

Clustering

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Clustering



- Unsupervised learning (no labels for training) Group data into similar classes that Maximize similarity within clusters

- Minimize similarity between clusters



Can be hard to define, but we know it when we see it.

What is Similarity?

What is a natural grouping?







Simpson's Family

School Employees

Choice of clustering criterion can be task-dependent



Females

Males

Defining Distance Measures



Similarity: $s(x_1, x_2)$

Common Distance Measures

• Euclidean Distance





Common Similarity Measures

Inner Product

 $\langle x, y \rangle = x_1 y_1 + x_2 y_2 + \dots + x_k y_k$

Cosine Similarity

 $cosine(x, y) = \frac{\langle x, y \rangle}{||x|| ||y||}$

Jaccard Similarity

 $J(x, y) = \frac{|x \cap y|}{|x \cup y|}$ If x and y are sets

Similarity: Kernel Functions

Formal Definition: Inner Product (in Hilbert space)

k(x, x')

Radial Basis Function (RBF

Squared Exponential (SE)

Automatic Relevance Determination (ARD)

$$= \langle \phi(x), \phi(x') \rangle \bullet \qquad \text{Feature map} \\ \phi: \mathbb{R}^{\mathsf{D}} \to \mathbb{R}^{\mathsf{E}}$$

In Practice: Can compute directly from x and x'

$$k(x, x') = \exp^{-\frac{1}{2}\gamma^{-2}||x-x'||^2}$$

$$k(\mathbf{x},\mathbf{x}') = \exp^{-\frac{1}{2}\mathbf{x}^{\top}\mathbf{\Sigma}^{-1}\mathbf{x}'}$$
$$k(\mathbf{x},\mathbf{x}') = \exp^{-\frac{1}{2}\sum_{i=1}^{d}\frac{(x_i-x_i')^2}{\sigma_i^2}}$$

Inner Product vs Distance Measure

Inner Product

- $\langle A, B \rangle = \langle B, A \rangle$
- $\langle \alpha A, B \rangle = \alpha \langle A, B \rangle$
- $\langle A, A \rangle \ge 0$, $\langle A, A \rangle = 0$ iff A = 0

Distance Measure

- D(A, B) = D(B, A)
- D(A, A) = 0
- D(A, B) = 0 iff A = B
- $D(A, B) \leq D(A, C) + D(B, C)$

Symmetry Linearity Postive-definiteness

Symmetry Constancy of Self-Similarity Positivity (Separation) Triangular Inequality



Centroid-based (K-means, K-medoids)



Notion of Clusters: Voronoi tesselation



Notion of Clusters: Cut off dendrogram at some depth

Connectivity-based (Hierarchical)



Density-based (DBSCAN, OPTICS)



Notion of Clusters: Connected regions of high density



Distribution-based (Mixture Models)





Notion of Clusters: Distributions over features



Clustering

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Algorithm and Objective



- Idea: Find Clusters with Smallest Variance
- Points: $X = [\mathbf{x}_1, ..., \mathbf{x}_N]$, where each $\mathbf{x}_n \in \mathbb{R}^D$
- Cluster assignments: $[z_1, ..., z_N]$, where each $z_n \in \{1, ..., K\}$
- Cluster means: $[\mu_1, ..., \mu_K]$, where each $\mu_k \in \mathbb{R}^D$
- Goal: find clusters with small variance (all points near their means)



K-means Algorithm

• Randomly initialize means $[\mu_1, ..., \mu_K]$ • Repeat until [μ_1 , ..., μ_K] unchanged • Assign all points to nearest cluster $z_n = \operatorname{argmin} ||\mathbf{x}_n - \boldsymbol{\mu}_k||^2$ • Update cluster means



Randomly initialize K means μ_k



Assign each point to closest cluster, then update means to average of points



Assign each point to closest cluster, then update means to average of points



Repeat until convergence (no points reassigned, means unchanged)



K-means Objective

Loss: Variance of All Clusters Combined/ Sum Square Error (SSE)/ Sum Square Distances.

 $L(z_1, \dots, z_N) = \sum_{k=1}^{n} N_k \sigma_k^2 - Variance of cluster k$

Number of points in cluster k (clusters with more points contribute more to the loss)

Goal: Minimize Loss with Respect to Assignments

 $\min_{z} L(z_1,\ldots,z_N)$



Mean and Variance of a Cluster



Number of Points in a Cluster

$$\sum_{n=1}^{N} I[z_n = k] \qquad I[z_n = k] = \begin{cases} 1 & z_n = k, \\ 0 & z_n \neq k. \end{cases}$$

Mean of a Cluster

$$\frac{1}{N_k} \sum_{n=1}^N I[z_n = k] \mathbf{x}_n$$

Variance of a cluster

 σ_k

$$\frac{1}{N_k} \sum_{n=1}^N I[z_n = k] ||x_n - \mu_k||^2$$

K-means Objective

Loss: Variance of Clusters (given assignments)



$$\sigma_{k} \sigma_{k}^{2} \qquad \sigma_{k} = \frac{1}{N_{k}} \sum_{n=1}^{N} I[z_{n} = k] ||x_{n} - \mu_{k}|$$

$$\int_{1}^{N} I[z_{n} = k] ||x_{n} - \mu_{k}||^{2} \quad \mu_{k} = \frac{1}{N_{k}} \sum_{n=1}^{N} I[z_{n} = k]$$

Goal: Minimize Loss with Respect to Assignments

min $L(z_1,\ldots,z_N)$

K^N possible combinations; can't solve via brute force









K-means Iteration

Solution: Define Loss in terms of μ and z

$$\sum_{k=1}^{N} \sum_{n=1}^{N} I[z_n = k] ||x_n - \mu_k||^2$$

- K-means Algorithm
- Randomly initialize μ
 - Repeat until L(μ , z) does not improve
 - Minimize L(μ, z) with respect to z (assign points to closest cluster)
 - 2. Minimize $L(\mu, z)$ with respect to μ (place clusters close to points)



K-means Algorithm

Randomly initialize means [μ₁, ..., μ_κ] **Repeat until L(μ, z) unchanged**

• Assign all points to nearest cluster

$$z_n = \underset{k}{\operatorname{argmin}} ||x_n - \mu_k||^2 = \underset{z_n}{\operatorname{argmin}} L(z, \mu)$$

Update cluster means

$$\boldsymbol{\mu}_{k} = \frac{1}{N_{k}} \sum_{\substack{n: z_{n} = k}} \boldsymbol{x}_{n} = \underset{\boldsymbol{\mu}_{k}}{\operatorname{argmin}} L(\boldsymbol{z}, \boldsymbol{\mu})$$

Each iteration reduces loss until (local) optimum is found







Choosing K

K=2, L=173

K=3, L=134





Choosing K



"Elbow finding" (a.k.a. "knee finding") Set K to value just above "abrupt" increase



Initialization, Speed-ups and Limitations

Choice of Initialization



Minimize L(μ, z) with respect to μ
 (place clusters close to points)

Loss: Sum of Squared Distances

$$= \sum_{k=1}^{K} \sum_{n=1}^{N} I[z_n = k] (x_n - \mu_k)^2$$

- Randomly initialize μ
- Alternate between two steps
 - Minimize L(μ, z) with respect to z
 (assign points to closest cluster)

Choice of Initialization



Loss: Sum of Squared Distances

$$= \sum_{k=1}^{K} \sum_{n=1}^{N} I[z_n = k] (x_n - \mu_k)^2$$

Randomly initialize μ What is a good choice?

Alternate between two steps

1. Minimize $L(\mu, z)$ with respect to z (assign points to closest cluster)

2. Minimize $L(\mu, z)$ with respect to μ (place clusters close to points)



"Good" Initialization of Centroids



"Bad" Initialization of Centroids





Importance of Initial Centroids

Good initialization: Pick one point in each cluster

What is the chance of *randomly* selecting one point from each of K clusters? (assume each cluster has size n = N/K)

 $\frac{\text{ways to select one from each cluster}}{\text{ways to select K centroids}} = \frac{K!n^{K}}{(Kn)^{K}} = \frac{K!}{K^{K}} \approx \sqrt{2\pi K} e^{-K}$

Implication: We will almost always have multiple initial centroids in same cluster. $\approx 10^{-4}$ for K = 10

 $\approx 10^{-8}$ for K = 20



Example: 10 Clusters



5 pairs of clusters, two initial points in each pair

Iteration 4



Example: 10 Clusters



Iteration 4


Picking the initialization cluster centers: a significant issue

 \hat{z} : cluster assignments returned by K-means, a local minimizer of the loss

 z_{opt} : the global minimizer of the loss

It is the speed and simplicity of the k-means method that make it appealing, not its accuracy. Indeed, there are many natural examples for which the algorithm generates arbitrarily bad clustering (i.e., $L(\hat{z})/L(z_{opt})$ is unbounded even when N and K are fixed). This does not rely on an adversarial placement of the starting centers, and in particular, it can hold with high probability if the centers are chosen uniformly at random from the data points.

Arthur, David, and Sergei Vassilvitskii. *k-means++: The advantages of careful seeding*. Stanford, 2006.

Importance of Initial Centroids

Initialization tricks

- Use multiple restarts
 - Helps, but probability is not on your side
- Initialize with hierarchical clustering
- Select more than K points, keep most widely separated points.
- Bisecting K-means
- K-means++

Furthest first

- Pick first center to be the mean of the data $M_1 \leftarrow \{\mu_1\}$
- to the closest center is largest.

$$\mu_{j+1} \leftarrow \operatorname{argmax}_{x \in X} [D_{min}(x \mid M_{j+1} \rightarrow M_j \cup \{\mu_{j+1}\}\}]$$

Problem: Outliers get chosen as centers.

• For the subsequent centers iteratively pick the point whose distance

 $D_{min}(x, M_j)$ distance of x to the closest center in M_j . (x, M_j)]

> M_j is the set of centroids at j^{th} step.



K-Means ++

1.Pick first center uniformly at random

$$M_1 \leftarrow \{\mu_1\}$$

2. For the subsequent centers iteratively pick a point $x \in X$ randomly with probability proportional to $D_{min}(x, M_i)$

$$\mu_{j+1} \leftarrow x \sim p(x) = \frac{D_{min}(x, M_j)^2}{\sum_{x \in X} D_{min}(x, M_j)^2}$$
$$M_{j+1} \rightarrow M_j \cup \{\mu_{j+1}\}$$

Here the outliers still have a high probability of being selected compared to other points individually. However, the cumulative probability of points having moderately large distances lying in a dense region dominate the probability as a group.

Arthur, David, and Sergei Vassilvitskii. *k-means++: The advantages of careful seeding*. Stanford, 2006.

 $D_{min}(x, M_j)$ distance of x to the closest center in M_j . M_i is the set of centroids at j^{th} step.

Theoretical guarantees when using K-Means++ $E[L(\hat{z})] \le (8 \log K + 2)L(z_{opt})$

	Ave	rage ϕ	Mini	$\operatorname{mum}\phi$	Average T		
k	k-means	k-means++	k-means	k-means++	k-means	k-means++	
10	135512	126433	119201	111611	0.14	0.13	
25	48050.5	15.8313	25734.6	15.8313	1.69	0.26	
50	5466.02	14.76	14.79	14.73	3.79	4.21	

Table 2: Experimental results on the Norm-25 dataset (n = 10000, d = 15)

	Ave	rage ϕ	Mini	$\operatorname{mum}\phi$	Average T		
k	k-means	k-means++	k-means	k-means++	k-means	k-means++	
10	7553.5	6151.2	6139.45	5631.99	0.12	0.05	
25	3626.1	2064.9	2568.2	1988.76	0.19	0.09	
50	2004.2	1133.7	1344	1088	0.27	0.17	

Table 3: Experimental results on the *Cloud* dataset (n = 1024, d = 10)

	Ave	$\operatorname{rage} \phi$	Mini	$\operatorname{mum}\phi$	Average T		
k	k-means	k-means++	k-means	k-means++	k-means	k-means++	
10	$3.45 \cdot 10^8$	$2.31 \cdot 10^{7}$	$3.25 \cdot 10^8$	$1.79 \cdot 10^{7}$	107.5	64.04	
25	$3.15 \cdot 10^8$	$2.53 \cdot 10^{6}$	$3.1 \cdot 10^8$	$2.06 \cdot 10^{6}$	421.5	313.65	
50	$3.08 \cdot 10^8$	$4.67 \cdot 10^{5}$	$3.08 \cdot 10^8$	$3.98 \cdot 10^{5}$	766.2	282.9	

Table 4: Experimental results on the *Intrusion* dataset (n = 494019, d = 35)

Here ϕ is same as the loss



K-means Clustering

Speed-ups

K-means Clustering

Finding new cluster assignments

To compute all point-center distances

O(KND) computational complexity (per iteration) for *K* clusters, *N* points, and *D* features.

Updating the cluster centers O(ND) computational

complexity (per iteration)

Can it be reduced further if only a few cluster assignments change?

K-means Algorithm

- Randomly initialize means [μ₁, ..., μ_κ]
- Repeat until L(μ, z) unchanged

Update cluster means

• Assign all points to nearest cluster

 $z_n = \operatorname{argmin} ||\mathbf{x}_n - \boldsymbol{\mu}_k||^2$



O(NKD) per iteration is prohibitive in high dimensions and large K!

The core idea for cutting on distance computation

When updating the cluster assignments not all pointcenter distances need be computed

Also true when

$$d(x, c_1) \le u \le \frac{d(c_1, c_2)}{2}$$
Upper bound
for $d(x, c_1)$

If distance between x and center c_1 is relatively small compared to that between c_1 and another center c_2 , the distance between x and c_2 need not be computed



 $d(x, c_1) \le \frac{d(c_1, c_2)}{2} \implies d(x, c_1) \le d(x, c_2)$

Exploit triangle inequality



 $d(x, z) \le d(x, y) + d(y, z)$



Elkan's accelerated K-means

Before cluster assignments. Right after -centers have moved. Closest center might not be the assigned center.

Conditions Checked: 1. $u(i) \le s(a(i))$

> i^{th} point cluster assignment need not be changed. No distance involving the i^{th} point needs to be computed.

2. $u(i) \le l(i,j)$ or $u(i) \le \frac{d(c(a(i)), c(j))}{2}$

 i^{th} point cluster assignment might change, but it won't be assigned to center j. Distance from the j^{th} center need not be computed.

a(i): contains the cluster index currently assigned to the i^{th} point.

u(i): contains an upper

bound to the distance of the

 i^{th} point to its current center

0

c(j): is the j^{th} center.

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S(j): is equal to half the distance of j^{th} center to its closest center

l(i, j): contains a lower bound of the distance of the i^{th} point to the j^{th} center

Bounding the distance of x from a center c after it moves to c^*

Distance computation: vector operation Upper and lower bound: scalar operation





Algorithm 3 Elkan's algorithm—using k lower bounds per point and k^2 centercenter distances procedure ELKAN(X, C) $a(i) \leftarrow 1, u(i) \leftarrow \infty, \forall i \in N$ {Initialize invalid bounds, all in one cluster.} $\ell(i, j) \leftarrow 0, \forall i \in N, j \in K$ while not converged do compute $||c(j) - c(j')||, \forall j, j' \in K$ 5: compute $s(j) \leftarrow \min_{j' \neq j} \|c(j) - c(j')\|/2, \forall j \in K$ for all $i \in N$ do if $u(i) \leq s(a(i))$ then continue with next *i r*: tells if the upper bound $r \leftarrow \text{True}$ needs to be tightened. for all $j \in K$ do 10: $z \leftarrow \max(\ell(i, j), \|c(a(i)) - c(j)\|/2)$ if j = a(i) or $u(i) \le z$ then continue with next j if r then $u(i) \leftarrow \|x(i) - c(a(i))\|$ 15: $r \leftarrow False$ if $u(i) \leq z$ then continue with next j $\ell(i, j) \leftarrow ||x(i) - c(j)||$ Both upper bound and the lower bound are tight on this step. if $\ell(i, j) < u(i)$ then $a(i) \leftarrow j \quad u(i) \leftarrow l(i, j)$ The upper bound should be updated at this step for all $j \in K$ do {Move the centers and track their movement} 20: move c(j) to its new location let $\delta(j)$ be the distance moved by c(j)for all $i \in N$ do {Update the upper and lower distance bounds} $u(i) \leftarrow u(i) + \delta(a(i))$ for all $j \in K$ do $\frac{\ell(i,j) \leftarrow \delta(j)}{\ell(i,j) - \delta(j)} \max(0,l(i,j) - \delta(j))$ 25:



Algorithm 3 Elkan's algorithm—using k lower bounds per point and k^2 centercenter distances procedure ELKAN(X, C) $a(i) \leftarrow 1, u(i) \leftarrow \infty, \forall i \in N$ {Initialize invalid bounds, all in one cluster.} $\ell(i, j) \leftarrow 0, \forall i \in N, j \in K$ while not converged do compute $||c(j) - c(j')||, \forall j, j' \in K$ 5: compute $s(j) \leftarrow \min_{j' \neq j} \|c(j) - c(j')\|/2, \forall j \in K$ for all $i \in N$ do if $u(i) \leq s(a(i))$ then continue with next i $r \leftarrow \text{True}$ for all $j \in K$ do 10: $z \leftarrow \max(\ell(i, j), \|c(a(i)) - c(j)\|/2)$ if j = a(i) or $u(i) \le z$ then continue with next j if r then $u(i) \leftarrow \|x(i) - c(a(i))\|$ $r \leftarrow False$ if $u(i) \leq z$ then continue with next j $\ell(i, j) \leftarrow \|x(i) - c(j)\|$ if $\ell(i, j) < u(i)$ then $a(i) \leftarrow j$ for all $j \in K$ do {Move the centers and track their movement} 20: move c(j) to its new location let $\delta(j)$ be the distance moved by c(j)for all $i \in N$ do {Update the upper and lower distance bounds} $u(i) \leftarrow u(i) + \delta(a(i))$ for all $j \in K$ do $\ell(i,j) \leftarrow \ell(i,j) - \delta(j) \quad \max(0,l(i,j) - \delta(j))$ 25:

Since the bounds are loose in the first iteration, all distances will be computed: O(NDK)

 $O(K^2D)$

O(N) $O(\alpha_1 NK)$ α_1 is the fraction of times the first condition is not satisfied satisfied

 $O(\alpha_1 \alpha_2 NKD)$

 α_2 is the fraction of times the second condition is not satisfied.

O(NK)





Running time of Elkan's K-means

Major computations

- Computing point-center distances
 - O(NKD) in the first/first-few iteration.
 - O(ND) over all later iterations combined. For most datasets with significant cluster structure.
- Computing pairwise center distances • $O(K^2 DE)$
- Updating the lower bound

• O(NKE)

Most points (in the core of the cluster) won't change cluster assignments after the first few iterations and will satisfy the pruning conditions. The more the clusters looks like gaussians, the more this true. This might no longer be true if the data lacks a cluster structure.

N: dataset size K: number of clusters D: number of dimensions E: number of iterations



Results for Elkan

		k = 3	k = 20	k = 100	name	cardinality	dimensionality	description
birch	iterations	17	38	56	birch	100000	2	10 by 10 grid of Gaussian clusters, DS1 in (Zhang et a
	standard	5 100e+06	7.600e+07	5 600e+08	covtype	150000	54	remote soil cover measurements, after (Moore, 2000)
	fact	1.100e+00	1.0850-06	1.5070106	kddcup	95413	56	KDD Cup 1998 data, un-normalized
	last	4.495e+05	1.0850+00	1.5970+00	mnist50	60000	50	random projection of NIST handwritten digit training
	speedup	11.3	70.0	351	mnist/84	60000	784	original NIST handwritten digit training data
covtype	iterations	18	256	152	random	10000	1000	uniform random data
	standard	8.100e+06	7.680e+08	2.280e+09				
	fast	9.416e+05	7.147e+06	7.353e+06	Table 2. Row	s labeled "standard w algorithm Row	l" and "fast" give the nu	The imperiation of the set of th
	speedup	8.60	107	310	distance calcu	alations.	s labeled speedup sh	low now many times faster the new argorithm is, when the unit of meas
kddcup	iterations	34	100	325				
	standard	9.732e+06	1.908e+08	3.101e+09				
	fast	6.179e+05	3.812e+06	1.005e+07				
	speedup	15.4	50.1	309				
mnist50	iterations	38	178	217				
	standard	6.840e+06	2.136e+08	1.302e+09				
	fast	1.573e+06	9.353e+06	3.159e+07				
	speedup	4.35	22.8	41.2				
mnist784	iterations	63	60	165				
	standard	1.134e+07	7.200e+07	9.900e+08				
	fast	1.625e+06	7.396e+06	3.055e+07				
	speedup	6.98	9.73	32.4				
random	iterations	52	33	18				
	standard	1.560e+06	6.600e+06	1.800e+07				
	fast	1.040e+06	3.020e+06	5.348e+06				
	speedup	1.50	2.19	3.37				
					-			



s algorithm surement is

Limitations of Elkan

for large K

Can a smaller set of lower bounds be used?

Storing and updating the lower bounds $(N \times K \text{ dimension})$ can be a bottleneck

Hamerly's accelerated K-means

Main difference from Elkan: l(i) instead of l(i,j)

Maintains one lower bound per point instead of *K*

Conditions Checked $u(i) \le s(a(i))$ or $u(i) \le l(a(i))$

 $u(i) \leq s(a(i))$ or $u(i) \leq l(i)$. No distance involving the i^{th} point needs to be computed.

Tradeoff

- Less memory for storing lower bounds.
- Fewer computations for updating lower bounds.
- However, there is less pruning and consequently more distance computation.

l(*i*): lower bound of the distance of the i^{th} point to the second closest centroid

O(N) instead of $O(N \times K)$ space for storing the lower bounds

oounds. Ind consequently

Alg	gorithm 4 Hamerly's algorithm—usi
	procedure HAMERLY(X, C)
	$a(i) \leftarrow 1, u(i) \leftarrow \infty, \ell(i) \leftarrow 0, \forall i \in$
	while not converged do
	compute $s(j) \leftarrow \min_{j' \neq j} \ c(j) - c(j)\ \le c(j) \le c(j) $
5:	for all $i \in N$ do
	$z \leftarrow \max(\ell(i), s(a(i)))$
	if $u(i) \leq z$ then continue with ne
	$u(i) \leftarrow x(i) - c(a(i)) $ {Tight
	if $u(i) \le z$ then continue with ne
10:	Find $c(j)$ and $c(j')$, the two closes
	if $j \neq a(i)$ then
	$a(i) \leftarrow j$
	$u(i) \leftarrow \ x(i) - c(a(i))\ $
	$\ell(i) \leftarrow \ x(i) - c(j')\ $
15:	for all $j \in K$ do {Move the centers
	move $c(j)$ to its new location
	let $\delta(j)$ be the distance moved by
	$\delta' \leftarrow \max_{i \in K} \delta(i)$
	for all $i \in N$ do {Update the upper
20:	$u(i) \leftarrow u(i) + \delta(a(i))$
	$\ell(i) \leftarrow \ell(i) - \delta' \max(0, l(i) - \delta)$

sing 1 lower bound per point

N {Initialize invalid bounds, all in one cluster.}

 $c(j')\|/2, \forall j \in K$

l(i) by definition is also a lower bound to the distances to other centers, except the closest one.

ext *i* ten the upper bound } ext *i*

sest centers to x(i), as well as the distances to each.

s and track their movement}

y c(j) of the second closest of the second closest cluster changes the lower bound is still valid.

and lower distance bounds }

′)

		Total user CPU Seconds (User CPU seconds per iteration)							
Dataset		1	c = 3	k =	= 20	k = 100		k =	500
uniform random	iterations		44	22	227		298		10
n = 1250000	lloyd	4.0	(0.058)	61.4	(0.264)	320.2	(1.070)	3486.9	(4.909)
d = 2	kd-tree	3.5	(0.006)	11.8	(0.035)	34.6	(0.102)	338.8	(0.471)
	elkan	7.2	(0.133)	75.2	(0.325)	353.1	(1.180)	2771.8	(3.902)
	hamerly	2.7	(0.031)	14.6	(0.058)	28.2	(0.090)	204.2	(0.286)
uniform random	iterations		121	3!	53	3	12	14	.05
n = 1250000	lloyd	21.8	(0.134)	178.9	(0.491)	660.7	(2.100)	13854.4	(9.857)
d = 8	kd-tree	117.5	(0.886)	622.6	(1.740)	2390.8	(7.633)	46731.5	(33.254)
	elkan	14.1	(0.071)	130.6	(0.354)	591.8	(1.879)	11827.9	(8.414)
	hamerly	10.9	(0.045)	40.4	(0.099)	169.8	(0.527)	1395.6	(0.989)
uniform random	iterations		137	41	20	20	96	24	.08
n = 1250000	lloyd	66.4	(0.323)	5479.5	(1.325)	12543.8	(5.974)	68967.3	(28.632)
d = 32	kd-tree	208.4	(1.324)	29719.6	(7.207)	74181.3	(35.380)	425513.0	(176.697)
	elkan	48.1	(0.189)	1370.1	(0.327)	2624.9	(1.242)	14245.9	(5.907)
	hamerly	46.9	(0.180)	446.4	(0.103)	1238.9	(0.581)	9886.9	(4.097)
birch	iterations		52	1'	79	1	10	9	9
n = 100000	lloyd	0.53	(0.004)	4.60	(0.024)	11.80	(0.104)	48.87	(0.490)
d = 2	kd-tree	0.41	(< 0.001)	0.96	(0.003)	2.67	(0.021)	17.68	(0.173)
	elkan	0.58	(0.005)	4.35	(0.023)	11.80	(0.104)	54.28	(0.545)
	hamerly	0.44	(0.002)	0.90	(0.003)	1.86	(0.014)	7.81	(0.075)
covtype	iterations		19	20	04	3	20	1	11
n = 150000	lloyd	3.52	(0.048)	48.02	(0.222)	322.25	(0.999)	564.05	(5.058)
d = 54	kd-tree	6.65	(0.205)	266.65	(1.293)	2014.03	(6.285)	3303.27	(29.734)
	elkan	3.07	(0.022)	11.58	(0.044)	70.45	(0.212)	152.15	(1.347)
	hamerly	2.95	(0.019)	7.40	(0.024)	42.83	(0.126)	169.53	(1.505)
kddcup	iterations		39	5	5	1	69	14	42
n = 95412	lloyd	4.74	(0.032)	12.35	(0.159)	116.63	(0.669)	464.22	(3.244)
d = 56	kd-tree	9.68	(0.156)	58.55	(0.996)	839.31	(4.945)	3349.47	(23.562)
	elkan	4.13	(0.012)	6.24	(0.049)	32.27	(0.169)	132.39	(0.907)
	hamerly	3.95	(0.011)	5.87	(0.042)	28.39	(0.147)	197.26	(1.364)
mnist50	iterations		37	24	49	1	90	8	1
n = 60000	lloyd	2.92	(0.018)	23.18	(0.084)	75.82	(0.387)	162.09	(1.974)
d = 50	kd-tree	4.90	(0.069)	100.09	(0.393)	371.57	(1.943)	794.51	(9.780)
	elkan	2.42	(0.005)	7.02	(0.019)	21.58	(0.101)	55.61	(0.660)
	hamerly	2.41	(0.004)	4.54	(0.009)	21.95	(0.104)	77.34	(0.928)

Table 3: These results show the fraction of times that each algorithm was able to skip the innermost loop on data of different dimensions (values closer to 1 are better). These results are averaged over runs using k =3, 20, 100, and 500 (one run for each k). The randX datasets are uniform random hypercube data with X dimensions.

dataset	rand2	rand8	rand32	rand128
elkan	0.56	0.01	0.00	0.00
hamerly	0.97	0.88	0.91	0.83
dataset	birch	covtype	kddcup	mnist50
dataset elkan	birch 0.52	covtype 0.34	kddcup 0.18	mnist50 0.22

Memory requirements

		Megabytes						
Dataset	Algorithm	k=3	k = 20	k = 100	k = 500			
uniform	lloyd	7.5	7.5	7.5	7.5			
random	kd-tree	32.1	32.1	32.1	32.1			
n = 1.25 M	elkan	19.8	60.3	251.0	1205.2			
d=2	hamerly	14.7	14.7	14.7	14.7			
uniform	lloyd	21.9	21.9	21.9	21.9			
random	kd-tree	54.8	54.8	54.8	54.8			
n = 1.25 M	elkan	34.1	74.6	265.3	1219.5			
d=8	hamerly	29.0	29.0	29.0	29.0			
uniform	lloyd	79.1	79.1	79.1	79.1			
random	kd-tree	145.2	145.2	145.2	145.3			
n = 1.25 M	elkan	91.3	131.8	322.6	1276.8			
d=32	hamerly	86.2	86.2	86.2	86.3			
birch	lloyd	1.4	1.1	1.1	1.3			
n = 100 K	kd-tree	2.9	2.9	2.8	2.7			
d=2	elkan	2.1	-5.2	20.6	97.3			
	hamerly	1.5	1.7	1.6	1.5			
covtype	lloyd	16.2	16.2	16.1	16.4			
n = 150 K	kd-tree	27.2	27.2	27.2	27.3			
d = 54	elkan	17.4	22.5	45.3	160.4			
	hamerly	17.0	17.0	16.8	17.2			
kddcup	lloyd	10.9	10.8	11.1	11.2			
n = 95412	kd-tree	18.8	18.9	19.1	19.0			
d = 56	elkan	11.9	15.1	29.6	103.1			
	hamerly	11.6	11.6	11.3	11.7			
mnist50	lloyd	6.3	6.6	6.4	6.8			
n = 60 K	kd-tree	10.5	10.4	10.6	10.7			
d = 50	elkan	7.0	9.1	18.4	64.8			
	hamerly	6.9	6.9	6.9	6.8			

Summary

- For moderate D (< 50) and K(< 100), Hamerly is well-suited (has smaller time and memory footprint).
- Large D (greater than 50), Elkan might be better (has smaller time footprint, in spite of large memory requirements).

Speed up with an approximate algorithm

Web-scale k-means clustering <u>D Sculley</u> - Proceedings of the 19th international conference on ..., 2010 - dl.acm.org Abstract We present two modifications to the popular k-means clustering algorithm to address the extreme requirements for latency, scalability, and sparsity encountered in userfacing web applications. First, we propose the use of mini-batch optimization for k-means ... Cited by 152 Related articles All 11 versions Cite Save

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Web-Scale K-Means Clustering

D. Sculley Google, Inc. Pittsburgh. PA USA dsculley@google.com

ABSTRACT

We present two modifications to the popular k-means clustering algorithm to address the extreme requirements for latency, scalability, and sparsity encountered in user-facing web applications. First, we propose the use of mini-batch optimization for k-means clustering. This reduces computation cost by orders of magnitude compared to the classic batch algorithm while yielding significantly better solutions than online stochastic gradient descent. Second, we achieve sparsity with projected gradient descent, and give a fast ϵ accurate projection onto the L1-ball. Source code is freely available: http://code.google.com/p/sofia-ml

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This paper proposes a mini-batch k-means variant that yields excellent clustering results with low computation cost on large data sets. We also give methods for learning sparse cluster centers that reduce storage and network cost.

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The k-means optimization problem is to find the set C of cluster centers $\mathbf{c} \in \mathbb{R}^m$, with |C| = k, to minimize over a set

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X of examples $\mathbf{x} \in \mathbb{R}^m$ the following objective function:

$$\min\sum_{\mathbf{x}\in X} ||f(C,\mathbf{x}) - \mathbf{x}||^2$$

Here, $f(C, \mathbf{x})$ returns the nearest cluster center $\mathbf{c} \in C$ to \mathbf{x} using Euclidean distance. It is well known that although this problem is NP-hard in general, gradient descent methods converge to a local optimum when seeded with an initial set of k examples drawn uniformly at random from X [1].

The classic batch *k*-means algorithm is expensive for large data sets, requiring O(kns) computation time where n is the number of examples and s is the maximum number of nonzero elements in any example vector. Bottou and Bengio proposed an online, stochastic gradient descent (SGD) variant that computed a gradient descent step on one example at a time [1]. While SGD converges quickly on large data sets, it finds lower quality solutions than the batch algorithm due to stochastic noise [1].

Algorithm 1 Mini-batch k-Means.

1: Given: k, mini-batch size b, iterations t, data set X
2: Initialize each $\mathbf{c} \in C$ with an \mathbf{x} picked randomly from X
$3: \mathbf{v} \leftarrow 0$
4: for $i = 1$ to t do
5: $M \leftarrow b$ examples picked randomly from X
6: for $\mathbf{x} \in M$ do
7: $\mathbf{d}[\mathbf{x}] \leftarrow f(C, \mathbf{x})$ // Cache the center nearest to \mathbf{x}
8: end for
9: for $\mathbf{x} \in M$ do
10: $\mathbf{c} \leftarrow \mathbf{d}[\mathbf{x}]$ // Get cached center for this \mathbf{x}
11: $\mathbf{v}[\mathbf{c}] \leftarrow \mathbf{v}[\mathbf{c}] + 1 // \text{ Update per-center counts}$
12: $\eta \leftarrow \frac{1}{\mathbf{v}[\mathbf{c}]}$ // Get per-center learning rate
13: $\mathbf{c} \leftarrow (1-\eta)\mathbf{c} + \eta \mathbf{x}$ // Take gradient step
14: end for
15: end for

We propose the use of mini-batch optimization for k-means clustering, given in Algorithm 1. The motivation behind this method is that mini-batches tend to have lower stochastic noise than individual examples in SGD (allowing convergence to better solutions) but do not suffer increased computational cost when data sets grow large with redundant examples. We use per-center learning rates for fast convergence, in the manner of [1]; convergence properties follow closely from this prior result [1].

Experiments. We tested the mini-batch k-means against both Lloyd's batch k-means [6] and the SGD variant of [1]. We used the standard RCV1 collection of documents [4] for

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Figure 1: Convergence Speed. The mini-batch method (blue) is orders of magnitude faster than the full batch method (green), while converging to significantly better solutions than the online SGD method (red).

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The results (Fig. 1) show a clear win for mini-batch kmeans. The mini-batch method converged to a near optimal value several orders of magnitude faster than the full batch method, and also achieved significantly better solutions than SGD. Additional experiments (omitted for space) showed that mini-batch k-means is several times faster on large data sets than batch k-means exploiting triangle inequality [3].

For small values of k, the mini-batch methods were able to produce near-best cluster centers for nearly a million documents in a fraction of a CPU second on a single ordinary 2.4 GHz machine. This makes real-time clustering practical for user-facing applications.

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We modify mini-batch k-means to find sparse cluster centers, allowing for compact storage and low network cost. The intuition for seeking sparse cluster centers for document clusters is that term frequencies follow a power-law distribution. Many terms in a given cluster will only occur in one or two documents, giving them very low weight in the cluster center. It is likely that for a locally optimal center \mathbf{c} , there is a nerby point \mathbf{c}' with many fewer non-zero values.

Sparsity may be induced in gradient descent using the projected-gradient method, projecting a given \mathbf{v} to the nearest point in an L1-ball of radius λ after each update [2]. Thus, for mini-batch k-means we achieve sparsity by performing an L1-ball projection on each cluster center **c** after each mini-batch iteration.

Algorithm 2 ϵ -L1: an ϵ -Accurate Projection to	L1	Ball.
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- 1: Given: ϵ tolerance, L1-ball radius λ , vector $\mathbf{c} \in \mathbb{R}^m$

Alg	orithm	2	<i>ϵ</i> -L1 :	an	ϵ -	-A	Accui	rate	Projec	tion t	o Ll	Ball.
			-	_	-				-		_	

- 2: if $||\mathbf{c}||_i \leq \lambda + \epsilon$ then exit
- 3: $upper \leftarrow ||\mathbf{c}||_{\infty}$; $lower \leftarrow 0$; $current \leftarrow ||\mathbf{c}||_1$
- 4: while $current > \lambda(1 + \epsilon)$ or $current < \lambda$ do
- 5: $\theta \leftarrow \frac{upper+lower}{2}$ // Get L1 value for this θ
- 6: current $\leftarrow \sum_{i=1}^{2.0}$ $\max(0, |\mathbf{c}_i| - \theta)$
- 7: **if** $current \leq \lambda$ **then** $upper \leftarrow \theta$ **else** $lower \leftarrow \theta$
- 8: end while
 - 9: for i = 1 to m do
 - 10: $\mathbf{c}_i \leftarrow sign(\mathbf{c}_i) \ast \max(0, |\mathbf{c}_i| \theta) // \text{ Do the projection}$ 11: end for

Fast L1 Projections. Applying L1 constraints to kmeans clustering has been studied in forthcoming work by Witten and Tibshirani [5]. There, a hard L1 constraint was applied in the full batch setting of maximizing betweencluster distance for k-means (rather than minimizing the k-means objective function directly); the work did not discuss how to perform this projection efficiently.

The projection to the L1 ball can be performed effectively using, for example, the linear time L1-ball projection algorithm of Duchi et al. [2], referred to here as LTL1P. We give an alternate method in Algorithm 2, observing that the exact L1 radius is not critical for sparsity. This simple approximation algorithm uses bisection to find a value θ that projects **c** to an L1 ball with radius between λ and $(1 + \epsilon)\lambda$. Our method is easy to implement and is also significantly faster in practice than LTL1P due to memory concurrency.

METHOD	λ	#NON-ZERO'S	TEST OBJECTIVE	CPUs
full batch	-	200,319	0 (baseline)	133.96
LTL1P	5.0	46,446	.004 (.002006)	0.51
ϵ -L1	5.0	44,060	.007 (.005008)	0.27
LTL1P	1.0	3,181	.018 (.016019)	0.48
ϵ -L1	1.0	2,547	.028 (.027029)	0.19

Results. Using the same set-up as above, we tested Duchi et al.'s linear time algorithm and our ϵ -accurate projection for mini-batch k-means, with a range of λ values. The value of ϵ was arbitrarily set to 0.01. We report values for k = 10, b = 1000, and t = 16 (results for other values qualitatively similar). Compared with the full batch method, we achieve much sparser solutions. The approximate projection is roughly twice as fast as LTL1P and finds sparser solutions, but gives slightly worse performance on the test set. These results show that sparse clustering may cheaply be achieved with low latency for user-facing applications.

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Algorithm 1 Mini-batch k-Means.

- 3: $\mathbf{v} \leftarrow \mathbf{0}$
- 4: for i = 1 to t do
- 5:
- for $\mathbf{x} \in M$ do 6:
- 7:
- end for 8:
- 9: for $\mathbf{x} \in M$ do

- end for 14:
- 15: **end for**

Here t is the number Complexity: O(N M K D t) of iterations

1: Given: k, mini-batch size b, iterations t, data set X2: Initialize each $\mathbf{c} \in C$ with an \mathbf{x} picked randomly from X

 $M \leftarrow b$ examples picked randomly from X

 $\mathbf{d}[\mathbf{x}] \leftarrow f(C, \mathbf{x})$ // Cache the center nearest to \mathbf{x}

10: $\mathbf{c} \leftarrow \mathbf{d}[\mathbf{x}]$ // Get cached center for this \mathbf{x} 11: $\mathbf{v}[\mathbf{c}] \leftarrow \mathbf{v}[\mathbf{c}] + 1$ // Update per-center counts 12: $\eta \leftarrow \frac{1}{\mathbf{v}[\mathbf{c}]}$ // Get per-center learning rate 13: $\mathbf{c} \leftarrow (1 - \eta)\mathbf{c} + \eta \mathbf{x}$ // Take gradient step





Clustering Jan-Willem van de Meent



K-means Clustering

Limitations

K-means Limitations: Differing Sizes



Original Points

K-means (3 clusters)

K-means Limitations: Different Densities



Original Points

K-means (3 clusters)

K-means Limitations: Non-globular Shapes



Original Points

K-means (2 clusters)

Overcoming K-means Limitations



Intuition: "Combine" smaller clusters into larger clusters

One Solution: Hierarchical Clustering • Another Solution: Density-based Clustering



Clustering

Shantanu Jain



Hierarchical Clustering

Dendrogram



(a.k.a. a similarity tree)
Dendrogram





(a.k.a. a similarity tree)

Example: Iris data







Iris Setosa

Iris versicolor



Iris virginica

https://en.wikipedia.org/wiki/Iris_flower_data_set

Hierarchical Clustering



(Euclidian Distance)

https://en.wikipedia.org/wiki/Iris_flower_data_set

Hamming Distance

Distance Patty and Selma

Change	dress color,	1	point
Change	earring shape,	1	point
Change	hair part,	1	point

D(Patty, Selma) = 3

Distance Marge and Selma

Change dress color,	1	point
Add earrings,	1	point
Decrease height,		point
Take up smoking,		point
Lose weight,	1	point

D(Marge,Selma) = 5



Can be defined for any set of discrete features

Edit Distance for Strings

- Transform string Q into string C, using only Substitution, Insertion and Deletion.
- Assume that each of these operators has a cost associated with it.
- The similarity between two strings can be defined as the cost of the *cheapest* transformation from Q to C.



Similarity "Peter" and "Piotr"?

Substitution	1 Unit
Insertion	1 Unit
Deletion	1 Unit

D(Peter, Piotr) is 3

Peter

Substitution (i for e) Piter Insertion (o) Pidter Deletion (e) Piotr

Hierarchical Clustering

Pedro (Portuguese)

Petros (Greek), Peter (English), Piotr (Polish), Peadar (Irish), Pierre (French), Peder (Danish), Peka (Hawaiian), Pietro (Italian), Piero (Italian Alternative), Petr (Czech), Pyotr (Russian)

Cristovao (Portuguese)

Christoph (German), Christophe (French), Cristobal (Spanish), Cristoforo (Italian), Kristoffer (Scandinavian), Krystof (Czech), Christopher (English)

Miguel (Portuguese)

Michalis (Greek), Michael (English), Mick (Irish)



(Edit Distance)

Meaningful Patterns

Edit distance yields clustering according to geography

Pedro

Petros (Greek), Peter (English), Piotr (Czech), Pyotr (Russian)



Spurious Patterns

In general clusterings will only be as meaningful as your distance metric



Spurious Patterns



Former UK colonies

In general clusterings will only be as meaningful as your distance metric

No relation

"Correct" Number of Clusters



"Correct" Number of Clusters



Determine number of clusters by looking at distance

Detecting Outliers



Bottom-up vs Top-down



Bottom-Up (agglomerative):

Starting with each item in its own cluster, find the best pair to merge into a new cluster. Repeat until all clusters are fused together.

Top-Down (divisive): Starting with all the data in a single cluster, consider every possible way to divide the cluster into two. Choose the best division and recursively operate on both sides.

Bottom-up: Distance Matrix

We begin with a distance matrix which contains the distances between every pair of objects in our database.





















How do we calculate the distance to a cluster?

Consider all possible merges... Consider all possible merges... Consider all possible merges...



Clustering Criteria

Single link: $d(A,B) = \min_{a \in A, b \in B} d(a,b)$ (Closest point)

 $d(A,B) = \max_{a \in A, b \in B} d(a,b)$ Complete link: (Furthest point)

Group average: (Average distance)

Centroid: (Distance of average)

 $x \in A \cup B$

Ward: (Intra-cluster variance)





Naive time complexity

Algorithm 8.3 Basic agglomerative hierarchical clustering algorithm.

- 1: Compute the proximity matrix, if necessary $O(N^2D)$
- 2: repeat
- Merge the closest two clusters. 3:
- 4: cluster and the original clusters.
- 5: **until** Only one cluster remains.

Naive approach $O(N^2D + N^3)$



N: number of points D: dimensionality



True Time complexity

Algorithm 8.3 Basic agglomerative hierarchical clustering algorithm.

- 1: Compute the proximity matrix, if necessary.
- 2: repeat
- Merge the closest two clusters. 3:
- Update the proximity matrix to reflect the proximity between the new 4:

O(1)

5: **until** Only one cluster remains.

Trick 1

Use Min heap

- Allows accessing the minimum distance in O(1)
- Insertion of new distance and deletion of old ones into the heap in step 4 takes $O(\log(N - i + 1))$ per distance



Trick 2

Recompute distances from merged cluster distances

• $d(AB, C) = \min(d(A, C), d(B, C))$ for single linkage, where AB denotes the merging of clusters A and B









Lance-Williams Methods

Clustering Method	$\alpha_{\mathbf{A}}$	$\alpha_{\mathbf{B}}$	β	γ
Single Link	1/2	1/2	0	-1/2
Complete Link	1/2	1/2	0	1/2
Group Average	$\frac{m_A}{m_A + m_B}$	$\frac{m_B}{m_A + m_B}$	0	0
Centroid	$\frac{m_A}{m_A + m_B}$	$\frac{m_B}{m_A + m_B}$	$rac{-m_Am_B}{(m_A+m_B)^2}$	0
Ward's	$\frac{m_A + m_Q}{m_A + m_B + m_Q}$	$\frac{m_B + m_Q}{m_A + m_B + m_Q}$	$\frac{-m_Q}{m_A + m_B + m_Q}$	0

 $p(R,Q) = \alpha_A p(A,Q)$ $+ \alpha_B p(B,Q)$ $+\beta p(A,B)$ $+\gamma |p(A,Q)-p(B,Q)|$

Recursively minimize/maximize proximity for a merger R:=AUB relative to all existing Q

Hierarchical Clustering Summary

- + Hierarchical structure maps nicely onto human intuition in some domains
- + No difficulty in choosing initial points
- Heuristic method: No global objective criteria to optimize. Optimizes local objective at each merge.
- Merging decisions are final: Prevents local optimization to from Can be improved becoming global optimization. For e.g., Ward methods optimized by initializing with several small klocal SSE doesn't translate to the optimized global SSE. means clusters.
- Scaling: Time complexity at least $O(N^2D + N^2 \log N)$, Space complexity: $O(N^2)$
- Susceptibility to noise
- Interpretation of results is (very) subjective -



Clustering

Shantanu Jain



DBScan

Density-based Clustering

DBSCAN



arbitrarily shaped clusters

[PDF] A density-based algorithm databases with noise.

M Ester, HP Kriegel, J Sander, X Xu - Kdd, 1996 - aaai.org Abstract Clustering algorithms are attractive for the task of class identification in spatial databases. However, the application to large spatial databases rises the following requirements for clustering algorithms: minimal requirements of domain knowledge to ... Cited by 8901 Related articles All 70 versions Cite Save More

(one of the most-cited clustering methods)

[PDF] A density-based algorithm for discovering clusters in large spatial

DBSCAN



arbitrarily shaped clusters

Intuition

• A *cluster* is a islands of *high* density Noise points lie in a sea of low density

Defining "High Density"

Naïve approach

For each point in a cluster there are at least a minimum number (MinPts) of points in an Eps-neighborhood of that point.



cluster

Defining "High Density"

Eps-neighborhood of a point p

$$N_{Eps}(p) = \{ q \in D \}$$

| dist (p, q) \leq Eps $\}$



Defining "High Density"

- In each cluster there are two kinds of points:
 - points inside the cluster (core points)
 - points on the border (border points)

An Eps-neighborhood of a border point contains significantly less points than an Eps-neighborhood of a core point.



cluster

Density Reachability

Definition

 $p \in N_{Eps}(q)$ 1)





A point p is directly density-reachable from a point q with regard to the parameters Eps and MinPts, if (reachability)

(core point condition)

Parameter: MinPts = 5

p directly density reachable from q

 $p \in N_{Eps}(q)$ $|N_{Eps}(q)| = 6 \ge 5 = MinPts$ (core point condition)

q **not** directly density reachable from p

 $|N_{Eps}(p)| = 4 < 5 = MinPts$ (core point condition)

Note: This is an asymmetric relationship

Density Reachability

Definition

A point p is density-reachable from a point q with regard to the parameters Eps and MinPts if there is a chain of points p_1, p_2, \dots, p_s with $p_1 = q$ and $p_s = p$ such that p_{i+1} is directly density-reachable from p_i for all 1 < i < s-1.



- MinPts = 5
- $|N_{Eps}(q)| = 5 = MinPts$ (core point condition) $|N_{Eps}(p_1)| = 6 \ge 5 = MinPts$ (core point condition) p_2
Density Connectivity

Definition (density-connected) A point p is density-connected to a point q with regard to the parameters Eps and MinPts



Note: This is a symmetric relationship

- if there is a point v such that both p and q are density-reachable from v.

Definition of a Cluster

A cluster with regard to the parameters Eps and MinPts is a non-empty subset C of the database D with 1) For all $p, q \in D$: If $p \in C$ and q is density-reachable from p with regard to the parameters Eps and MinPts, then $q \in C$. 2) For all p, q \in C:

The point p is density-connected to q with regard to the parameters Eps and MinPts.

(Maximality)

(Connectivity)

Definition of Noise

Let C_1, \ldots, C_k be the clusters of the database D with regard to the parameters Eps_i and MinPts₁ (i=1,...,k).

The set of points in the database D not belonging to any cluster C₁,...,C_k is called **noise**:

Noise = { $p \in D$ | $p \notin C_i$ for all i = 1,...,k }



DBSCAN Algorithm

- (1) Start with an arbitrary point p from the database and retrieve all points density-reachable from p with regard to Eps and MinPts.
 The set of points reached from p may include points previously labeled as noise, but are in reality border points
- (2) If p is a core point, the procedure yields a cluster with regard to Eps and MinPts and all points in the cluster are classified.
- (3) If p is a border point, label it as noise
 (3) If p is a border point, no points are density-reachable from p
 - and DBSCAN visits the next unclassified point in the database. and go to step 1

DBSCAN Complexity

- Time complexity: O(N²D) if done naively, O(DN log N) when using a spatial index such as K-D tree. (*works in relatively low dimensions*)
- Space complexity: O(ND)

DBSCAN Algorithm





Point types: core, border and noise

DBSCAN strengths



Original Points

+ Resistant to noise
+ Can handle arbitrary shapes



Clusters



Ground Truth

- Varying densities _
- -

DBSCAN Weaknesses

MinPts = 4, Eps=9.75MinPts = 4, Eps=9.92

High dimensional data Cannot give overlapping clusters



Determining EPS and MINPTS



- Calculate distance of k-th nearest neighbor for each point

- Set Minpts to k.

 Plot in ascending / descending order Set EPS to max distance before "jump"



K-means vs DBSCAN