Machine Learning 520 Advanced Machine Learning

Lesson 6: Unsupervised Learning



Today's Agenda

- Clustering
 - Concept of Clustering
 - Distance Measures
 - Hierarchical Clustering
 - K-means Clustering
 - Clustering Evaluation



Learning Objectives

By the end of this session, you should be able to:

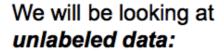
- Identify use cases for unsupervised learning.
- Explain the effects of applying different distance metrics.
- Apply K-means to benchmark data and evaluate the quality of the clusters.
- Apply hierarchical clustering to benchmark data and evaluate the quality of the clusters.



Unsupervised Learning

So far, our data has been in this form:

$$\begin{bmatrix} x_1^1, x_2^1, x_3^1, ..., x_m^1 & y^1 \\ x_1^2, x_2^2, x_3^2, ..., x_m^2 & y^2 \\ & ... \\ & ... \\ x_1^n, x_2^n, x_3^n, ..., x_m^n & y^n \end{bmatrix}$$



$$x_1^1, x_2^1, x_3^1, ..., x_m^1$$
 $x_1^2, x_2^2, x_3^2, ..., x_m^2$
...
...
 $x_1^n, x_2^n, x_3^n, ..., x_m^n$

- > What do we expect to learn from such data?
- > I have tons of data (web documents, gene data, etc) and need to:
 - organize it better e.g., find subgroups
 - understand it better e.g., understand interrelationships
 - find regular trends in it e.g., If A and B, then C



Clustering

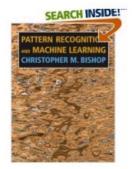
- > **Clustering:** Organization of unlabeled data into similar groups (subsets).
- Cluster: A collection of data where the items in the collection are similar to one another and are dissimilar to other collections of data.

> What are good clusters?

- Maximize the similarity within objects in the same group.
- Maximize the difference between objects in different groups.



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Image compression: Vector quantization





Group all pixels into self-similar groups, instead of storing all pixel values, store the means of each group

701,554 bytes



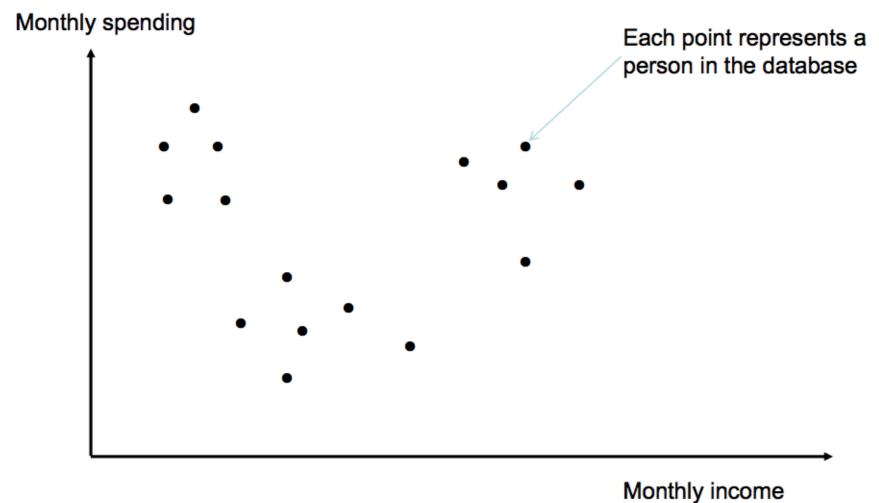
127,292 bytes



Applications

- > Information retrieval: cluster retrieved documents to present more organized and understandable results
- Consumer market analysis: cluster consumers into different interest groups so that marketing plans can be specifically designed for each individual group
- > Image segmentation: decompose an image into regions with coherent color and texture
- > Vector quantization for data (i.e., image) compression: group vectors into similar groups, and use group mean to represent group members
- Computational biology: group gene into co-expressed families based on their expression profile using different tissue samples and different experimental conditions

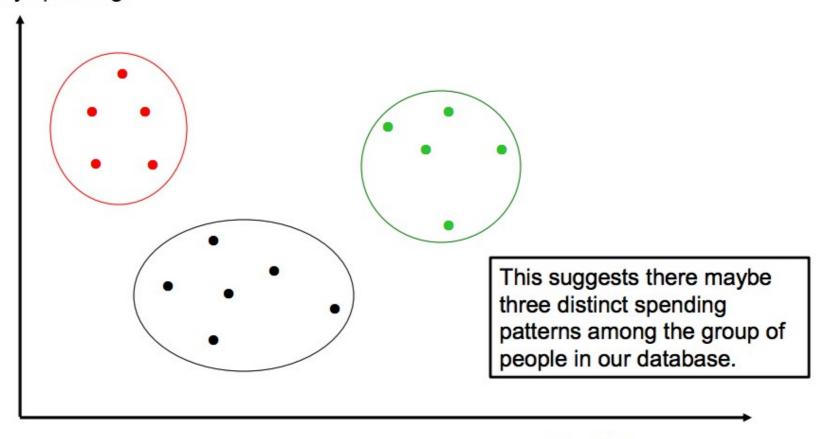
A Hypothetical Clustering Example





A Hypothetical Clustering Example

Monthly spending

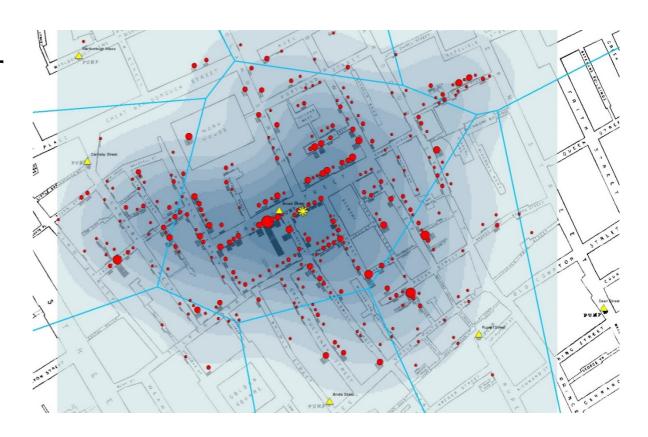


Monthly income



John Snow's Cholera Study (1854)

- One of the earliest known examples of using clustering for data analysis is the pioneering study of cholera outbreak in Soho, London in 1854.
- Collected data on cholera instances and their proximity to water pumps.
- > Outbreaks were clustered around water pumps with some exceptions.





Important Components in Clustering

- > Distance/similarity measures (aka proximity measures)
 - Measures to determine how similar or different are instances to one another.
- > Clustering algorithm
 - Algorithm to find the clusters based on the distance/similarity measures.
- > Evaluation Criteria
 - Metrics to tell if one form of clustering is better than another form.



Distance/similarity Measures

- > One of the most important question in unsupervised learning, often more important than the choice of clustering algorithms.
- > What is similarity?
 - Similarity is hard to define, but we know it when we see it.

- More pragmatically, there are many mathematical definitions of

distance/similarity







Distance/Similarity Measures

> Manhattan Distance:

$$d_1(\mathbf{p},\mathbf{q}) = \|\mathbf{p}-\mathbf{q}\|_1 = \sum_{i=1}^n |p_i-q_i|_i.$$

> Euclidean Distance:

$$egin{split} d(\mathbf{p},\mathbf{q}) &= d(\mathbf{q},\mathbf{p}) = \sqrt{(q_1-p_1)^2 + (q_2-p_2)^2 + \dots + (q_n-p_n)^2} \ &= \sqrt{\sum_{i=1}^n (q_i-p_i)^2}. \end{split}$$

> Minkowski Distance

$$D\left(X,Y
ight) = \left(\sum_{i=1}^{n}\left|x_{i}-y_{i}
ight|^{p}
ight)^{1/p}$$



Distance/Similarity Measures

> Inner Product Space: The angle between two vectors as a distance metric. It is especially useful when clustering high dimens $\sum_{n=1}^{n} A_{n} B_{n}$

$$\mathbf{S} ext{similarity} = \cos(heta) = rac{\mathbf{A} \cdot \mathbf{B}}{\|\mathbf{A}\| \|\mathbf{B}\|} = rac{\sum\limits_{i=1}^n A_i B_i}{\sqrt{\sum\limits_{i=1}^n A_i^2} \sqrt{\sum\limits_{i=1}^n B_i^2}}$$

> **Chebychev Distance:** Two vectors are different if they are different on any one of the attributes.

We can always transform between distance and similarity using a monotonically decreasing function. For example, $e^{-\alpha D(x_1,x_2)^2}$

Distance Metrics on Nominal Values

> Hamming Distance:

The minimum number of *substitutions* required to change one string into the other

$$d_{ham}(karolin, kathrin) = 3, d_{ham}(1010, 1000) = 1$$

> Convert to Numeric using one-hot encoding:

ID	Fruit	
1	Apple	
2	Apple	
3	Orange	
4	Banana	
5	Orange	
6	Apple	
7	Orange	



ID	Apple	Orange	Banana
1	1	0	0
2	1	0	0
3	0	1	0
4	0	0	1
5	0	1	0
6	1	0	0
7	0	1	0



How to decide which to use?

- > It is application dependent.
- Consider your application domain, you need to ask questions such as:
 - What does it mean for two consumers to be similar to each other? Or for two genes to be similar to each other?
- > For example, for text domain, we typically use cosine similarity.
- > This may or may not give you the answer you want depends on your existing knowledge of the domain.
- > Clustering is an exploratory procedure and it is important to explore i.e., try different options and see what makes sense.



Clustering Algorithms

- > **Hierarchical algorithms** build a tree-based hierarchical taxonomy (dendrogram).
 - Bottom up
 - Top down
- > **Partition (Flat) algorithms** produce a single partition of the unlabeled data.
 - K-means
 - Mixture of Gaussian

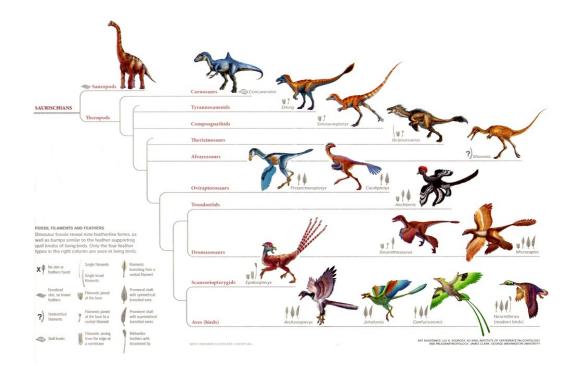


Hierarchical Clustering



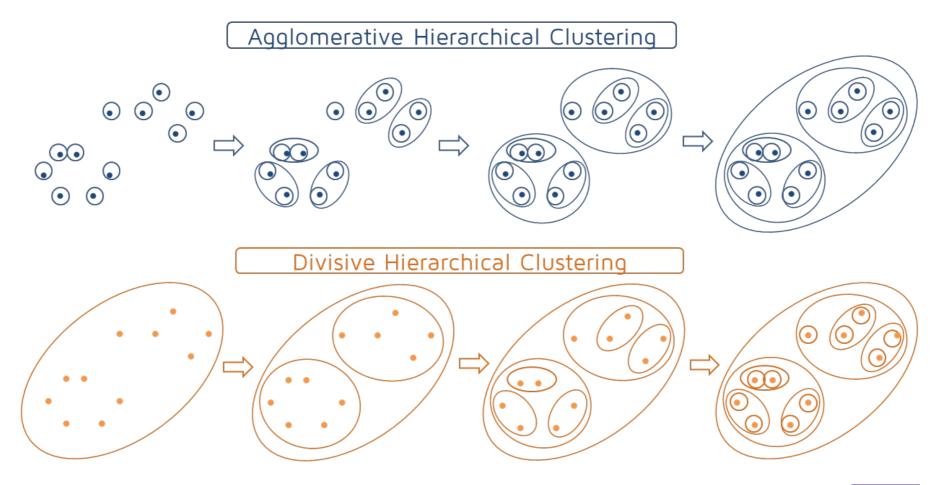
Hierarchical Clustering

- > **Goal:** Build a hierarchy of clusters
- > **Agglomerative Clustering**: (Bottom up approach)
 - Each instance is its own cluster
 - Pairs of clusters are merged as one moves up the hierarchy until there is only one cluster
- > **Divisive Clustering**: (Top Down approach)
 - All observations start as one cluster
 - Recursively split the data as one moves down the hierarchy until each instance is a cluster





Types of Hierarchical Clustering





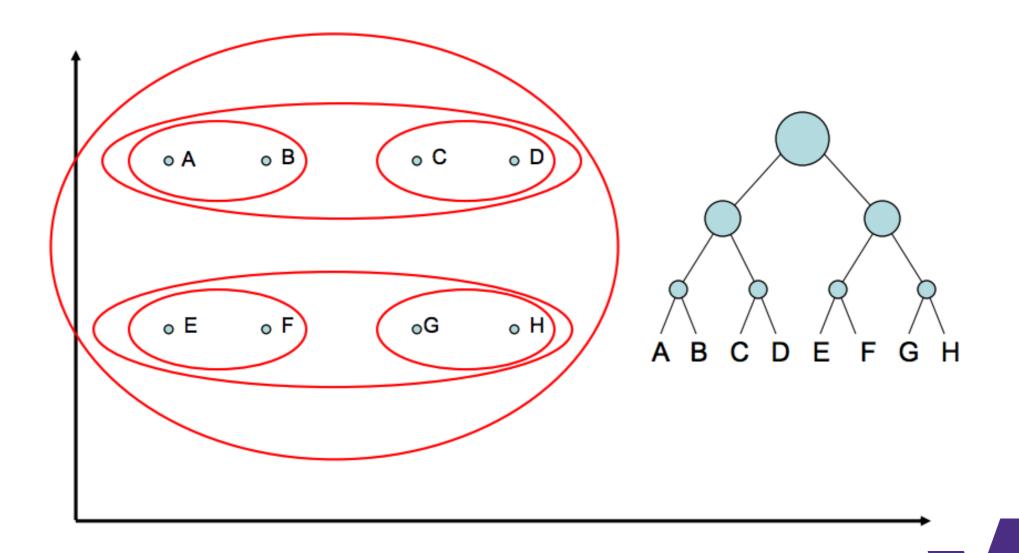
Algorithm

Start with all objects in their own cluster. Repeat until there is only one cluster: Among the current clusters, determine the two clusters, c_i and c_j , that are closest Replace c_i and c_j with a single cluster $c_i \cup c_j$

Problem: we assume a distance/similarity function that computes distance/similarity between examples, but here we also need to compute distance between clusters.

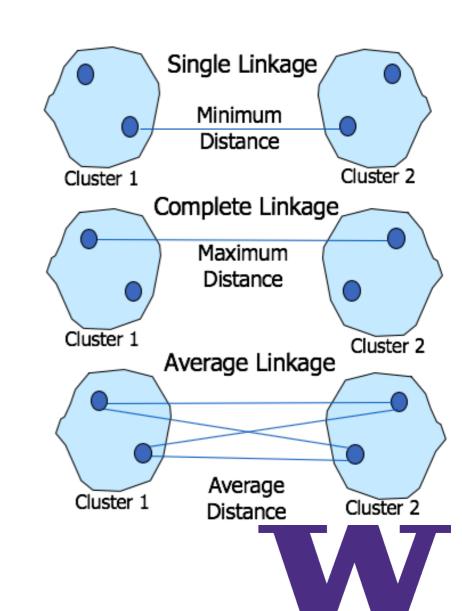


HAC Example



Distance Between Clusters

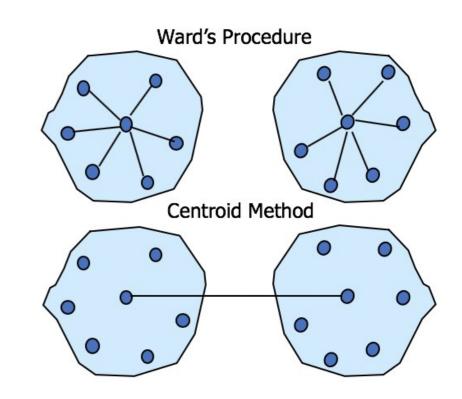
- > **Single Link:** The distance between two clusters is the distance between two closest points in the two clusters, one from each cluster. Can result in long chains of clusters
- > **Complete Link:** The distance between two clusters is the distance of two furthest data points in the two clusters. Sensitive to outliers
- > **Average Link:** the distance between two clusters is the average distance of all pair-wise distances between the data



Distance Between Clusters

- > Ward's Procedure: For each cluster calculate the sum of squares. The two clusters with the smallest increase in the overall sum of squares within cluster distances are combined.
- > **Centroids Method:** The distance between two clusters is the distance between their centroids.

In general, the average linkage and Ward's methods have been shown to perform better than others.





Updating the Cluster Distances

- > After merging c_i and c_j , the distance of the resulting cluster to any other cluster, c_k , can be computed by:
 - Single Link:

$$D((c_i \cup c_j), c_k) = \min(D(c_i, c_k), D(c_j, c_k))$$

– Complete Link:

$$D((c_i \cup c_j), c_k) = \max(D(c_i, c_k), D(c_j, c_k))$$



Updating the Cluster Distances con't

- > Average Link: average similarity between members of the two clusters.
 - Averaged across all pairs between the original two clusters

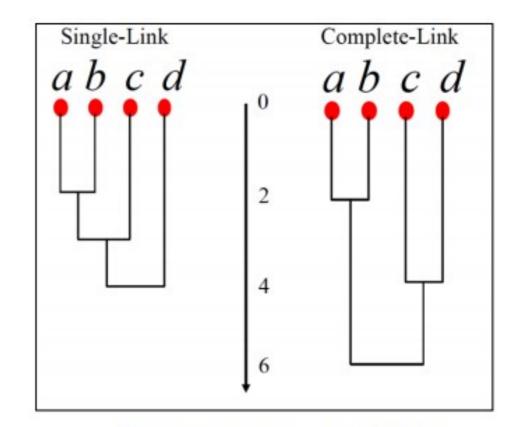
$$D(c_i, c_j) = \frac{1}{|c_i||c_j|} \sum_{\mathbf{x} \in c_i} \sum_{\mathbf{x'} \in c_j} D(\mathbf{x}, \mathbf{x'})$$

- > Compared to single link and complete link:
 - Computationally more expensive O(n₁n₂)
 - Achieves a compromise between single and complete link



Dendrogram: Cluster Visualization

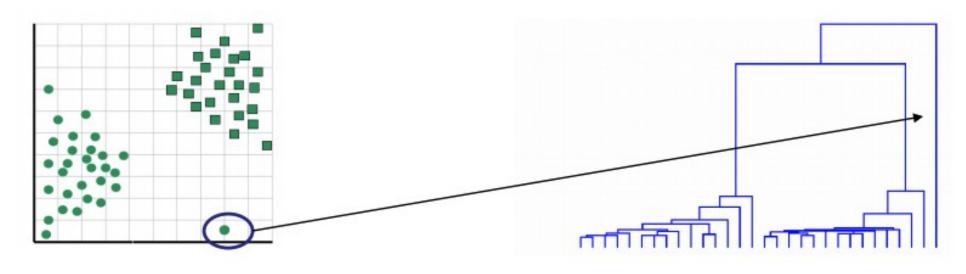
- > Height of the joint = the distance between the two merge clusters.
- > The merge distance monotonically increases as we merge more and more for
 - Single, complete and average linkage methods
 - Not for the centroid method
- > This can provide some understanding about how many natural groups there are in the data.
- > A drastic height change indicates that we are merging two very different



This example is shown upside down.



Interpreting Dendrogram



- > Dendrogram can be used to identify
 - The number of clusters in data
 - Well-formed clusters
 - Outliers



K-Means Clustering



Goal of Clustering

- > Given a data set $D = \{x_1, x_2, \dots, x_n\}$
- > We need to partition D into k disjoint clusters, such that
 - Examples are self-similar in the same cluster
 - Examples are dissimilar across different clusters

> How do we quantify this?



Objective: Sum of Squared Errors

> Given a partition of the data into k clusters, we can compute the **center** (i.e., mean, center of mass) of each cluster.

$$\mu_i = \frac{1}{n_i} \sum_{\mathbf{x} \in C_i} \mathbf{x}$$

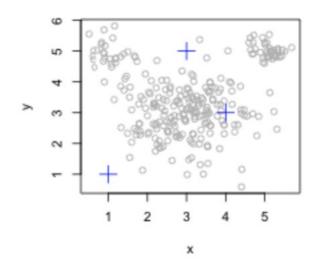
> For a well-formed cluster, its points should be close to its center. We measure this with sum of squared error (SSE), and formulate our objective to find a partition C* that minimizes sum of squared error:

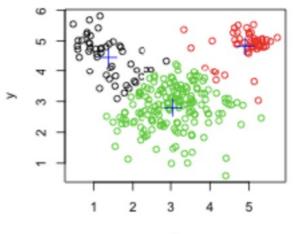
$$\mathbb{C}^* = \underset{\mathbb{C} = \{C_1, \dots, C_k\}}{\operatorname{argmin}} \sum_{i=1}^{N} \sum_{x \in C_i} ||x - \mu_i||^2$$



Basic Idea

- > We assume the number of desired clusters, k, is given.
- > Randomly choose k examples as seeds, one for each cluster.
- > Form initial clusters based on these seeds.
- > Iterate by repeatedly re-allocating instances to different clusters to improve the overall clustering.
- > Stop when clustering converges or after a fixed number of iterations.







The K-means algorithm

Input: $D = \{x_1 x_2 ... x_n\}$ and desired number of clusters k

Output: a partition of D into k disjoint clusters $c_1 \dots c_k$ (s.t. D = $c_1 \cup c_2 \cup \dots \cup c_k$)

Let d be the distance function between examples

- 1. Select k random samples from D as centers $\{\mu_1 \dots \mu_k\}$ //Initialization
- 2. Do
- 3. for each example x_i
- 4. assign x_i to c_j such that $d(\mu_j, x_1)$ is minimized // the Assignment step
- 5. for each cluster *j*, update cluster center
- 6. $\mu_j = \frac{1}{|c_j|} \sum_{\mathbf{x} \in c_j} \mathbf{x}$ // the update step
- 7. Until convergence



Convergence Criterions

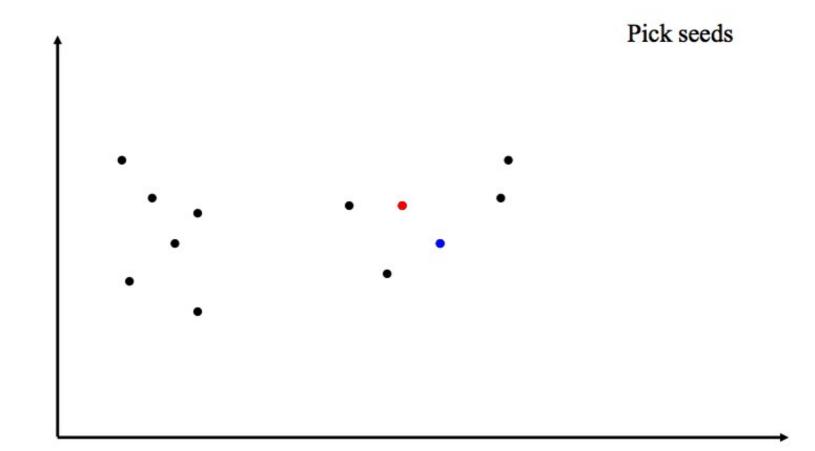
- > No (or minimum) reassignments of data to different clusters
- > No (or minimum) change of centroids
- > Minimum decrease in the sum of squared error (Optimization Criteria)

$$J = \sum_{j=1}^{K} \sum_{n \in \mathcal{S}_j} \left| x_n - \mu_j \right|^2$$

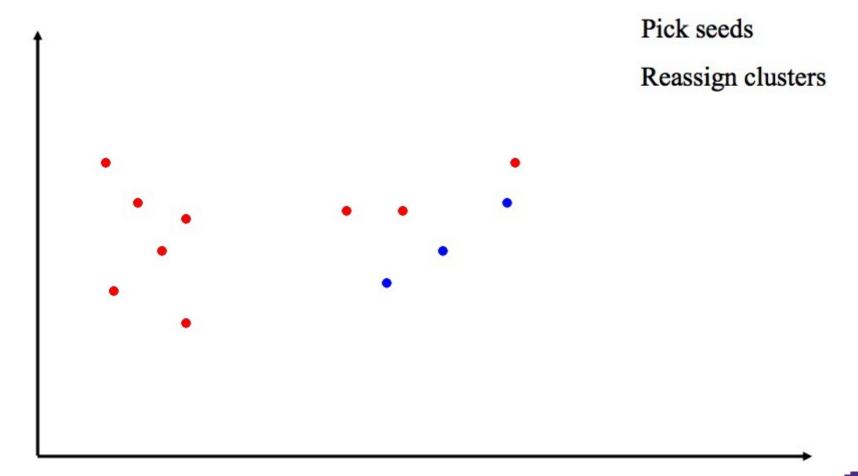


K-Means Example

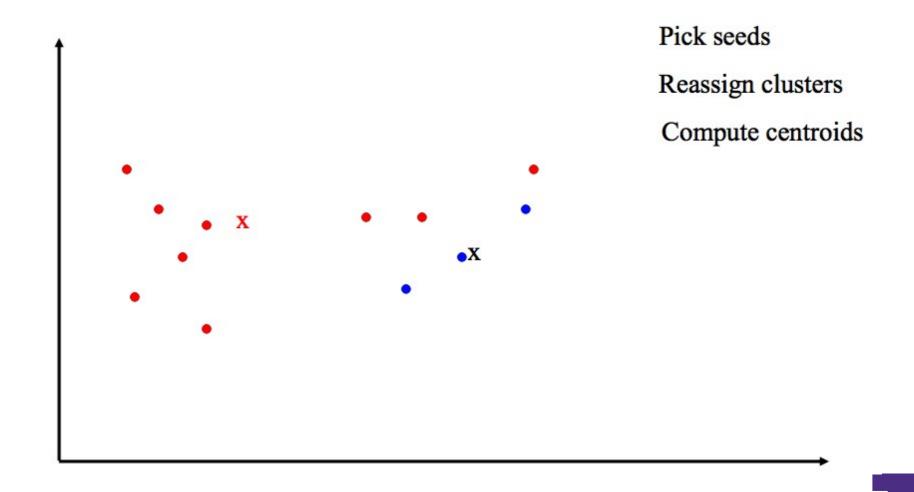


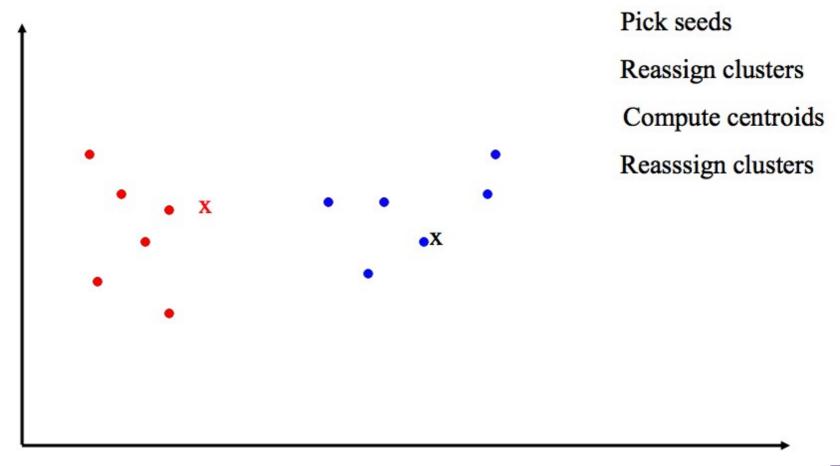




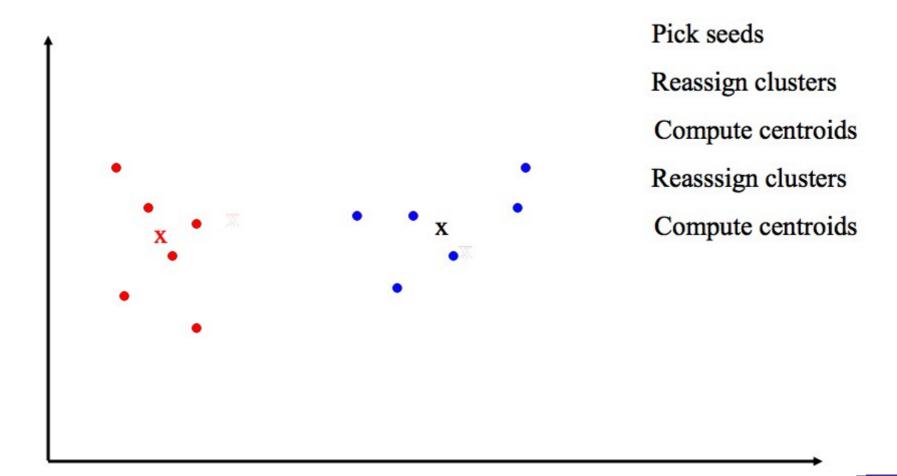


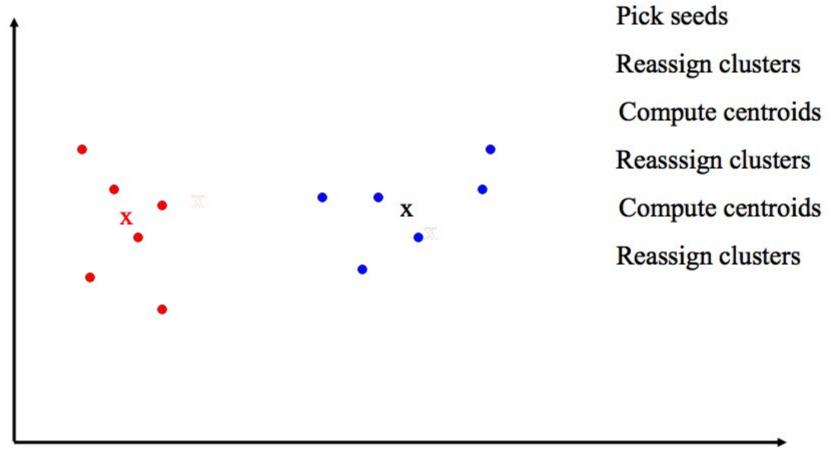




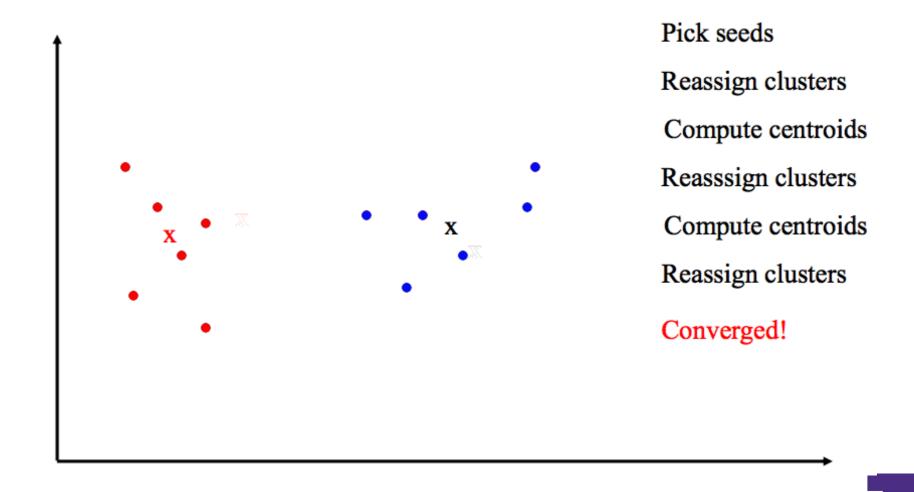












Convergence of K-means

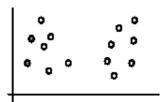
- > Monotonicity Property: Each iteration of K-means strictly decreases the SSE until convergence.
- K-means always converges in a finite number of steps. Typically converges very fast.
- > Time complexity:
 - Assume computing distance between two instances is O(d) where d is the dimensionality of the vectors.
 - Reassigning clusters: O(kn) distance computations, or O(knd).
 - Computing centers: Each instance vector gets added once to some center: O(nd).
 - Assume these two steps are each done once for l iterations: O(lknd).

Weaknesses of K-Means: Local Minimal

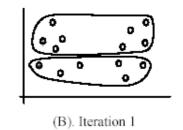
- > K-means is very sensitive to initial conditions i.e., the initial assignment will determine the final set of clusters that one will get.
- > This is because SSE has many local minimal solutions.

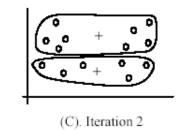
Solutions

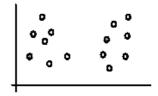
- > Run multiple trials and choose the one with the best SSE.
- > Heuristics. Try to choose initial centers to be far apart (e.g. K-means++).



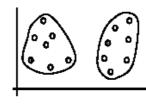
(A). Random selection of seeds (centroids)

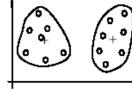






(A). Random selection of k seeds (centroids)



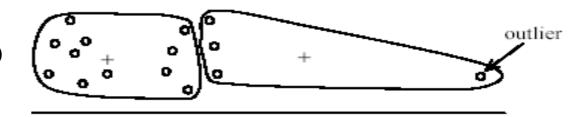


(B). Iteration 1



Weaknesses of K-Means: Outliers

- > K-means is very sensitive to outliers.
- > The presence of outliers can lead to very *unreasonable* clusters.



(A): Undesirable clusters

- > Solution:
 - Remove possible outliers before running K-means.
 - K-medoids



(B): Ideal clusters



K-medoids

> K-medoids – use the medoid for each cluster, i.e., the data point that is closest to other points in the cluster.

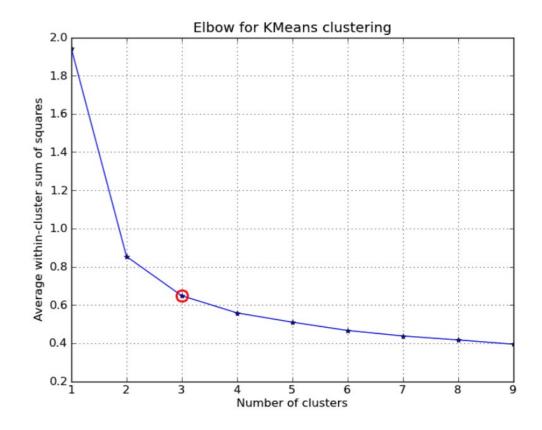
$$\mu = \sum_{\mathbf{X} \in C} \mathbf{X} \qquad \qquad \mu = \underset{\mathbf{X} \in C}{\operatorname{argmin}} \sum_{\mathbf{Z} \in C} \|\mathbf{x} - \mathbf{z}\|^2$$

> K-medoids is computationally more expensive but more robust to outliers



Selection of K

- > What if we don't know how many clusters there are in the data?
- Can we use SSE to decide k by choosing k that gives the smallest SSE?
 - We will always favor larger k values
- > Heuristic: find the knee



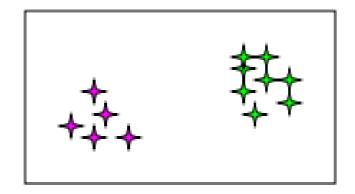


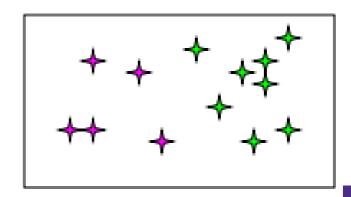
Evaluating clustering



Evaluating Clusters: Internal Evaluation

- > By user interpretation
 - does a document cluster seem to correspond to a specific topic?
- Internal criterion: a good clustering will produce high quality clusters
 - high within-cluster similarity:
 - Low between-cluster similarity:





External Indexes: Rand Index

- > If true class labels (ground truth) are known, the validity of a clustering can be verified by comparing the class labels and clustering labels.
- > Given partition (P) and ground truth (G), measure the number of vector pairs that are:
 - a: in the same class both in P and G.
 - b: in the same class in P, but in the different class in G.
 - c: in different classes in P, but in the same class in G.
 - d: in different classes both in P and G.

$$RI = \frac{a+d}{a+b+c+d}$$



$$NMI(Y,C) = \frac{2 \times I(Y;C)}{[H(Y) + H(C)]}$$

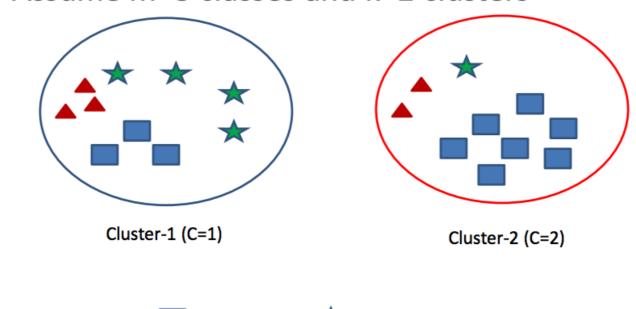
where,

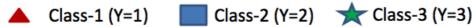
- 1) Y = class labels
- 2) C = cluster labels
- 3) H(.) = Entropy
- 4) I(Y;C) = Mutual Information b/w Y and C

Note: All logs are base-2.

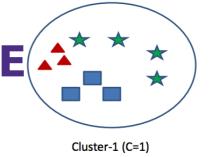


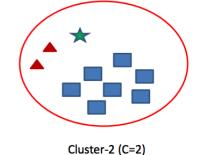
Assume m=3 classes and k=2 clusters











H(Y) = Entropy of Class Labels

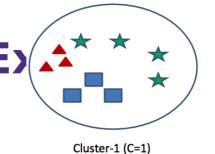
•
$$P(Y=1) = 5/20 = \frac{1}{4}$$

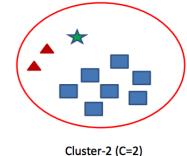
•
$$P(Y=2) = 5/20 = \frac{1}{4}$$

•
$$P(Y=3) = 10/20 = \frac{1}{2}$$

•
$$H(Y) = -\frac{1}{4}\log\left(\frac{1}{4}\right) - \frac{1}{4}\log\left(\frac{1}{4}\right) - \frac{1}{2}\log\left(\frac{1}{2}\right) = 1.5$$







H(C) = Entropy of Cluster Labels

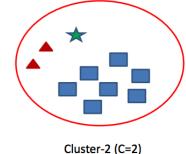
- P(C=1) = 10/20 = 1/2
- $P(C=2) = 10/20 = \frac{1}{2}$

• H(Y) =
$$-\frac{1}{2}\log(\frac{1}{2}) - \frac{1}{2}\log(\frac{1}{2}) = 1$$

This will be calculated every time the clustering changes. You can see from the figure that the clusters are balanced (have equal number of instances).







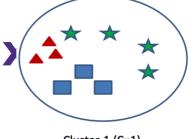
Cluster-1 (C=1)

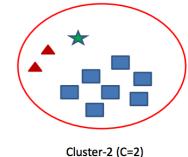
H(Y|C): conditional entropy of class labels for clustering C

- Consider Cluster-1:
 - -P(Y=1|C=1)=3/10 (three triangles in cluster-1)
 - -P(Y=2|C=1)=3/10 (three rectangles in cluster-1)
 - -P(Y=3|C=1)=4/10 (four stars in cluster-1)
 - Calculate conditional entropy as:

$$H(Y|C=1) = -P(C=1) \sum_{y \in \{1,2,3\}} P(Y=y|C=1) \log(P(Y=y|C=1))$$
$$= -\frac{1}{2} \times \left[\frac{3}{10} \log\left(\frac{3}{10}\right) + \frac{3}{10} \log\left(\frac{3}{10}\right) + \frac{4}{10} \log\left(\frac{4}{10}\right) \right] = 0.7855$$







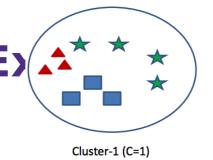
Cluster-1 (C=1)

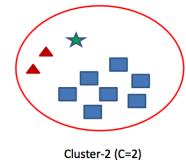
H(Y|C): conditional entropy of class labels for clustering C

- Now, consider Cluster-2:
 - -P(Y=1|C=2)=2/10 (two triangles in cluster-1)
 - -P(Y=2|C=2)=7/10 (seven rectangles in cluster-1)
 - P(Y=3 | C=2)=1/10 (one star in cluster-1)
 - Calculate conditional entropy as:

$$H(Y|C=2) = -P(C=2) \sum_{y \in \{1,2,3\}} P(Y=y|C=2) \log(P(Y=y|C=2))$$
$$= -\frac{1}{2} \times \left[\frac{2}{10} \log\left(\frac{2}{10}\right) + \frac{7}{10} \log\left(\frac{7}{10}\right) + \frac{1}{10} \log\left(\frac{1}{10}\right) \right] = 0.5784$$







I(Y;C)

Finally the mutual information is:

$$I(Y;C) = H(Y) - H(Y|C)$$

= 1.5 - [0.7855 + 0.5784]
= 0.1361

The NMI is therefore,

$$NMI(Y,C) = \frac{2 \times I(Y;C)}{[H(Y) + H(C)]}$$

$$NMI(Y,C) = \frac{2 \times 0.1361}{[1.5+1]} = 0.1089$$



Summary on Clustering Evaluation

- > Internal evaluation
 - Within-cluster similarity, larger the better
 - Between-cluster similarity, smaller the better
 - Potential issue: Dependent on how similarity is measured
- > External evaluation (compare against a ground truth clustering)
 - Rand Index (very sensitive to the number of clusters)
 - Normalized mutual information (less sensitive to the number of clusters)
 - Potential issue: there may not be only one way to cluster the data



Conclusion

- > There are a massive number of clustering algorithms.
- > Clustering is hard to evaluate, but very useful in practice.
- > Clustering is highly application dependent and to some extent subjective.
- > There is no one universal recipe for choosing a clustering technique and its associated parameters.



Appendix

