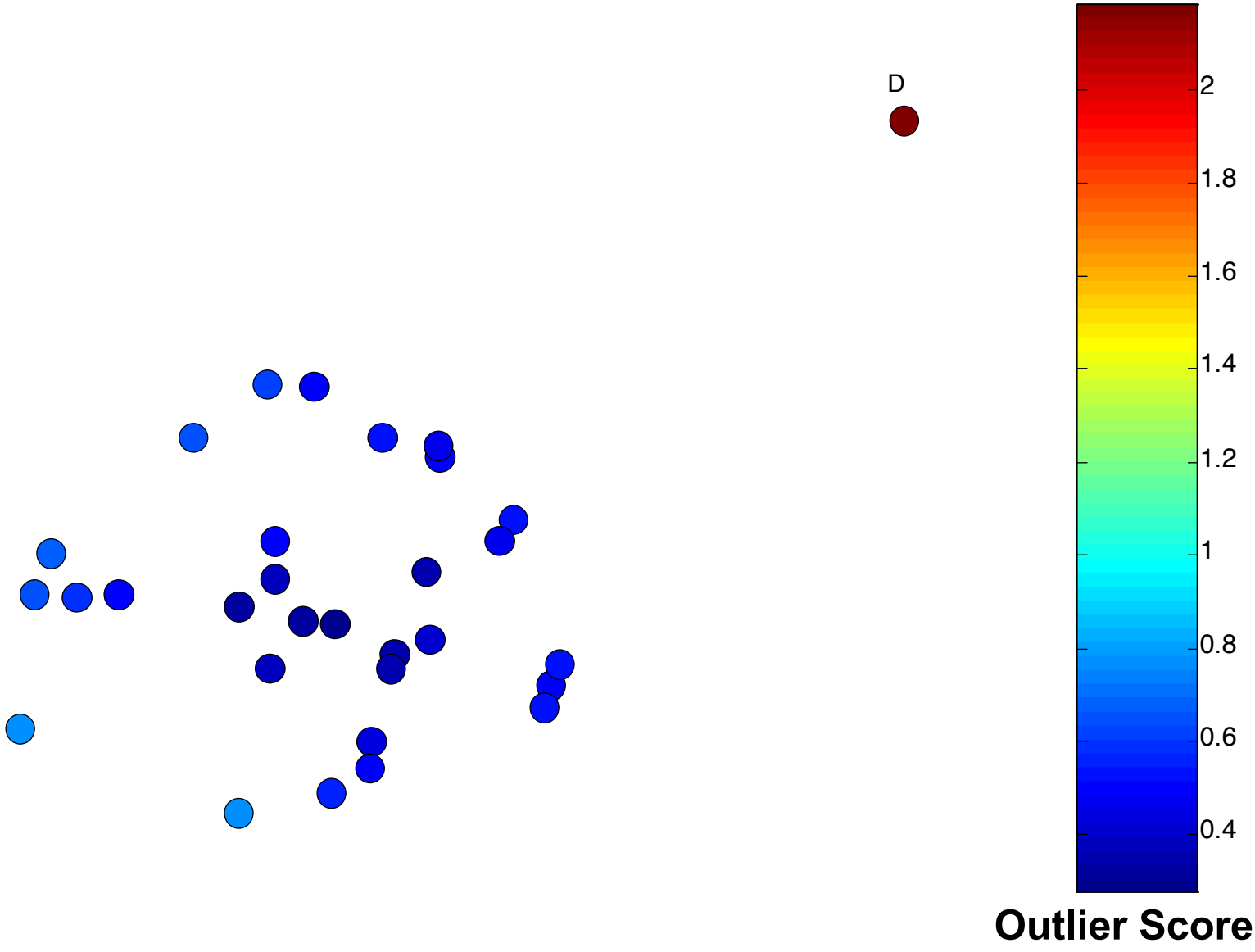
Techniques for unsupervised anomaly detection

- Proximity-based
- Density-based
- Clustering-based
- Isolation forest
- Auto Encoder
- Deep One-Class Classification
- Deep isolation forest

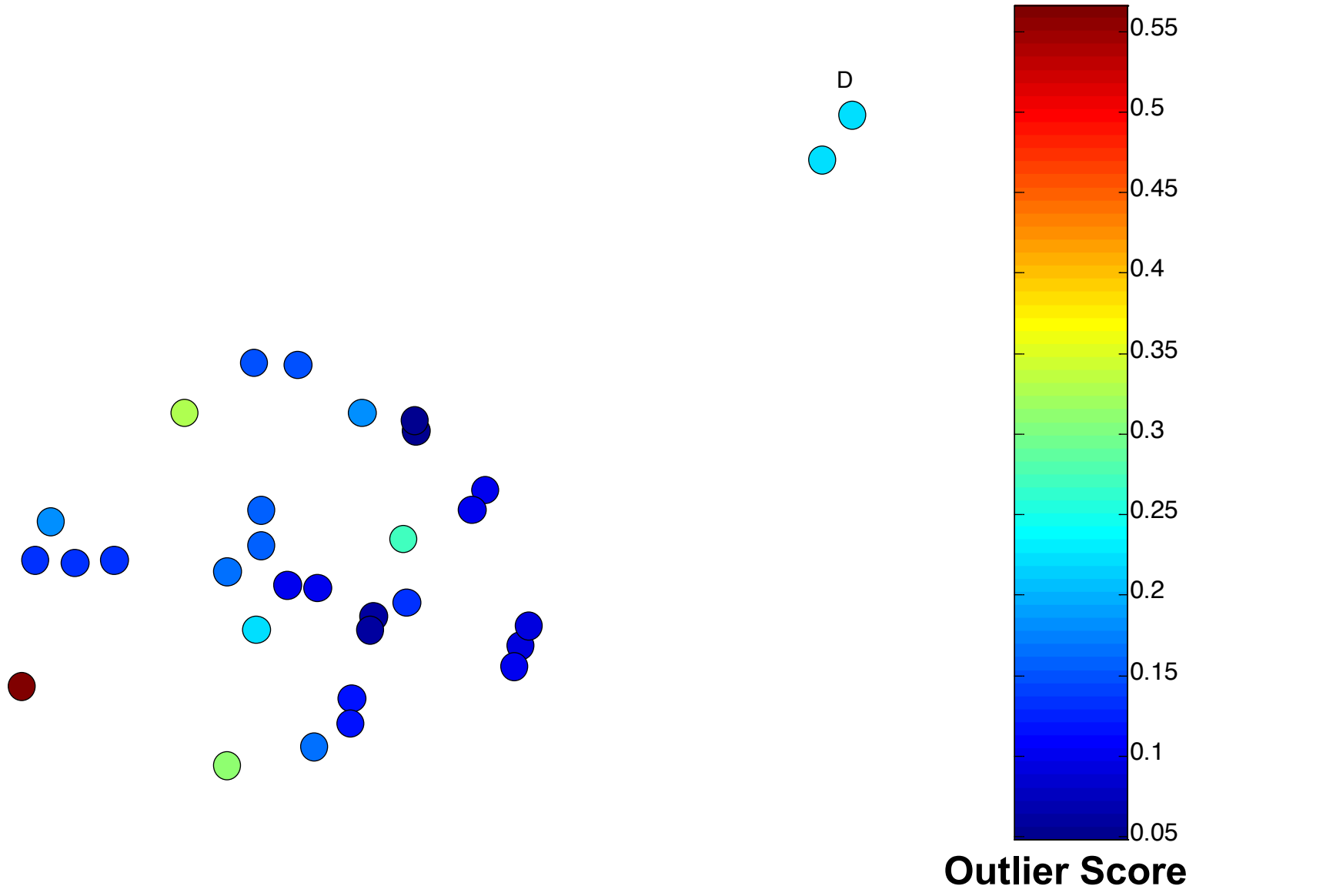
Distance-Based Approaches

- An object is an outlier if a specified fraction of the objects is more than a specified distance away (Knorr, Ng 1998)
  - Some statistical definitions are special cases of this
- The outlier score of an object is the distance to its kth nearest neighbor

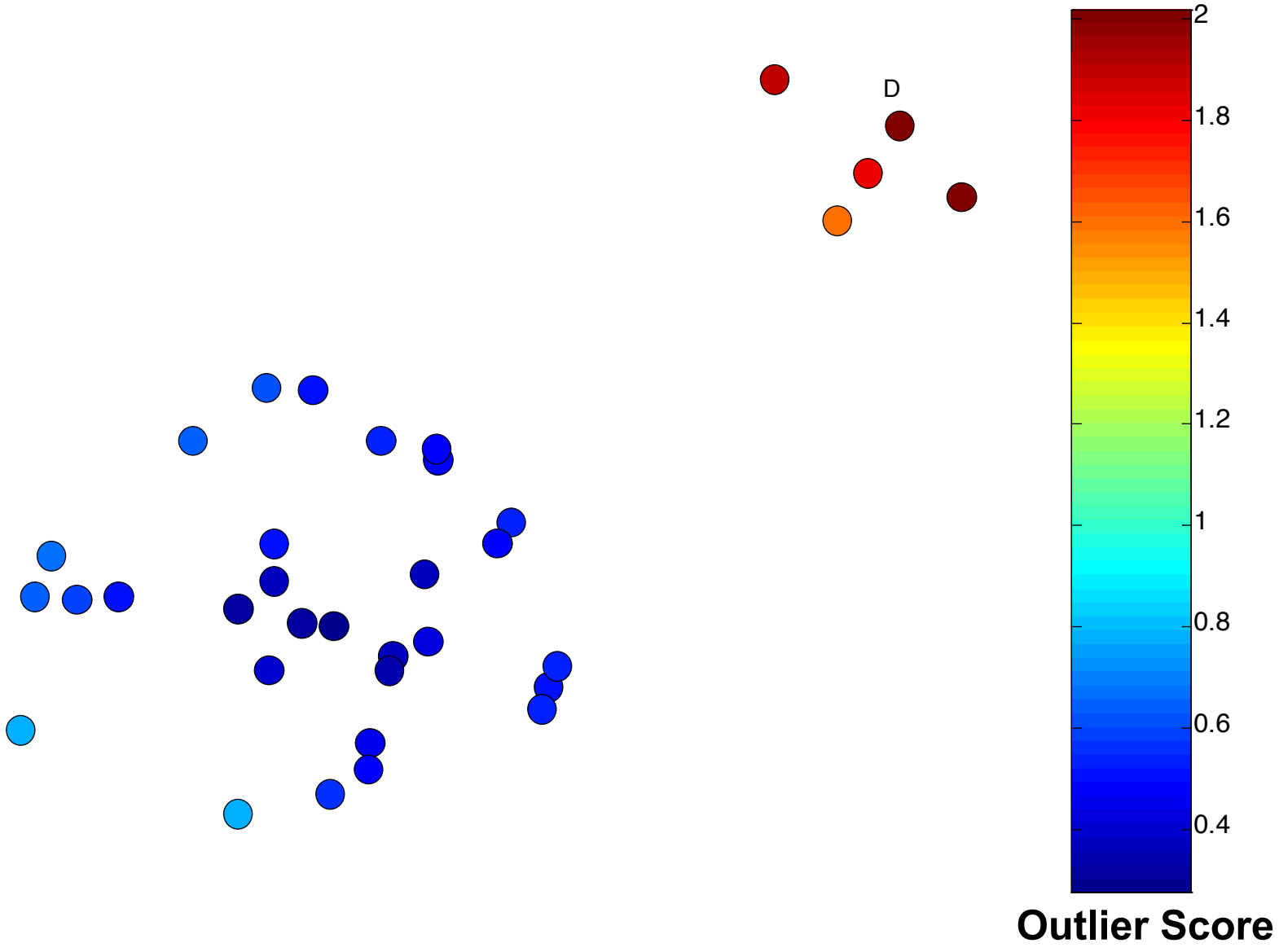
Nearest Neighbor – K=5



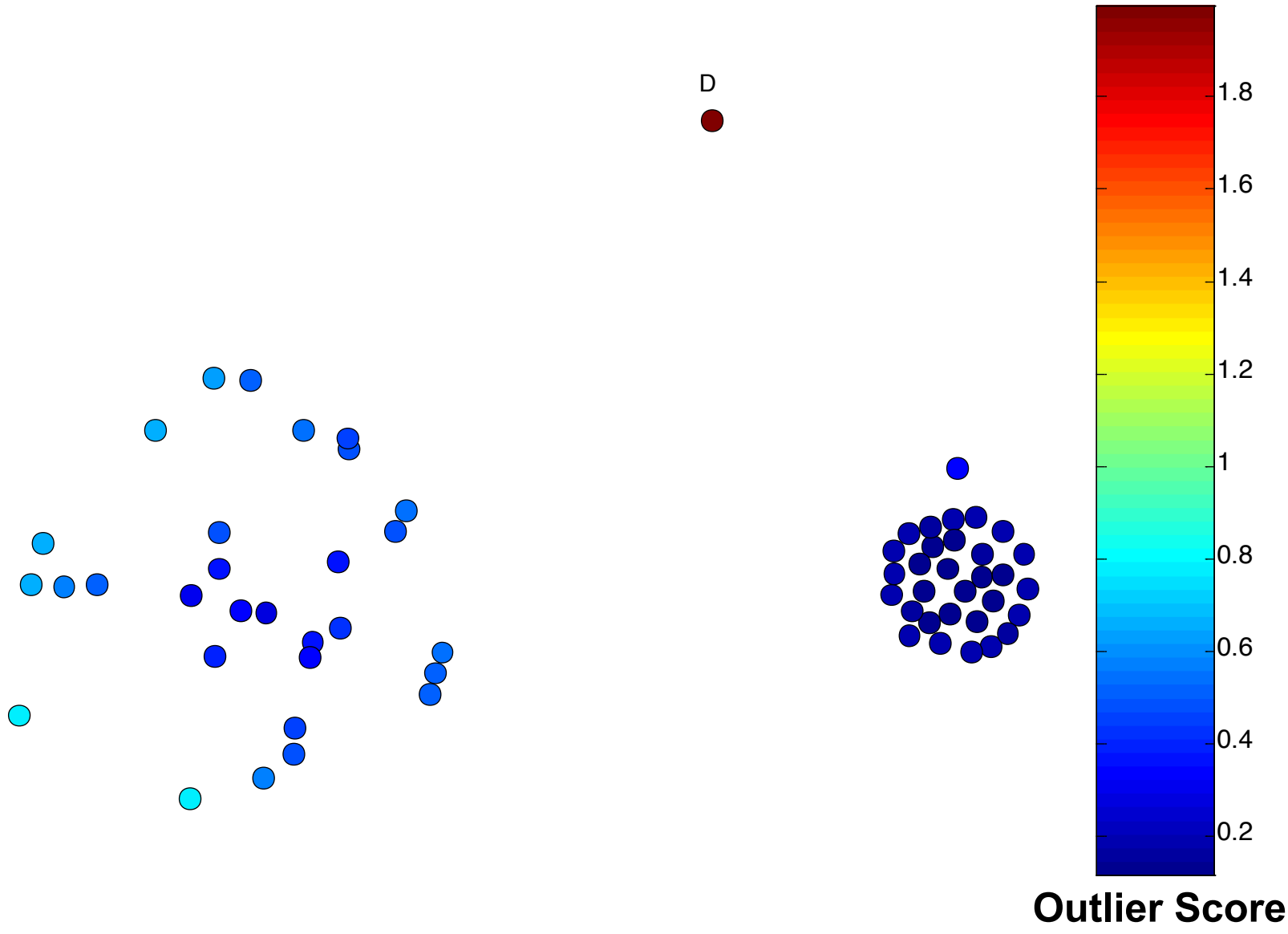
Nearest Neighbor – K=1



Five Nearest Neighbors - Small Cluster



Five Nearest Neighbors - Differing Density



Strengths/Weaknesses of Distance-Based Approaches

- Simple
- Expensive – $O(n^2)$
- Sensitive to parameters
- Sensitive to variations in density
- Distance becomes less meaningful in high-dimensional space

Density-Based Approaches

- **Density-based Outlier:** The outlier score of an object is the inverse of the density around the object.
  - Can be defined in terms of the k nearest neighbors
  - One definition: Inverse of distance to the k^{th} neighbor
  - Another definition: Inverse of the average distance to k neighbors
  - DBSCAN definition

- If there are regions of different density, this approach can have problems

Relative density outlier score (Local Outlier Factor, LOF)

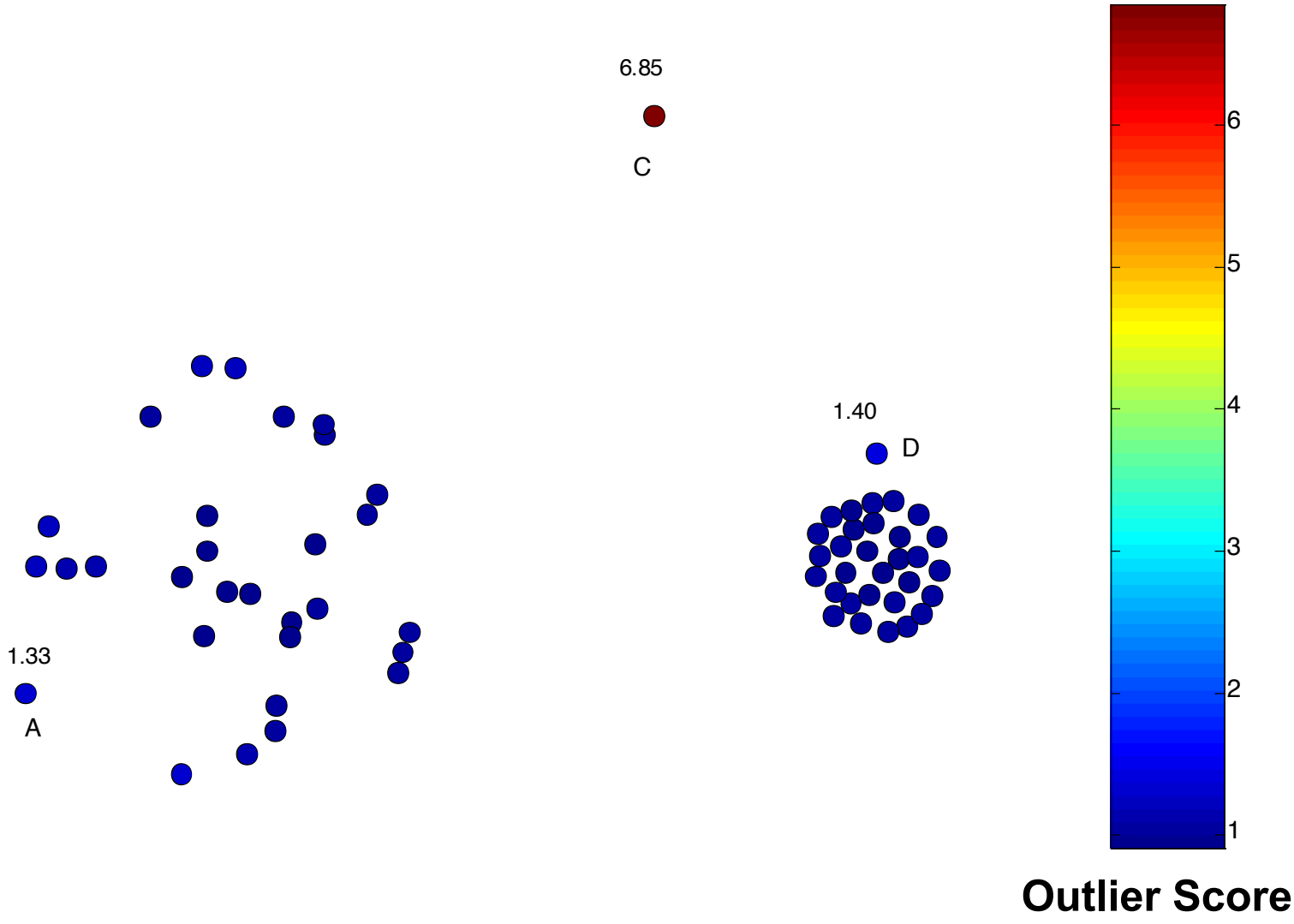
- Consider the density of a point relative to that of its k nearest neighbors

$$average\ relative\ density(\mathbf{x}, k) = \frac{density(\mathbf{x}, k)}{\sum_{\mathbf{y} \in N(\mathbf{x},k)} density(\mathbf{y}, k)/|N(\mathbf{x}, k)|}. \quad (10.7)$$

Algorithm 10.2 Relative density outlier score algorithm.

1: $\{k$ is the number of nearest neighbors$\}$
2: **for all** objects $\mathbf{x}$ **do**
3: Determine $N(\mathbf{x}, k)$, the k-nearest neighbors of $\mathbf{x}$.
4: Determine $density(\mathbf{x}, k)$, the density of $\mathbf{x}$, using its nearest neighbors, i.e., the objects in $N(\mathbf{x}, k)$.
5: **end for**
6: **for all** objects $\mathbf{x}$ **do**
7: Set the $outlier\ score(\mathbf{x}, k) = average\ relative\ density(\mathbf{x}, k)$ from Equation 10.7.
8: **end for**

Relative Density Outlier Scores



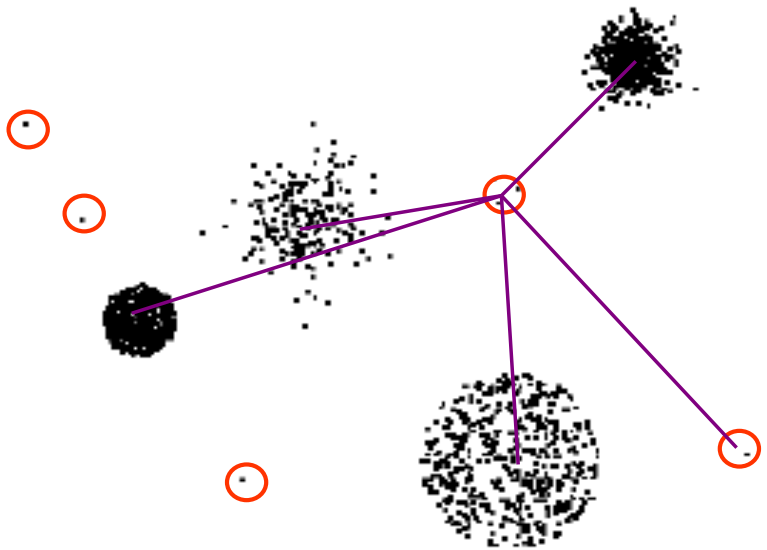
Density-Based Approaches

- Pros
  - Quantitative measure of degree to which object is an outlier.
  - Can work well even if data has variable density.

- Cons
  - $O(n^2)$ complexity
  - Must choose parameters
    - k for nearest neighbor
    - d for distance threshold

Clustering-Based Approaches

- **Clustering-based Outlier:** An object is a cluster-based outlier if it does not strongly belong to any cluster
  - For prototype-based clusters, an object is an outlier if it is not close enough to a cluster center
  - For density-based clusters, an object is an outlier if its density is too low
  - For graph-based clusters, an object is an outlier if it is not well connected
- Other issues include the impact of outliers on the clusters and the number of clusters



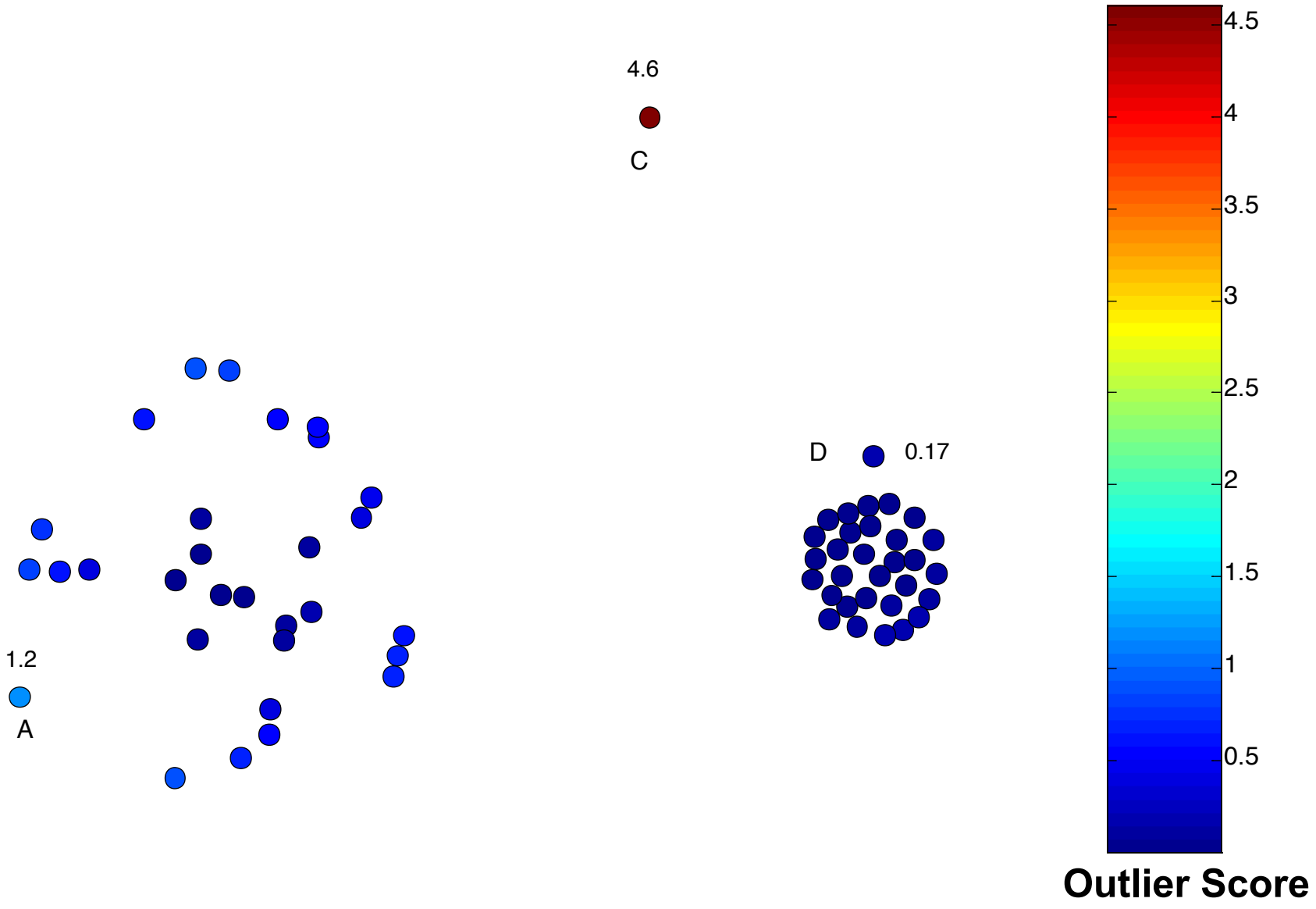
Clustering-Based Approaches

Assess degree to which object belongs to any cluster.

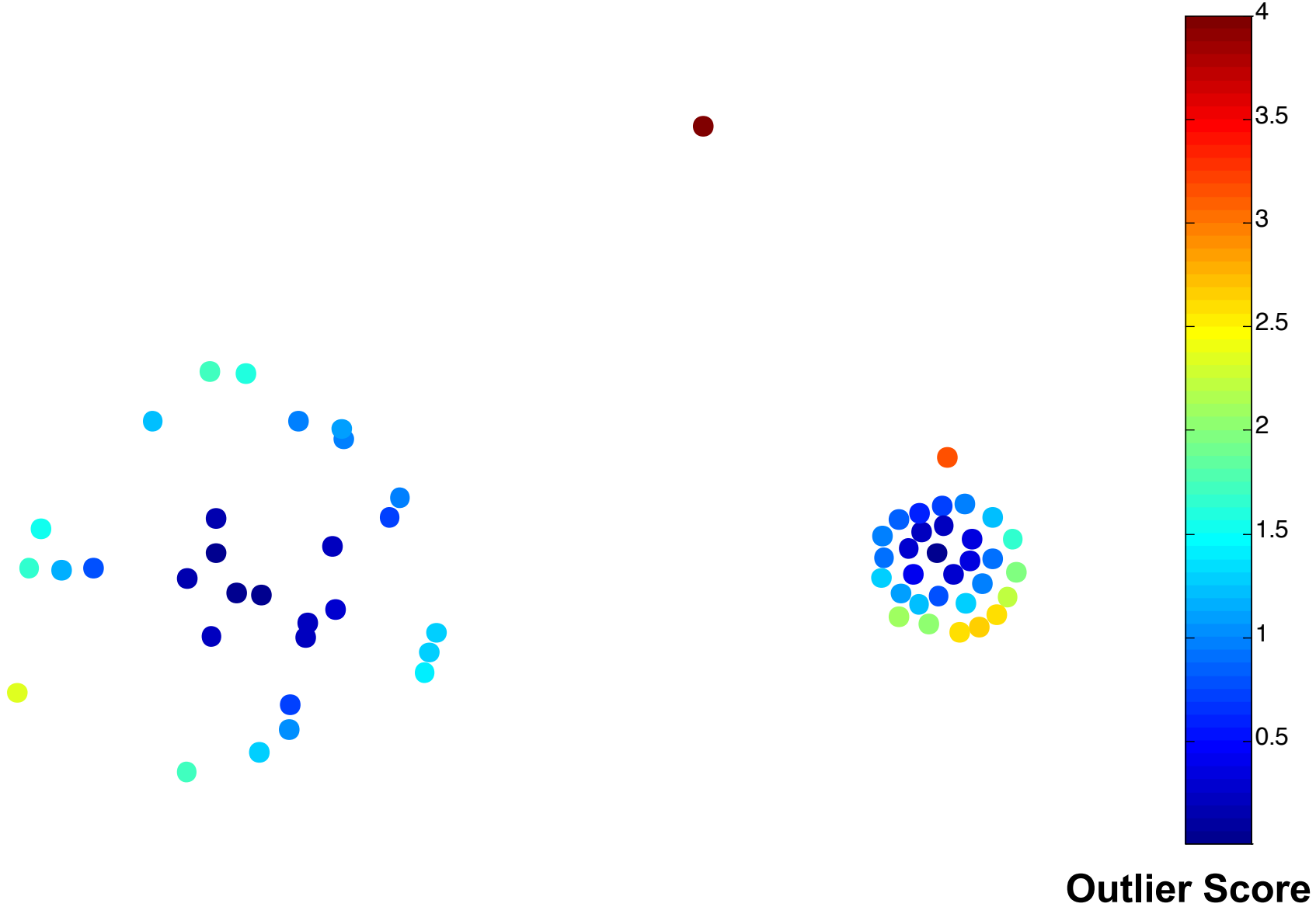
- For prototype-based clustering (e.g. k-means), use distance to cluster centers.
  - To deal with variable density clusters, use relative distance:

$$\frac{\text{distance}(\mathbf{x}, centroid_C)}{\text{median}(\{\forall_{x' \in C} \text{distance}(\mathbf{x}', centroid_C)\})}$$

Distance of Points from Closest Centroids



Relative Distance of Points from Closest Centroid



Strengths/Weaknesses of Distance-Based Approaches

- Simple
- Many clustering techniques can be used
- Can be difficult to decide on a clustering technique
- Can be difficult to decide on number of clusters
- Outliers can distort the clusters

Drawback of the existing approaches

- Many existing methods are constrained to low dimensional data and small data size because of their high computational complexity.

Isolation Forest

Isolation Forest

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Liu, F.T., Ting, K.M. and Zhou, Z.H., 2008, December. Isolation forest. In International Conference on Data Mining (ICDM), pp. 413-422

Isolation Forest

- This paper proposes a different type of model-based method that explicitly isolates anomalies rather than profiles normal instances.

- The proposed method takes advantage of two anomalies' quantitative properties:
  - they are the minority consisting of fewer instances
  - they have attribute-values that are very different from those of normal instances. (Anomalies are 'few and different', which make them more susceptible to isolation than normal points.)

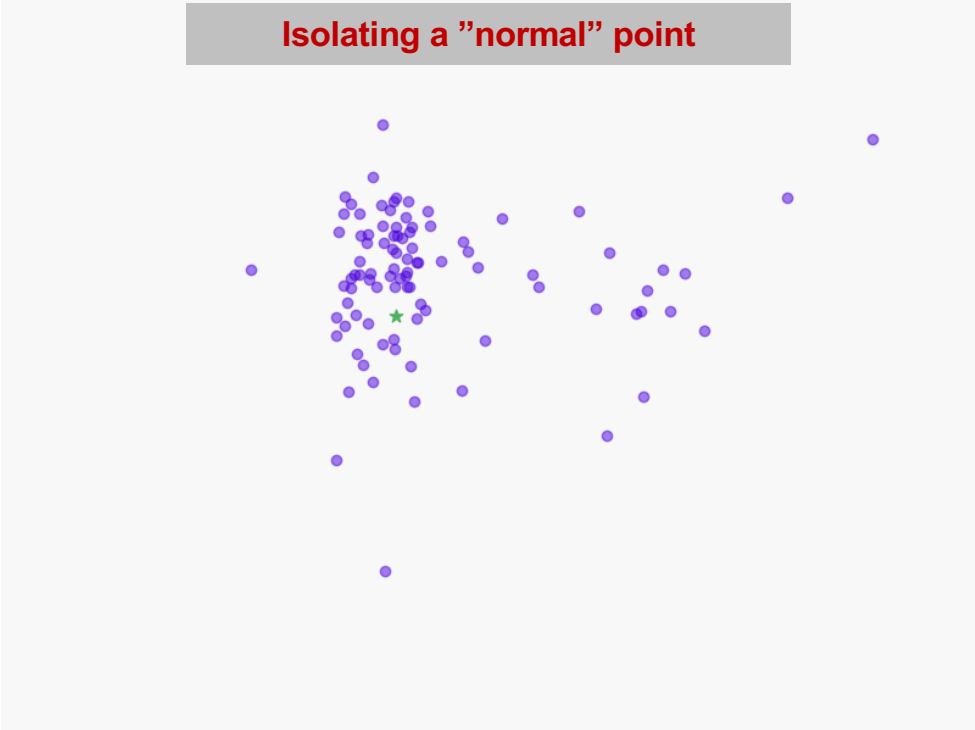
Isolation Forest

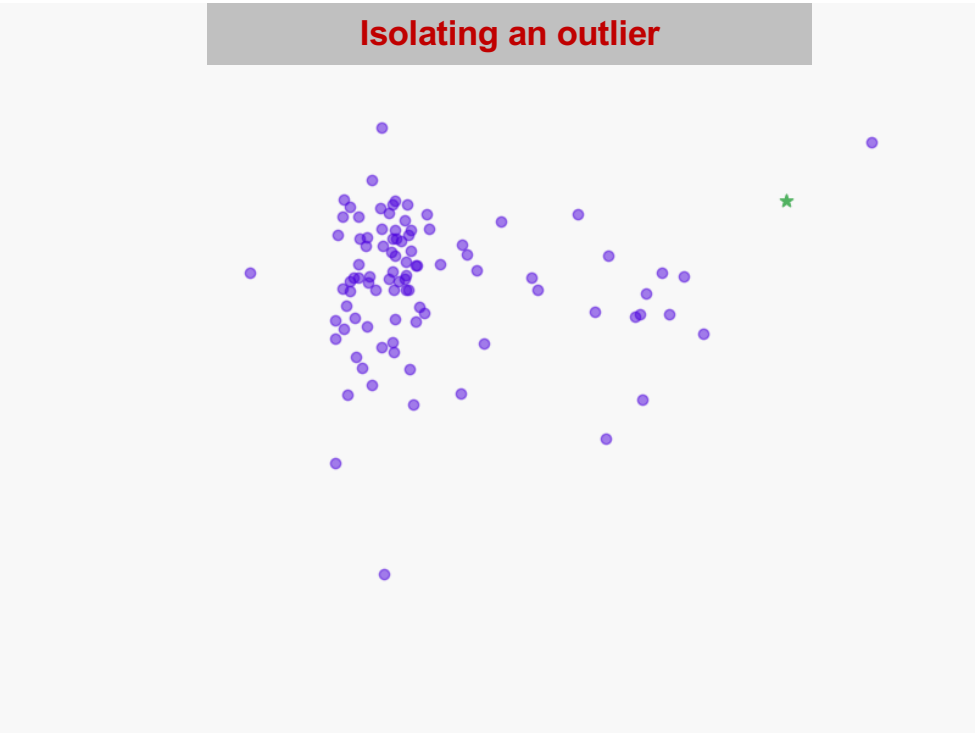
Definition : **Isolation Tree.** Let T be a node of an isolation tree. T is either an external-node with no child, or an internal-node with one test and exactly two daughter nodes (T_l,T_r). A test consists of an attribute q and a split value p such that the test $q < p$ divides data points into T_l and T_r.

Definition : **Path Length** $h(x)$ of a point x is measured by the number of edges x traverses an iTree from the root node until the traversal is terminated at an external node.

Isolation Forest

- Selects a feature, randomly selects a split between minimum and maximum values of the selected parameter
- Many splits are required in order to isolate a “normal” point
  - small number of splits: anomaly!

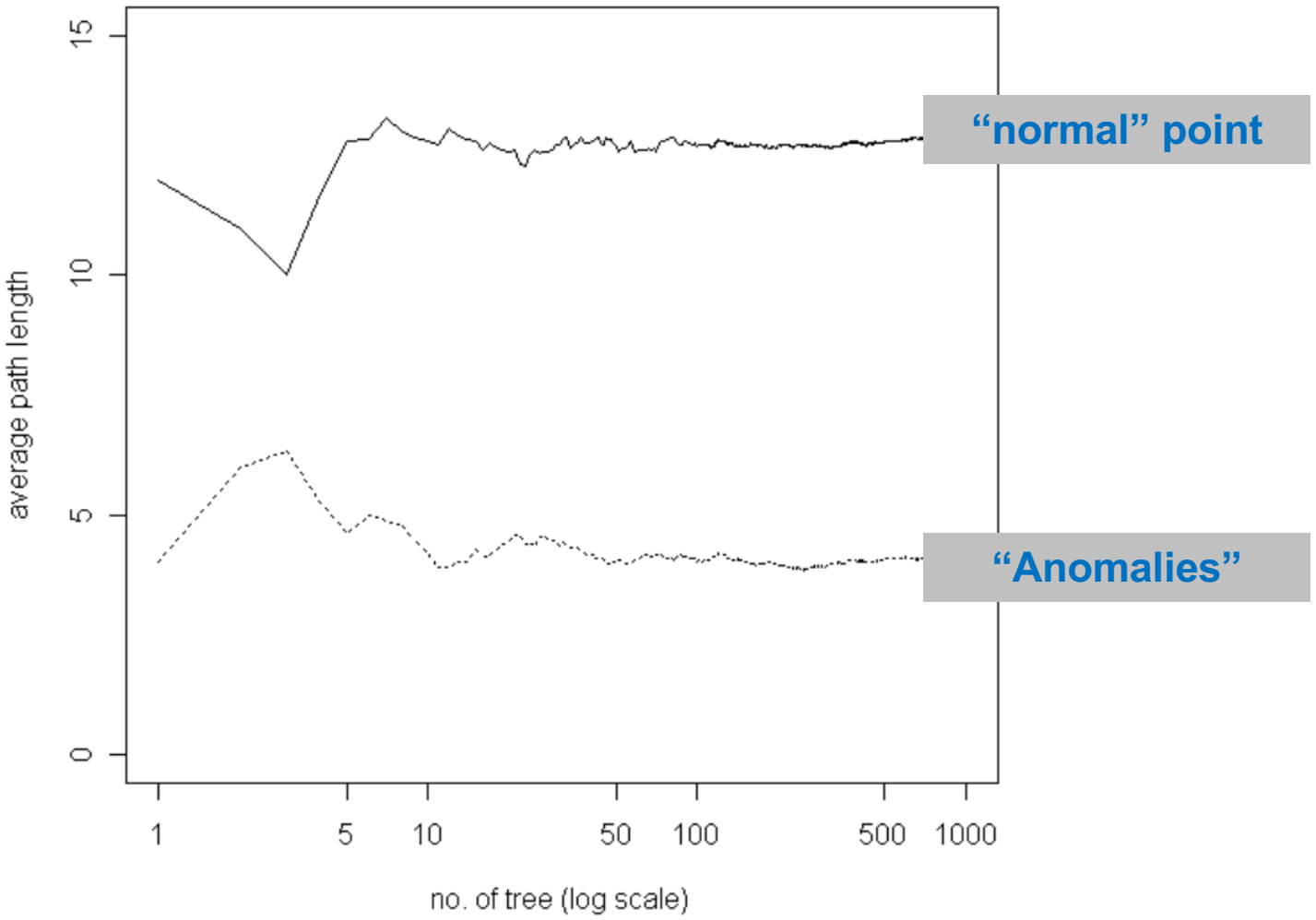




Isolation Forest

- The random partitioning produces noticeable shorter paths for anomalies since
  - the fewer instances of anomalies result in a smaller number of partitions – shorter paths in a tree structure;
  - instances with distinguishable attribute-values are more likely to be separated in early partitioning.

Isolation Forest



(c) Average path lengths converge

Isolation Forest

Algorithm 2 : $iTree(X, e, l)$

Inputs: X - input data, e - current tree height, l - height limit

Output: an iTree

1: **if** $e \geq l$ or $|X| \leq 1$ **then**
2: return *exNode*$\{Size \leftarrow |X|\}$
3: **else**
4: let Q be a list of attributes in X
5: randomly select an attribute $q \in Q$
6: randomly select a split point p from max and min values of attribute q in X
7: $X_l \leftarrow filter(X, q < p)$
8: $X_r \leftarrow filter(X, q \geq p)$
9: return *inNode*$\{Left \leftarrow iTree(X_l, e + 1, l),$
10: $Right \leftarrow iTree(X_r, e + 1, l),$
11: $SplitAtt \leftarrow q,$
12: $SplitValue \leftarrow p\}$
13: **end if**

Isolation Forest

Algorithm 1 : $iForest(X, t, \psi)$

Inputs: X - input data, t - number of trees, ψ - sub-sampling size

Output: a set of t *iTrees*

1: **Initialize** $Forest$
2: set height limit $l = ceiling(\log_2 \psi)$
3: **for** $i = 1$ to t **do**
4: $\quad X' \leftarrow sample(X, \psi)$
5: $\quad Forest \leftarrow Forest \cup iTree(X', 0, l)$
6: **end for**
7: **return** $Forest$

Isolation Forest

The anomaly score s of an instance x is defined as:

$$s(x, n) = 2^{-\frac{E(h(x))}{c(n)}}$$

- c(n) is the average of h(x) given n
- E(h(x)) is the average of h(x) from a collection of isolation trees
- s is monotonic to h(x)
- when $E(h(x)) \to c(n)$, $s \to 0.5$;
- when $E(h(x)) \to 0$, $s \to 1$;
- and when $E(h(x)) \to n - 1$, $s \to 0$.
- If instances return s very close to 1, then they are definitely anomalies;
- If instances have s much smaller than 0.5, then they are quite safe to be regarded as normal instances;
- If all the instances return s ≈ 0.5, then the entire sample does not really have any distinct anomaly.

Characteristics of iForest

- iForest utilizes no distance or density measures to detect anomalies. This eliminates major computational cost of distance calculation in all distance-based methods and density-based methods.

- iForest has a linear time complexity with a low constant and a low memory requirement.

- iForest has the capacity to scale up to handle extremely large data size and high-dimensional problems with a large number of irrelevant attributes.