidly, thus we need a method that is very efficient computationally
- We strive to react quickly to an intrusion, thus we are interested in **online** processing and detection
- Intrusions patterns change over time, thus the IDS must deal with **concept drift**
- An IDS may contain multiple observation sensors and if the sensors fail the dataset will contain missing features. Thus the trained IDS must be **robust** for such scenarios.

LODA

LODA idea:

- To achieve efficiency we must avoid using a single complex model/classifier
- Instead we should use an **ensemble** of simple detectors that we aggregate into a strong detector

- The same idea formed also the basis for the iForest algorithm which is an ensemble of simple iTrees
- LODA simplifies the approach even more by using sparse **projections** and **histograms**

LODA

LODA projection:

- Very often we must process multi-dimensional datasets
- To achieve efficiency LODA applies a **projection** on every datapoint and reduces its dimension to 1

- Assume a d-dimensional datapoint $\mathbf{x}$ and a projection vector $\mathbf{w}$ of the same dimension

$$\mathbf{x} = \begin{bmatrix} x^0 \\ x^1 \\ \vdots \\ x^{d-1} \end{bmatrix}, \qquad \mathbf{w} = \begin{bmatrix} w^0 \\ w^1 \\ \vdots \\ w^{d-1} \end{bmatrix}, \qquad \mathbf{x}, \mathbf{w} \in \mathbb{R}^d$$

LODA

LODA projection:

- To reduce the dimension of datapoint $\mathbf{x}$ we compute the following inner product denoted as z:

$$z = \mathbf{x}^\mathsf{T} \cdot \mathbf{w} = \begin{bmatrix} x^0 & x^1 & \dots & x^{d-1} \end{bmatrix} \begin{bmatrix} w^0 \\ w^1 \\ \vdots \\ w^{d-1} \end{bmatrix} = \sum_{i=0}^{d-1} x^i w^i$$

- The projection vector $\mathbf{w}$ is a sparse projection initialized in the following manner
  1. $\mathbf{w} = \begin{bmatrix} 0 & 0 & \dots & 0 \end{bmatrix}, \quad \mathbf{w} \in \mathbb{R}^d$
  2. Select randomly $\left\lceil \sqrt{d} \right\rceil$ elements in vector $\mathbf{w}$
  3. Initialize the selected elements with values sampled from the standard normal distribution $\mathcal{N}(0, 1)$

LODA

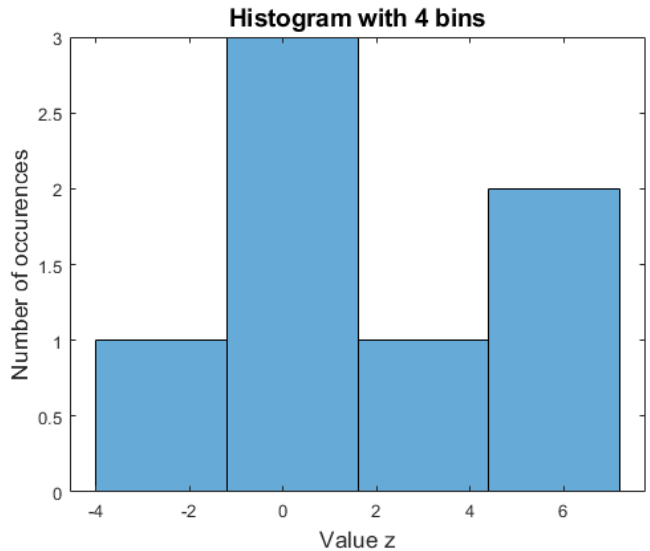
LODA histogram:

- We create a **histogram** h that models the projected values z
- The histogram h approximates the probability density function (pdf) of z

- Assume that we project 7 datapoints $\mathbf{x}_i$ to the respective scalars z_i

$$\{\mathbf{x}_0, \mathbf{x}_1, \ldots, \mathbf{x}_6\} \xrightarrow{\mathbf{w}} \{z_0, z_1, \ldots, z_6\} = \begin{bmatrix} 5.1 & -3.2 & 7.0 & 0.4 & 0.2 & -1.1 & 2.9 \end{bmatrix}$$

- Applying e.g. the `histogram(z,4)` function we bin the z values using 4 bins



- LODA will use an ensemble of multiple histograms

LODA

LODA training algorithm

- Training LODA uses n d-dimensional datapoints $\{\mathbf{x}_0, \mathbf{x}_1, \ldots, \mathbf{x}_{n-1}\}$ as the training set
- The training procedure requires 2 hyper-parameters
  - The number of histograms k used, i.e. the ensemble size
  - The number of bins b in every histogram

```
1 LodaTrain({x_0, x_1, ..., x_{n-1}}, k, b)
2 Initialize k projection vectors {w_1, w_2, ..., w_k}
3 Initialize k histograms {h_1, h_2, ..., h_k} with b bins
4 for j=0 until n-1 do
5 |   for i=1 until k do
6 |   |   z_i = x_j^T · w_i
7 |   |   update histogram h_i with z_i
8 |   end
9 end
```

- The outputs are the k projection vectors $\{\mathbf{w}_1, \mathbf{w}_2, \ldots, \mathbf{w}_k\}$ and the k trained histograms $\{h_1, h_2, \ldots, h_k\}$

LODA

LODA score function:

- We want to compute the **anomaly score** of a d-dimensional datapoint $\mathbf{x}$
  1. First we apply the projection $\mathbf{w}$

$$z = \mathbf{x}^\intercal \cdot \mathbf{w}$$

  2. A trained histogram h provides an approximate pdf for value z

$$p = h(z) \approx pdf(z)$$

- The process is repeated for all k projections $\mathbf{w}_i$ and trained histograms h_i.

$$z_i = \mathbf{x}^\intercal \cdot \mathbf{w}_i, \quad p_i = h_i(z_i), \quad i = 1, 2, \ldots, k$$

- The *log* function is applied to the estimated likelihoods p_i and the score is computed as the average.

$$score(\mathbf{x}) = -\frac{1}{k} \sum_{i=1}^{k} log(p_i)$$

LODA

LODA Testing Algorithm

- Testing LODA uses m d-dimensional datapoints $\{\mathbf{x}_0, \mathbf{x}_1, \ldots, \mathbf{x}_{m-1}\}$ as the test set
- LodaTest also receives the k projection vectors $\mathbf{w}_i$ and trained histograms h_i as inputs

```
1 LodaTest({x_0, x_1, ..., x_{m-1}}, {w_1, ..., w_k}, {h_1, h_2, ..., h_k})
2 for j=0 until m-1 do
3 |   for i=1 until k do
4 |   |   z_i = x_j^T · w_i
5 |   |   p_i = h_i(z_i)
6 |   end
7 |   score(x_j) = -(1/k) Σ_{i=1}^{k} log(p_i)
8 end
```

LODA

Final notes on LODA:

- LODA uses a computationally efficient one-dimensional histograms to detect intrusions. Histograms typically require only 'counting' operations
- The histogram can be updated on-the-fly enabling online detection and resistance to drifting
- In the case of a missing feature, LODA can apply only the projections $\mathbf{w}_i$ that ignore the particular feature. Thus we can use a part of the ensemble that guarantees robustness and avoids the failing sensors.