Index Clustering: A Map-reduce Clustering Approach using Numba

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Abstract: Clustering high-dimensional data is often a crucial step of many applications. However, the so called "Curse of dimensionality" is a challenge for most clustering algorithms. In such high-dimensional spaces, distances between points tend to be less meaningful and the spaces become sparse. Such sparsity needs more data points to characterize the similarities so more distance comparisons are computed. Many approaches have been proposed for reduction of dimensionality, such as sub-space clustering, random projection clustering, and feature selection technique. However, approaches like these become unfeasible in scenarios where data is geographically distributed or cannot be openly used across sites. To deal with the location and privacy issues as well as mitigate the expensive distance computation, we propose an index-based clustering algorithm that generates a spatial *index* for each data point across all dimensions without needing an explicit knowledge of the other data points. Then it performs a conceptual Map-Reduce procedure in the index space to form a final clustering assignment. Our results show that this algorithm is linear and can be parallelized and executed independently across points and dimensions. We present a Numba implementation and preliminary study of this algorithm's capabilities and limitations.

1 INTRODUCTION

Clustering technology has been challenged by the rapid growing of data. In domains where data volume is continuously growing (e.g., climate simulations - 32 PB, astronomy - 200 GB/day to 30 TB/day, and high-energy physics - 500 EB/day), data movement and centralized processing represent performance bottlenecks that increase resource pressure on storage, bandwidth, memory, and CPU (Tiwari et al., 2012). The problem becomes even more challenging as the number of distributed locations increases, or as privacy and management impose restrictions to data access. Two scenarios are of relevance for this work: (1) In-situ data analysis of HPC simulations. Analysis has to be done on site, using local data, in real time, along with as little communication as possible. (2) Medical data analysis. Data volume may not be too large to be efficiently moved across locations, but privacy issues may restrict data sharing. In both scenarios, a global model has to be computed at run time using only an incomplete view of the data. Our question is *if data cannot be moved, or shared, how can we still learn from it?*.

From the standpoint of scalability in parallel and distributed environments and privacy bound applications, state of the art clustering techniques lack in one or more of the following crucial aspects: (1) Traditional machine learning and data mining approaches rely on expensive training phases and often require gathering data in a centralized (Šíma and Orponen, 2003), (Salakhutdinov and Hinton, 2009) or semi-centralized (Kargupta et al., 2001), (Boyd et al., 2011) way. (2) Existing distributed approaches either require synchronized communication (Bandyopadhyay et al., 2006), are tied to a particular domain and do not generalize (Estrada and Taufer, 2012), (Kawashima et al., 2008), sacrifice accuracy for the sake of scalability (Liu et al., 2013), (Gionis et al., 1999), (Aggarwal et al., 1999), or are affected by the *curse of dimensionality* (Quiroz et al., 2012) (i.e., scaling the number of data features negatively affects an algorithm's predictive capabilities (Indyk and Motwani, 1998)). None of these methods are all, scalable, accurate, and general enough to be useful in privacy bound or distributed scenarios of Big Data.

Our goal is to build a clustering algorithm that is able to organize large dimensional datasets without relying on a global knowledge of the data or expensive distance computations. This is a key step that may eventually lead to a solution for location and privacy restricted situations: the clustering can be done locally on each distributed site by exchanging only summarized information, like bins and frequencies,

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with other sites. Compared to moving the whole raw dataset around, the summarized information is extremely small. Individual data points cannot be reproduced from such limited information on other sites so that the privacy is well protected. With this in mind, we propose *Index Clustering*, a new data clustering approach based on indexing individual data points across their whole high dimensional space, and then using only the indexes to build final clusters. Without distance computation, our algorithm has a linear time complexity with regards to both the number of points and dimensions. More specifically, the processing of each point can be done in a constant time. Finally, unlike most density-based clustering methods, our algorithm can benefit from a large number of dimensions. This paper's contributions are as follow:

- A linear time complexity clustering approach that is able to group data across multiple dimensions even with a very limited view of the data.
- A parallel implementation of our algorithm in GPU using Numba.
- A preliminary evaluation of our algorithm's scalability and generality using synthetic and real datasets.

The remainder of this paper is organized as follows: in section 2, we briefly summarize some algorithms that have influence on our algorithm as well as other related approaches. Section 3 presents our index-based clustering algorithm, which combines a map-reduce like approach with Numba to accomplish the parallel clustering tasks. In section 4 we explain the experimental results. Section 5 presents our discussion regarding our algorithm's limitations, reasoning behind parameter selection, and overview of future works that can improve the robustness of our method. Finally, section 6 concludes the paper.

2 RELATED WORK

Scalable methods, closely related to our techniques, are **density-based clustering**. One of the first approaches is DBSCAN (Ester et al., 1996). Another successful example is the Decentralized Online Clustering (Quiroz et al., 2012) that was used in the context of distributed systems monitoring and resource provisioning. Our approach is similar to these techniques in the sense that it groups points in a density-based way; but it is different in that we use indexed bins to define dense regions that contain enough points instead of defining some core points that have enough neighbors.

Other methods have been proposed to capture low-dimensional semantics of data features with the final purpose of accelerating searches for similar items. Successful methods in this category include Latent Semantic Analysis (LSA), Semantic Hashing, and Lazy Learning (Indyk and Motwani, 1998; Barrena et al., 2010; Omercevic et al., 2007). **Latent Semantic Analysis** (Deerwester et al., 1990) uses the SVD decomposition to extract low dimensional semantic structure of the word-document co-occurrence matrix. LSA enables document retrieval engines to base their searches on semantic structure, rather than using individual word counts. This property greatly reduces the time complexity of the algorithms. However, computing the SVD decomposition becomes unfeasible as data size grows large.

Sub-space Clustering algorithms gave inspiration to our algorithm. Grid-based hierarchical clustering algorithms that use bottom-up search strategies are most related and influential to us. CLIQUE (Agrawal et al., 1998) and MAFIA (Goil et al., 1999) first find dense regions in lower-dimensional spaces. Then they merge these lower-dimensional regions into bigger higher-dimensional hyper-cubes if they can find a common-face between two regions. The limitation of these two algorithms is the expensive combinations of all possible lower dimensional regions so they didn't show scalability when the dimensionality goes to several hundred.

3 ALGORITHM

Most traditional clustering techniques rely on computing pairwise distances between points or regions to form clusters. These computations are exponentially expensive as the number of points and the number of dimensions grow. Other more efficient techniques such as dimensionality reduction, need prior knowledge of the data (e.g. its principal components, covariance matrix, or some other statistical properties). However, when data needs to be analyzed as a stream, *in situ*, or on different geographical locations, and the i.i.d.(independent and identically distributed) property cannot be guaranteed, then these methods fail.

For an algorithm to work in such circumstances, the main question is: if we cannot compute pairwise distances, how can we decide whether two points are similar? To efficiently answer this question, we took inspiration from Locality Sensitive Hashing (Gionis et al., 1999). Similar to the family of hashed values, we map data points to indexes along every dimensions. By organizing these indexes into bins and

merging bins to primary clusters, we get a list of primary cluster identifiers like the *fingerprints* for each point which we call it a *index*. Then, forming clusters can be done in this projected space, and is almost as easy as performing a reduction on fingerprints. The A-priori algorithm for mining frequent patterns (Agrawal et al., 1994) is behind our final grouping approach: Points belong to one higher dimensional cluster also stay together in each lower dimensional regions; Points with different fingerprints belongs to different clusters. Two crucial aspects of this process are: (1) the space of indexes represents summarized knowledge of the raw data, which allows us to preserve privacy, and (2) the reduction on fingerprints instead of distance comparisons, which allows us to improve scalability.

3.1 Methods

We want to cluster a dataset m of size $M \times N$, where M is the number of data points and N is the number of features. We denote $m = \{cor_{i,j} | i < M, j < N\}$, with i being the unique identity of a data point and j its jth feature. Without lack of generality we could assume $M = 1$ for a data stream scenario or multiple m's for a distributed case. For descriptive purposes we will call m as our *raw data* for the rest of the paper. The steps of our method are as follows:

1. Assign a list of indexes to a point. Every index is associated with a bin in the specific dimension. As points get their indexes, bins update their density. This step only involves the point itself and the value range of each dimension. In the distributed scenario this can be done with only local data.
2. Building primary clusters. A primary cluster is a partial clustering assignment viewed from one particular dimension. This step merge adjacent bins into what we call primary clusters if they exceed the density threshold.
3. Assigning points to final clusters. Once primary clusters are built, every point can be mapped to a specific set of primary clusters in all of its dimensions. They use their indexes to get a index. This leads to a final global clustering assignment.

3.1.1 Assigning a List of Indexes to a Point

A point$_i$'s *coordinate* are converted to *idx*, a list of indexes indicating a relative location along each dimension. The number of bits per index is defined by the user as the $depth$ of our algorithm. This depth also determines the number of bins per dimension as $B = 2^{depth}$. Then, $idx_{i,j}$, which is the index for $x_{i,j}$ is in range of $[0, 2^{depth} - 1]$.

The function *getindex* as shown in Algorithm 1, receives as parameters the $depth$ of indexes, an estimated $lower$ and $upper$ boundaries of the specific dimension, and the point's *coordinate*. Then, it recursively divides the range on one dimension into equal halves for $depth$ number of steps. This procedure is conceptually building a $depth$ deep binary tree to accommodate the range. Each leaf contains a sub region of the bounded dimension. The point's *coordinate*s are then converted into indexes of leaves. The *getindex* function is applied to $x_{i,j} \forall i, j$ independently. Thus, it can be efficiently implemented in parallel, not only per data point but also per feature.

Algorithm 1: getindex.

```
1:  procedure GETIDX(max_depth, lower, upper, x_{i,j})
2:      for depth < max_depth do
3:          μ_{j,depth} ← 1/2(lower + upper)
4:          if x_{i,j} ≥ μ_{j,depth} then
5:              append 1 to idx_{i,j}
6:              lower ← μ_{j,depth}
7:          else
8:              append 0 to idx_{i,j}
9:              upper ← μ_{j,depth}
10:     return idx_{i,j}                ▷ return leaf index
```

3.1.2 Building Primary Clusters

Primary clusters are sets of bins organized in a partial clustering assignment for a single dimension. Our algorithm follows a bottom-up strategy. Unlike CLIQUE(Agrawal et al., 1998) and MAFIA(Goil et al., 1999), we build primary clusters on each dimension then directly reduce to the entire dimensional clusters and skip all intermediate lower-dimensional dense regions. A bin is instantiated only when there is a data point whose index on this dimension is associated to that bin. $bins = \{dbin_{b,j} | b < B, j < N\}$. $dbin_{b,j}$ is the density of bin b on the jth dimension.

To build primary clusters we merge adjacent bins if their density is larger than a predefined threshold *minDensity*. For very sparse clustering, this threshold can be set to zero. A primary cluster represents an agglomeration of points viewed from one particular dimension. We refer them as *pc* where $\{pc_{b,j} | b < B, j < N\}$ contains a unique identifier (e.g. *PCid*) for the primary cluster in that dimension, with B and N being the number of bins and the number of dimensions respectively. Algorithm 2 shows the procedure for building primary clusters. A while loop for generating point's indexes and updating bins' density, and a for loop for merging adjacent bins forming primary

clusters. The only communication needed would be the final bin densities, which is considerably smaller than raw data and has no sensitive information that could compromise privacy.

Algorithm 2: Build Primary Clusters.

```
M = numberOfPoints
N = numberOfDimension
minD = minimumDensityInBin
depth = depthOfindex
B = 2^depth numberOfBins
while not EOF do                          ▷ generate indexes, fill bins
    cor ← one data point from raw data
    idx ← getindex(depth, cor)
    for j = 1 to N do
        dbin_{j,idx_j} += 1               ▷ increase bin density
PCid ← 0                                  ▷ initialize for noise
for i = 1 to N do                         ▷ merge bins
    k ← 1, flag ← false
    while k ≤ B do
        if dbin_{i,k} > minD AND not flag then
            PCid ← k
            flag ← true
        else if dbin_{i,k} <= minD AND flag then
            PCid ← 0
            flag ← false
        pc_{i,k} ← PCid
        k ← k + 1
```

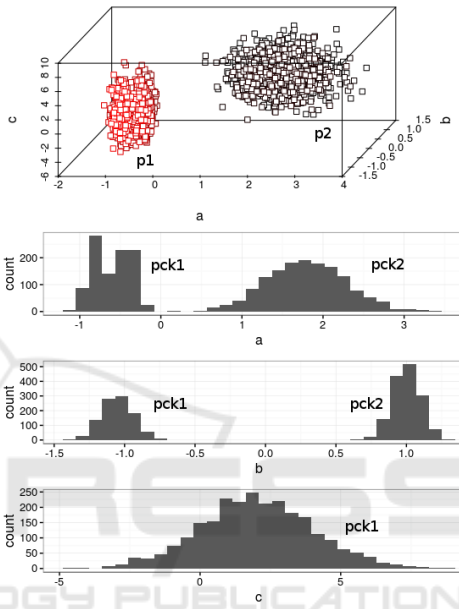
3.1.3 Assigning Points to Final Clusters

The final step makes a final assignment of points to their respective clusters. The aggregated clusters are represented as $FC = \{fc_m | m < M\}$. The index for a *final cluster* is just the concatenation of *PCid*s of each one-dimensional primary cluster. The intuition being that if points belong together in a high dimensional cluster, they will be together with high frequency in lower dimensional clusters. Although the possible combination of primary cluster indexes is vast, the real worst case is each point forms a unique "group". So we can bound the maximum number of *final clusters* to be M. Algorithm 3 shows the procedure of building final clusters. This procedure consists on concatenating the set of primary clusters assigned to a point to build a global index which determines the point membership to a specific final cluster.

In figure 1(a) we illustrate the algorithm with an intuitive example. Two *primary cluster*s are formed on dimension$_a$,dimension$_b$, and one *primary cluster* forms on dimension$_c$. *Final cluster*s are built upon points sharing the same concatenation of their *PCid*s. p_1, p_2 are from the red and black group respectively. Figure 1(b) shows their specific primary clusters

Algorithm 3: Final clustering.

```
M = numberOfPoints
N = numberOfDimensions
pc = primaryClusters
for i = 1 to M do                         ▷ concatenate PCids
    for k = 1 to N do
        fcindex ← concatenate pc_{i,k}
    fc_{fcindex} += 1                     ▷ increase cluster density
```



(a) 2 final clusters and bin densities.

pointID	PCid$_a$	PCid$_b$	PCid$_c$	fcindex
p_1	1	1	1	111
p_2	2	2	1	221

(b) Example of primary clusters and final clusters indexes

Figure 1: Didactic example of how our algorithm will merge adjacent bins into *primary clusters* and reduce on PCid*s* to form a global arrangement.

across the three dimensions. The column *fcindex* shows their final clustering assignments. Note that with this arrangement, it is very easy to collapse a particular dimension and form completely different clustering assignments without having to reiterate through the data.

3.2 Parallel Implementation with Numba

We used **Numba** to accelerate the above algorithm. Numba is an Open Source NumPy-aware optimizing compiler for Python that generates machine code for

both CPUs and NVIDIA GPUs. To Assign indexes is the most time consuming section. We parallelized the function *getindexGPU* and *fillBinsGPU* with one GPU thread per coordinate. To build *primary clusters*, the *buildPClustersGPU* function is implemented in a limited parallel manner. The algorithm only launches one thread per dimension. The location to merge bins starts from the lowest bin. Since this step is not the most computationally expensive in our method, we leave it in a simple parallel approach. The Numba sequence of steps is described in Algorithm 4.

Algorithm 4: Parallel map-reduce clustering algorithm.

1: M = numberOfPoints
2: N = numberOfDimension
3: B = numberOfBins
4: $wt \leftarrow rand(w_1, w_2, ..., w_N)^T \| w_i \in (0,1)$
5: $m \leftarrow$ readFile ▷ get $\text{cor}_{i,j}$
6: $k \leftarrow$ getindexGPU ▷ get $\text{idx}_{i,j}$
7: $dbin \leftarrow$ fillBinsGPU ▷ get $\text{dbin}_{i,k}$
8: $pc \leftarrow$ buildPClustersGPU ▷ get $\text{pc}_{i,k}$
9: $cg \leftarrow$ getPrimaryClusterindex ▷ additional step
10: $cm \leftarrow cg \cdot wt$ ▷ additional step
11: $ck \leftarrow$ getindexGPU ▷ additional step
12: $hc \leftarrow$ fillBinsGPU ▷ additional step
13: **for** $i = 1$ to M **do** ▷ output final clusters
14: **if** $\text{hc}_{fcindex} \geq$minThreshold **then**
15: output final $\text{cluster}_{fcindex}$

The current version of Numba has no direct string operations. Our implementation uses four additional steps (lines 9 to 12 in Algorithm 4) to accomplish the final clustering assignment. To emulate the serial implementation of concatenating each of the primary cluster indexes in a point's dimensions, we first fetch the *primary cluster indexes* into a matrix $cg = \{cid_{i,j} | i < M, j < N\}$. Then we multiply c with a random N dimensional real vector $wt = (w_1, w_2, ..., w_N)^T, w_i \in (0,1)$. The result is a column vector $cm = \{hk_i | i < M\}$. So we get an unique real number hk_i to replace the concatenation of primary cluster indexes. We will discuss the correctness of this later in section 5.

The above two steps generate a 1 dimensional array of real number *final cluster index*s for every points. We use an additional *generate index* step to scatter these indexes onto a deeper binary tree. This converts the vector $cm = \{hk_i \in \mathbb{R}\}$ of real numbers into the integer vector $ck = \{ck_i \in \mathbb{I}\}$ with unique integers per bin. Our worst case is still when each point has an unique final cluster index. To assure each of the resulting leaf indexes are unique, the additional *getindex* step uses a new $depth > log(M)$. The last additional step consists on keeping track of the density of bins in ck.

3.3 Time Complexity

In Algorithm 1, *getindex* uses a constant $depth$ steps to convert coordinates to indexes. The while loop in Algorithm 2 goes one pass through all M points to convert coordinates to indexes and accumulate the bin densities on all N dimensions. This pass will be $O(M \times N)$. The for loop goes one pass through bins on N dimensions to merge them into *Primary Clusters*. The number of bins is 2^{depth}. This adds up to $O(2^{depth} \times N)$. The Algorithm 3 goes through all M points on all N dimensions adds up to $O(M \times N)$. The overall time complexity will be $O(M \times N) + O(2^{depth} \times N)$. Normally, we set $depth$ to 10 to 15 so $M > 2^{depth}$. The time complexity is still $O(M \times N)$. The Numba implementation can parallelize the above computations to the number of GPU threads P. So The overall time complexity reduces to $O(M \times \frac{N}{P})$. As P and N are fixed for a given dataset, our algorithm can be seen as linear to the number of data points with time complexity $= O(M)$.

4 EXPERIMENTS AND RESULTS

We empirically evaluate the scalability and generality of our Index Clustering algorithm through three tests. First we compare performance between the serial and the GPU implementations to quantify gains obtained from the algorithm's parallelization. Then, we perform controlled scalability tests to quantify performance when we varied the number of points or the number of dimensions. Finally, we use the algorithm on real datasets to understand its predictive capabilities. All the experiments ran on an 8 core Intel Haswell 2.4GHz machine with a 640 Maxwell core 0.9GHz SMM graphic card. The host RAM is 8G and the device RAM is 2G.

4.1 Performance Gain from GPU

Our first experiment is to quantify the improvement of performance of GPU parallelization. We used simple synthetic data to allow us control over the dimensionality and size of the datasets. We used the data generator from gpumafia(Canonizer,) to generate 1 million *20*-dimensional points grouped into 5 hypercubic clusters with 10% uniformly distributed noises. We sum up the additional steps on the GPU implementation to get an equivalent timing for the *final clustering* step on CPU. Figure 2 shows the time for clustering 1 million 20 dimensional points into 5 groups. The algorithm successfully found five groups with recall and precision equal to 1.0. The GPU implementation

is about 30 time faster than CPU. Performance is expected to plateau as the number of data dimensions approach the maximum number of threads. However, this is a limitation of the hardware rather than of the algorithm.

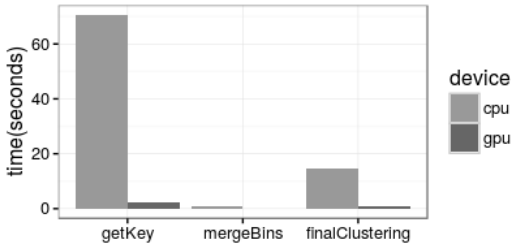


Figure 2: Elapsed time consumed by each step on CPU and GPU in clustering 1 million low dimensional points.

4.2 Scalability

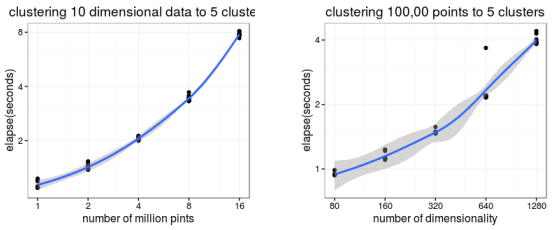
Our second set of experiments are designed to test the algorithm's weak scalability as the number of points or the number of dimensions grow.

We first fixed the dimensions to 10 and number of clusters to 6. Then we varied the number of points from 1 million to 16 million with intermediate measures at 2, 4, and 8 million. Figure 3(a) shows the relationship between time and size of the datasets is close to linear. Through experimentation we observed that the $depth = 15$ and $minpt = 10$ produced accurate clusters for the 1 million dataset, and $minpt = 100$ for the 16 million dataset. Even though it is apparent that the $depth$ parameter is weakly correlated to the data size, its relative growth is so small that it does not have a considerable effect on the time complexity of the algorithm.

Next we fixed the number of points to 100,000 and varied the number of dimensions from 80 to 1280(i.e, 80, 160, 320, 640, 1280). Again, the algorithm successfully divided the points into 5 groups. Figure 3(b) shows that the relationship between time and dimensionality is close to linear.

4.3 Comparison with K-means

It's better to compare with density-based algorithms. However, DBSCAN failed to finish 1 million data points due to its quadratic complexity. So we compare our algorithm with the K-Means due to its high performance and widely acceptance in many disciplines. We picked the implementation of K-means in scikit-learn package 0.17.1. To avoid hardware difference, only accuracy is compared. We simply give K-means the ground truth value of k. Table 1 contains averaged recall and precision of 10 runs for each row. This comparison shows the generated separable boundaries of synthetic hypercubes help our algorithm achieve high accuracy. But the pairwise distances trick K-Means to lower accuracy.



(a) Scalability as data points increases

(b) Scalability as dimensionality increases

Figure 3: Scalability as dataset size and dimensionality increase. Above: time for clustering 10 dimensional data with size of 1, 2, 4, 8,and 16 million points. Below: time for clustering 100,000 points with 80, 160, 320, 640 and 1280 dimensions.

Table 1: Index Clustering (idxc) VS. K-Means (kms).

	Recall		Precision	
	idxc	kms	idxc	kms
1m-10d	0.999	0.798	1.0	0.788
2m-10d	0.999	0.799	1.0	0.841
4m-10d	0.999	0.800	0.999	0.791
8m-10d	0.999	0.799	1.0	0.806
16m-10d	0.999	0.800	1.0	0.601
100k-80d	0.999	0.800	1.0	0.984
100k-160d	0.999	0.804	1.0	0.746
100k-320d	0.998	0.799	1.0	0.738
100k-640d	0.998	0.797	1.0	0.736
100k-1280d	0.996	0.801	1.0	0.741

4.4 Clustering Real Data

We tested our algorithm on the Daily and Sports Activities Data Set(Altun et al., 2010) from the UCI Machine Repository. The data set contains 45-dimensional signals measured from different physical activities performed by eight persons.

The first experiment is to identify different activities of the same person. We considered *sitting*, *walking on a treadmill* and *jumping*. Each activity contains $7,500$ records. The total observations per person are $22,500$. Without further preprocessing, our algorithm separates the signals into three well defined groups. The algorithm discards a few observations (in the order of 20 per person) as noise. However, it correctly assigns 99.9% of the data to the correct activities.

The second experiment aims to identify different people doing a particular activity. In this case total 60,000 points per activity for 8 persons. Our algorithm consistently identified nine distinct clus-

ters. The nine-th cluster can be explained as noisy inputs and inconsistencies of participants performing the physical activity during the data collection.

5 DISCUSSION

In this section, we discuss the limitations of our algorithm. This will help us to decide whether and when the algorithm can accomplish its tasks.

Our algorithm works well with the assumption that all dimensions are orthogonal to each other. Adding one orthogonal dimension only stretches points farther. However, adding one non orthogonal dimension may compress points closer. To avoid this problem, our algorithm makes it easy to collapse dimensions. If the collapse produces radically different clustering assignments, it is possible to determine that some dimensions are not orthogonal and need to be revised.

Another limitation is the situation where the dense bins of two clusters overlap. Figure 4 shows a common situation in a 2 dimensional space, where the projected dense bins of cluster$_1$ and cluster$_2$ overlap on both dimensions. Our algorithm would fail if they overlap in all dimensions. If p_i is the probability of overlapping on the ith dimension, then the probability that our algorithm fails is $\prod_{i=1}^{N} p_i$, which becomes small quickly as dimensionality increases. Thus, our algorithm is likely to perform better with high dimensional data. To ameliorate the overlapping problem, we can check dimension$_b$ in Figure 4 to observe a bimodal distribution of densities. An analysis of the modes per range would give us indications that the data is actually forming two clusters instead of one. Again, as the number of dimensions increase, the probability of successfully identifying this phenomena just increases.

Unique Final Cluster indexes. In Section 3.2, we convert the row vector of primary cluster into a real value as the final index. We accomplish this goal by multiplying this row vector with a random column weight vector $wt = (w_1, w_2, .., w_N)^T, w_i \in (0,1)$. In Table 2, the column PCid$_1$ and PCid$_2$ are primary cluster indexes. We can generalize the number of primary clusters in dimension$_1$ and dimension$_2$ to be X and Y. The maximum number final cluster indexes. is $X \times Y$.

Let the weight vector be $wt = (\frac{1}{a}, \frac{1}{a+1})$ where a is an integer and $a \cdot (a+1) \geq X \cdot Y$. The dot product of the matrix of *PCid*s with wt is an 1-dimensional column vector of real values. The results are within the range of $[\frac{2a+1}{a(a+1)}, \frac{X(a+1)+aY}{a(a+1)}]$. The minimum step between two values will be $\frac{1}{a(a+1)}$. This value range

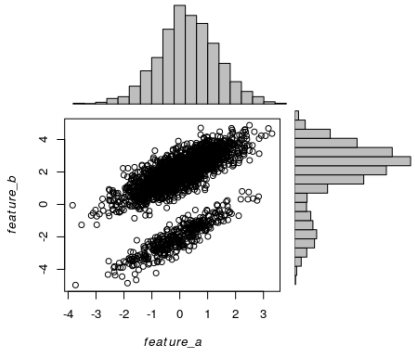


Figure 4: Algorithm cannot separate two clusters when histograms overlap on both dimensions. This happens more often in lower dimensional spaces.

Table 2: Generate unique cluster indexes.

PCid$_1$	PCid$_2$	Weight	Result
1	1	$(1/2, 1/3)^T$	5/6
1	2	$(1/2, 1/3)^T$	7/6
1	3	$(1/2, 1/3)^T$	9/6
2	1	$(1/2, 1/3)^T$	8/6
2	2	$(1/2, 1/3)^T$	10/6
2	3	$(1/2, 1/3)^T$	12/6

contains $a(X+Y-2)+X$ points. Solve the above inequality we have $a \geq \sqrt{XY + \frac{1}{4}} - \frac{1}{2}$. Given X, Y, a are all integers, we can simplify the inequality to be $a > min(X,Y)$. This will give us the lower bounds of the number of unique points $XY + (X^2 - X), (X \geq Y)$ or $XY + (Y^2 - Y), (Y \geq X)$. For both cases, the lower bound will be larger than the maximum number of all possible final cluster indexes. In the above example, $X = 2, Y = 3$. We choose $a = 2$ such that $a(a+1) \geq XY$. Then $wt = (1/2, 1/3)^T$. The result final cluster indexes are all unique. We can choose $wt = (\frac{1}{a}, \frac{1}{b})^T$ instead of $(\frac{1}{a}, \frac{1}{a+1})^T$ as long as $|a-b|$ is still small, and $a \cdot b \geq X \cdot Y$. Our algorithm uses random real numbers within $(0,1)$ to simulate such a weight vector. For the purpose of querying a new point's cluster index, we can generate a fixed weight vector as the index generator.

6 CONCLUSIONS

In this paper we presented the Index Clustering algorithm, a parallel clustering algorithm tailored for scenarios with very limited view of the data. Our algorithm, is able to organize large dimensional datasets without pair-wise point comparisons. This enables us to form clusters under location and privacy restricted situations. The communication is extremely small compared to the whole raw dataset and indi-

vidual data points cannot be reproduced from it. Our algorithm shows weak scalability with the number of points/dimensions. The limitation of dimension orthogonality and overlapping is discussed. Such situation shall be rare as dimensionality grows higher. Domain knowledge can benefit our algorithm by providing guidelines for collapsing particularly noisy or non-orthogonal dimensions. Finally, this work shows the potential power of Numba in high-dimensional data analysis.

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