Clustering

Instructor: Jesse Davis

Slides from: Colin Dewey, Pedro Domingos, Ray Mooney, David Page, Sofus Macskassy, Dan Weld



- No class final week
 - Office hours June 1st from 5:30-7:30 or 8
 - Homework 4 will be due @ midnight June 1st
- Andrey is out of town
 - He has access to email at funny times
 - Email both of us
- Clustering reading (Chapters 16+17): <u>http://nlp.stanford.edu/IR-book/</u>
- Lecture notes are available online



Homework 4: VC-Dimension problem

Clustering

Definition: Shattering

- A hypothesis space is said to shatter a set of instances iff for every partition of the instances into positive and negative, there is a hypothesis that produces that partition
- Example: Consider 2 instances with a single real-valued feature being shattered by intervals





The Vapnik-Chervonenkis dimension, VC(*H*). of hypothesis space *H* defined over instance space *X* is the size of the largest finite subset of *X* shattered by *H*. If arbitrarily large finite subsets of *X* can be shattered then VC(*H*) = ∞



VC-Dim of rectangles in 2-D space Part 1: For VC-dim, show ONE configuration of examples that can be separated regardless of labels

Part 2: For VC-dim+1, show that for ANY configuration of examples, there exists a labeling of the examples that can't be separated





Therefore VC-dim at least 3

Example Justification

Case 1: 3 or more points co-linear Obviously can't label

Case 2: Other allignments Form a regular polygon with points Examples not connected get same label Single line won't be able to separate (XOR)





Homework 4: VC-Dimension problem

Clustering

- Unsupervised learning, clustering intro
- Hierarchical clustering
- Partitional clustering
- Model-based clustering
- Applications

Unsupervised Learning

- In supervised learning, we have data in the form of pairs <x,y>, where y=f(x). The goal is to approximate f
- In unsupervised learning, the data just contains x!
- The main goal is to find structure in the data
- The definition of ground truth is often missing (no clear error function, like in supervised learning)

Uses of Unsupervised Learning

- Visualization of the data
- Data compression
- Density estimation: what distribution generated the data?
- Pre-processing step for supervised learning
- Partition data
- Novelty detection

Unsupervised Learning: Clustering

- In many problems there are no class labels
- Humans: How do we form categories of objects?
- Humans are good at creating groups/categories/clusters from data
- Image analysis finding groups in data is very useful
 - e.g., can find pixels with similar intensities
 - e.g., can find images that are similar -> can automatically find classes/clusters of images



Cluster: a collection of data objects

- Similar to one another within the same cluster
- Dissimilar to the objects in other clusters
- Cluster analysis: Grouping objects into clusters
- Clustering is unsupervised classification
- Clusterings are usually not right or wrong
 - Different clusterings can reveal different things about the data
 - More direct measure of goodness if it is a first step towards supervised learning, or data compression

How is Clustering Used

- Clustering is grouping similar objects together
 - To establish prototypes or detect outliers
 - To simplify data for further analysis/learning
 - To visualize data
 - As a stand-alone tool to get insight into data distribution
 - As a preprocessing step for other algorithms

Example: Two Clusters



Example: Gene Expression

(Green = up-regulated, Red = down-regulated)



Experiments (Samples)

Clustering Applications

- <u>Marketing</u>: Help marketers discover distinct groups in their customer bases, and then use this knowledge to develop targeted marketing programs
- Land use: Identification of areas of similar land use in an earth observation database
- <u>Insurance</u>: Identifying groups of motor insurance policy holders with a high average claim cost
- <u>Urban planning</u>: Identifying groups of houses according to their house type, value, and geographical location
- <u>Seismology</u>: Observed earth quake epicenters should be clustered along continent faults

What Is a Good Clustering?

- A good clustering method will produce clusters with
 - High <u>intra-class</u> similarity
 - Low inter-class similarity
- Precise definition of clustering quality is difficult
 - Application-dependent
 - Ultimately subjective

Requirements for Clustering in Data Mining

- Scalability
- Ability to deal with different types of attributes
- Discovery of clusters with arbitrary shape
- Minimal domain knowledge required to determine input parameters
- Ability to deal with noise and outliers
- Insensitivity to order of input records
- Robustness wrt high dimensionality
- Incorporation of user-specified constraints
- Interpretability and usability

The Clustering Problem

- Let <u>x</u> = (x₁, x₂,..., x_d,) be a d-dimensional feature vector
- Let D be a set of <u>x</u> vectors,

$$D = \{ \underline{x}_1, \underline{x}_2, \dots, \underline{x}_N \}$$

 Given data D, group the N vectors into K groups such that the grouping is "optimal"

Basic Concept: Distances/Similarities

- Clustering methods use a distance (similarity) measure to assess the distance between
 - a pair of instances
 - a cluster and an instance
 - a pair of clusters
- Given a distance value, can convert it into a similarity value: sim(i,j) = 1/[1+dist(i,j)]
- Not always straightforward to go the other way
- We'll describe our algorithms in terms of distances

Distances Between Instances

- Same we used for IBL (e.g, Lp norm)
- Euclidean distance (p = 2):

$$d(i,j) = \sqrt{\left(\left|x_{i_{1}} - x_{j_{1}}\right|^{2} + \left|x_{i_{2}} - x_{j_{2}}\right|^{2} + \dots + \left|x_{i_{p}} - x_{j_{p}}\right|^{2}\right)}$$

- Properties of a metric d(i,j):
 - *d(i,j)* ≥ 0
 - $\bullet d(i,i) = 0$
 - d(i,j) = d(j,i)
 - $d(i,j) \leq d(i,k) + d(k,j)$

Basic Concept: Clusters Structure



Basic Concept: Cluster Assignment

Hard clustering:

- Each item in only one cluster
- Soft clustering:
 - Each item has a probability of membership in each cluster
- Disjunctive / overlapping clustering:
 - An item can be in more than one cluster

Major Clustering Approaches

- <u>Hierarchical</u>: Create a hierarchical decomposition of the set of objects using some criterion
- <u>Partitioning</u>: Construct various partitions and then evaluate them by some criterion
- Model-based: Hypothesize a model for each cluster and find best fit of models to data
- <u>Density-based</u>: Guided by connectivity and density functions



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Hierarchical Clustering

- Can do top-down (divisive) or bottom-up (agglomerative)
- In either case, we maintain a matrix of distance (or similarity) scores for all pairs of
 - Instances
 - Clusters (formed so far)
 - Instances and clusters



Bottom-Up Hierarchical Clustering

Given: instances x_1, \dots, x_n For i = 1 to n, $c_i = \{x_i\}$ $C = \{C_1, ..., C_n\}$ j = n While |C| > 1j = j + 1 $(c_a, c_b) = \operatorname{argmin} \operatorname{dist}(c_u, c_v)$ $c_i = c_a U c_v$ add node to tree joining a and b $C = C - \{c_a, c_b\} \cup c_i$ Return tree with root node j





Distance Between Two Clusters

- The distance between two clusters can be determined in several ways
 - Single link: distance of two most similar instances: dist(c_u, c_v) = min{dist(a, b) | a∈c_u, b∈c_v}
 - Complete link: distance of two least similar instances: dist(c_u, c_v) = max{dist(a, b) | a∈c_u, b∈c_v}
 - Average link: average distance between instances: dist(c_u, c_v) = avg{dist(a, b) | a∈c_u, b∈c_v}



Cluster similarity = similarity of two most similar members





Cluster similarity = similarity of two least similar members





Cluster similarity = average similarity of all pairs



Note: Picture doesn't show all connections

- If we merged and c_u and c_v into c_j, we can determine distance to each other cluster:
 - Single link: dist(c_j, c_k) = min{dist(c_u, c_k), dist(c_v, c_k)}
 - Complete link: dist(c_j, c_k) = max{dist(c_u, c_k), dist(c_v, c_k)}
 - Average link: $dist(c_j, c_k) = \frac{|c_u| * dist(c_u, c_k) + |c_v| * dist(c_v, c_k)}{|c_u| + |c_v|}$

Naïve implementation has O(n³) time complexity, where n is the number of instances

- Compute initial distances: O(n²)
- Merge steps: O(n), each step
 - Update distance matrix: O(n)
 - Select next pair of clusters: O(n²)
Computational Complexity

- Single link: Can update and pick pair in O(n), which results in O(n²) algorithm
- Complete and average link: Can do these steps in O(n log n), which yields an O(n² log n) algorithm



Chaining:





Chaining:





Chaining:







- Bottom line:
 - Simple, fast
 - Often low quality



- Worst case O(n³)
- Fast algorithm: Requires O(n²) space
- No chaining
- Bottom line:
 - Typically much faster than O(n³)
 - Often good quality

Divisive or Top-Down Clustering

Initialize: All items one cluster Iterate:

select a cluster c_j (least coherent)
 divide c_j into two clusters
 Halt: When have required # of clusters

Note: Step 2 requires another clustering algorithm!



Other Hierarchical Clustering Methods

- Major weakness of agglomerative clustering methods
 - <u>Do not scale</u> well: time complexity of at least $O(n^2)$, where *n* is the number of total objects
 - Can never undo what was done previously
- Integration of hierarchical with distance-based clustering
 - <u>BIRCH</u>: uses CF-tree and incrementally adjusts the quality of sub-clusters
 - <u>CURE</u>: selects well-scattered points from the cluster and then shrinks them towards the center of the cluster by a specified fraction



- BIRCH: Balanced Iterative Reducing and Clustering using Hierarchies (Zhang, Ramakrishnan & Livny, 1996)
- Incrementally construct a CF (Clustering Feature) tree
 - Parameters: max diameter, max children
 - Phase 1: scan DB to build an initial in-memory CF tree (each node: #points, sum, sum of squares)
 - Phase 2: use an arbitrary clustering algorithm to cluster the leaf nodes of the CF-tree
- Scales linearly: finds a good clustering with a single scan
- Weaknesses: handles only numeric data, sensitive to order of data records



• **Centroid:**
$$\vec{X0} = \frac{\sum_{i=1}^{N} \vec{X_i}}{N}$$

• Radius: average distance from member points to cluster centroid $R = (\frac{\sum_{i=1}^{N} (\vec{X_i} - \vec{X0})^2}{N})^{\frac{1}{2}}$

Cluster Feature Vector

- Given: X₁,...,X_n, data points in a cluster where each with d-dimensions
- We define CF = (N, LS, SS), where
 - *N*: Number of data points
 - $LS: \sum_{i=1}^{N} X_i$
 - SS: $\sum_{i=1}^{N} X_i^2$
- Note: CFs are additive!
 - E.g., $CF_1 + CF_2 = (N_1 + N_2, LS_1 + LS_2, SS_1 + SS_2)$



Cluster Feature Tree

- A CF-tree is a height-balanced tree with two parameters:
 - Branching factor (non leaf nodes B, leaf nodes, L)
 Threshold T
- Each non leaf node has the form [CF_i, child_i]
- Each leaf node has CF
 - Set of CFs
 - Two pointers: prev and next
- Diameter of a subcluster under a leaf node can not exceed the threshold T



CF-Tree Construction

- Scan data set and insert the incoming data instances into the CF tree one by one
- Each instance is inserted into the closest subcluster under a leaf node
- If insertion causes subcluster diameter to exceed threshold, then create new subcluster

CF-Tree Construction

- The new subcluster may cause its parent to exceed branching factor
- If so, split leaf node
 - Identifying the pair of subclusters with largest intercluster distance
 - Divide by proximity to these two subclusters
- If this split clause non-leaf node to exceed branching fact, then recursively split
- If the root node is split, then the height of the CF tree is increased by one



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Partitioning Algorithms

- <u>Partitioning method</u>: Construct a partition of a database
 D of *n* objects into a set of *k* clusters
- Given a k, find a partition of k clusters that optimizes the chosen partitioning criterion
 - Global optimal: exhaustively enumerate all partitions
 - Heuristic methods: k-means, k-medoids algorithms
 - <u>k-means</u> (MacQueen, 1967): Each cluster is represented by the center of the cluster
 - <u>k-medoids</u> or PAM (Partition around medoids) (Kaufman & Rousseeuw, 1987): Each cluster is represented by one of the objects in the cluster



- Divide instances into disjoint clusters
 Flat vs. tree structure
- Key issues:
 - How many clusters should there be?
 - How should clusters be represented?

Partitional Clustering from a Hierarchical Clustering

Can generate a partitional clustering from a hierarchical clustering by "cutting" the tree at some level



K-Means Clustering

A commonly-used clustering algorithm

- Easy to implement
- Quick to run
- Assumes
 - Objects are n-dimensional vectors
 - Distance/similarity measure between these instances
- Goal: Partition the data in K disjoint subsets
- Ideally: Partition reflects the structure of the data

K-Means Overview

- Inputs:
 - A set of n-dimensional real vectors {x1,..., xm}
 - K, the desired number of clusters
- Output: A mapping of the vectors into k clusters (disjoint subsets), C: {1,...,m} -> {1,...,k}
- The k cluster centers are in the same space as instances
- Each cluster is represented by a vector



Let *d* be the distance measure between instances Pick *k* random centroids, s_1, \dots, s_j

Until clustering converges or other stopping criterion: For each instance x_i : Assign x_i to the cluster c_i s.t. $d(x_i, s_i)$ is minimal

Update the centroid of each cluster For each cluster c_j $s_j = \mu(c_j)$

Algorithmic Details

Initializing the centroids

- Pick points randomly
- Pick points from data instances

• $\mu(C_j) = [1/|C_j|] * [\Sigma_i X_i]$

- $|c_j|$ is number of examples assigned to cluster c_j
- $i \in C_j$, i.e., examples that are assigned to cluster C_j
- Note: This is a vector [calculate the mean along each dimension]



- Results vary based on seed selection
- Some seeds can result in poor convergence rate, or convergence to sub-optimal clusterings
- Select good seeds using a heuristic or the results of another method
- Do many runs of k-means, each from a different random start configuration

K-Means W/K=2



Pick seeds Reassign clusters Compute centroids Reassign clusters Compute centroids Reassign clusters **Converged!**





Distance function: Manhattan



Step 1a $X_1 = \langle 4, 1 \rangle$ $Dist(X_1, C_1) = 2$ $X_2 = \langle 4, 3 \rangle$ $Dist(X_2, C_1) = 2$ $X_3 = \langle 6, 2 \rangle$ $Dist(X_3, C_1) = 3$ $X_4 = \langle 8, 8 \rangle$ $Dist(X_4, C_1) = 11$ $C_1 = \langle 3, 2 \rangle$ $Dist(X_1, C_2) = 5$ $C_2 = \langle 7, 3 \rangle$ $Dist(X_2, C_2) = 3$ $Dist(X_3, C_2) = 2$ $Dist(X_4, C_2) = 6$



$X_1 = \langle 4, 1 \rangle$ Dist $(X_1, C_1) = 2$ $X_2 = \langle 4, 3 \rangle$ Dist $(X_2, C_1) = 2$ $X_3 = \langle 6, 2 \rangle$ Dist $(X_3, C_1) = 3$ $X_4 = \langle 8, 8 \rangle$ Dist $(X_4, C_1) = 11$ $Dist(X_1, C_2) = 5$ C₁= <3,2> $Dist(X_2, C_2) = 3$ C₂= <7,3> $Dist(X_3, C_2) = 2$ $Dist(X_4,C_2) = 6$ $C_1 = \langle \frac{4+4}{2}, \frac{1+3}{2} \rangle = \langle 4, 2 \rangle$ $C_{2} = \langle \frac{6+8}{2}, \frac{2+8}{2} \rangle = \langle 7, 5 \rangle$

Step 1b



Step 2a $X_1 = \langle 4, 1 \rangle$ $Dist(X_1, C_1) = 1$ $X_2 = \langle 4, 3 \rangle$ $Dist(X_2, C_1) = 1$ $X_3 = \langle 6, 2 \rangle$ $Dist(X_3, C_1) = 2$ $X_4 = \langle 8, 8 \rangle$ $Dist(X_4, C_1) = 10$ $C_1 = \langle 4, 2 \rangle$ $Dist(X_1, C_2) = 7$ $C_2 = \langle 7, 5 \rangle$ $Dist(X_2, C_2) = 5$ $Dist(X_3, C_2) = 4$ $Dist(X_4, C_2) = 4$







Step 3a	
X ₁ = <4,1> X ₂ = <4,3> X ₃ = <6,2> X ₄ = <8,8>	Dist $(X_1, C_1) = 1.67$ Dist $(X_2, C_1) = 1.67$ Dist $(X_3, C_1) = 1.67$ Dist $(X_4, C_1) = 10.33$
C ₁ = <4.67,2> C ₂ = <8,8>	Dist $(X_1, C_2) = 11$ Dist $(X_2, C_2) = 9$ Dist $(X_3, C_2) = 8$ Dist $(X_4, C_2) = 0$



Assignment are unchanged -> converged

Note: Not showing centroid recomputatoin

Time Complexity

- Distance between two instances: O(n), where n is the dimensionality of the vectors
- Reassigning clusters: O(*km*) distance computations, or O(*kmn*)
- Computing centroids: Each instance vector gets added once to some centroid: O(*nm*)
- Assume these two steps are each done once for *I* iterations: O(*Iknm*)
- Linear in all relevant factors, with fixed number of iterations, more efficient than O(m²) HAC

Comments on the K-Means Method

Strengths

- *Relatively efficient*: O(*Ikmn*), where *m* is # objects, *k* is # clusters, and *I* is # iterations. Normally, *k*, *I* << *m*
- Often terminates at a *local optimum*. The *global optimum* may be found using techniques such as *simulated annealing* and *genetic algorithms*

Weaknesses

- Applicable only when *mean* is defined (what about categorical data?)
- Need to specify *k*, the *number* of clusters, in advance
- Trouble with noisy data and *outliers*
- Not suitable to discover clusters with *non-convex shapes*


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Model-Based Clustering

- Basic idea: Clustering as probability estimation
- One model for each cluster
- Generative model:
 - Probability of selecting a cluster
 - Probability of generating an object in cluster
- Find max. likelihood or MAP model
- Missing information: Cluster membership
- Use EM algorithm
- Quality of clustering: Likelihood of test objects



- In k-means, instances are assigned to exactly one cluster
- We can do "soft" k-means with an Expectation Maximization algorithm
 - Each cluster represented by a distribution
 - E step: Determine how likely it is that each that each cluster generated each instance
 - M step: Adjust cluster parameters to maximize likelihood

Mixtures of Gaussians

- Cluster model: Normal distribution (mean, covariance)
- Assume: diagonal covariance, known variance, same for all clusters
- Max. likelihood: mean = avg. of samples
- But what points are samples of a given cluster?
- Estimate prob. that point belongs to cluster
- Mean = weighted avg. of points, weight = prob.
- But to estimate probs. we need model
- "Chicken and egg" problem: use EM algorithm

EM Algorithm for Mixtures

- Initialization: Choose means at random
- E step:
 - For all points and means, compute Prob(point|mean)
 - Prob(mean|point) = Prob(mean) Prob(point|mean) / Prob(point)

M step:

- Each mean = Weighted avg. of points
- Weight = Prob(mean|point)
- Repeat until convergence

Representing Clusters

Represent clusters with a Gaussian

$$N_{j}(x_{i}) = \frac{1}{(2\pi\sigma^{2})^{0.5}} e^{\frac{-1}{2} \left[\frac{(x_{i} - \mu_{j})}{\sigma}\right]^{2}}$$

Where

- μ_j is the mean
- σ^2 is the variance
- $N_j(x_i) = \text{probability}(x_i | \mu_j)$

EM Clustering: Hidden Variables

- On each iteration of *k-means clustering, we* had to assign each instance to a cluster
- In the EM approach, we'll use hidden variables to represent this idea
- For each instance x_i we have a set of hidden variables z_{i1},...,z_{ik}
- We can think of z_{ij} as being 1 if is a member of cluster j and 0 otherwise



- Recall that z_{ij} is a hidden variable which is 1 if N_j generated x_i and 0 otherwise
- In the E-step, we compute h_{ij}, the expected value of this hidden variable

$$h_{ij} = \frac{P_j * N_j(x_i)}{\Sigma_l P_l * N_l(x_i)}$$



 Given the expected values h_{ij}, we re-estimate the means of the Gaussians and the cluster probabilities

$$\mu_{j} = \frac{\Sigma_{i} x_{i} * h_{ij}}{\Sigma_{i} h_{ij}}$$
$$\Sigma_{i} h_{ij}$$

$$P_j = \frac{Z_i n_i}{n}$$

Note: i goes over examples

EM Clustering Example

- Consider a one-dimensional clustering problem:
 - x1 = -4
 - $x^2 = -3$
 - x3 = -1
 - x4 = 3
 - x5 = 5
- Settings
 - $\mu 1 = 0, \mu_2 = 2$, both have $\sigma = 2$
 - Density function is: $f(x, \mu) = \frac{1}{(8\pi)^{0.5}} e^{\frac{-1}{2} \left[\frac{(x-\mu)}{2}\right]^2}$ Initially, we set D1
 - Initially, we set P1 = P2 = 0.5

EM Clustering Example

F(-4,
$$\mu_1$$
) = $\frac{1}{(8\pi)^{0.5}} e^{\frac{-1}{2} \left[\frac{(4-0)}{2}\right]^2}$

- f(-4, μ₁) = 0.0269
- f(-3, μ₁) = 0.0646
- f(-1, μ₁) = 0.176
- $f(3, \mu_1) = 0.0646$
- $f(5, \mu_1) = 0.00874$

- f(-4, μ₂) = 0.0022
- f(-3, μ₂) = 0.00874

•
$$f(-1, \mu_2) = 0.0646$$

- $f(3, \mu_2) = 0.176$
- $f(5, \mu_2) = 0.0646$

EM Clustering Example: E Step

$$h_{11} = \frac{P_1 * f(x_1, \mu_1)}{P_1 * f(x_1, \mu_1) + P_2 * f(x_1, \mu_2)} = \frac{0.5 * .0269}{0.5 * 0.0269 + 0.5 * 0.0022} = 0.924$$

•
$$h_{21} = 0.881$$

•
$$h_{31} = 0.732$$

•
$$h_{41} = 0.268$$

•
$$h_{51} = 0.119$$

•
$$h_{12} = 0.076$$

•
$$h_{32} = 0.268$$

•
$$h_{52} = 0.881$$

EM Clustering Example: M Step

$$\mu_{1} = \frac{\sum_{i} x_{i} * h_{i1}}{\sum_{i} h_{i1}} \qquad \mu_{2} = \frac{\sum_{i} x_{i} * h_{i2}}{\sum_{i} h_{i2}}$$

$$\mu_{1} = \frac{-4*0.924 + -3*0.881 + -1*0.732 + 3*0.268 + 5*0.119}{0.924 + 0.881 + 0.732 + 0.268 + 0.119} = -1.94$$

$$\mu_{2} = \frac{-4*0.076 + -3*0.119 + -1*0.268 + 3*0.732 + 5*0.881}{0.076 + 0.119 + 0.268 + 0.732 + 0.881} = 3.39$$

$$P_{1} = \frac{\sum_{i} h_{i1}}{n} = \frac{0.924 + 0.881 + 0.732 + 0.268 + 0.119}{5} = 0.58$$

$$P_{2} = \frac{\sum_{i} h_{i2}}{n} = \frac{0.076 + 0.119 + 0.268 + 0.732 + 0.881}{5} = 0.42$$



- Will converge to a local maximum
- Sensitive to initial means of clusters
- Have to choose the number of clusters in advance
- k-means is a special case of EM clustering

Evaluating Cluster Results

- Given random data without any "structure", clustering algorithms will still return clusters
- The gold standard: do clusters correspond to natural categories?
- Do clusters correspond to categories we care about? (there are lots of ways to partition the world)

Approaches to Cluster Evaluation

- External validation
 - e.g. do genes clustered together have some common function?
- Internal validation
 - How well does clustering optimize intra-cluster similarity and inter-cluster dissimilarity?
- relative validation
 - How does it compare to other clusterings?
 - e.g. with a probabilistic method (such as EM) we can ask: how probable does held-aside data look as we vary the number of clusters.



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Low Quality of Web Searches

- System perspective:
 - small coverage of Web (<16%)</p>
 - dead links and out of date pages
 - Iimited resources
- IR perspective (relevancy of doc ~ similarity to query):
 - very short queries
 - huge database
 - novice users



- User receives many (200 5000) documents from Web search engine
- Group documents in clusters
 - by topic
- Present clusters as interface

web news images wikipedia blogs jobs more »	
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At the conclusion of the **NCAA** men's and women's Division I **basketball** championships (the "Final Four" **tournaments**), the Associated Press selects a Most Outstanding Player. The MOP need not be, but almost always is a member of the Championship team. The last man to win the award despite not being on the Championship team was Hakeem Olajuwon in 1983; the last woman to do so was Dawn Staley in 1991. en.wikipedia.org/wiki/NCAA Basketball Tournament Most Outstanding Player - [cache] - Live, Ask



Q: Need Way to Compare Queries and Documents

Vector space model:

- How to determine important words in a document?
- How to determine the degree of importance of a term within a document and within the entire collection?
- How to determine the degree of similarity between a document and the query?
- In the case of the web, what is a collection and what are the effects of links, formatting information, etc.?

- Assume t distinct terms remain after preprocessing: vocabulary
- These "orthogonal" terms form a vector space Dimension = t = |vocabulary|
- Each term, *i*, in a document or query, *j*, is given a real-valued weight, *w_{ij}*.
- Both documents and queries are expressed as *t*-dimensional vectors:

$$d_{j} = (W_{1j}, W_{2j}, ..., W_{tj})$$

Graphical Representation



Document Collection

- Vector space model represents a collection of n documents by a term-document matrix
- Each entry: "weight" of a term in the document

Term Weights: Term Frequency

- More frequent terms in a document are more important, i.e. more indicative of the topic
 f_{ij} = frequency of term *i* in document *j*
- May want to normalize *term frequency* (*tf*) by dividing by the frequency of the most common term in the document:

$$tf_{ij} = f_{ij} / max_i \{f_{ij}\}$$

Term Weights: Inverse Document Frequency

 Terms that appear in many *different* documents are *less* indicative of overall topic

 df_i = document frequency of term *i*

= number of documents containing term *i*

 idf_i = inverse document frequency of term *i*,

= $\log_2 (N/df_i)$ (*N*: number of documents)

An indication of a term's *discrimination* power

Log used to dampen the effect relative to tf

TF-IDF Weighting

A typical combined term importance indicator is *tf-idf weighting*:

 $w_{ij} = tf_{ij} idf_i = tf_{ij} \log_2 (N/df_i)$

- A term occurring frequently in the document but rarely in the rest of the collection is given high weight
- Many other ways of determining term weights have been proposed
- Experimentally, *tf-idf* works well



Given a document containing terms with given frequencies:

A(3), B(2), C(1)

Assume collection contains 10,000 documents and document frequencies of these terms are:

A(50), B(1300), C(250)

Then:

A: tf = 3/3; $idf = log_2(10000/50) = 7.6$; tf-idf = 7.6

B: tf = 2/3; $idf = log_2(10000/1300) = 2.9$; tf-idf = 2.0

C: tf = 1/3; $idf = log_2(10000/250) = 5.3$; tf-idf = 1.8



- Query vector is typically treated as a document and also tf-idf weighted
- Alternative is for the user to supply weights for the given query terms

- Inner product: $sim(d_j,q) = \Sigma w_{ij} * w_{iq}$
 - w_{ij} = weight of term i in doc j
 - w_{iq} is weight of term i in query

• Cosine similarity: sim(d_j,q) =
$$\frac{\Sigma_i w_{ij} * w_{iq}}{\Sigma_i (w_{ij})^2 \Sigma_i (w_{iq})^2}$$

- Measures the cosine of the angle between two vectors
- Inner product normalized by the vector lengths

Cosine Similarity Visually

Take cosine of this angle as similarity between query and document



 t_3

 θ_1

Comparison

- $D_1 = 2T_1 + 3T_2 + 5T_3$
- $D_2 = 3T_1 + 7T_2 + 1T_3$
- $Q = 0T_1 + 0T_2 + 2T_3$
- Weighted inner product
 - $sim(D_1, Q) = 2*0 + 3*0 + 5*2 = 10$
 - $sim(D_2, Q) = 3*0 + 7*0 + 1*2 = 2$

Cosine

- $sim(D_1, Q) = 10 / \sqrt{(4+9+25)(0+0+4)} = 0.81$
- $sim(D_2, Q) = 2 / \sqrt{(9+49+1)(0+0+4)} = 0.13$

 D_1 is 6 times better than D_2 using cosine similarity but only 5 times better using inner product.

Comments On Vector Space Model

- Simple, mathematically based approach
- Considers both local (*tf*) and global (*idf*) word occurrence frequencies
- Provides partial matching and ranked results.
- Tends to work quite well in practice despite obvious weaknesses
- Allows efficient implementation for large document collections

Weakness with Vector Space Model

- Missing semantic information (e.g. word sense)
- Missing syntactic information (e.g. phrase structure, word order, proximity information)
- Assumption of term independence (e.g. ignores synonomy)

Analyzing Microarray Data

- Microarrays allow us to measure gene expression
- Central Dogma:
 - Genes encode proteins
 - DNA transcribed into messenger RNA
 - mRNA translated into proteins
 - Triplet code (codons)




Two Views of Microarray Data

Data points are genes

- Represented by expression levels across <u>different samples</u> (ie, features=samples)
- **Goal**: categorize new genes
- Data points are samples (eg, patients)
 - Represented by expression levels of <u>different</u> <u>genes</u> (ie, features=genes)
 - **Goal**: categorize new samples

Unsupervised Learning Task

- Given: a set of microarray experiments under different conditions
- Do: <u>cluster</u> the genes, where a gene described by its expression levels in different experiments

Example (Green = up-regulated, Red = down-regulated)



Experiments (Samples)

Unsupervised Learning Task 2

- Given: a set of microarray experiments (samples) corresponding to different conditions or patients
- Do: <u>cluster</u> the experiments



- Cluster samples from mice subjected to a variety of toxic compounds (Thomas *et al.*, 2001)
- Cluster samples from cancer patients, potentially to discover different subtypes of a cancer
- Cluster samples taken at different time points



- Unsupervised learning technique: Gain insight into the data
- Clustering approaches
 - Hierarchical methods
 - Partitioning methods
 - Model-based methods
- Used in many applications
 - Information retrieval
 - Bioinformatics



Association rule mining

Reading: <u>http://infolab.stanford.edu/~ullman/mining/assocrules.pdf</u>

