Alternatives to the k-means algorithm that find better clusterings

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ABSTRACT

We investigate here the behavior of the standard k-means clustering algorithm and several alternatives to it: the k-harmonic means algorithm due to Zhang and colleagues, fuzzy k-means, Gaussian expectation-maximization, and two new variants of k-harmonic means. Our aim is to find which aspects of these algorithms contribute to finding good clusterings, as opposed to converging to a low-quality local optimum. We describe each algorithm in a unified framework that introduces separate cluster membership and data weight functions. We then show that the algorithms do behave very differently from each other on simple low-dimensional synthetic datasets and image segmentation tasks, and that the k-harmonic means method is superior. Having a soft membership function is essential for finding high-quality clusterings, but having a non-constant data weight function is useful also.

Categories and Subject Descriptors

H.3.3 [**Information Systems**]: Information Search and Retrieval; I.5.3 [**Computing Methodologies**]: Pattern Recognition

General Terms

Clustering quality k-means k-harmonic means unsupervised classification

1. INTRODUCTION

Data clustering, which is the task of finding natural groupings in data, is an important task in machine learning and pattern recognition. Typically in clustering there is no one perfect solution to the problem, but algorithms seek to minimize a certain mathematical criterion (which varies between algorithms). Minimizing such criteria is known to be NP-hard for the general problem of partitioning d-dimensional data into k sets [6]. Algorithms like k-means seek local rather than the global minimum solutions, but can get stuck at poor solutions. In these cases we consider that a solution which better minimizes the mathematical criterion (for the same number of centers) to be a better-quality clustering.

We use the term "center-based clustering" to refer to the family of algorithms such as k-means and Gaussian expectation-maximization, since they use a number of "centers" to represent and/or partition the input data. Each center defines a cluster with a central point and perhaps a covariance matrix. Center-based clustering algorithms begin with a guess about the solution, and then refine the positions of centers until reaching a local optimum. These methods can work well, but they can also converge to a local minimum that is far from the global minimum, i.e. the clustering that has the highest quality according to the criterion in use. Converging to bad local optima is related to sensitivity to initialization, and is a primary problem of data clustering.

The goal of this work is to understand and extend center-based clustering algorithms to find good-quality clusterings in spatial data. Recently, many wrapper methods have been proposed to improve clustering solutions. A wrapper method is one that transforms the input or output of the clustering algorithm, and/or uses the algorithm multiple times. One commonly used wrapper method is simply running the clustering algorithm several times from different starting points (often called random restart), and taking the best solution. Algorithms such as used in [10] push this technique to its extreme, at the cost of computation. Another wrapper method is searching for the best initializations possible; this has been looked at in [16, 12, 3]. This is fruitful research, as many clustering algorithms are sensitive to their initializations. Other research [15, 17] has been looking at finding the appropriate number of clusters, and analyzing the difference between the cluster solution and the dataset. This is useful when the appropriate number of centers is unknown, or the algorithm is stuck at a sub-optimal solution.

These approaches are beneficial, but they are attempting to fix the problems of clustering algorithms externally, rather than to improve the clustering algorithms themselves. We are interested in improving the clustering algorithms directly to make them less sensitive to initializations and give better solutions. Of course, any clustering algorithm developed could benefit from wrapper methods.

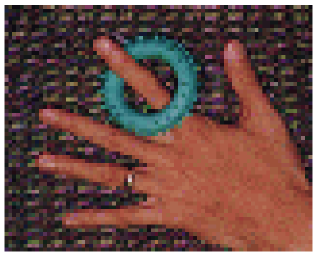

Figure 1: The original "hand" image used for segmentation. The image size is 80x64 pixels and is full color.

Recently, Zhang *et al.* introduced a new clustering algorithm called k-harmonic means (KHM) that arises from an optimization criterion based on the harmonic mean [22, 21]. This algorithm shows promise in finding good clustering solutions quickly, and outperforms k-means (KM) and Gaussian expectation-maximization (GEM) in many tests. The KHM algorithm also has a novel feature that gives more influence to data points that are not well-modeled by the clustering solution, but is unknown how important this feature is. Our work is a first answer to this question.

In this paper, we present a unified framework for looking at center-based clustering algorithms, and then derive two new algorithms that are based on properties of KM and KHM. The algorithms are compared analytically and empirically.

2. IMAGE SEGMENTATION

We motivate the need for good-quality clustering algorithms with an image segmentation example. Image segmentation is the task of grouping the pixels of an image according to color, texture, and location. Clustering is an important part of image segmentation. There are two parts to image segmentation. First, we define a set of useful features on image pixels (such as position, color, and texture) that are used as an input to a clustering algorithm. Second, we feed the data into a clustering algorithm, and cluster it to produce the segmentation.

We use the image "hand" (see Figure 1) from computer vision literature [4]. Rather than using complicated features such as texture or color histograms, we simply convert the image to a dataset with 5 dimensions. The first two dimensions are the pixel coordinates (x, y), and the last three dimensions are the color values (l, u, v) in LUV color space. LUV is a standard in computer graphics for representing a perceptually-uniform colors. Other image attributes may be more appropriate (e.g. texture similarity or color histogram windows around each pixel), but we are interested in the clustering algorithm, and not the inputs to the algorithm. Other image segmentation methods [4, 19] also use similarity metrics for spatial (x and y), color, and texture information.

We normalize each dimension to zero-mean and unit variance, and then cluster the data using two algorithms (KM and KHM), two different initializations (Forgy and Random Partition, described later in the paper), and $k = 5$ clusters.

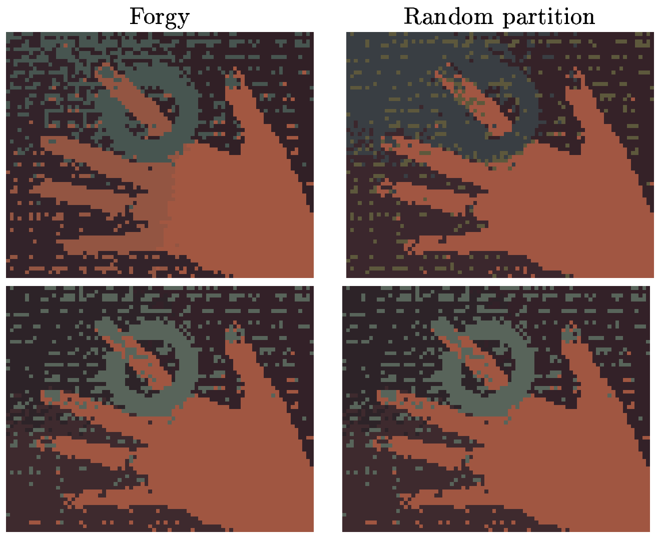

Figure 2: Image segmentation results. From top to bottom: KM, KHM. We chose $k = 5$ clusters on the data (x, y, l, u, v) of the original input image "hand". Each segment is colored by the average color of the segment. Please see a full-color version of this paper for the correct view. Note that KHM has more clearly segmented the hand from the background, and its segmentation is the same for both initializations. The KM segmentation varies depending on its initialization, and its segmentations are poorer. Notice that the hand is split into two segments by KM with Forgy initialization, and the differences around the tip of the index finger.

We found that KHM was able to find best-quality clusterings compared with KM, according to the KM quality metric. Table 1 shows the KM quality metric for both KM and KHM (lower is better). Also, KHM found the same segmentation for both types of initializations, while KM behaved very differently depending on the initialization.

Figure 2 shows the outputs for the image segmentation task, with $k = 5$ clusters. Each segment in the output image is colored by the average color within the segment. Please see a full-color version of this paper for the correct view. The segmentation by KM does poorly because it splits the hand into two segments with Forgy initialization, and it has a poor segmentation of the index finger with Random Partition initialization. However, KHM does a better job of clearly segmenting the hand away from the background and has a visually consistent segmentation across initializations. Thus we see that the better-quality clustering (according to the KM quality metric) has given a better-quality image segmentation (upon visual inspection).

Several recent algorithms in image segmentation [19, 13] are based on eigenvector computations on distance matrices. These "spectral" algorithms still use k-means as a post-processing step to find the actual segmentation, usually in a lower-dimensional space than the original input. Thus there is a great need to have good-quality clustering algorithms like k-means. Additionally, these spectral algorithms are expensive to use, costing $O(n^3)$ time to use, where n is the number of input data points. Another class of clustering algorihtms, agglomerative clustering algorithms, cost $O(n^2)$ time to compare the distances between all pairs of points. For large images, or real-time video segmentation, speed is essential. We are interested in linear-time $O(n)$ clustering algorithms, which is what we consider in this paper.

Table 1: Quality of solutions for image segmentation. Numbers are for the k-means quality metric; lower values are better. The KHM algorithm found better-quality clusterings than KM, and found the same clustering regardless of initialization.

	Forgy	Random Partition
KM	10398	10244
KHM	10137	10137

3. CENTER-BASED CLUSTERING

The algorithms k-means, Gaussian expectation-maximization, fuzzy k-means, and k-harmonic means are in the family of center-based clustering algorithms. They each have their own objective function, which defines how good a clustering solution is. The goal of each algorithm is to minimize its objective function. Since these objective functions cannot be minimized directly, we use iterative update algorithms which converge on local minima.

3.1 General iterative clustering

We can formulate a general model for the family of clustering algorithms that use iterative optimization, following [8], and use this framework to make comparisons between algorithms. Define a d-dimensional set of n data points $X = \{x_1, \ldots, x_n\}$ as the data to be clustered. Define a d-dimensional set of k centers $C = \{c_1, \ldots, c_k\}$ as the clustering solution that an iterative algorithm refines.

A membership function $m(c_j|x_i)$ defines the proportion of data point x_i that belongs to center c_j with constraints $m(c_j|x_i) \geq 0$ and $\sum_{j=1}^{k} m(c_j|x_i) = 1$. Some algorithms use a *hard* membership function, meaning $m(c_j|x_i) \in \{0,1\}$, while others use a *soft* membership function, meaning $0 \leq m(c_j|x_i) \leq 1$. Kearns and colleagues have analyzed the differences between hard and soft membership from an information-theoretic standpoint [9]. One of the reasons that k-means can converge to poor solutions is due to its hard membership function. However, the hard membership function makes possible many computational optimizations that do not affect accuracy of the algorithm, such as using kd-trees [14].

A weight function $w(x_i)$ defines how much influence data point x_i has in recomputing the center parameters in the next iteration, with constraint $w(x_i) > 0$. A dynamic, or changing, weight function was introduced in [21]. Giving variable influence to data in clustering has analogies to boosting in supervised learning [7]. Each approach gives more weight to data points that are not "well-covered" by the current solution. Unlike boosting, this approach does not create an ensemble of solutions.

Now we can define a general model of iterative, center-based clustering. The steps are:

1. Initialize the algorithm with guessed centers C.
2. For each data point x_i, compute its membership $m(c_j|x_i)$ in each center c_j and its weight $w(x_i)$.
3. For each center c_j, recompute its location from all data points x_i according to their memberships and weights:
$$c_j = \frac{\sum_{i=1}^{n} m(c_j|x_i)w(x_i)x_i}{\sum_{i=1}^{n} m(c_j|x_i)w(x_i)} \quad (1)$$
4. Repeat steps 2 and 3 until convergence.

Now we can compare algorithms based on their membership and weight functions. An alternative initialization procedure is to guess an initial partition, and then start the algorithm from step 3. The computational complexity of each algorithm in this paper is $O(nkd)$ for each update iteration (Equation 1). The algorithms vary by constant factors but have the same order complexity.

3.2 K-means

The k-means algorithm (KM) [11] partitions data into k sets. The solution is then a set of k centers, each of which is located at the centroid of the data for which it is the closest center. For the membership function, each data point belongs to its nearest center, forming a Voronoi partition of the data. The objective function that the KM algorithm optimizes is

$$KM(X,C) = \sum_{i=1}^{n} \min_{j\in\{1\ldots k\}} ||x_i - c_j||^2 \quad (2)$$

This objective function gives an algorithm which minimizes the within-cluster variance (the squared distance between each center and its assigned data points).

The membership and weight functions for KM are:

$$m_{KM}(c_l|x_i) = \begin{cases} 1\ ; & \text{if } l = \arg\min_j ||x_i - c_j||^2 \\ 0\ ; & \text{otherwise} \end{cases} \quad (3)$$

$$w_{KM}(x_i) = 1 \quad (4)$$

KM has a hard membership function, and a constant weight function that gives all data points equal importance. KM is easy to understand and implement, making it a popular algorithm for clustering.

3.3 Gaussian expectation-maximization

The Gaussian expectation-maximization (GEM) algorithm for clustering uses a linear combination of d-dimensional Gaussian distributions as the centers. It minimizes the objective function

$$GEM(X,C) = -\sum_{i=1}^{n} \log\left(\sum_{j=1}^{k} p(x_i|c_j)p(c_j)\right) \quad (5)$$

where $p(x_i|c_j)$ is the probability of x_i given that it is generated by the Gaussian distribution with center c_j, and $p(c_j)$ is the prior probability of center c_j. We use a logarithm to make the math easier (while not changing the solution), and we negate the value so that we can minimize the quantity (as we do with the other algorithms we investigate). See [2, pages 59–73] for more about this algorithm. The membership and weight functions of GEM are

$$m_{GEM}(c_j|x_i) = \frac{p(x_i|c_j)p(c_j)}{p(x_i)} \quad (6)$$

$$w_{GEM}(x_i) = 1 \quad (7)$$

Bayes' rule is used to compute the soft membership, and m_{GEM} is a probability since the factors in Equation 6 are probabilities. GEM has a constant weight function that gives all data points equally importance, like KM. Note that $w_{GEM}(x_i)$ is not the same as $p(x_i)$.

3.4 Fuzzy k-means

The fuzzy k-means algorithm (FKM; also called fuzzy c-means) [1] is an adaptation of the KM algorithm that uses a soft membership function. Unlike KM which assigns each data point to its closest center, the FKM algorithm allows a data point to belong partly to all centers, like GEM.

$$FKM(X,C) = \sum_{i=1}^{n}\sum_{j=1}^{k} u_{ij}^{r}||x_i - c_j||^2 \quad (8)$$

The parameter u_{ij} denotes the proportion of data point x_i that is assigned to center c_j, and is under the constraints $\sum_{j=1}^{k} u_{ij} = 1$ for all i and $u_{ij} \geq 0$. The parameter r has the constraint $r \geq 1$. A larger value for r makes the method "more fuzzy."

Bezdek and others give separate update functions for u_{ij} and c_j. The u_{ij} update equation depends only on C and X, so we incorporate its update function into the update for c_j. Then we can represent FKM in the form of the general iterative update of Equation 1. The membership and weight functions for FKM are:

$$m_{FKM}(c_j|x_i) = \frac{||x_i - c_j||^{-2/(r-1)}}{\sum_{j=1}^{k}||x_i - c_j||^{-2/(r-1)}} \quad (9)$$

$$w_{FKM}(x_i) = 1 \quad (10)$$

FKM has a soft membership function, and a constant weight function. As r tends toward 1 from above, the algorithm behaves more like standard k-means, and the centers share the data points less.

3.5 K-harmonic means

The k-harmonic means algorithm (KHM) is a method similar to KM that arises from a different objective function [21]. The KHM objective function uses the harmonic mean of the distance from each data point to all centers.

$$KHM(X,C) = \sum_{i=1}^{n} \frac{k}{\sum_{j=1}^{k}\frac{1}{||x_i - c_j||^p}} \quad (11)$$

Here p is an input parameter, and typically $p \geq 2$. The harmonic mean gives a good (low) score for each data point when that data point is close to any one center. This is a property of the harmonic mean; it is similar to the minimum function used by KM, but it is a smooth differentiable function.

The membership and weight functions for KHM are:

$$m_{KHM}(c_j|x_i) = \frac{||x_i - c_j||^{-p-2}}{\sum_{j=1}^{k}||x_i - c_j||^{-p-2}} \quad (12)$$

$$w_{KHM}(x_i) = \frac{\sum_{j=1}^{k}||x_i - c_j||^{-p-2}}{\left(\sum_{j=1}^{k}||x_i - c_j||^{-p}\right)^2} \quad (13)$$

Note that KHM has a soft membership function, and also a varying weight function. This weight function gives higher weight to points that are far away from every center, which aids the centers in spreading to cover the data.

The implementation of KHM needs to deal with the case where $x_i = c_j$. In this case we follow Zhang using $\max(||x_i - c_j||, \epsilon)$ and use a small positive value of ϵ. We also apply this technique for FKM and the algorithms discussed in Section 3. We have not encountered any numerical problems in any of our tests.

4. NEW CLUSTERING ALGORITHMS

We are interested in the properties of the new algorithm KHM. It has a soft membership function and a varying weight function, which makes it unique among the algorithms we have encountered. KHM has been shown to be less sensitive to initialization on synthetic data [21].

Here we analyze two aspects of KHM (the membership and the weight functions) and define two new algorithms we call Hybrid 1 and Hybrid 2. They are named for the fact that they are hybrid algorithms that combine features of KM and KHM. The purpose for creating these algorithms is to find out what effects the membership and weight functions of KHM have by themselves.

4.1 Hybrid 1: hard membership, varying weights

Hybrid 1 (H1) uses the hard membership function of KM. Every point belongs only to its closest center. However, H1 uses the KHM weight function, which gives more weight to points that are far from every center. We expect that this algorithm should converge more quickly than KM due to the weights, but will still have problems related to the hard membership function. As far as we know, adding weights in this manner to KM is a new idea.

The definitions of the membership and weight functions for H1 are:

$$m_{H1}(c_l|x_i) = \begin{cases} 1\ ;\ \text{if } l = \arg\min_j ||x_i - c_j||^2 \\ 0\ ;\ \text{otherwise} \end{cases} \quad (14)$$

$$w_{H1}(x_i) = \frac{\sum_{j=1}^{k}||x_i - c_j||^{-p-2}}{\left(\sum_{j=1}^{k}||x_i - c_j||^{-p}\right)^2} \quad (15)$$

4.2 Hybrid 2: soft membership, constant weights

Hybrid 2 (H2) uses the soft membership function of KHM, and the constant weight function of KM. The definitions of the membership and weight functions for H2 are:

$$m_{H2}(c_j|x_i) = \frac{||x_i - c_j||^{-p-2}}{\sum_{j=1}^{k} ||x_i - c_j||^{-p-2}} \quad (16)$$

$$w_{H2}(x_i) = 1 \quad (17)$$

Note that H2 resembles FKM. In fact, for certain values of r and p they are mathematically equivalent. It is interesting to note, then, that the membership function of KHM (from which we get H2) and FKM are also very similar. We investigate H2 and FKM as separate entities to keep clear the fact that we are investigating the membership and weight functions of KHM separately.

5. EXPERIMENTAL SETUP

We perform two sets of experiments to demonstrate the properties of the algorithms described in Sections 3 and 4. We want to answer several questions: how do different initializations affect each algorithm, what is the influence of soft versus hard membership, and what is the benefit of using varying versus constant weights.

Though each algorithm minimizes a different objective function, we measure the quality of each clustering solution by the square-root of the k-means objective function in Equation 2. It is a reasonable metric by which to judge cluster quality, and by using a single metric we can compare different algorithms. We use the square root because the squared distance term can exaggerate the severity of poor solutions. We considered running KM on the output of each algorithm, so that the KM objective function could be better minimized. We found that this did not help significantly, so we do not do this here.

Our experiments use two datasets already used in recent empirical work on clustering algorithms [23, 14], and a photograph of a hand from [4]. The algorithms we test are KM, KHM, FKM, H1, H2, and GEM. The code for each of these algorithms is our own (written in Matlab), except for GEM (FastMix code provided by [18]). We need to supply the the KHM, H1, and H2 with the parameter p, and FKM with r. We set $p = 3.5$ for all tests, as that was the best value found by Zhang. We set $r = 1.3$, as that is the best value we found based on our preliminary tests.

The two initializations we use are the Forgy and Random Partition methods [16]. The Forgy method chooses k data points from the dataset at random and uses them as the initial centers. The Random Partition method assigns each data point to a random center, then computes the initial location of each center as the centroid of its assigned points. The Forgy method tends to spread centers out in the data, while the Random Partition method tends to place the centers in a small area near the middle of the dataset. Random Partition was found to be a preferable initialization method for its simplicity and quality in [16, 12]. For GEM, we also initialize $p(c_j) = 1/k$ and initialize the covariance to be $0.2I$, where I is the identity matrix.

Before clustering, all datasets used in both experiments are shifted and re-scaled to give each dimension zero mean and unit variance. This is the standard z-score transformation. This can be a good idea before using algorithms based on

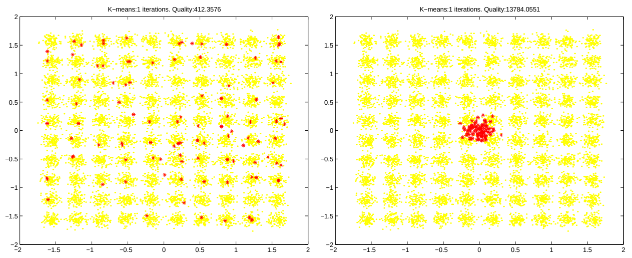

Figure 3: Experiment 1: Forgy (left) and Random Partition (right) initializations for the BIRCH dataset. Centers are shown in the dark color, data points in the light color. This dataset has a grid of 10x10 natural clusters.

distance metrics, as it gives the same influence to each dimension.

5.1 Experiment 1: BIRCH

The purpose of our first experiment is to illustrate the convergence properties of the different algorithms, and to show the need to improve clustering algorithms. We use a randomly generated synthetic dataset we call BIRCH, as defined by [23]. This dataset has $k = 100$ true clusters arranged in a 10x10 grid in $d = 2$ dimensions. Each cluster generates 100 data points from its own Gaussian distribution, for a total of $n = 10,000$ data points. The distance between two adjacent cluster means is $4\sqrt{2}$ with cluster radius of $\sqrt{2}$ (meaning the variance in each dimension is 1). We run each algorithm twice, once with the Forgy initialization, and once with the Random Partition initialization. Figure 3 shows the two initializations. We use the same randomly chosen initializations for all algorithms. Our results are similar for other random initializations.

5.2 Experiment 2: Pelleg and Moore data

The second experiment uses a synthetic dataset based on work by [14]. Here we run many tests to determine the average-case behavior of the algorithms. We test datasets of dimensions 2, 4, and 6 to show that all these algorithms work well in low dimensions. Each dataset has $k = 50$ true natural clusters which generate $n = 2500$ total data points. The true cluster centers are chosen at random in the unit hypercube, then 2500 data points are generated by choosing a cluster randomly, and generating a data point according to a Gaussian distribution with standard deviation $s = d \times 0.012$ and mean at the true cluster center. We generate data that is more separated (clusters have less overlap) than the work by Pelleg and Moore (who used $s = d \times 0.025$), because this presents a more difficult task to the clustering algorithms. This is because it is harder for centers to move freely through the whole dataset due to gaps between natural clusters.

For each $d \in \{2, 4, 6\}$ we generate 100 datasets, and two initializations (Random Partition and Forgy) for each dataset. Then we test each algorithm from both of these initializations. For each algorithm we allow it to run for 100 iterations, which is plenty for the algorithms to converge.

Table 2: Experiment 1: Quality of solutions for one run on the BIRCH dataset, using Forgy and Random Partition initializations. Lower quality scores are better. "Clusters found" is the number of true clusters (maximum 100) in which the algorithm placed at least one center.

	$\sqrt{KM}$ quality		Clusters found	
	Forgy	RP	Forgy	RP
GEM	15.530	24.399	77	49
KM	12.771	18.396	83	60
H1	12.159	15.242	86	72
FKM	11.612	10.441	89	93
H2	10.670	9.908	92	95
KHM	10.255	9.999	94	95

6. EXPERIMENTAL RESULTS

6.1 Experiment 1: BIRCH

Running each algorithm on the BIRCH dataset once gives an intuition for how each behaves. Figure 3 shows the two initializations we use. The results of KM, GEM, and KHM's runs are shown in Figure 4 and the cluster qualities for all are shown in Table 2. FKM, H2, and KHM all found good clusterings for both types of initializations, and they are all soft membership algorithms.

The two hard membership algorithms, KM and H1, have distinctly different behavior for the two initializations. Starting from Forgy initialization these two algorithms perform reasonably well, but starting from the Random Partition these algorithms converge with many centers remaining in the middle of the dataset, "trapped" there by hard assignment. This is because the hard membership function prevents centers from moving if they do not own enough points. In Table 2 we show the number of true clusters found, which is the number of true clusters (out of 100) that received a center by the algorithm.

Although GEM has a soft membership function, it does poorly on this dataset due to some centers having variance that is too large and taking over several clusters. The output of GEM initialized by Random Partition appears to have more centers concentrated in the middle of the dataset, where the centers began. This is similar to the hard membership results. The FastMix implementation we used for GEM started with 100 centers and removes centers whose prior became too small. For this reason, it ended with 98 (Forgy) and 81 (Random Partition) centers depending on the initialization. FastMix has the ability to search for the number of centers using density estimation. We tried starting FastMix without a pre-defined number of centers, and it found 23.

6.2 Experiment 2: Pelleg and Moore data

Our second experiment shows the average performance of the algorithms compared over many randomly generated data sets in several dimensions. For each dataset $X_{d,i}$ where $d \in \{2, 4, 6\}$ and $1 \leq i \leq 100$ we compute the optimal KM partition $O_{d,i}$ by running KM to convergence starting with

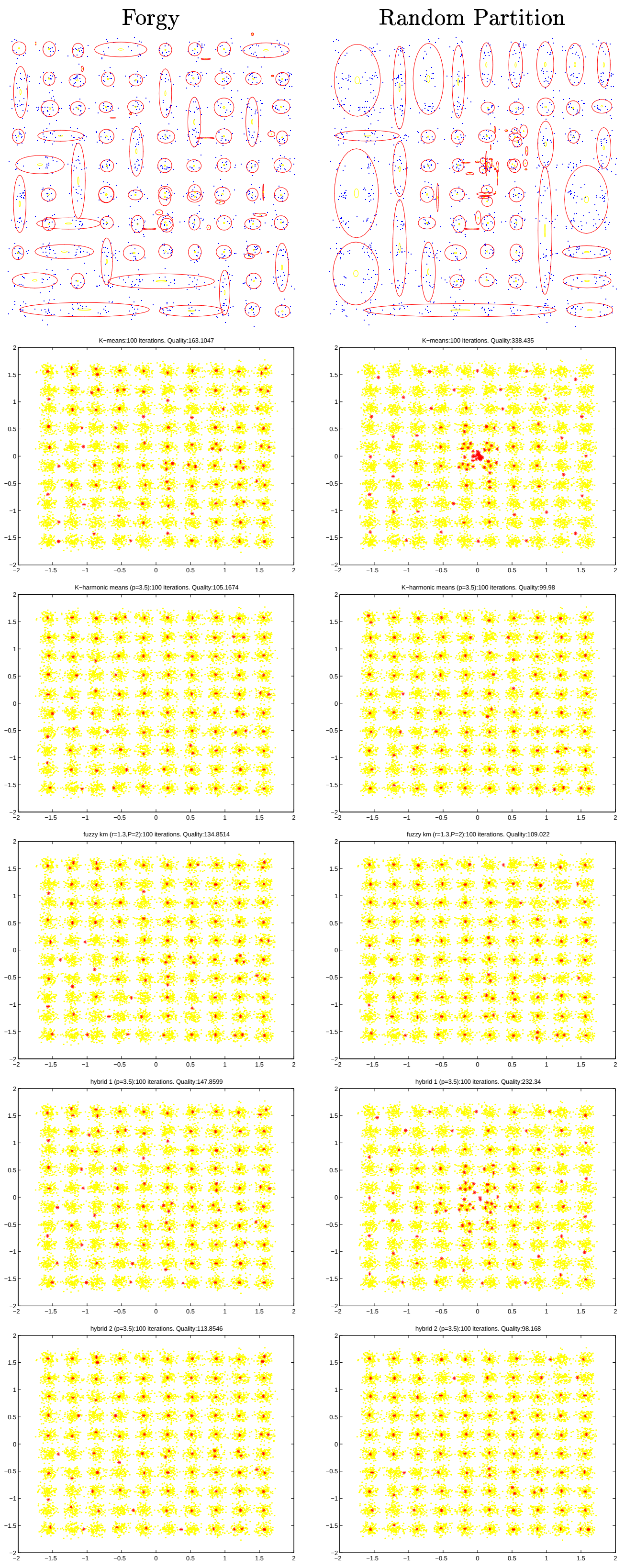

Figure 4: Experiment 1: Convergence on the BIRCH dataset. From top to bottom: GEM, KM, KHM, FKM, H1, H2. GEM and KM both converge to very low-quality optima, while KHM does not. FastMix software generated the plots for GEM, showing the 1-sigma contours.

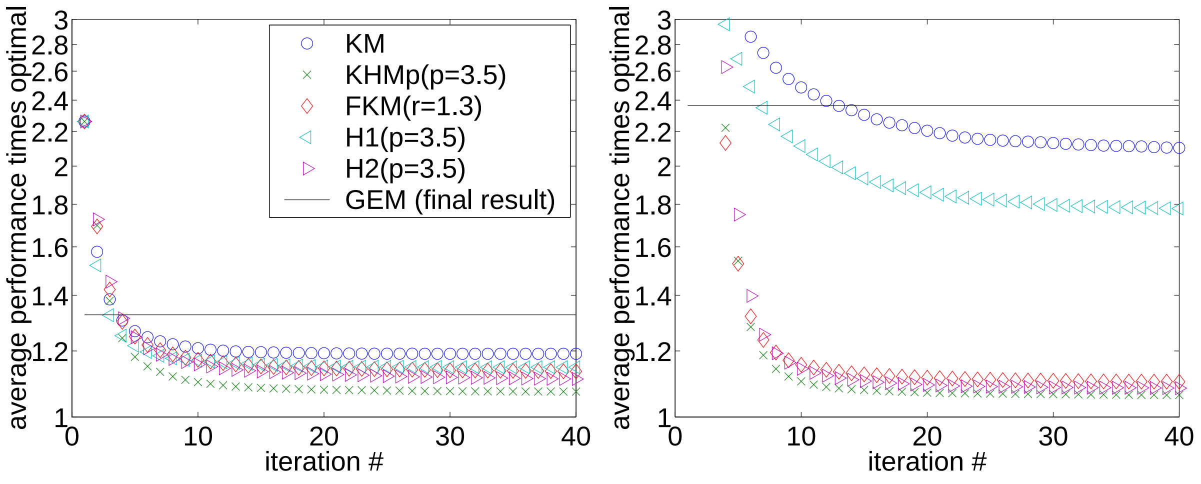

Figure 5: Experiment 2: Convergence curves starting from Forgy (top) and Random Partition (bottom) initializations on 2-d synthetic data. The x-axis shows the number of iterations, and the y-axis (log scale) shows average clustering quality score, where lower values are better. Only the final results for GEM are shown. Note that KM and GEM perform worse than every other algorithm.

the centers that generated the data sets. Then we compute the score of a clustering $C_{d,i}$ as the ratio

$$R_{d,i} = \sqrt{\frac{KM(X_{d,i}, C_{d,i})}{KM(X_{d,i}, O_{d,i})}} \qquad (18)$$

Table 4 shows the mean and standard deviation of $R_{d,i}$ for each algorithm, computed using 100 datasets in 2 dimensions. Table 3 shows the point-wise comparison of each algorithm for the same experiment. It is clear from this as well that soft membership algorithms (KHM, FKM, H2) perform better than hard membership algorithms (KM, H1) in both average performance and variance. The results for 4 and 6 dimensional datasets are very similar, so we do not report them here.

Figure 5 shows the speed of convergence of each algorithm for $d = 2$ dimensions. The x-axis shows the iteration number, and the y-axis shows the average k-means quality ratio at that iteration, computed using the 100 datasets. We can see that GEM and KM are uniformly inferior to every other algorithm, and that the soft membership algorithms KHM, H2, and FKM move quickly to find good solutions. Only the final result for GEM is plotted as we cannot capture clustering progress before the FastMix software terminates.

FastMix has the ability to add and remove centers to better fit its data. FastMix adds a center if the model underpredicts the data and removes a center if its prior probability is too low. We expect that FastMix's ability to add centers would be helpful in a dataset in which clusters are well-separated. For experiment 2, FastMix began with 50 centers and only removed centers. FastMix converged with an average of 48.39 centers (Forgy) and 40.13 centers (Random Partition) in the 2-dimension test. This shows that GEM is also sensitive to poor initializations.

Table 4: Experiment 2: The mean and standard deviation of $R_{2,i}$, the ratio between the k-means quality and the optimum, over 100 datasets, in 2 dimensions. Lower values are better. Results for 4 and 6 dimensions are similar, and have the same ranking.

	Forgy	Random Partition
GEM	1.3262 +/- 0.1342	2.3653 +/- 0.4497
KM	1.1909 +/- 0.0953	2.0905 +/- 0.2616
H1	1.1473 +/- 0.0650	1.7644 +/- 0.2403
FKM	1.1281 +/- 0.0637	1.0989 +/- 0.0499
H2	1.1077 +/- 0.0536	1.0788 +/- 0.0416
KHM	1.0705 +/- 0.0310	1.0605 +/- 0.0294

7. CONCLUSIONS

Our experiments clearly show the superiority of the k-harmonic means algorithm (KHM) for finding clusterings of high quality in low dimensions. Our algorithms H1 and H2 let us study the effects of the KHM weight and membership separately. They show that soft membership is essential for finding good clusterings, as H2 performs nearly as well as KHM, but that varying weights are beneficial with a hard membership function, since H1 performs better than KM. Varying weights are intuitively similar to the weights applied to training examples by boosting [7]. It remains to be seen whether this analogy can be made precise.

Previous work in initialization methods has concluded that the Random Partition method is good for GEM and for KM, but our experiments do not confirm this conclusion. The Forgy method of initialization (choosing random points as initial centers) works best for GEM, KM, and H1. Overall, our results suggest that the best algorithms available today are FKM, H2, and KHM, initialized by the Random Partition method.

Table 3: Experiment 2: Competition matrix for 2-d data starting from Forgy (left) and Random Partition (right) initializations. Each entry shows the number of times (maximum 100) that the algorithm in the column had a better-quality clustering than the algorithm in the row. The results for 4 and 6 dimensions are similar, so we do not report them here. In particular, KHM is better than KM for 99 to 100 of 100 times in each dimension tested.

	GEM	KM	KHM	FKM	H1	H2
GEM		97	100	100	98	100
KM	3		99	91	73	91
KHM	0	1		15	7	24
FKM	0	9	85		19	62
H1	2	27	93	81		90
H2	0	9	76	38	10	
sum:	5	143	453	325	207	367

	GEM	KM	KHM	FKM	H1	H2
GEM		100	100	100	100	100
KM	0		100	100	100	100
KHM	0	0		21	0	34
FKM	0	0	79		0	70
H1	0	0	100	100		100
H2	0	0	66	30	0	
sum:	0	100	445	351	200	404

Clustering in high dimensions has been an open problem for many years. However, recent research has shown that it may be preferable to use dimensionality reduction techniques before clustering, and then use a low-dimensional clustering algorithm such as k-harmonic means, rather than clustering in the high dimension directly. In [5] the author shows that using a simple, inexpensive linear projection preserves much of the properties of data (such as cluster distances), while making it easier to find the clusters. Thus there is a need for good-quality, fast clustering algorithms for low-dimensional data, such as k-harmonic means.

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