



K-means Clustering

Speed-ups

K-means Clustering

Finding new cluster assignments

compute all point-center distances

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

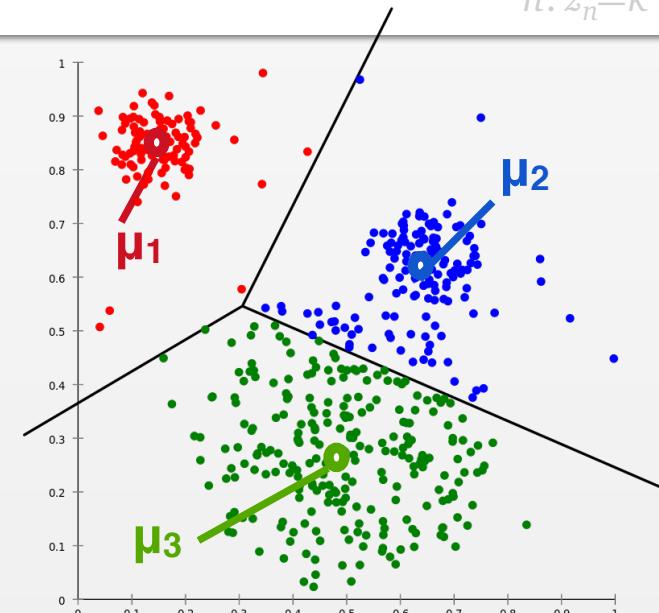
Updating the cluster centers

$O(ND)$ computational complexity (per iteration)

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

K-means Algorithm

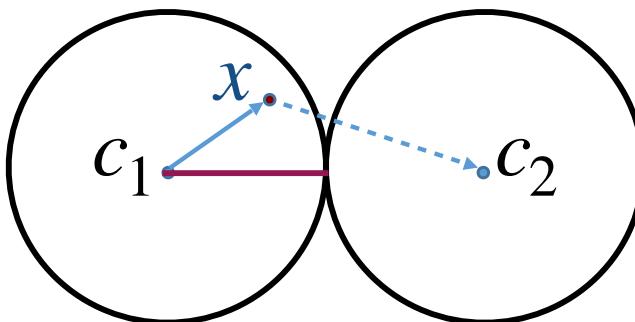
- Randomly initialize means $[\mu_1, \dots, \mu_K]$
- Repeat until $L(\mu, z)$ unchanged
 - Assign all points to *nearest* cluster
$$z_n = \operatorname{argmin}_k \|x_n - \mu_k\|^2$$
 - Update cluster means
$$\mu_k = \frac{1}{N_k} \sum_{n: z_n=k} x_n$$



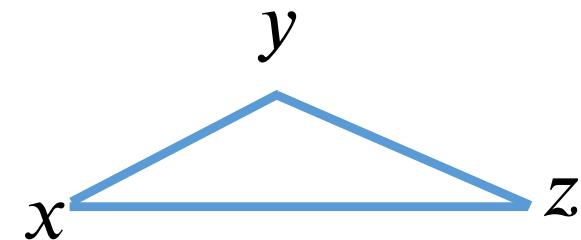
$O(NKD)$ per iteration is
prohibitive in high dimensions
and large K!

The core idea for cutting on distance computation

When updating the cluster assignments not all point-center distances need be computed



Exploit triangle inequality



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

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

Also true when

$$d(x, c_1) \leq u \leq \frac{d(c_1, c_2)}{2}$$

↑
Upper bound
for $d(x, c_1)$

$$d(x, c_1) \leq \frac{d(c_1, c_2)}{2} \Rightarrow d(x, c_1) \leq d(x, c_2)$$

Elkan's accelerated K-means

Conditions Checked:

$$1. \ u(i) \leq s(a(i))$$

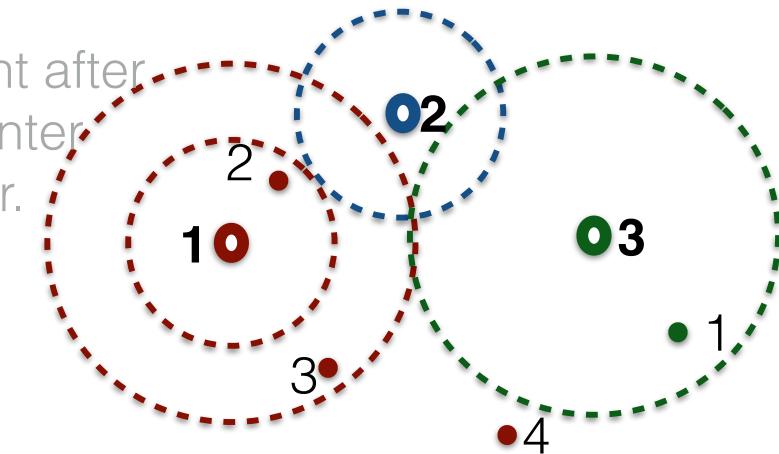
i^{th} point cluster assignment need not be changed. No distance involving the i^{th} point needs to be computed.

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

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.

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



$a(i)$: 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

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

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

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

Lower bound

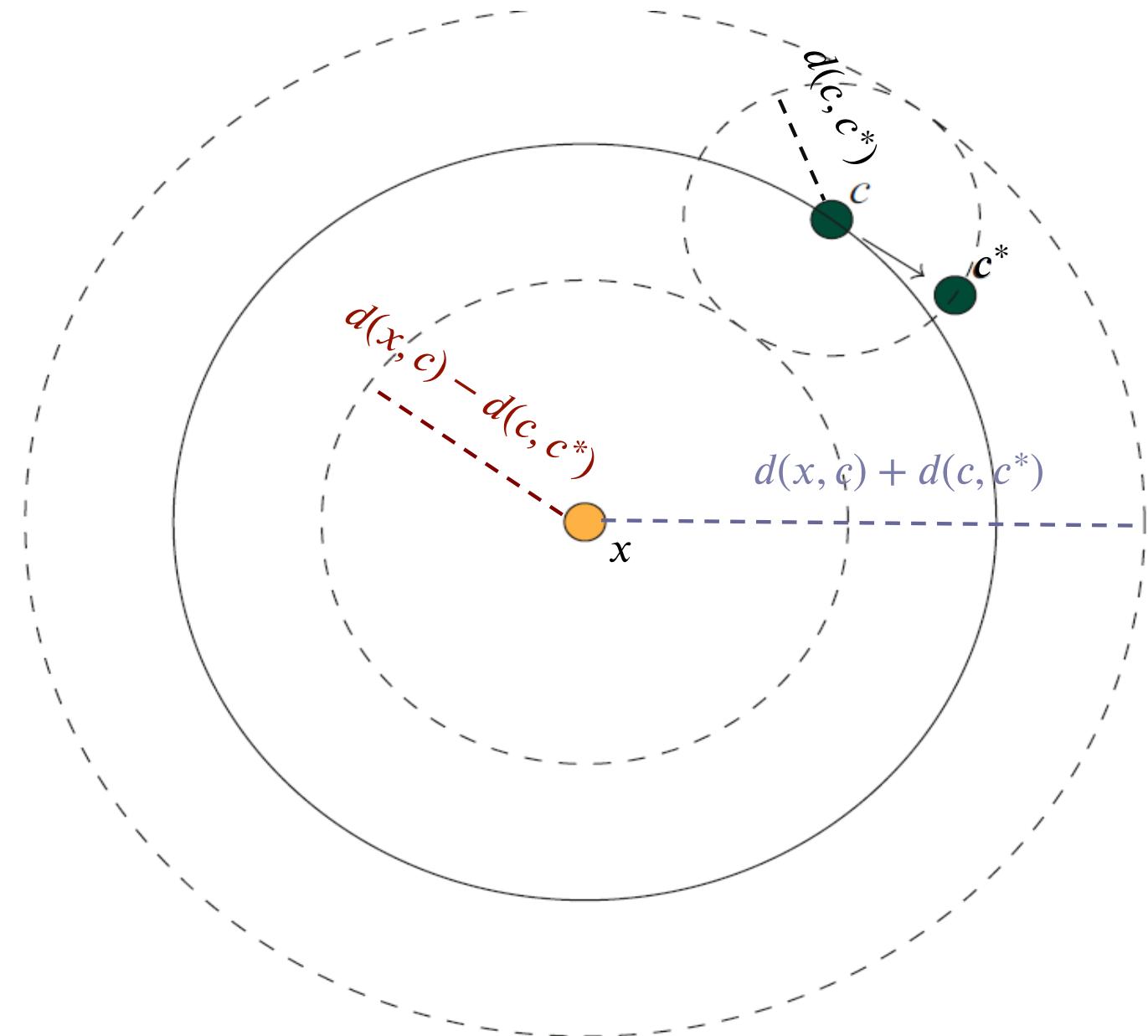
$$\begin{aligned} d(x, c^*) &\geq \max(0, d(x, c) - d(c, c^*)) \\ &\geq \max(0, l - d(c, c^*)) \\ &= l^* \end{aligned}$$

New lower bound Old lower bound

Upper bound

$$\begin{aligned} d(x, c^*) &\leq d(x, c) + d(c, c^*) \\ &\leq u + d(c, c^*) \\ &= u^* \end{aligned}$$

New upper bound Old upper bound



Algorithm 3 Elkan's algorithm—using k lower bounds per point and k^2 center-center 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**5: compute $\|c(j) - c(j')\|, \forall j, j' \in K$ 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 $r \leftarrow \text{True}$ r : tells if the upper bound
needs to be tightened.10: **for all** $j \in K$ **do** $z \leftarrow \max(\ell(i, j), \|c(a(i)) - c(j)\|/2)$ **if** $j = a(i)$ or $u(i) \leq z$ **then** continue with next j **if** r **then** $u(i) \leftarrow \|x(i) - c(a(i))\|$ $r \leftarrow \text{False}$ **if** $u(i) \leq z$ **then** continue with next j 15: $\ell(i, j) \leftarrow \|x(i) - c(j)\|$ Both upper bound and the lower bound are tight on this step. **if** $\ell(i, j) < u(i)$ **then** $a(i) \leftarrow j$ $u(i) \leftarrow \ell(i, j)$

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**25: $\ell(i, j) \leftarrow \max(0, l(i, j) - \delta(j))$

Algorithm 3 Elkan's algorithm—using k lower bounds per point and k^2 center-center 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**

5: compute $\|c(j) - c(j')\|, \forall j, j' \in K$

$O(K^2D)$

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

$O(N)$

$r \leftarrow \text{True}$

$O(\alpha_1 NK)$

10: **for all** $j \in K$ **do**

$z \leftarrow \max(\ell(i, j), \|c(a(i)) - c(j)\|/2)$

if $j = a(i)$ **or** $u(i) \leq z$ **then** continue with next j

if r **then**

$u(i) \leftarrow \|x(i) - c(a(i))\|$

$r \leftarrow \text{False}$

if $u(i) \leq z$ **then** continue with next j

$O(\alpha_1 \alpha_2 N K D)$

$\ell(i, j) \leftarrow \|x(i) - c(j)\|$

if $\ell(i, j) < u(i)$ **then** $a(i) \leftarrow j$

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

20: **for all** $j \in K$ **do** {Move the centers and track their movement}

 move $c(j)$ to its new location

$O(KD)$

 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**

$\ell(i, j) \leftarrow \max(0, l(i, j) - \delta(j))$

$O(NK)$

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

15:

16:

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
 - $O(K^2DE)$
- 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

		$k = 3$	$k = 20$	$k = 100$
birch	iterations	17	38	56
	standard	5.100e+06	7.600e+07	5.600e+08
	fast	4.495e+05	1.085e+06	1.597e+06
	speedup	11.3	70.0	351
covtype	iterations	18	256	152
	standard	8.100e+06	7.680e+08	2.280e+09
	fast	9.416e+05	7.147e+06	7.353e+06
	speedup	8.60	107	310
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

name	cardinality	dimensionality	description
birch	100000	2	10 by 10 grid of Gaussian clusters, DS1 in (Zhang et al., 1996)
covtype	150000	54	remote soil cover measurements, after (Moore, 2000)
kddcup	95413	56	KDD Cup 1998 data, un-normalized
mnist50	60000	50	random projection of NIST handwritten digit training data
mnist784	60000	784	original NIST handwritten digit training data
random	10000	1000	uniform random data

Table 2. Rows labeled “standard” and “fast” give the number of distance calculations performed by the unaccelerated k -means algorithm and by the new algorithm. Rows labeled “speedup” show how many times faster the new algorithm is, when the unit of measurement distance calculations.

Limitations of Elkan

Storing and updating the lower bounds ($N \times K$ dimension) can be a bottleneck for large K

Can a smaller set of lower bounds be used?

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

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

Conditions Checked

$u(i) \leq s(a(i))$ or $u(i) \leq l(i)$.

No distance involving the i^{th} point needs to be computed.

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

Tradeoff

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

Algorithm 4 Hamerly's algorithm—using 1 lower bound per point

procedure HAMERLY(X, C) $a(i) \leftarrow 1, u(i) \leftarrow \infty, \ell(i) \leftarrow 0, \forall i \in N$ {Initialize invalid bounds, all in one cluster.}**while** not converged **do** compute $s(j) \leftarrow \min_{j' \neq j} \|c(j) - c(j')\|/2, \forall j \in K$ 5: **for all** $i \in N$ **do** $z \leftarrow \max(\ell(i), s(a(i)))$ **if** $u(i) \leq z$ **then** continue with next i $u(i) \leftarrow \|x(i) - c(a(i))\|$ {Tighten the upper bound} **if** $u(i) \leq z$ **then** continue with next i 10: Find $c(j)$ and $c(j')$, the two closest centers to $x(i)$, as well as the distances to each. **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 and track their movement} move $c(j)$ to its new location let $\delta(j)$ be the distance moved by $c(j)$ $\delta' \leftarrow \max_{j \in K} \delta(j)$ **for all** $i \in N$ **do** {Update the upper and lower distance bounds}20: $u(i) \leftarrow u(i) + \delta(a(i))$ $\ell(i) \leftarrow \ell(i) - \delta'$

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

δ' ensures that if the second closest cluster changes the lower bound is still valid.

Dataset		Total user CPU Seconds (User CPU seconds per iteration)			
		$k = 3$	$k = 20$	$k = 100$	$k = 500$
uniform random $n = 1250000$ $d = 2$	iterations	44	227	298	710
	lloyd	4.0 (0.058)	61.4 (0.264)	320.2 (1.070)	3486.9 (4.909)
	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 $n = 1250000$ $d = 8$	iterations	121	353	312	1405
	lloyd	21.8 (0.134)	178.9 (0.491)	660.7 (2.100)	13854.4 (9.857)
	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 $n = 1250000$ $d = 32$	iterations	137	4120	2096	2408
	lloyd	66.4 (0.323)	5479.5 (1.325)	12543.8 (5.974)	68967.3 (28.632)
	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 $n = 100000$ $d = 2$	iterations	52	179	110	99
	lloyd	0.53 (0.004)	4.60 (0.024)	11.80 (0.104)	48.87 (0.490)
	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 $n = 150000$ $d = 54$	iterations	19	204	320	111
	lloyd	3.52 (0.048)	48.02 (0.222)	322.25 (0.999)	564.05 (5.058)
	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 $n = 95412$ $d = 56$	iterations	39	55	169	142
	lloyd	4.74 (0.032)	12.35 (0.159)	116.63 (0.669)	464.22 (3.244)
	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 $n = 60000$ $d = 50$	iterations	37	249	190	81
	lloyd	2.92 (0.018)	23.18 (0.084)	75.82 (0.387)	162.09 (1.974)
	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)

Memory requirements

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
elkan	0.52	0.34	0.18	0.22
hamerly	0.94	0.89	0.82	0.82

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

Mini-batch K-means

Web-scale k-means clustering

[D Sculley](#) - 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 user-facing web applications. First, we propose the use of mini-batch optimization for k-means ...

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Mini-batch K-means

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Web-Scale K-Means Clustering

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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 L_1 -ball. Source code is freely available: <http://code.google.com/p/sfia-m>

Categories and Subject Descriptors

1.5.3 [Computing Methodologies]: Pattern Recognition—Clustering

General Terms

Algorithms, Performance, Experimentation

Keywords

unsupervised clustering, scalability, sparse solutions

1. CLUSTERING AND THE WEB

Unsupervised clustering is an important task in a range of web-based applications, including grouping search results, near-duplicate detection, and news aggregation to name but a few. Lloyd's classic k -means algorithm remains a popular choice for real-world clustering tasks [6]. However, the standard batch algorithm is slow for large data sets. Even optimized batch k -means variants exploiting triangle inequality [3] cannot cheaply meet the latency needs of user-facing applications when clustering results on large data sets are required in a fraction of a second.

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.

2. MINI-BATCH K-MEANS

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

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

Here, $f(C, x)$ returns the nearest cluster center $c \in C$ to 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 non-zero 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  $c \in C$  with an  $x$  picked randomly from  $X$ 
3:  $v \leftarrow 0$ 
4: for  $i = 1$  to  $t$  do
5:    $M \leftarrow b$  examples picked randomly from  $X$ 
6:   for  $x \in M$  do
7:      $d[x] \leftarrow f(C, x)$  // Cache the center nearest to  $x$ 
8:   end for
9:   for  $x \in M$  do
10:     $c \leftarrow d[x]$  // Get cached center for this  $x$ 
11:     $v[c] \leftarrow v[c] + 1$  // Update per-center counts
12:     $\eta \leftarrow \frac{1}{v[c]}$  // Get per-center learning rate
13:     $c \leftarrow (1 - \eta)c + \eta x$  // 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 our experiments. To assess performance at scale, the set of 781,265 examples were used for training and the remaining 23,149 examples for testing. On each trial, the same random initial cluster centers were used for each method. We evaluated the learned cluster centers using the k -means objective function on the held-out test set; we report fractional error from the best value found by the batch algorithm run to convergence. We set the mini-batch b to 1000 based on separate initial tests; results were robust for a range of b .

The results (Fig. 1) show a clear win for mini-batch k -means. 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.

3. SPARSE CLUSTER CENTERS

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 c , there is a nearby point c' with many fewer non-zero values.

Sparcity may be induced in gradient descent using the projected-gradient method, projecting a given v to the nearest point in an L_1 -ball of radius λ after each update [2]. Thus, for mini-batch k -means we achieve sparsity by performing an L_1 -ball projection on each cluster center c after each mini-batch iteration.

Algorithm 2 ϵ -L1: an ϵ -Accurate Projection to L_1 Ball.

```

1: Given:  $\epsilon$  tolerance,  $L_1$ -ball radius  $\lambda$ , vector  $c \in \mathbb{R}^m$ 
2: if  $\|c\|_1 \leq \lambda + \epsilon$  then exit
3:  $upper \leftarrow \|c\|_\infty$ ;  $lower \leftarrow 0$ ;  $current \leftarrow \|c\|_1$ 
4: while  $current > \lambda(1 + \epsilon)$  or  $current < \lambda$  do
5:    $\theta \leftarrow \frac{upper + lower}{2.0}$  // Get  $L_1$  value for this  $\theta$ 
6:    $current \leftarrow \sum_{c_i \neq 0} \max(0, |c_i| - \theta)$ 
7:   if  $current \leq \lambda$  then  $upper \leftarrow \theta$  else  $lower \leftarrow \theta$ 
8: end while
9: for  $i = 1$  to  $m$  do
10:   $c_i \leftarrow sign(c_i) * max(0, |c_i| - \theta)$  // Do the projection
11: end for

```

Fast L_1 Projections. Applying L_1 constraints to k -means clustering has been studied in forthcoming work by Witten and Tibshirani [5]. There, a hard L_1 constraint was applied in the full batch setting of maximizing between-cluster 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 L_1 ball can be performed effectively using, for example, the linear time L_1 -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 L_1 radius is not critical for sparsity. This simple approximation algorithm uses bisection to find a value θ that projects c to an L_1 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 (.002-.006)	0.51
ϵ -L1	5.0	44,060	.007 (.005-.008)	0.27
LTL1P	1.0	3,181	.018 (.016-.019)	0.48
ϵ -L1	1.0	2,547	.028 (.027-.029)	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.

4. REFERENCES

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(2-page abstract)

Mini-batch K-means

WWW 2010 • Poster

April 26-30 • Raleigh • NC • USA

Web-Scale K-Means Clustering

D. Sculley
Google, Inc. Pittsburgh, PA USA
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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>

Categories and Subject Descriptors

I.5.3 [Computing Methodologies]: Pattern Recognition
Clustering

General Terms

Algorithms, Performance, Experimentation

Keywords

unsupervised clustering, scalability, sparse solutions

1. CLUSTERING AND THE WEB

Unsupervised clustering is an important task in a range of web-based applications, including grouping search results, near-duplicate detection, and news aggregation to name but a few. Lloyd's classic k -means algorithm remains a popular choice for real-world clustering tasks [6]. However, the standard batch algorithm is slow for large data sets. Even optimized batch k -means variants exploiting triangle inequality [3] cannot cheaply meet the latency needs of user-facing applications where clustering results on large data sets are required in a fraction of a second.

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.

2. MINI-BATCH K-MEANS

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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ACM 978-1-60558-799-8/10/04.

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

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

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 non-zero 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 less accurate solutions than the batch k -means 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  $\mathbf{x}$ 
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9:   for  $\mathbf{x} \in M$  do
10:     $\mathbf{c} \leftarrow \mathbf{d}[\mathbf{x}]$  // Get cached center for this  $\mathbf{x}$ 
11:     $\mathbf{v}[\mathbf{c}] \leftarrow \mathbf{v}[\mathbf{c}] + 1$  // Update per-center counts
12:     $\eta \leftarrow \frac{1}{|\mathbf{v}|}$  // Get per-center learning rate
13:     $\mathbf{c} \leftarrow (1 - \eta)\mathbf{c} + \eta\mathbf{x}$  // Take gradient step
14:  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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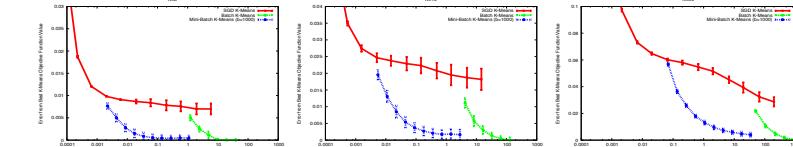


Figure 1: Convergence Speed. The mini-batch method (blue) is orders of magnitude faster than the full batch method (green), while converging to significantly better solutions than the online SGD method (red).

our experiments. To assess performance at scale, the set of 781,265 examples were used for training and the remaining 23,149 examples for testing. On each trial, the same random initial cluster centers were used for each method. We evaluated the learned cluster centers using the k -means objective function on the held-out test set; we report fractional error from the best value found by the batch algorithm run to convergence. We set the mini-batch b to 1000 based on separate initial tests; results were robust for a range of b .

The results (Fig. 1) show a clear win for mini-batch k -means. 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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(2-page abstract)

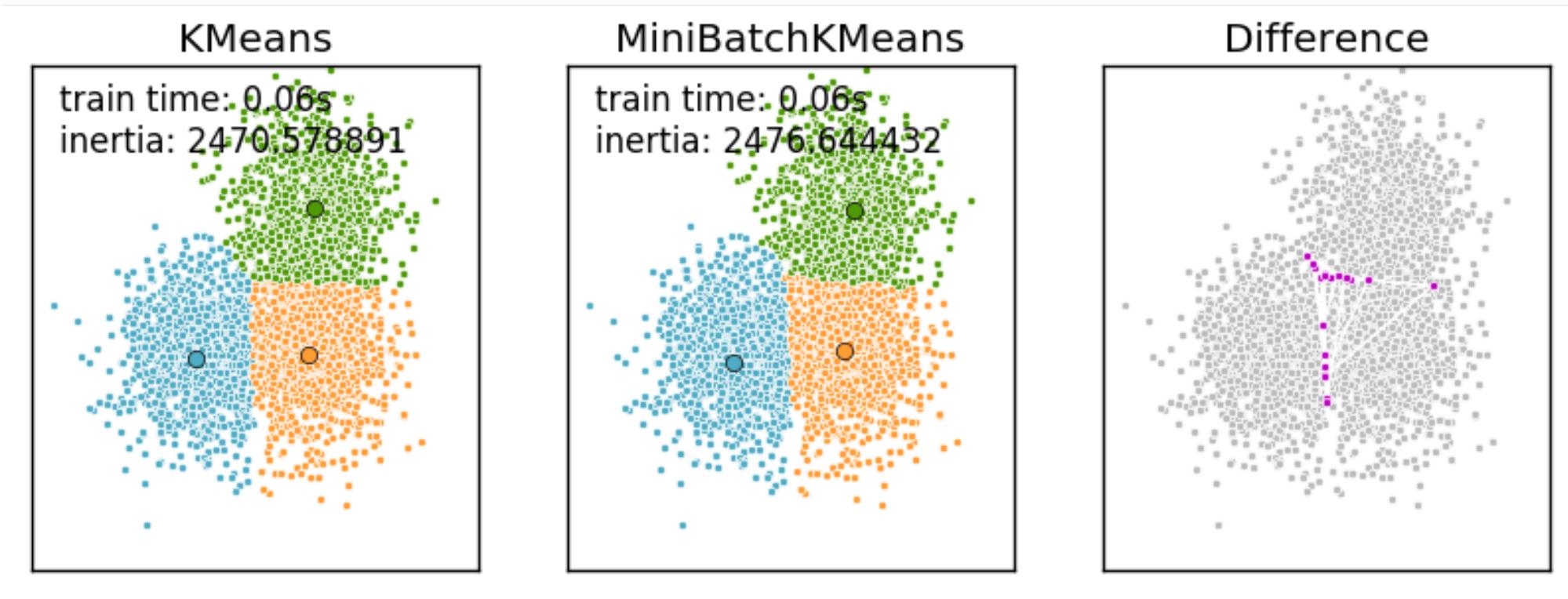
Mini-batch K-means

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13:     $\mathbf{c} \leftarrow (1 - \eta)\mathbf{c} + \eta\mathbf{x}$  // Take gradient step
14:   end for
15: end for
```

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

Mini-batch K-means





Clustering

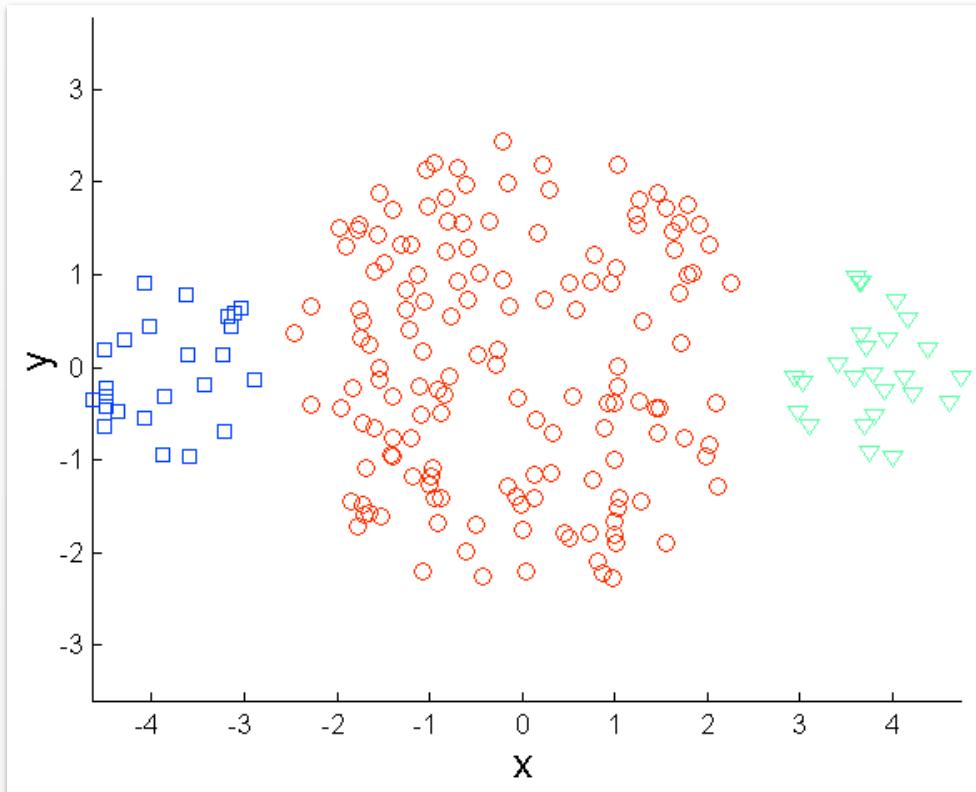
Shantanu Jain



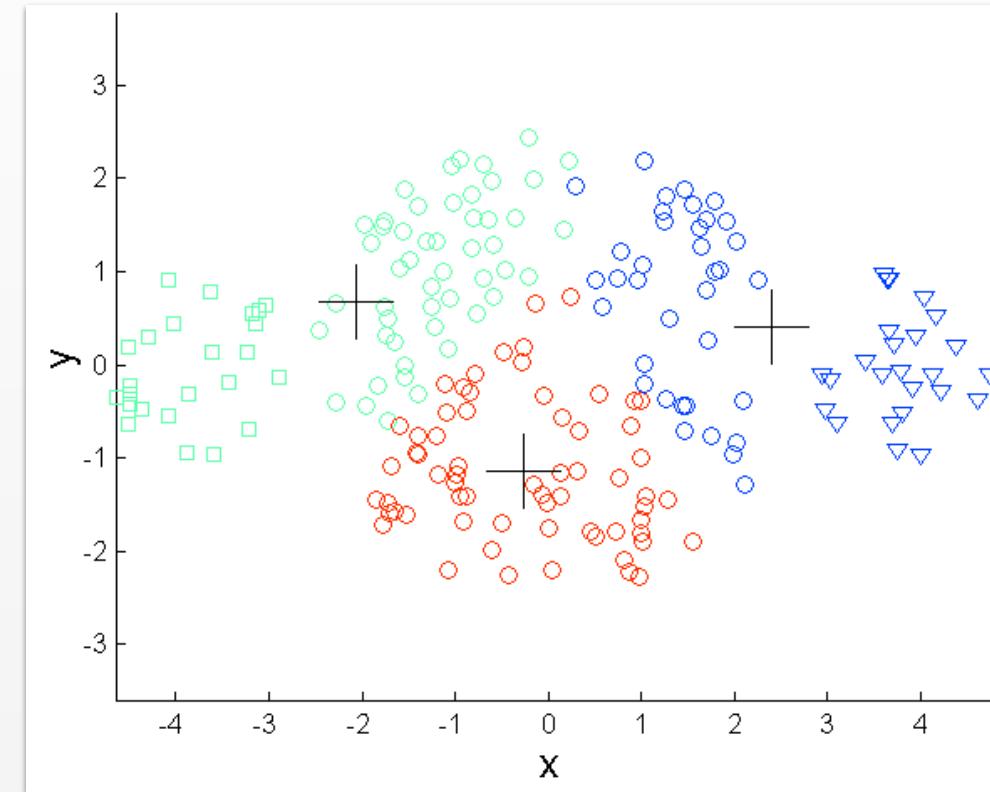
K-means Clustering

Limitations

K-means Limitations: Differing Sizes

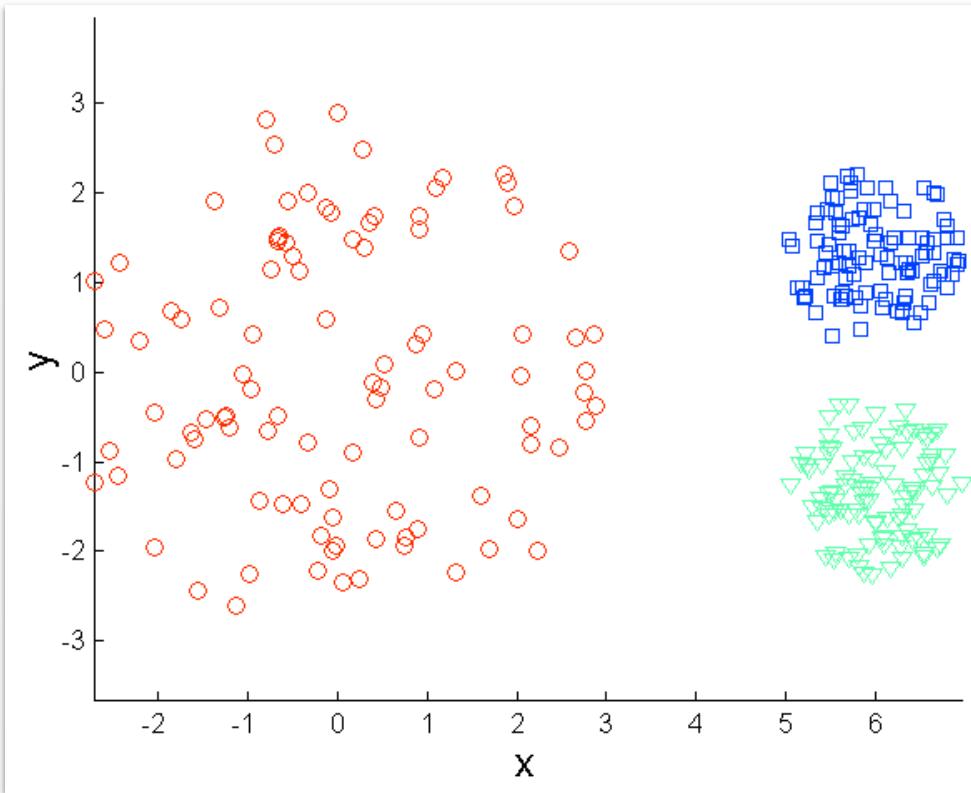


Original Points

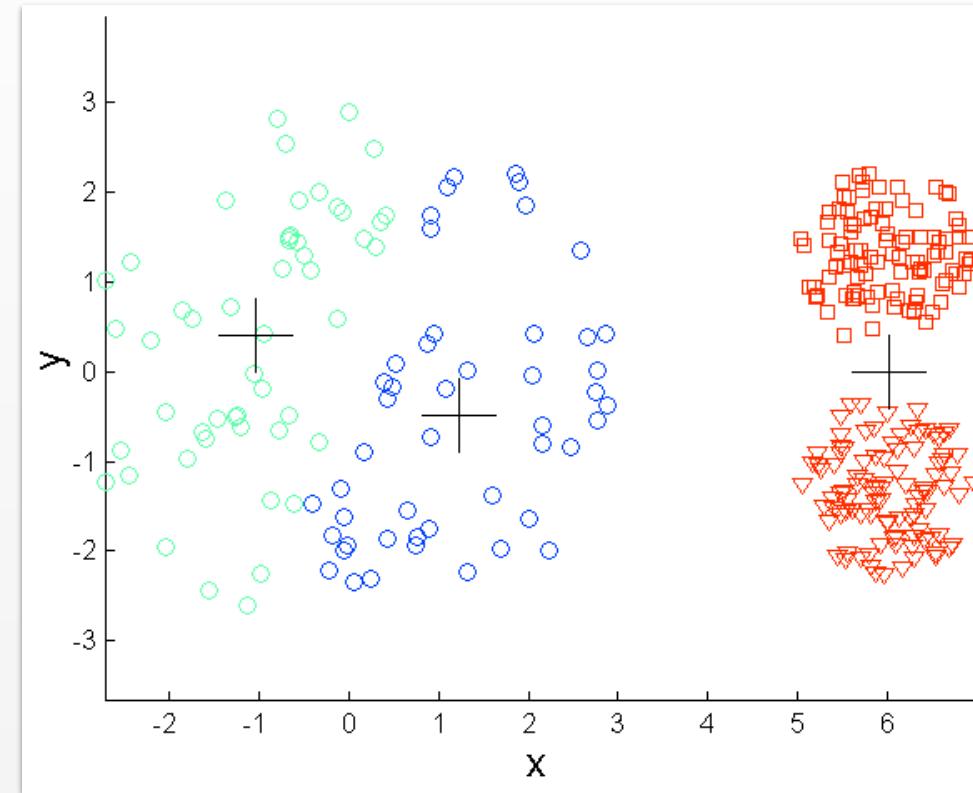


K-means (3 clusters)

K-means Limitations: Different Densities

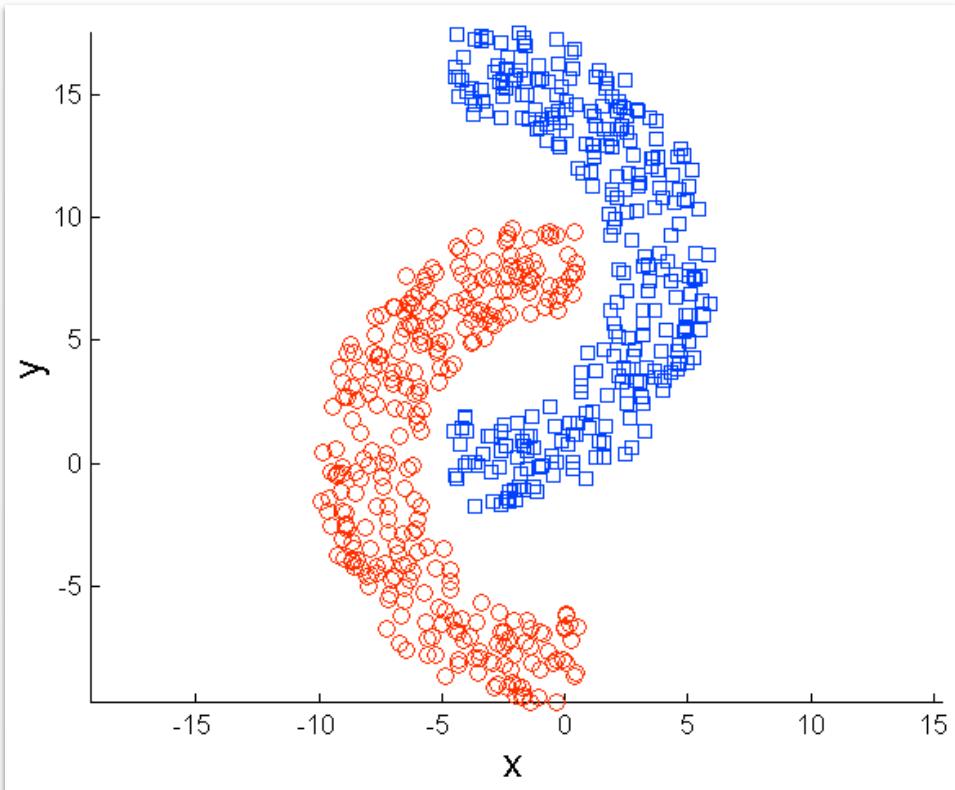


Original Points

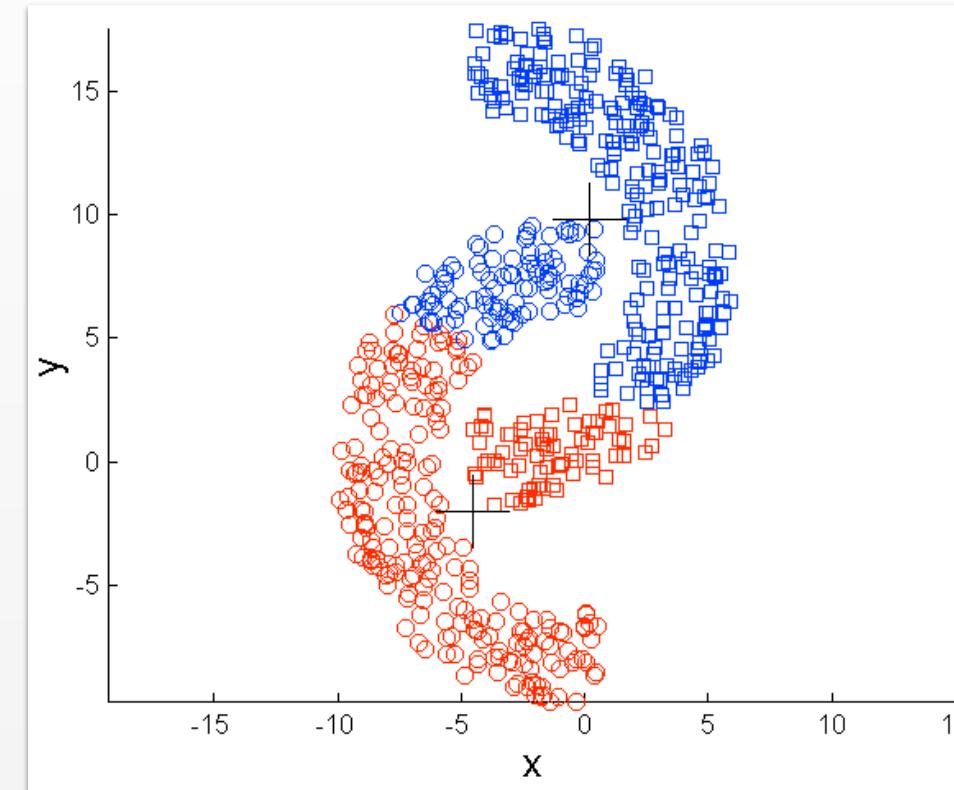


K-means (3 clusters)

K-means Limitations: Non-globular Shapes

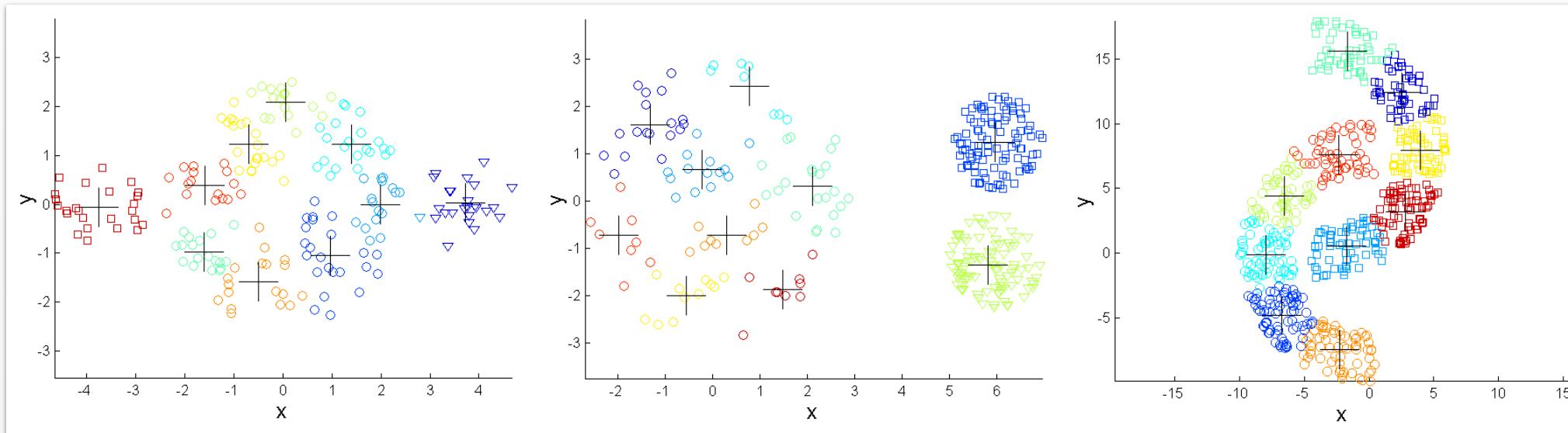


Original Points



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

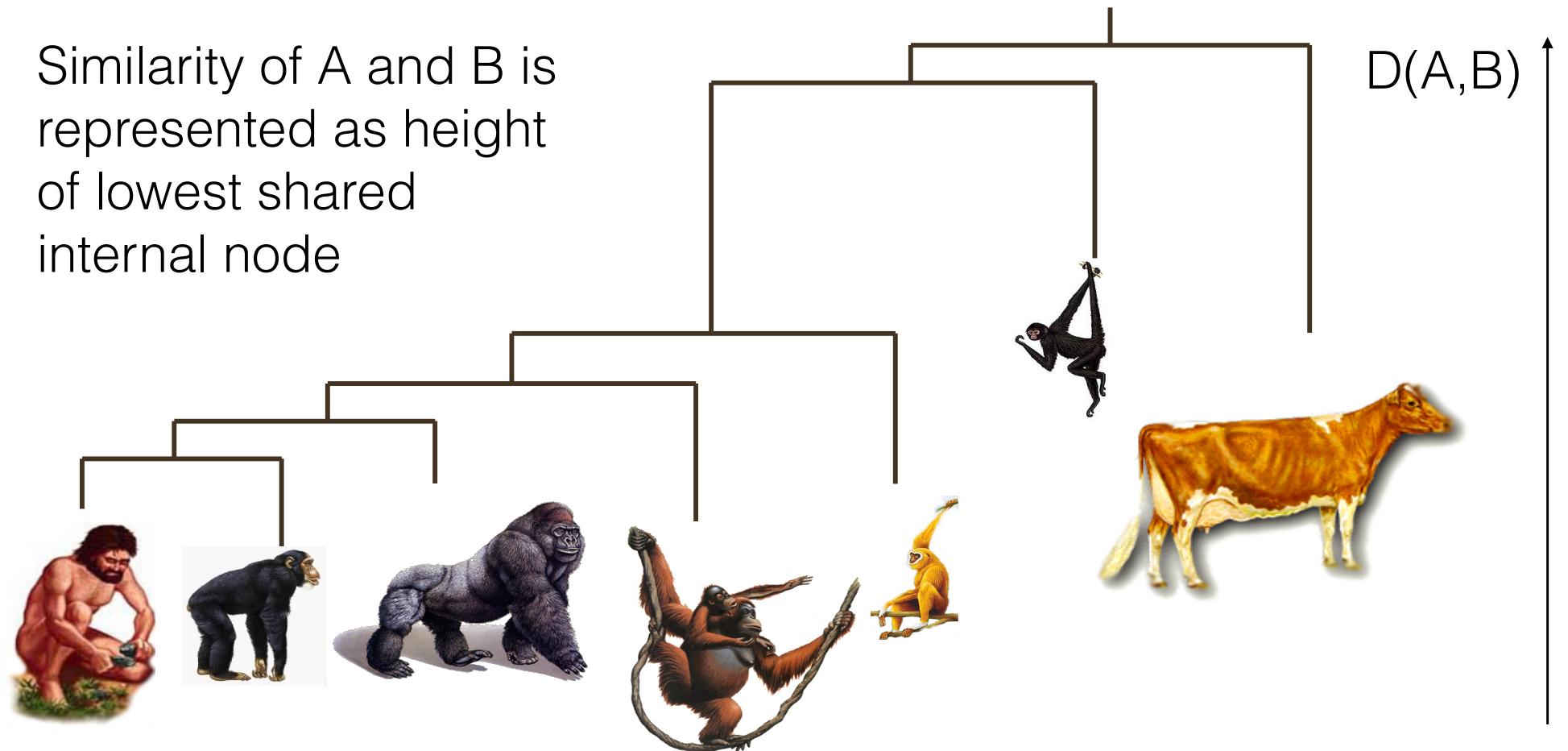


Hierarchical Clustering

Dendrogram

(a.k.a. a *similarity tree*)

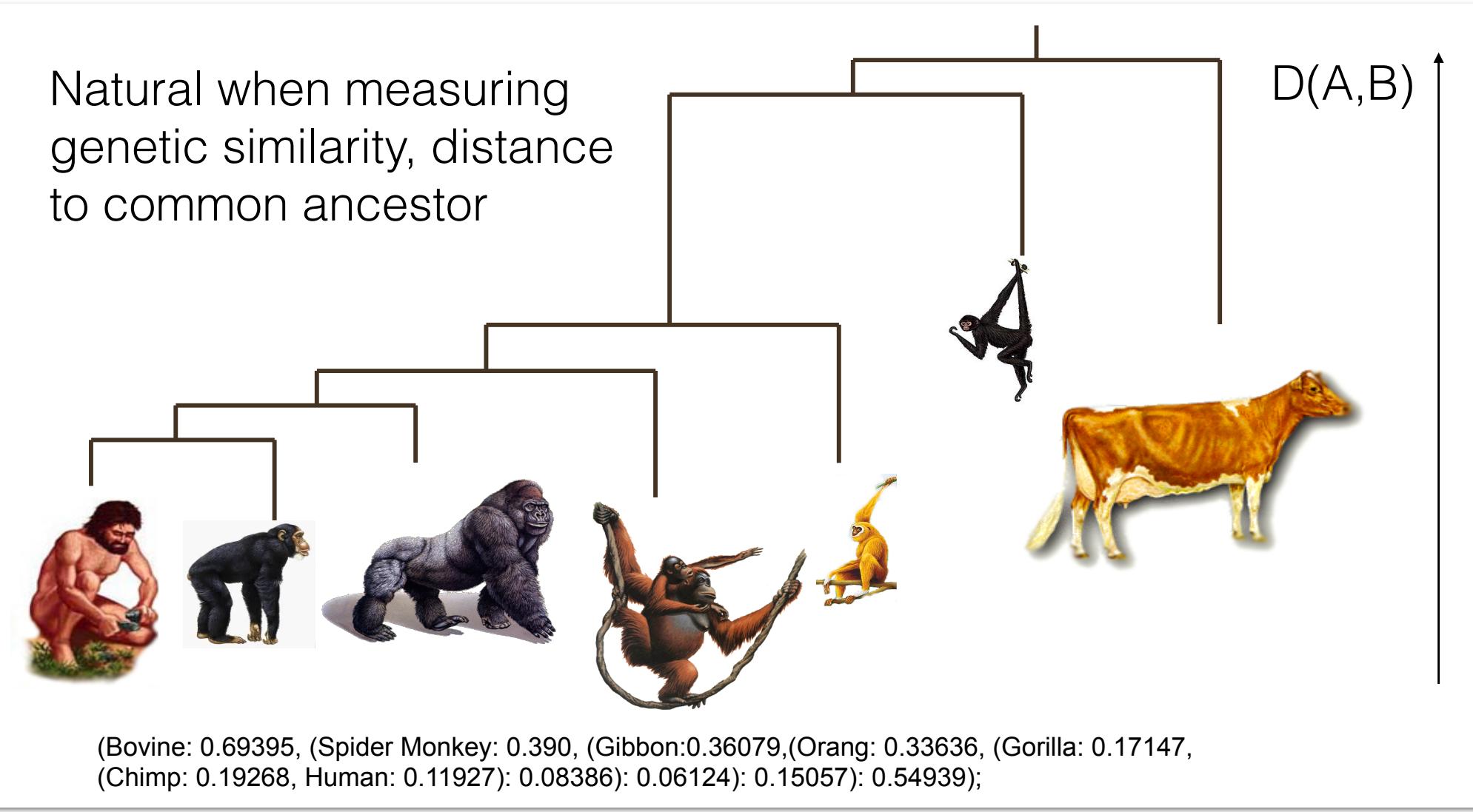
Similarity of A and B is represented as height of lowest shared internal node



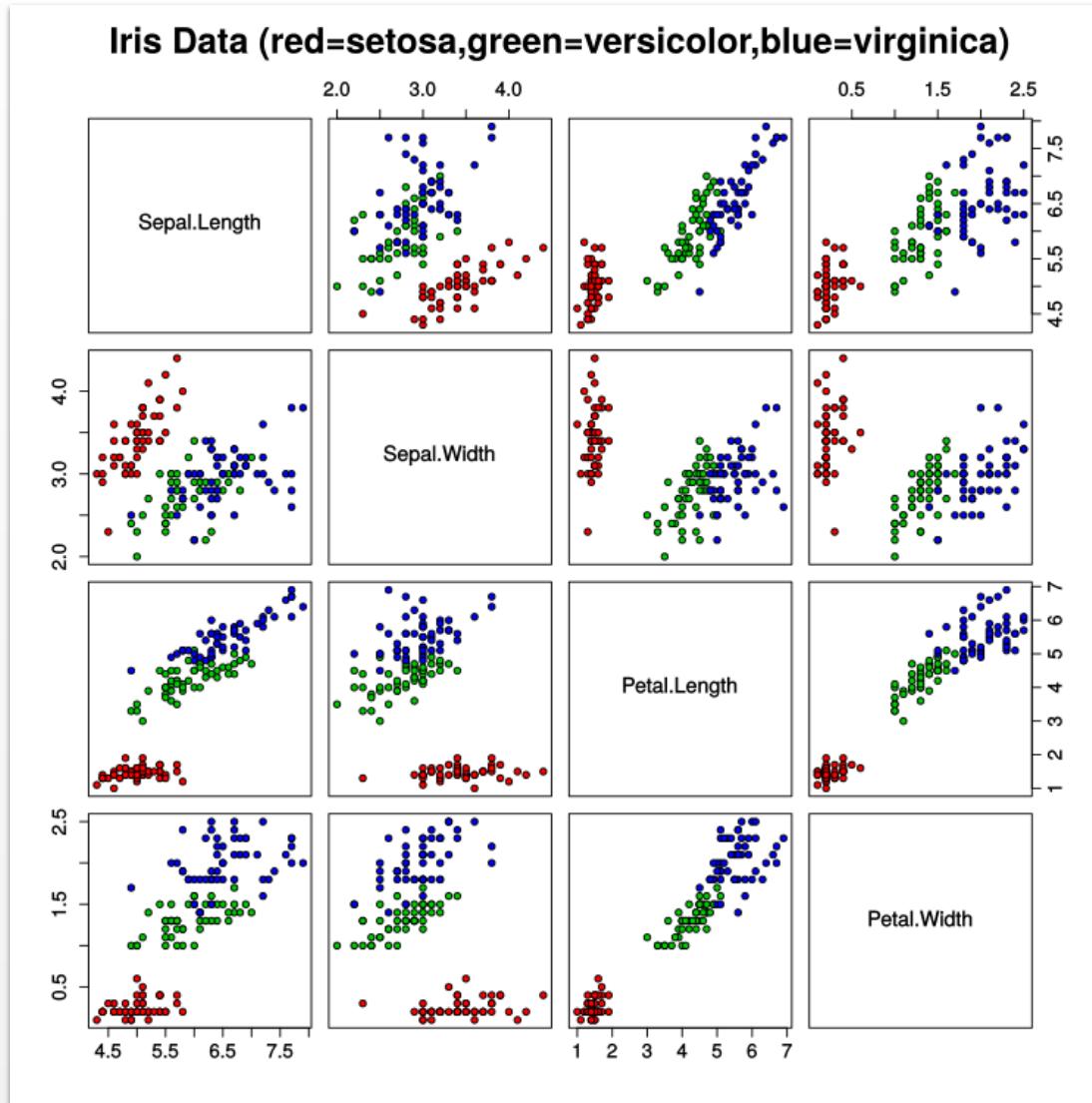
(Bovine: 0.69395, (Spider Monkey: 0.390, (Gibbon:0.36079,(Orang: 0.33636, (Gorilla: 0.17147,
(Chimp: 0.19268, Human: 0.11927): 0.08386): 0.06124): 0.15057): 0.54939);

Dendrogram

(*a.k.a. a similarity tree*)



Example: Iris data



Iris
Setosa



Iris
versicolor

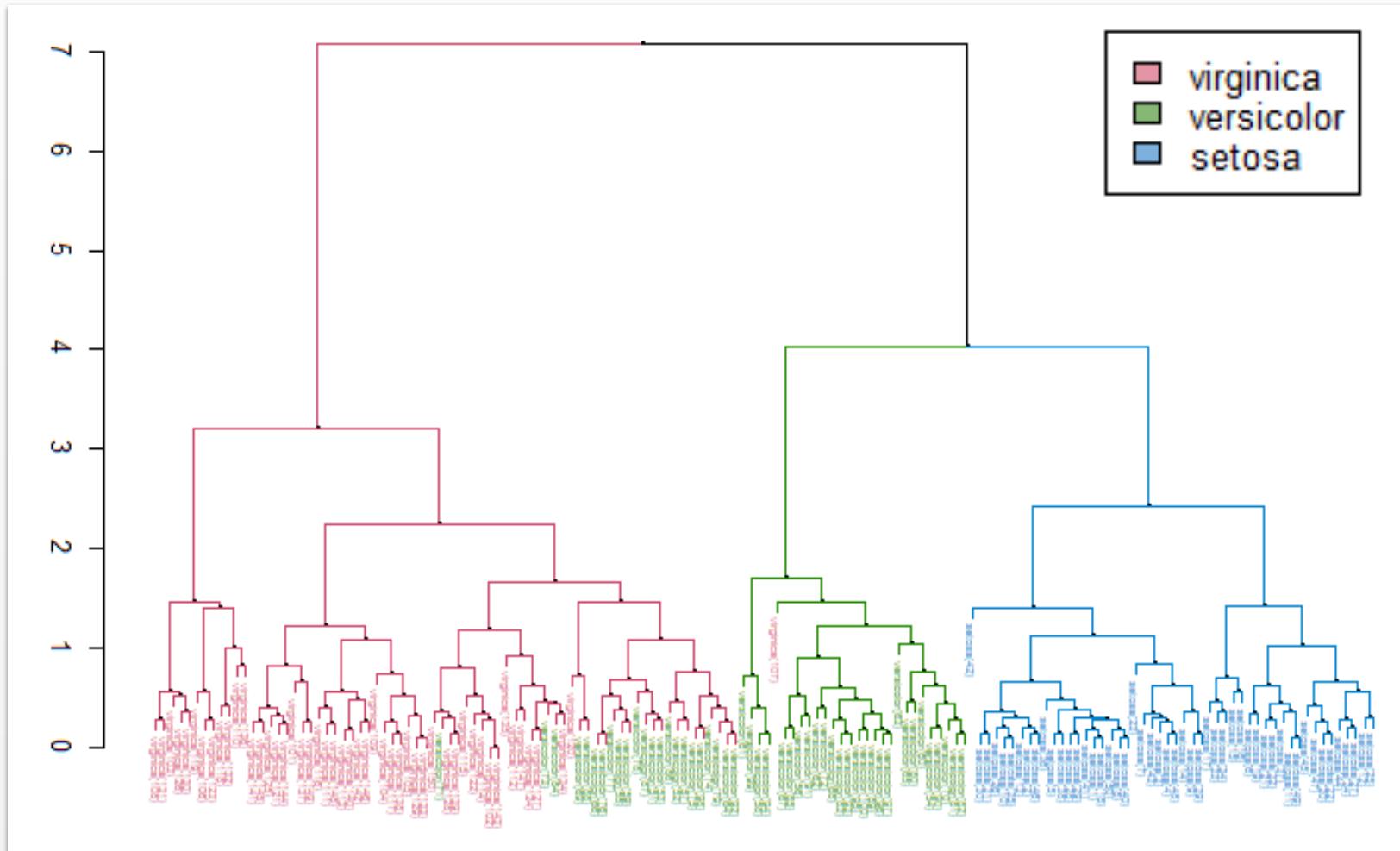


Iris
virginica

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

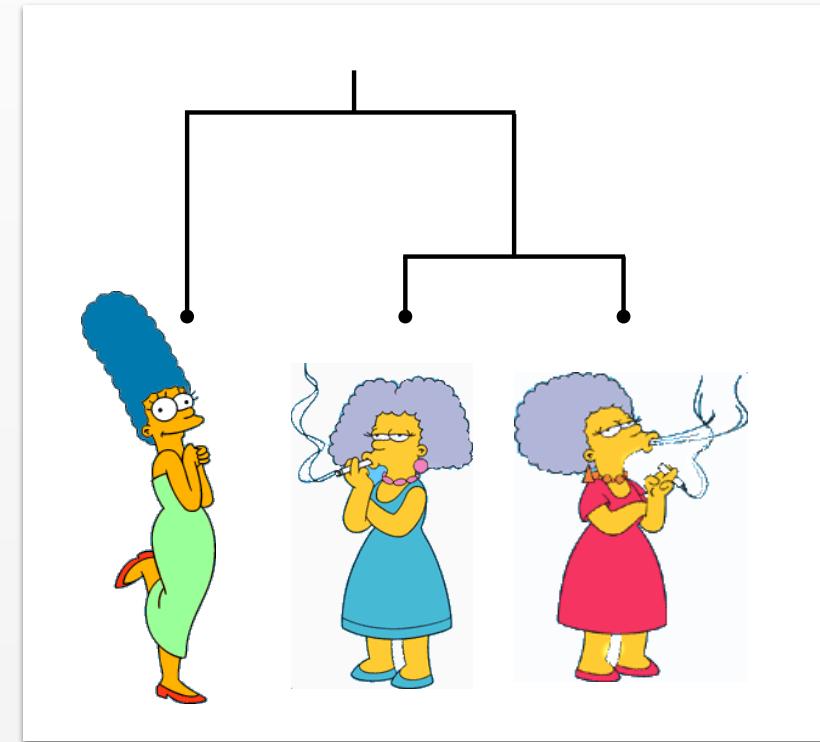
Change dress color, 1 point
Change earring shape, 1 point
Change hair part, 1 point

$$D(\text{Patty}, \text{Selma}) = 3$$

Distance Marge and Selma

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

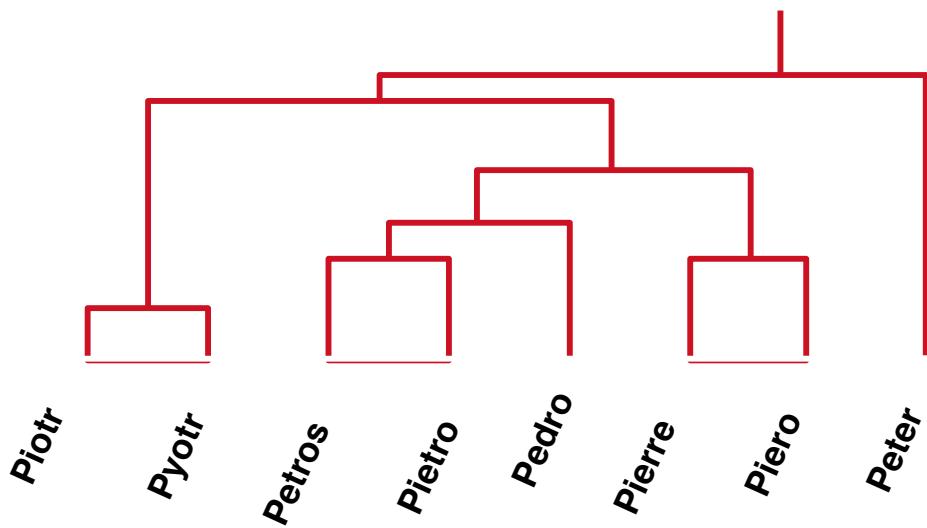
$$D(\text{Marge}, \text{Selma}) = 5$$



Can be defined for any set of discrete features

Edit Distance for Strings

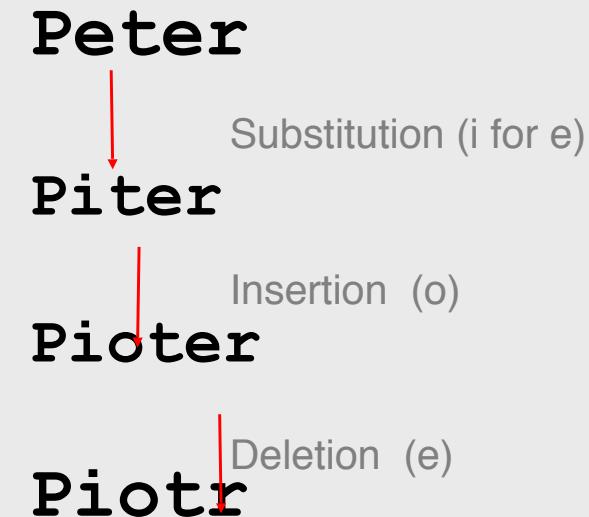
- Transform string Q into string C , using only ***Substitution***, ***Insertion*** and ***Deletion***.
- Assume that each of these operators has a **cost** associated with it.
- The similarity between two strings can be defined as the cost of the ***cheapest*** transformation from Q to C .



Similarity “Peter” and “Piotr”?

Substitution 1 Unit
Insertion 1 Unit
Deletion 1 Unit

$D(\text{Peter}, \text{Piotr})$ is 3



Hierarchical Clustering

(*Edit Distance*)

Pedro (Portuguese)

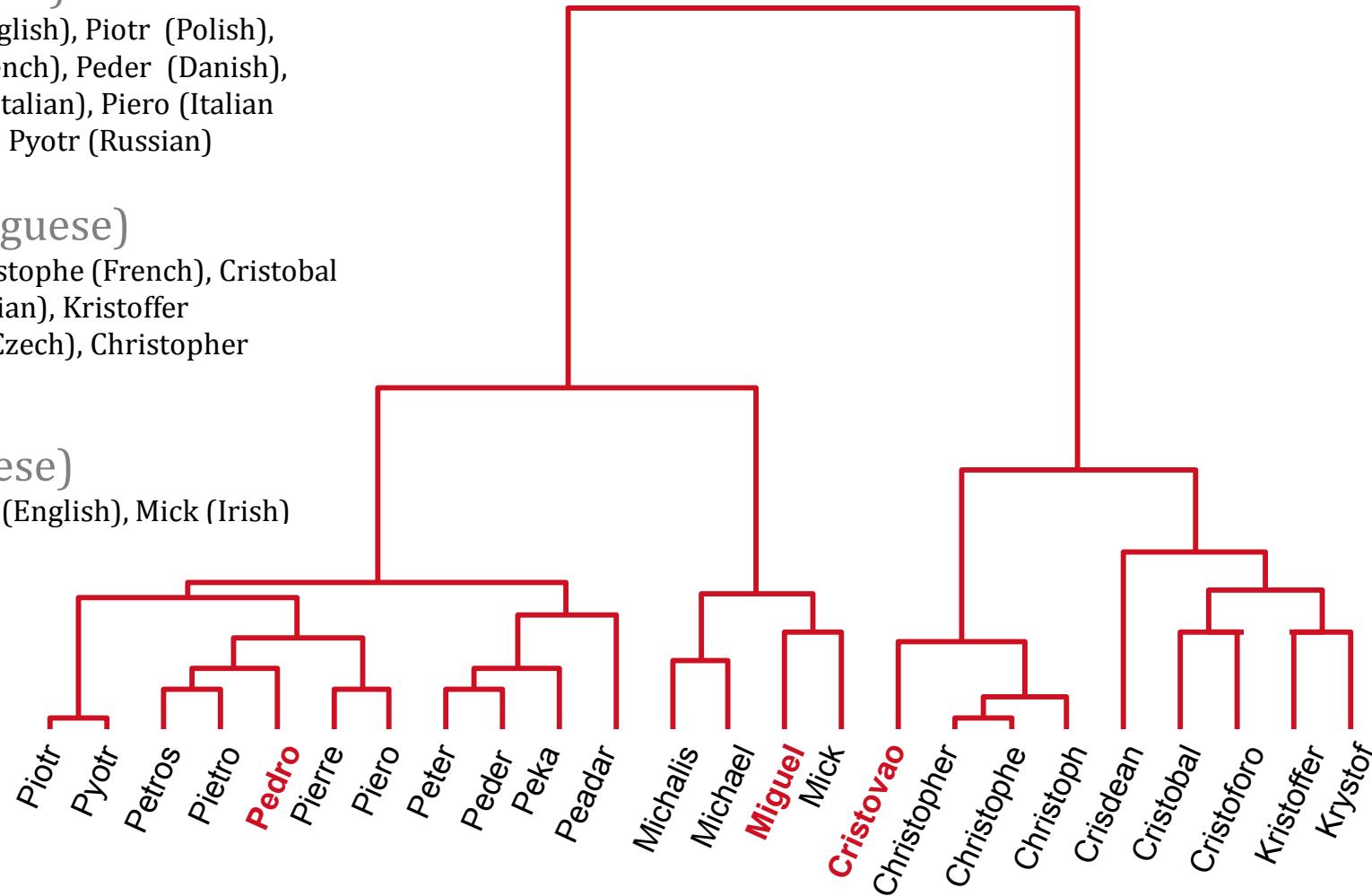
Petros (Greek), Peter (English), Piotr (Polish),
Peadar (Irish), Pierre (French), Peder (Danish),
Peka (Hawaiian), Pietro (Italian), Piero (Italian
Alternative), Petr (Czech), Pyotr (Russian)

Cristovao (Portuguese)

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

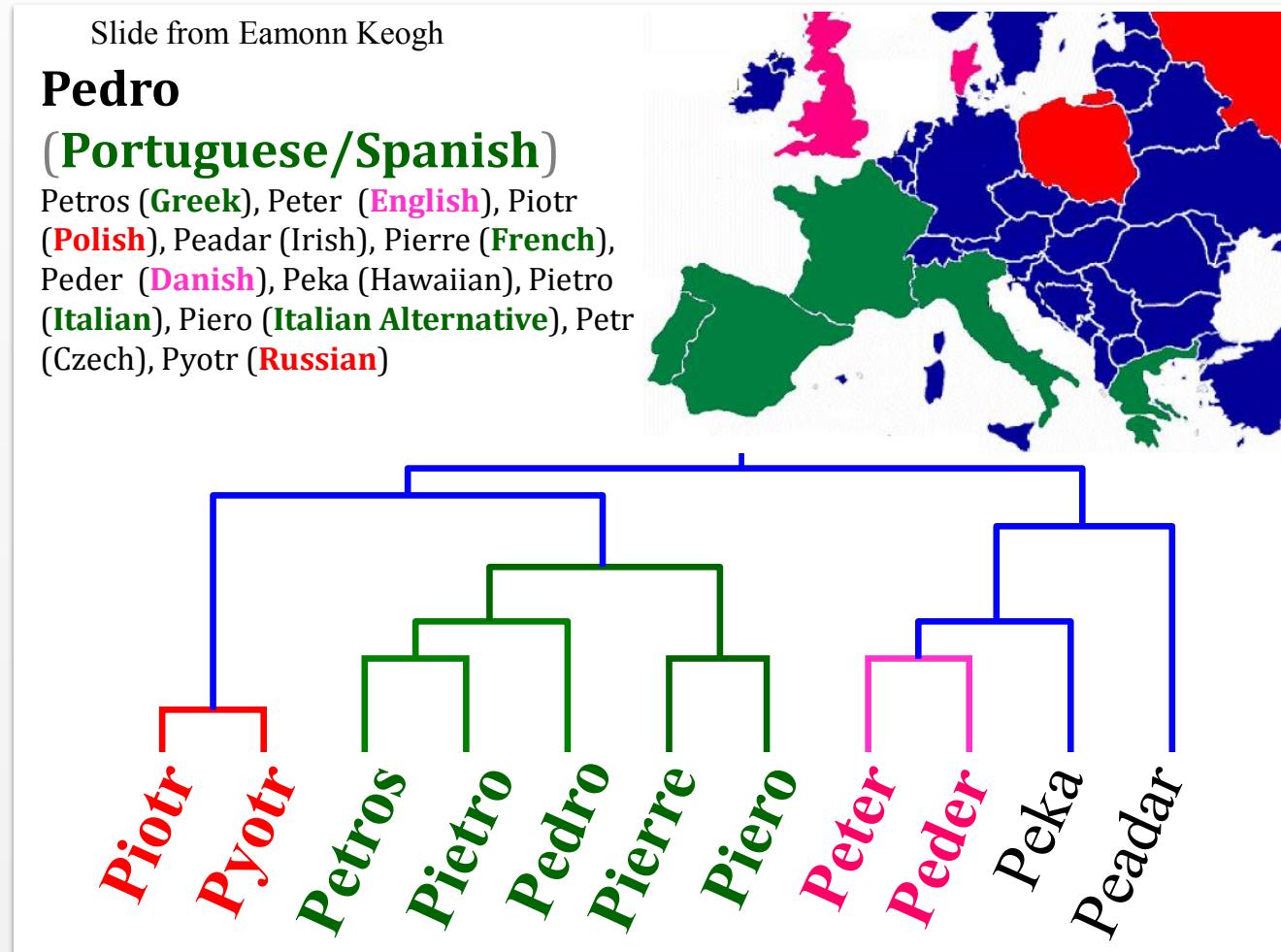
Miguel (Portuguese)

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



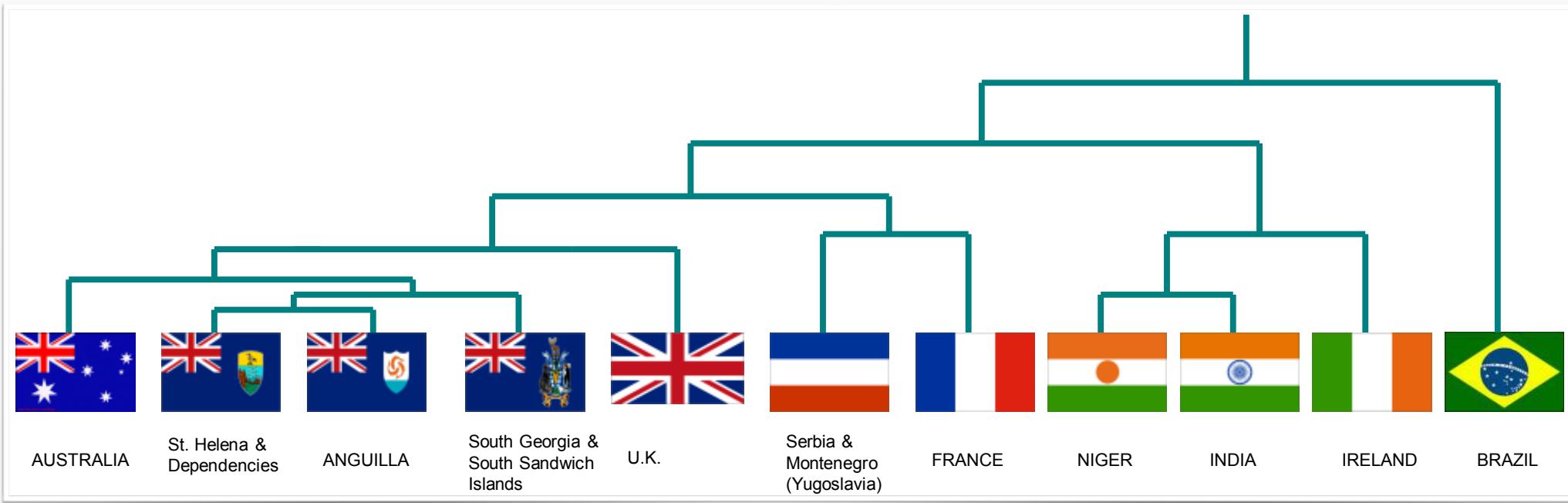
Meaningful Patterns

Edit distance yields clustering according to geography



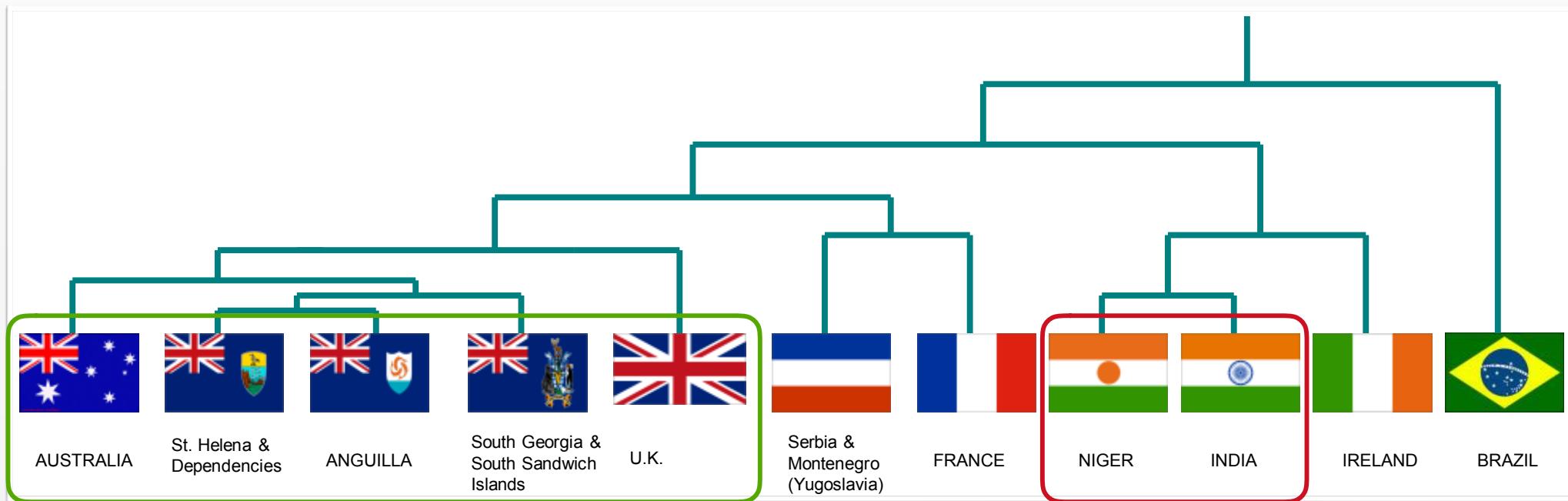
Spurious Patterns

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



Spurious Patterns

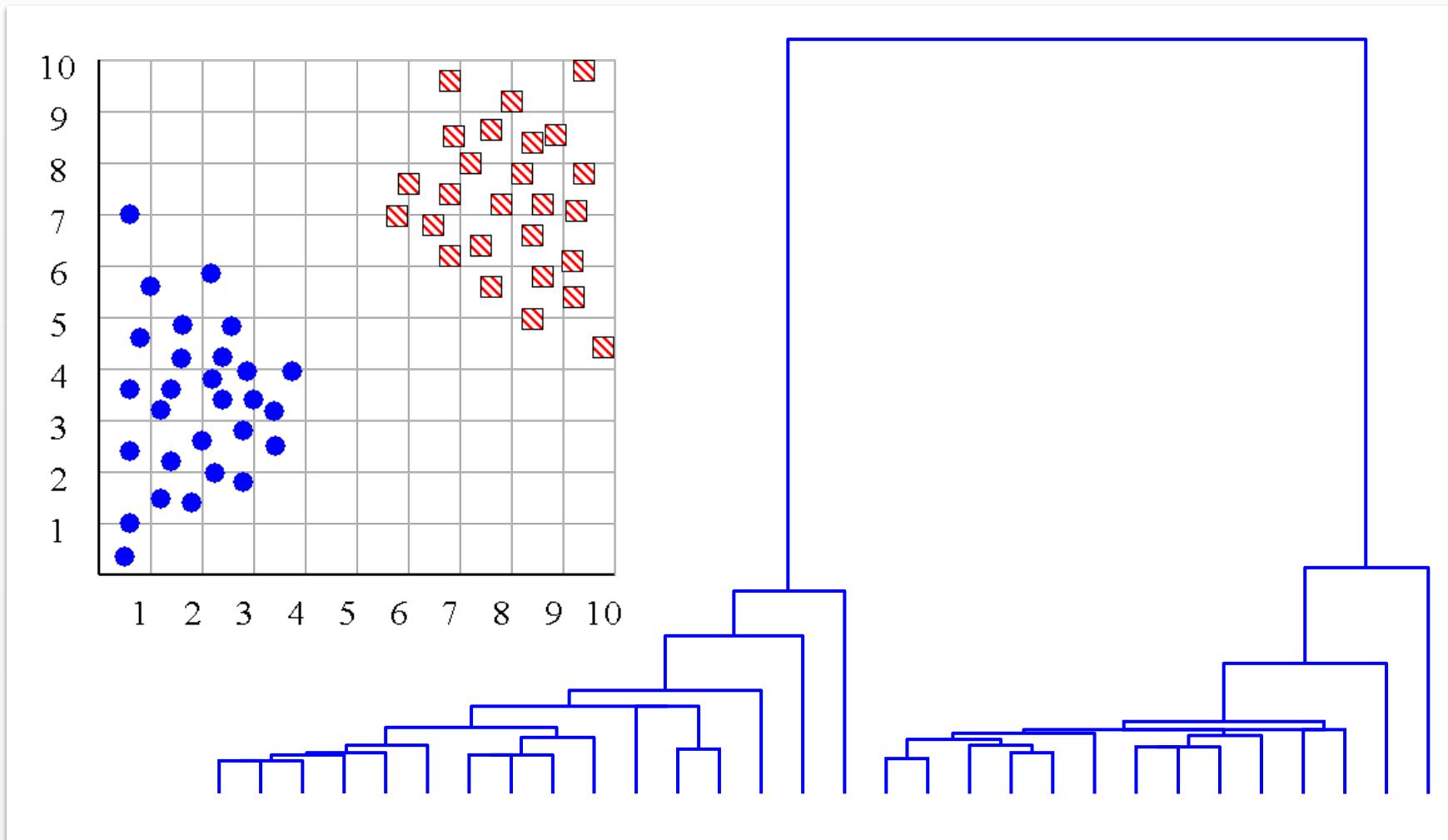
In general clusterings will only be as meaningful as your distance metric



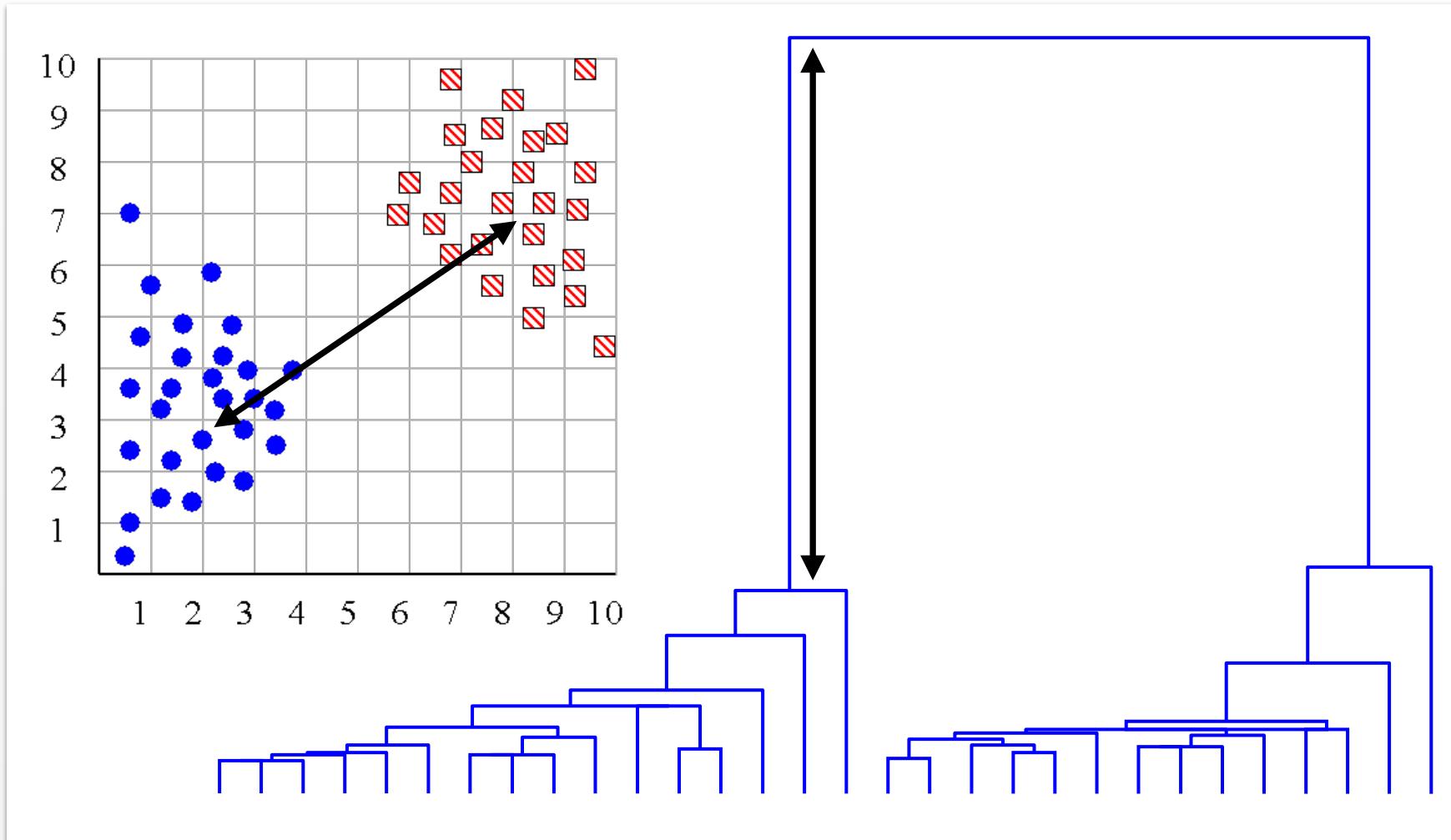
Former UK colonies

No relation

“Correct” Number of Clusters



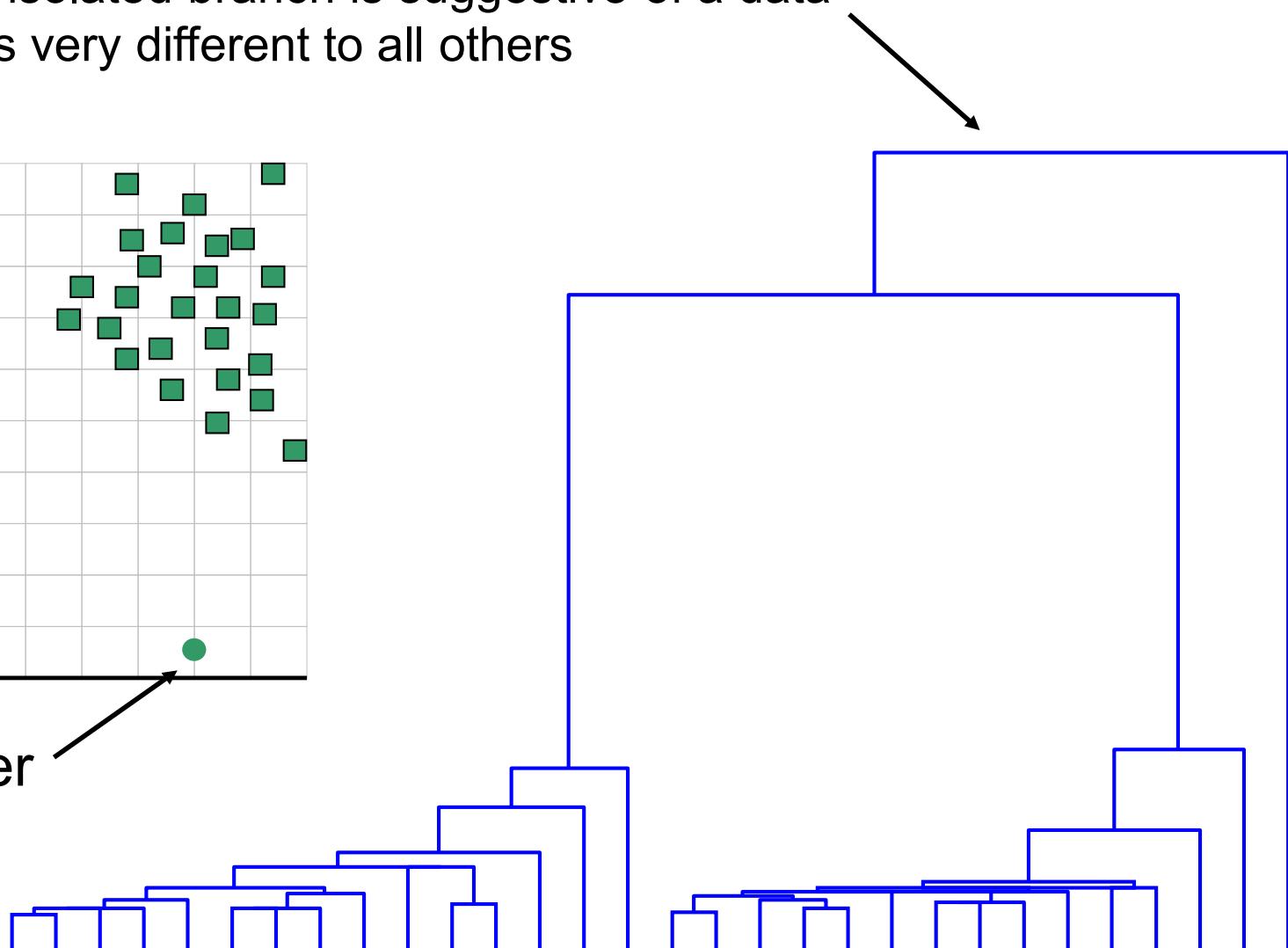
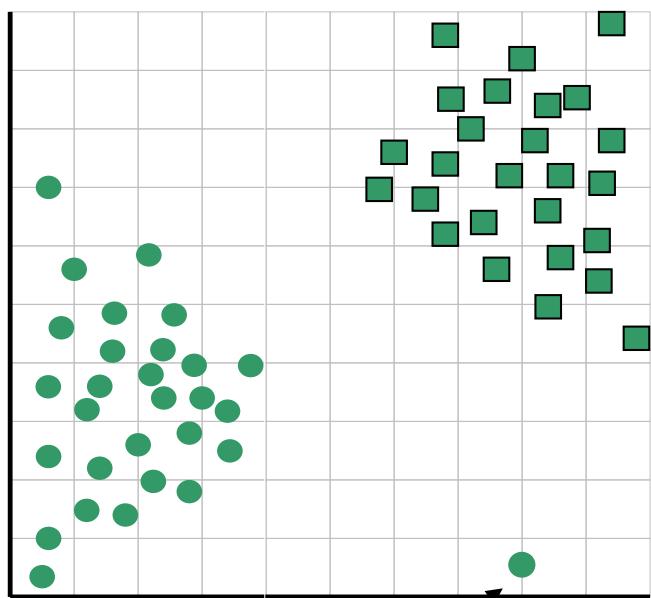
“Correct” Number of Clusters



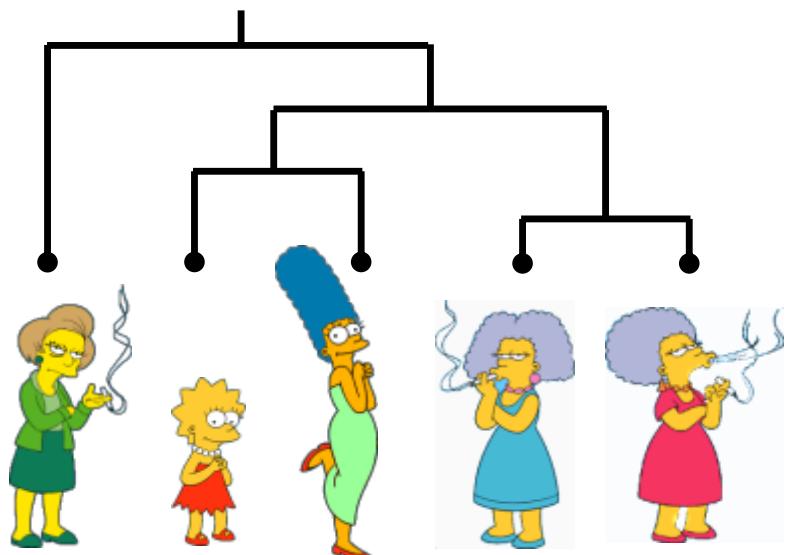
Determine number of clusters by looking at distance

Detecting Outliers

The single isolated branch is suggestive of a data point that is very different to all others



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

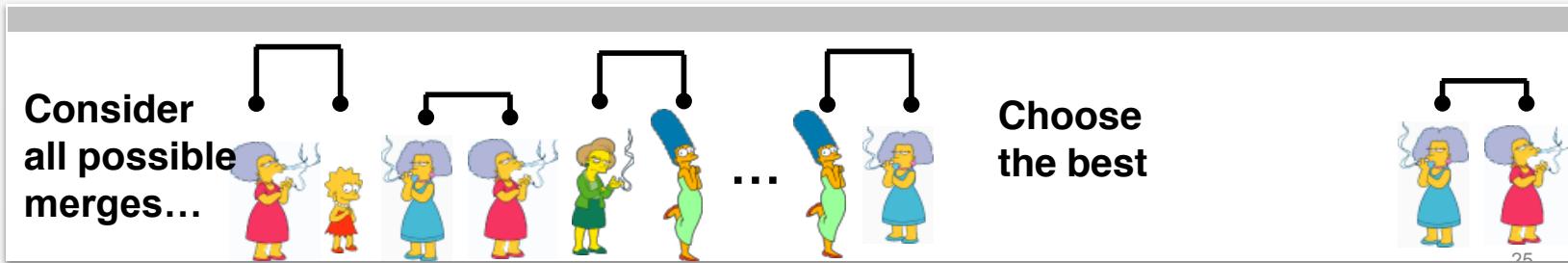
We begin with a distance matrix which contains the distances between every pair of objects in our database.

$$D(\text{Marge}, \text{Lisa}) = 8$$

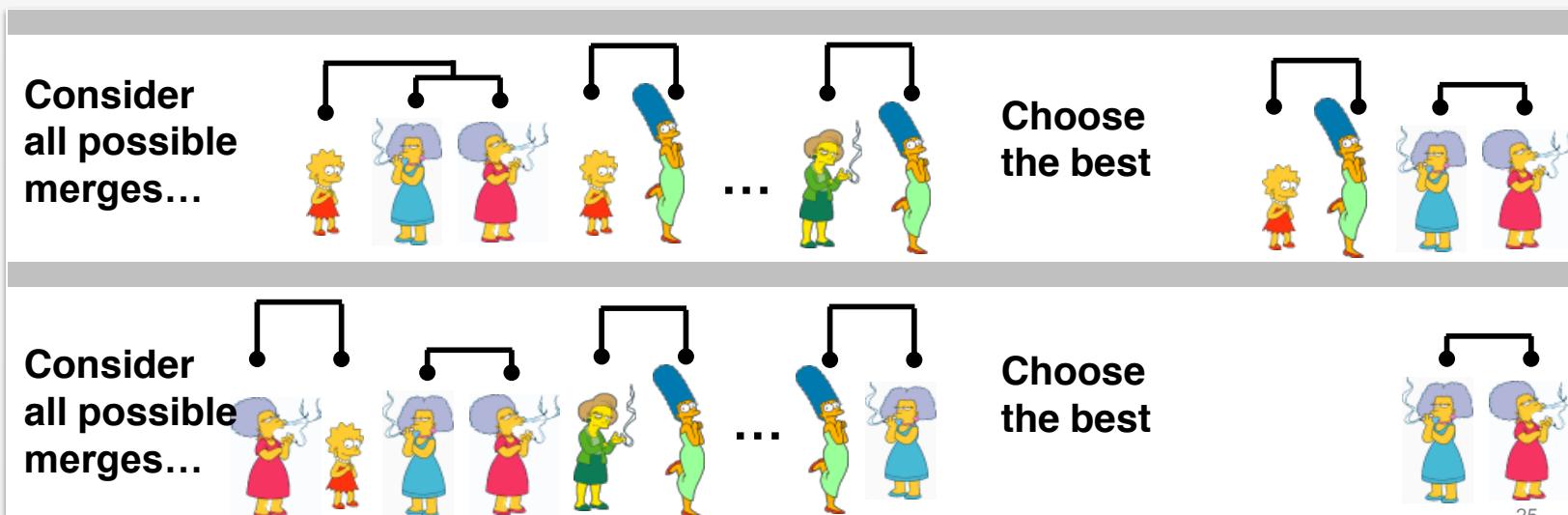
$$D(\text{Edna}, \text{Marge}) = 1$$

	0	8	8	7	7
	0	2	4	4	
		0	3	3	
			0	1	
				0	

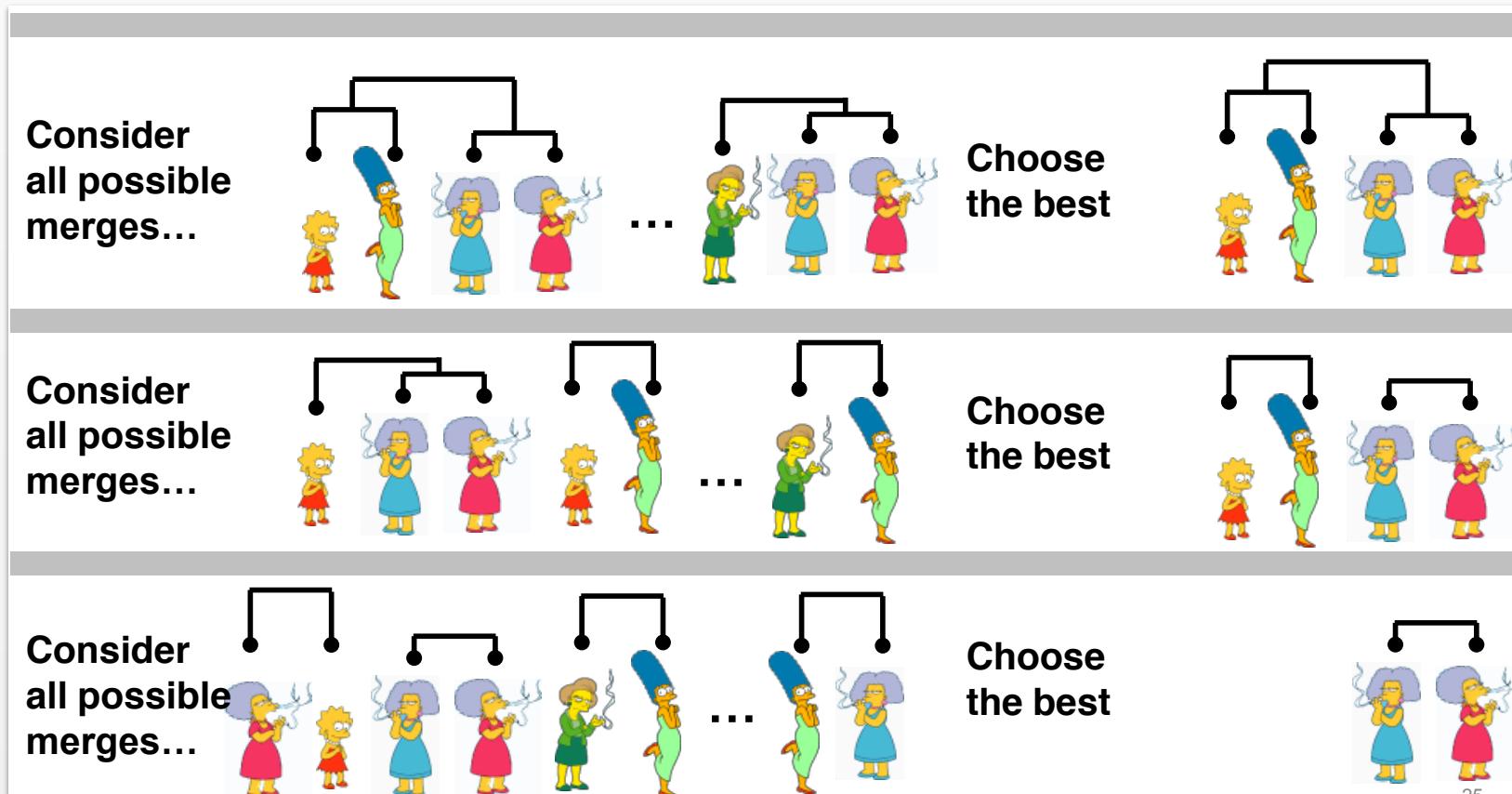
Bottom-up (Agglomerative Clustering)



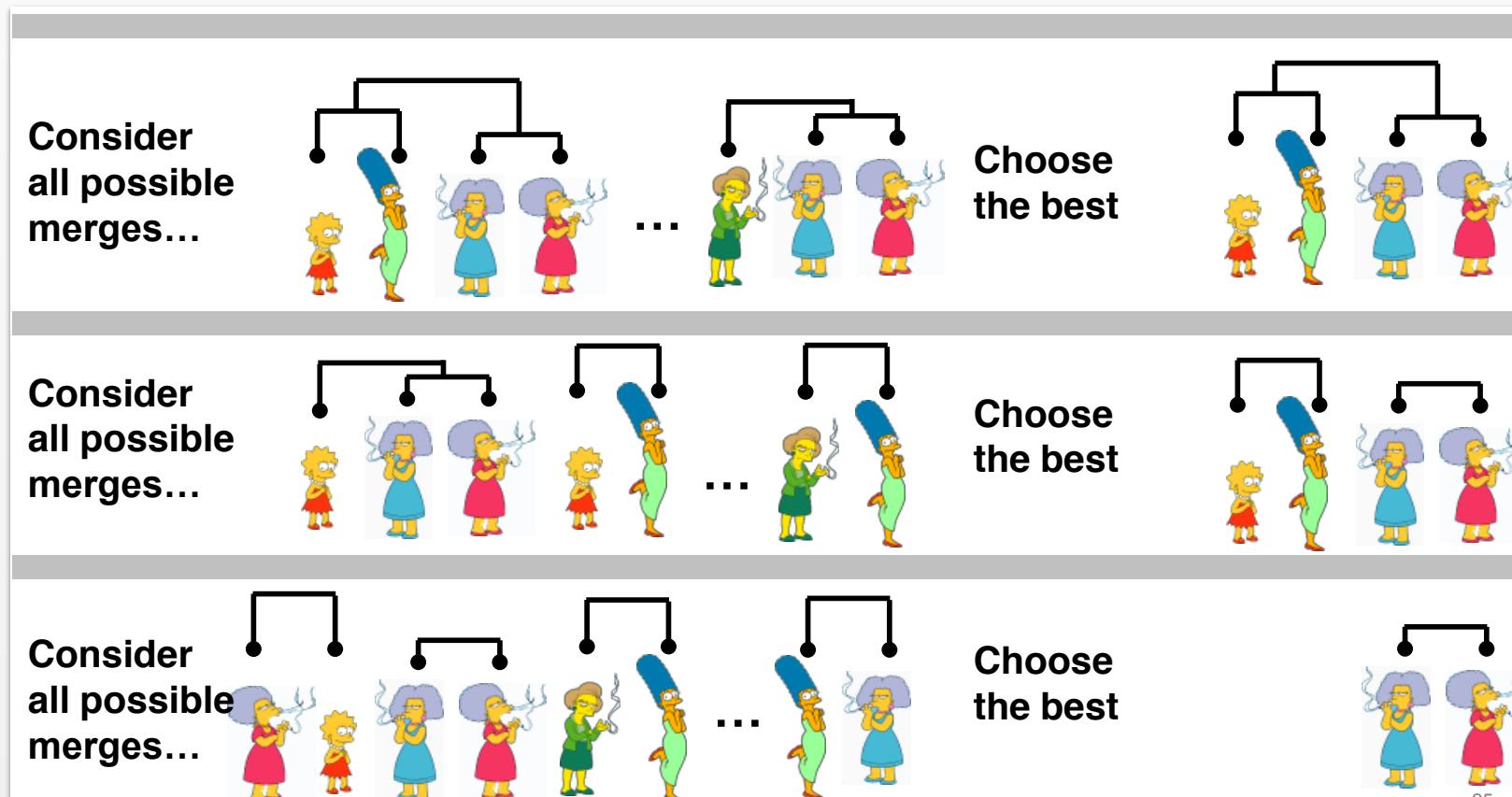
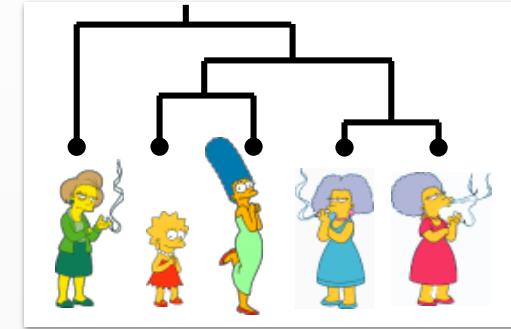
Bottom-up (Agglomerative Clustering)



Bottom-up (Agglomerative Clustering)

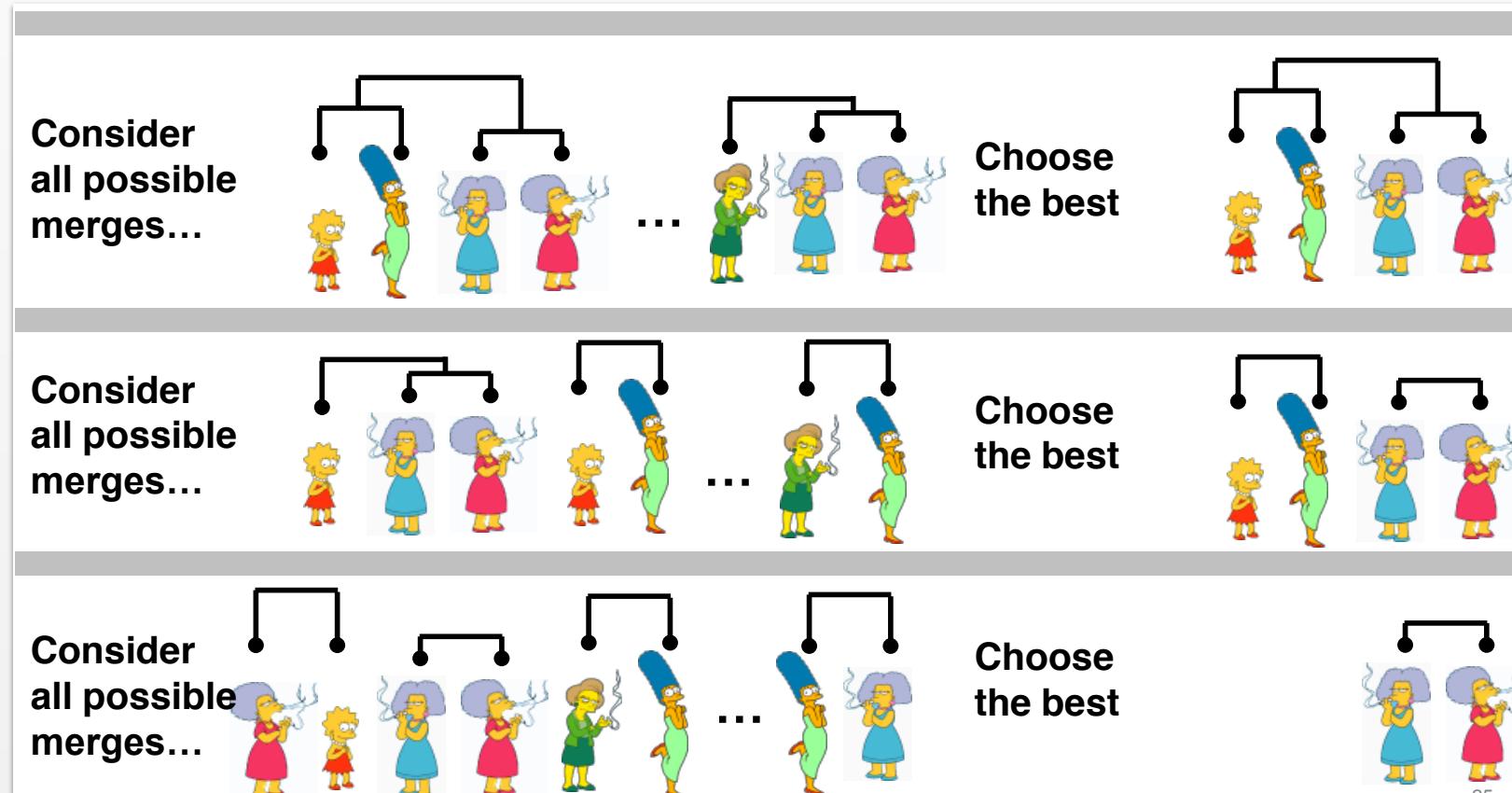
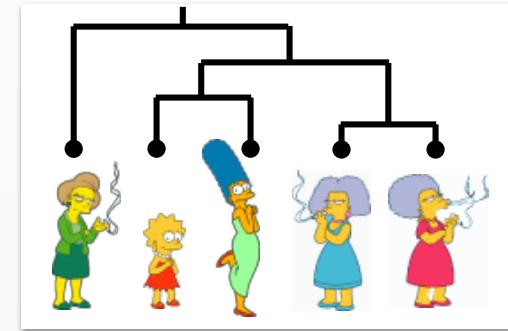


Bottom-up (Agglomerative Clustering)



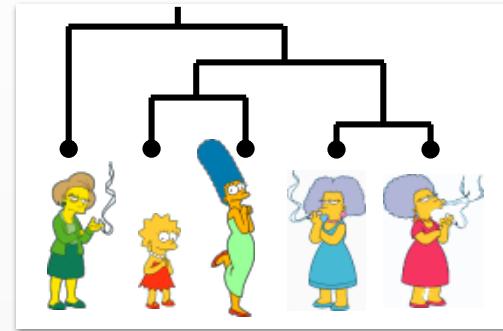
Bottom-up (Agglomerative Clustering)

Can you now implement this?

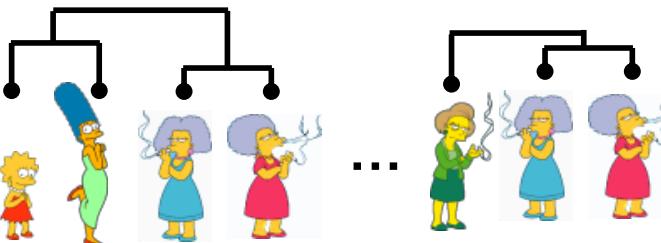


Bottom-up (Agglomerative Clustering)

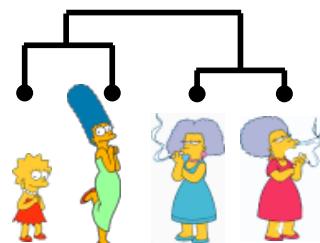
Distances between examples (can calculate using metric)



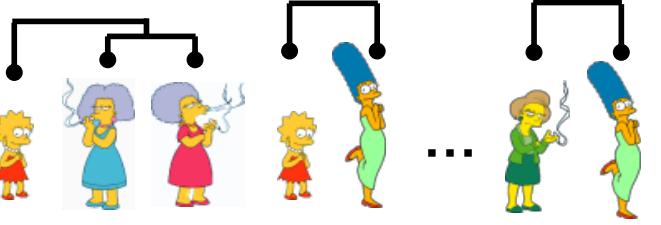
**Consider
all possible
merges...**



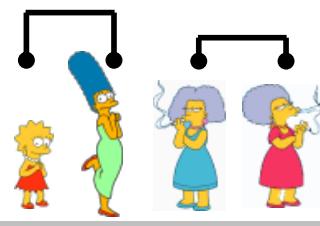
Choose the best



**Consider
all possible
merges...**



Choose the best



**Consider
all possible
merges...**

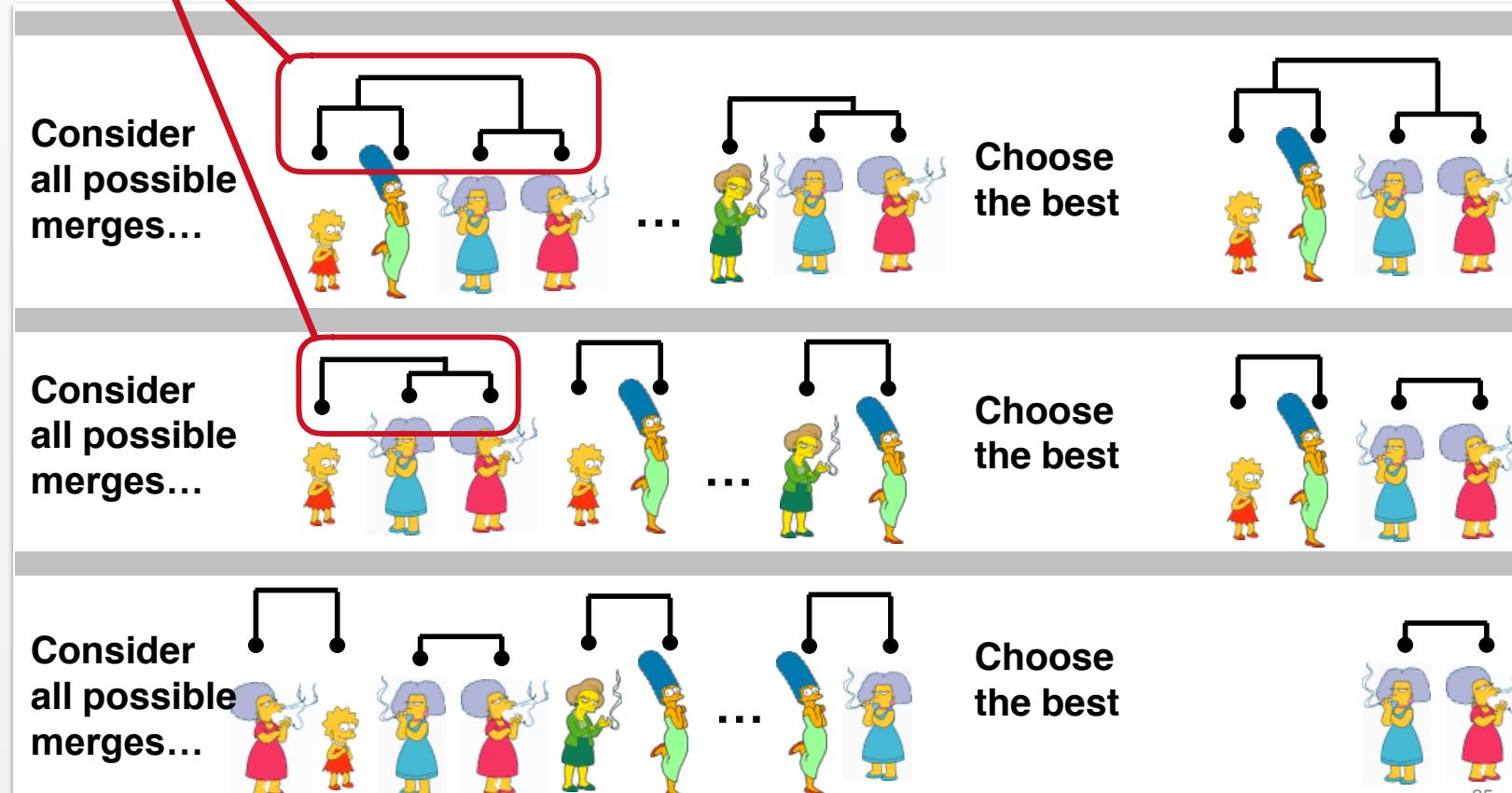
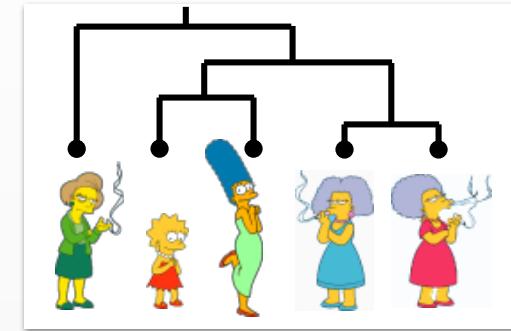


Choose the best



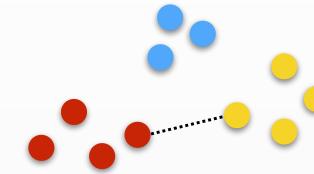
Bottom-up (Agglomerative Clustering)

How do we calculate the distance to a cluster?

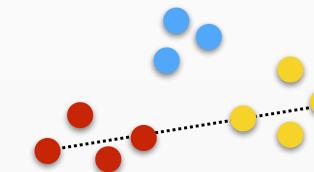


Clustering Criteria

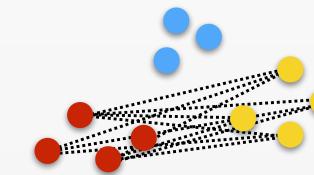
Single link: $d(A, B) = \min_{a \in A, b \in B} d(a, b)$



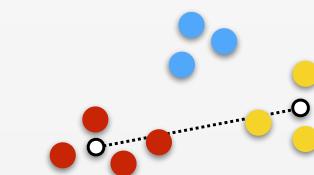
Complete link: $d(A, B) = \max_{a \in A, b \in B} d(a, b)$



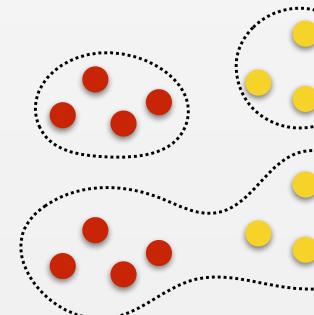
Group average: $d(A, B) = \frac{1}{|A||B|} \sum_{a \in A, b \in B} d(a, b)$

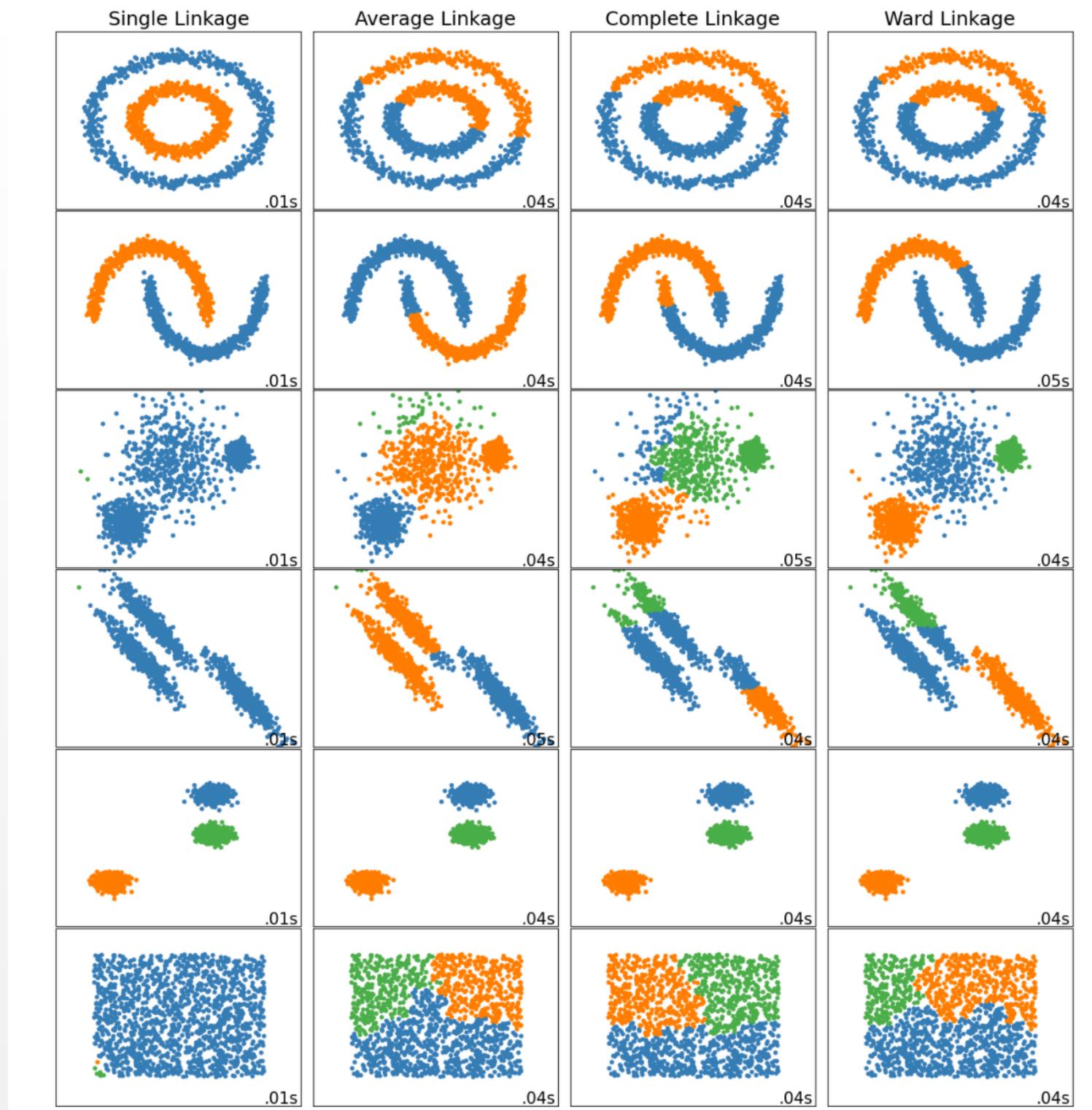


Centroid: $d(A, B) = d(\mu_A, \mu_B)$ $\mu_X = \frac{1}{|X|} \sum_{x \in X} x$



Ward: $S_{A \cup B} = \sum_{x \in A \cup B} d(x, \mu_{A \cup B})^2$





Naive time complexity

Algorithm 8.3 Basic agglomerative hierarchical clustering algorithm.

- 1: Compute the proximity matrix, if necessary. $O(N^2D)$
 - 2: **repeat**
 - 3: Merge the closest two clusters. $O((N - i + 1)^2)$
 - 4: Update the proximity matrix to reflect the proximity between the new cluster and the original clusters. $O((N - i - 1)D)$
 - 5: **until** Only one cluster remains.
- Performed $O(N)$ iterations
-

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. $O(N^2D)$
 - 2: **repeat**
 - 3: Merge the closest two clusters. $O(1)$
 - 4: Update the proximity matrix to reflect the proximity between the new cluster and the original clusters. $O((N - i)\log(N - i + 1))$ and $O(N - i - 1)$
 - 5: **until** Only one cluster remains.
-

Performed $O(N)$

iterations

Overall complexity
 $O(N^2D + N^2 \log N)$

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	α_A	α_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	$\frac{m_A}{m_A+m_B}$	$\frac{m_B}{m_A+m_B}$	$\frac{-m_A m_B}{(m_A+m_B)^2}$	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

$$d(x,y) = |x-y|$$

$$d(x,y) = |x-y|^2$$

Recursively minimize/maximize proximity for a merger $R := A \cup B$ relative to all existing Q

$$\begin{aligned}
 p(R, Q) = & \alpha_A p(A, Q) \\
 & + \alpha_B p(B, Q) \\
 & + \beta p(A, B) \\
 & + \gamma |p(A, Q) - p(B, Q)|
 \end{aligned}$$

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 from becoming global optimization. For e.g., Ward methods optimized local SSE doesn't translate to the optimized global SSE.
 - *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*
- Can be improved by initializing with several small k-means clusters



Clustering

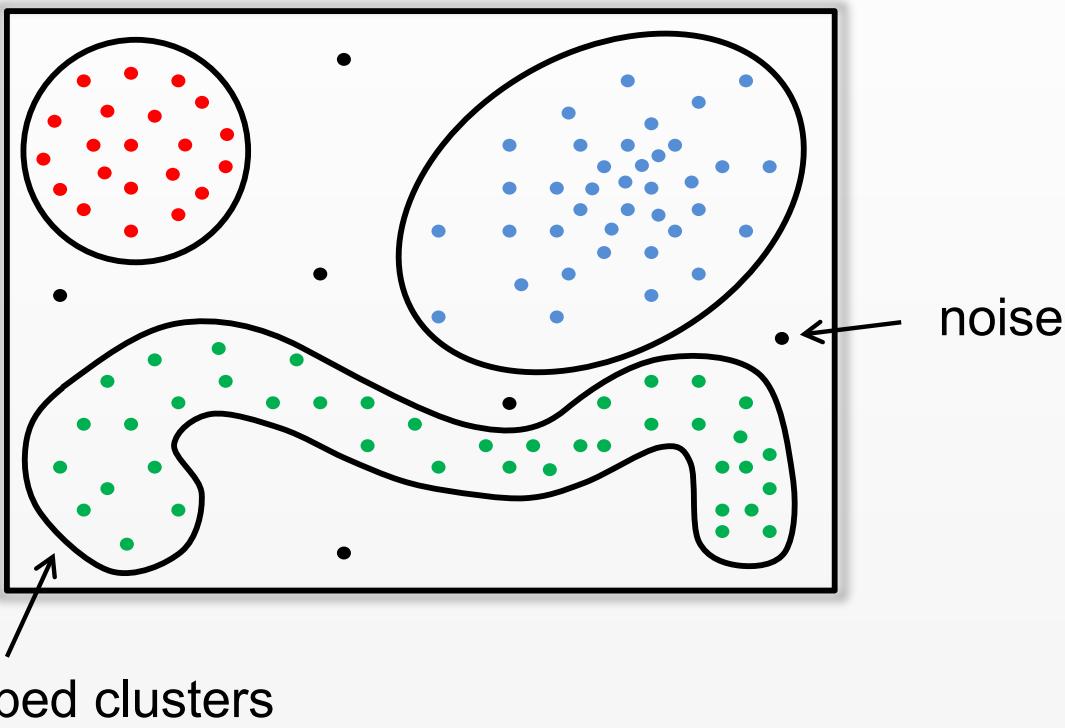
Shantanu Jain



DBScan

Density-based Clustering

DBSCAN



[PDF] A density-based algorithm for discovering clusters in large spatial databases with noise.

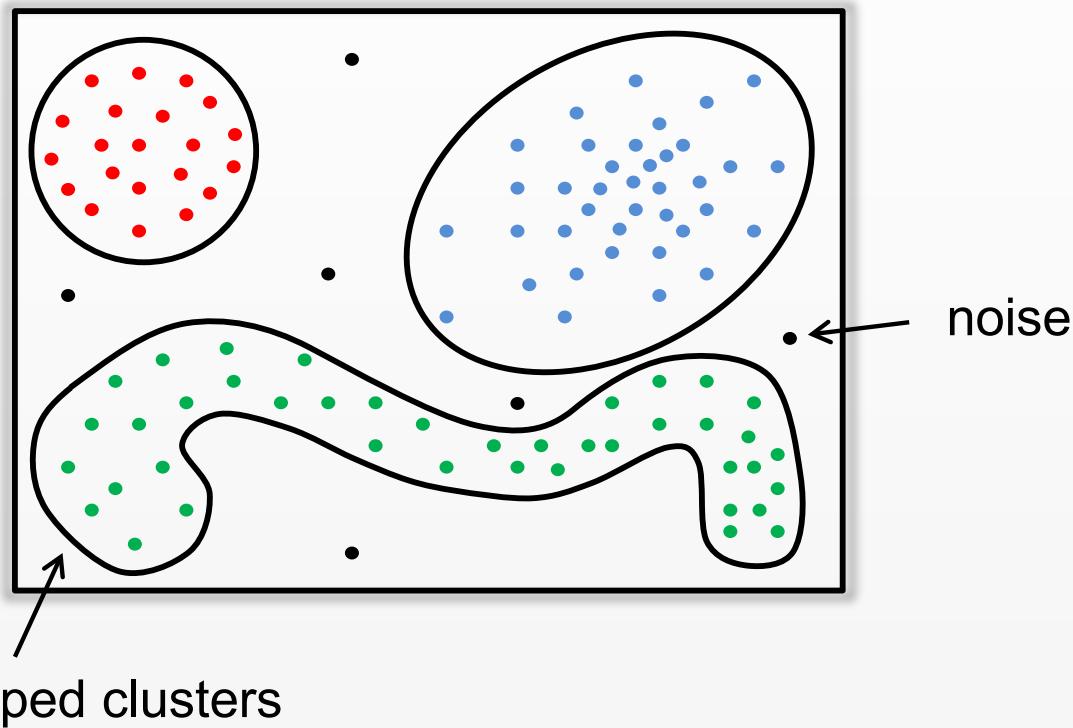
M Ester, HP Kriegel, J Sander, X Xu - Kdd, 1996 - aaai.org

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)

DBSCAN



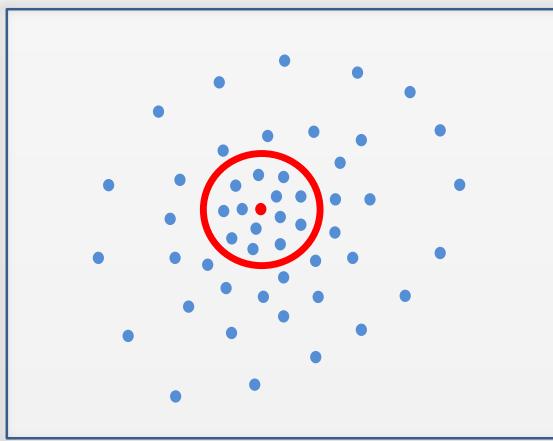
Intuition

- 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.

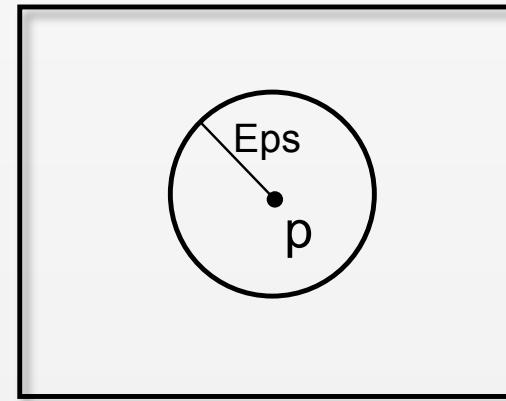


cluster

Defining “High Density”

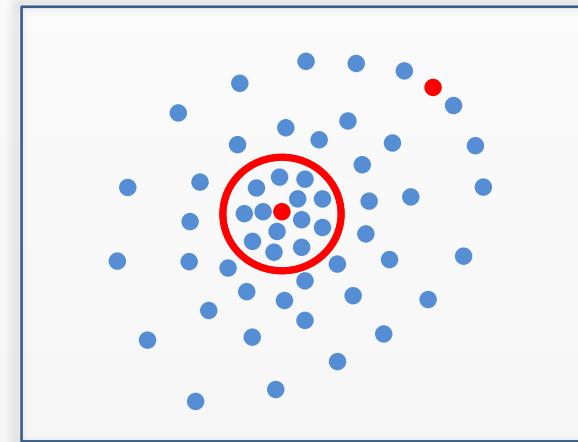
Eps-neighborhood of a point p

$$N_{Eps}(p) = \{ q \in D \mid \text{dist}(p, q) \leq Eps \}$$



Defining “High Density”

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



cluster

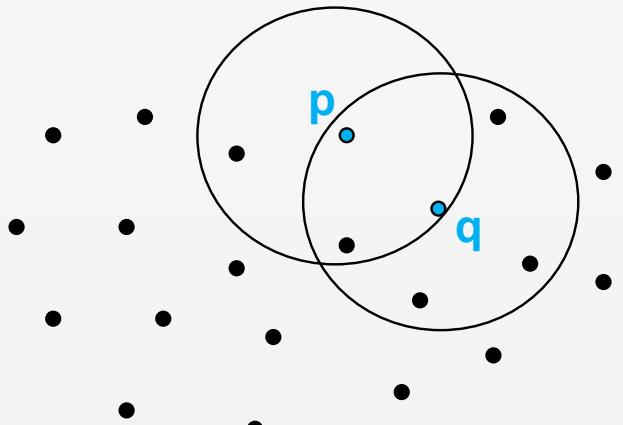
An Eps-neighborhood of a border point contains significantly less points than an Eps-neighborhood of a core point.

Density Reachability

Definition

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

- 1) $p \in N_{Eps}(q)$ (reachability)
- 2) $|N_{Eps}(q)| \geq MinPts$ (core point condition)



Parameter: $MinPts = 5$

p directly density reachable from q

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

$$|N_{Eps}(q)| = 6 \geq 5 = MinPts \quad (\text{core point condition})$$

q not directly density reachable from p

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

Note: This is an asymmetric relationship

Density Reachability

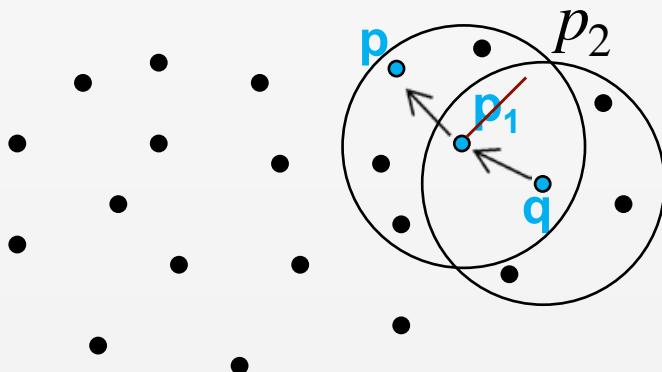
Definition

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 $1 < i < s-1$.



$$\text{MinPts} = 5$$

$$|N_{\text{Eps}}(q)| = 5 = \text{MinPts} \quad (\text{core point condition})$$

$$|N_{\text{Eps}}(\cancel{p_1})| = 6 \geq 5 = \text{MinPts} \quad (\text{core point condition})$$

$$p_2$$

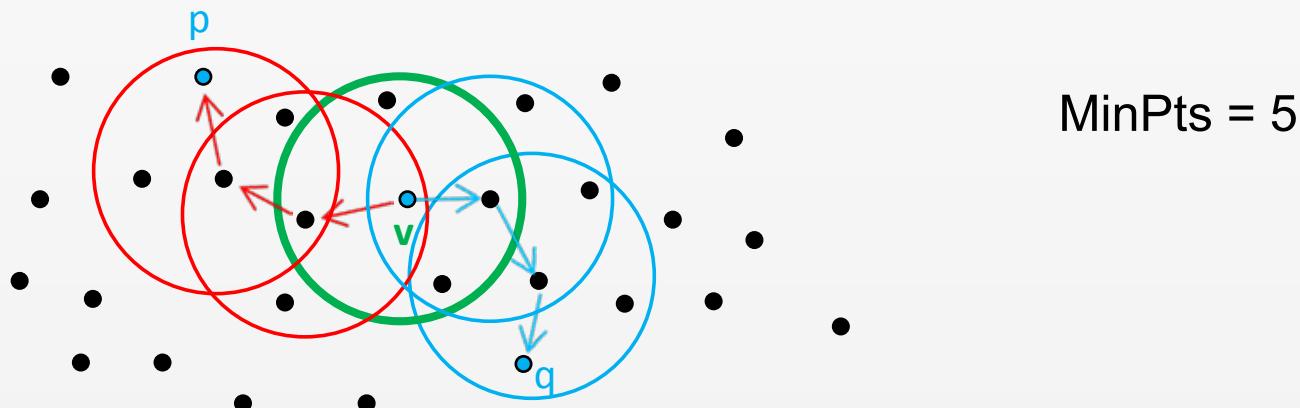
Density Connectivity

Definition (density-connected)

A point p is **density-connected** to a point q

with regard to the parameters Eps and MinPts

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



Note: This is a symmetric relationship

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 $p, q \in D$: (Maximality)

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 $p, q \in C$: (Connectivity)

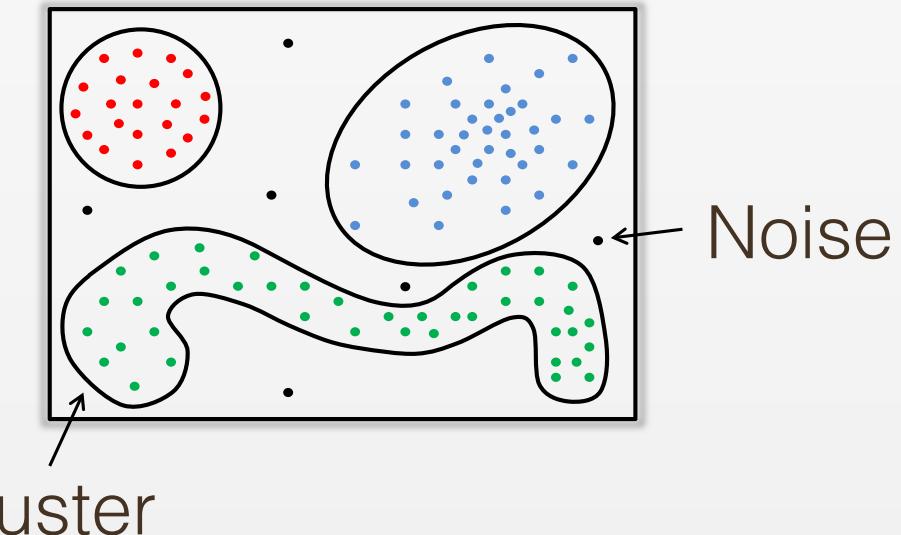
The point p is density-connected to q with regard to the parameters Eps and MinPts.

Definition of Noise

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

The set of points in the database D not belonging to any cluster C_1, \dots, C_k
is called **noise**:

$$\text{Noise} = \{ p \in D \mid p \notin C_i \text{ for all } i = 1, \dots, k \}$$



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.

- Low density 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:* $O(N^2D)$ 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

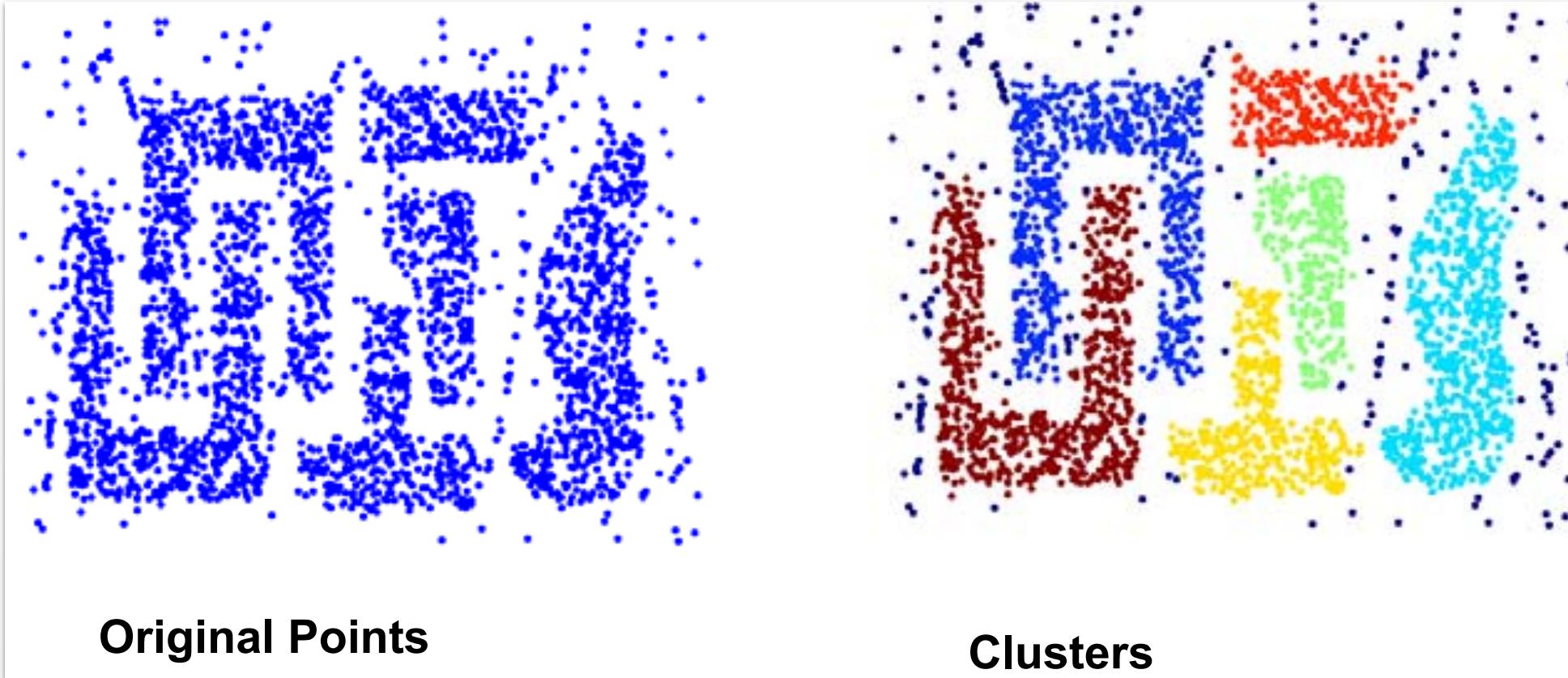


Original Points



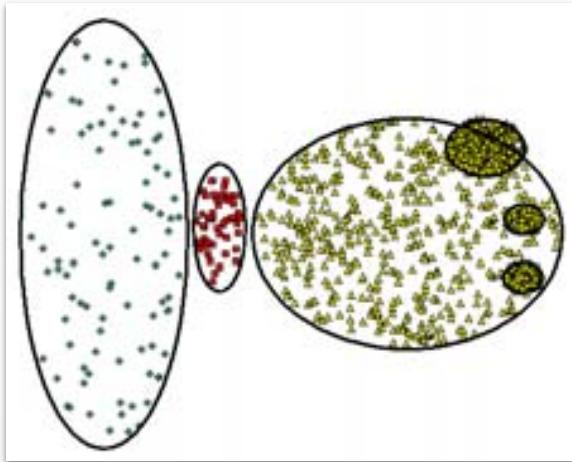
Point types: **core**,
border and **noise**

DBSCAN strengths

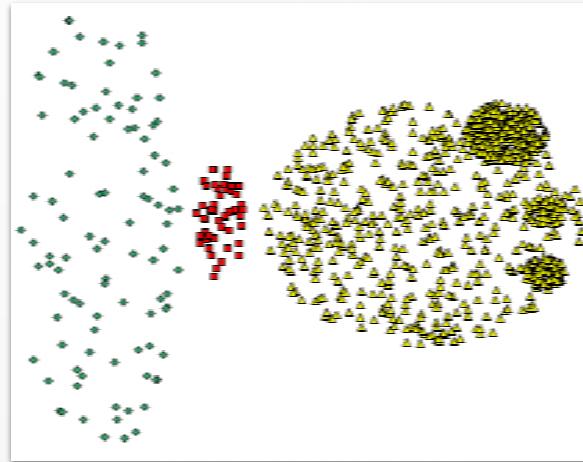


- + Resistant to noise
- + Can handle arbitrary shapes

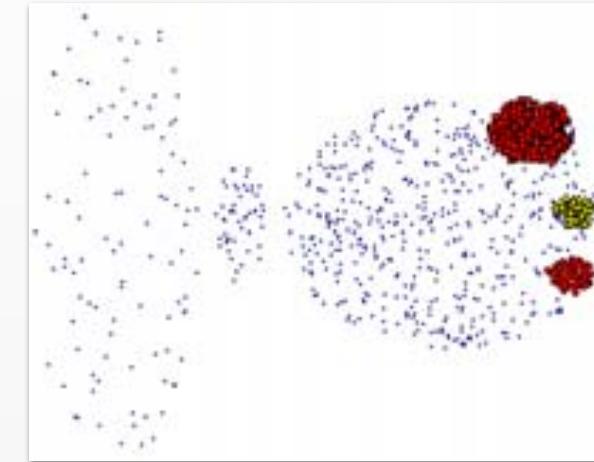
DBSCAN Weaknesses



Ground Truth



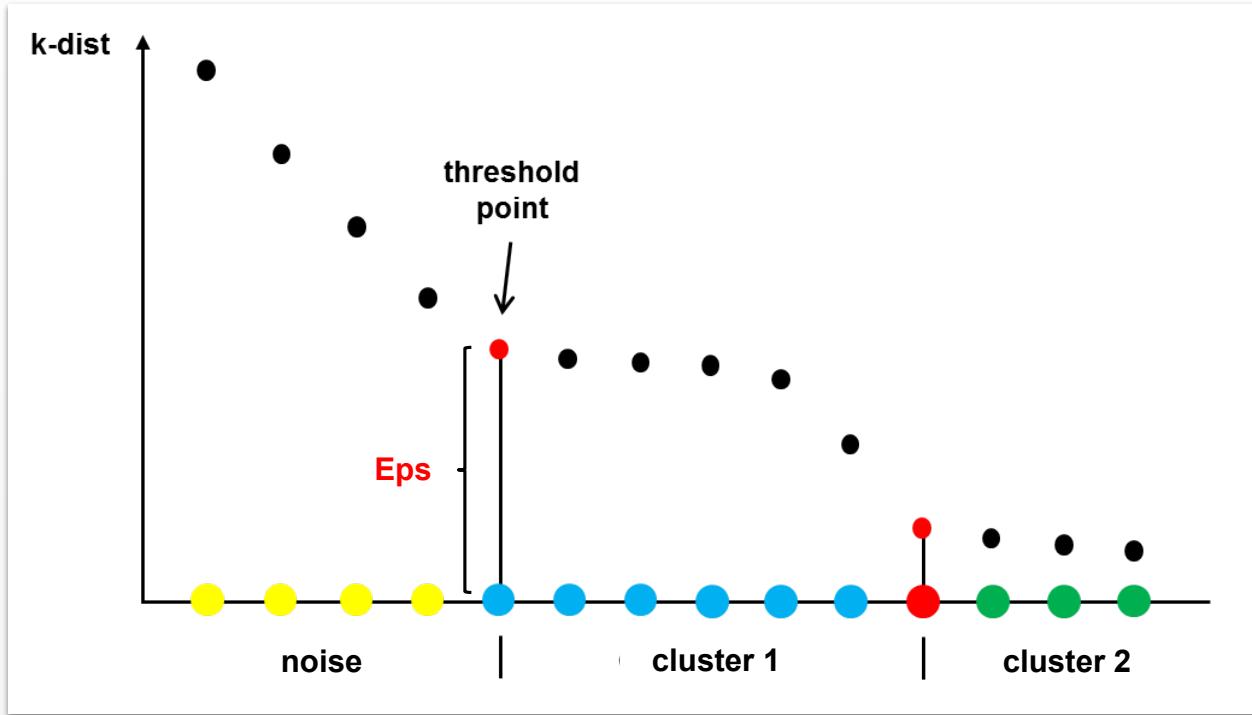
MinPts = 4, Eps=9.92



MinPts = 4, Eps=9.75

- Varying densities
- High dimensional data
- Cannot give overlapping clusters

Determining EPS and MINPTS



- Calculate distance of k -th nearest neighbor for each point
- Plot in ascending / descending order
- Set **EPS** to max distance before “jump”
- Set Minpts to k .

K-means vs DBSCAN

