CSC2515 – Machine Learning Sam Roweis

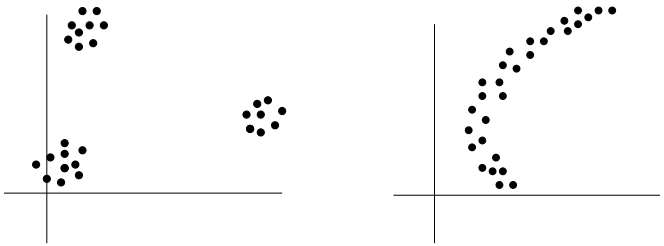
Lecture 7:

Clustering and Tree Models

October 25, 2005

Unsupervised Learning 1

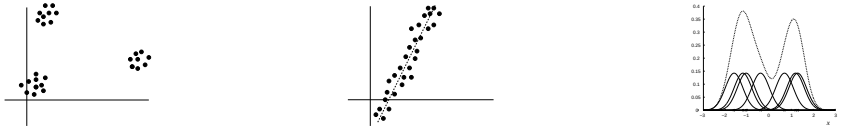
- So far we have only discussed *supervised learning* in which there are both inputs and desired outputs.
  For *regression*, the output(s) were continuous values.
  For *classification*, the output was a discrete (categorical) label.
- Another very important problem in machine learning is *unsupervised learning*, in which there are no outputs, only inputs.



- What should we do here?

Three Unsupervised Models 2

- The three canonical problems in unsupervised learning are *clustering*, *dimensionality reduction*, and *density modeling*:
  - Clustering: grouping similar training cases together and identifying a "prototype" example to represent each group.
  - Dimensionality reduction: learning to represent each training case using a small number of continuous variables from which the original data can be almost exactly reconstructed.
  - Density modeling: learning a density function from a few samples. This is like quantitative novelty detection: we want to produce a large signal when data similar to training data appears and a small signal when different data appears.

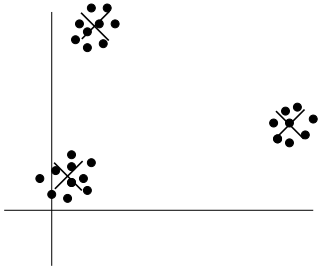


Missing Outputs 3

- You can think of unsupervised learning as supervised learning in which all the outputs are *missing*:
  - Clustering == classification with missing labels.
  - Dimensionality reduction == regression with missing targets.

- Density estimation is actually very general and encompasses the two problems above and a whole lot more.
- Let's start off by talking about clustering

- Clustering: grouping similar training cases together and identifying a "prototype" example to represent each group.



- Several approaches: partitional (find a fixed number of clusters), ... heirarchical (agglomerative, divisive),
- All require a way to measure distance between two data points, e.g. Euclidean distance $\|\mathbf{x}-\mathbf{y}\|^2$,
  Mahanalobis distance $(\mathbf{x}-\mathbf{y})^\top\mathbf{V}^{-1}(\mathbf{x}-\mathbf{y})$,
  ...

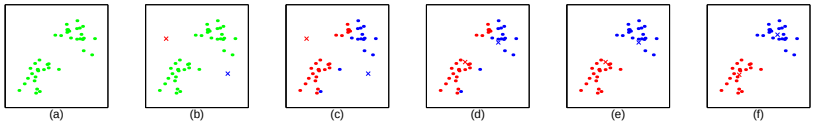
- Select a number of clusters K (and possible a covariance $\mathbf{V}$.
  Start with initial cluster centres $\mu_1^0, \mu_2^0, \ldots, \mu_K^0$.
- Alternate between two steps.
  Assign each datapoint to the cluster whose centre is closest:

$$c_n^{t+1} = \text{argmin}_k (\mathbf{x}^n - \mu_k^t)^\top \mathbf{V}^{-1} (\mathbf{x}^n - \mu_k^t)$$

  Update cluster centres to the mean of all points assigned to them:

$$\mu_k^{t+1} = \frac{\sum_n [c_k^{t+1} = n] \mathbf{V}\mathbf{x}^n}{\sum_n [c_k^{t+1} = n]}$$

- If a cluster becomes empty, use a heuristic to reposition its mean.
  Break ties in distance using cluster of smallest size.



- Q: What cost function is K-means minimizing?
  A: Average squared distance from each datapoint to the nearest cluster centre:

$$E(\{\mu_k\}) = \frac{1}{N} \sum_n \min_k \left[(\mathbf{x}^n - \mu_k)^\top \mathbf{V}^{-1} (\mathbf{x}^n - \mu_k) \right]$$

- The K-means algorithm does coordinate descent in a function $F(\{\mu_k\}, \{c_n\})$ which is an upper bound on this error:

$$F(\{\mu_k\}, \{c_n\}) = \frac{1}{N} \sum_n \left[(\mathbf{x}^n - \mu_{c_n})^\top \mathbf{V}^{-1} (\mathbf{x}^n - \mu_{c_n}) \right]$$

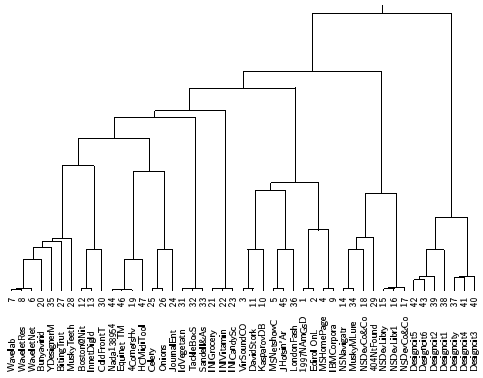
  This upper bound is valid for *any* setting of the c_n.
  After the assignment step for c_n, $F(\mu, c) = E(\mu)$.
  The assignment step lowers this bound as much as possible with respect to $\{c_n\}$ keeping μ fixed, the update step minimizes it with with respect to $\{\mu_k\}$, keeping c fixed.

- K-means clustering is also called *vector quantization* in the engineering/signal processing literature, because the problem is like quantization but for multivariate objects.
- The cluster centres are called *codebook vectors*.
- More correctly, K-means (or VQ) is an *optimization problem*, and the algorithm above, which is (just) one potential solution to it is called the *Lloyd-Max algorithm*.
- However, sometimes, we want to apply this algorithm to complex data that cannot be expressed easily as a vector (eg gene sequence).
- As long as we have a distance measure between data items, we can still perform the assignment step, but for the update step, we cannot "average" so we restrict the centres to lie on one of the original data items (could be expensive to find the best one).
- This is the *K-mediods/K-medians* problem.

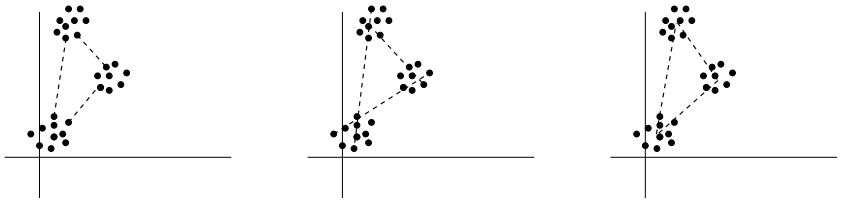
- K-means (and other clustering methods) require tricks to work well.
- Initialization: set μ_k^0 to be K randomly chosen points, or else to the first K points from *furthest-first* clustering (see later).
- Picking number of clusters: use cross validation on the error function evaluated on a validation set.
- Unused clusters: set to points with biggest errors.
- Ties in distance: add points to smaller clusters first.
- Robust errors: use squared error up to some maximum error then constant error beyond that. (Affects both steps.)
- Local minima: use random restarts, split and merge clusters.

- If we change the distance function, the assignment step is still easy, but updating the cluster centres might be hard.
- Some common distances, their names, and their cost functions:
  K-means (average squared distance)
  $E(\{\mu_k\}) = \frac{1}{N}\sum_n \min_k \left[(\mathbf{x}^n - \mu_k)^\top \mathbf{V}^{-1}(\mathbf{x}^n - \mu_k)\right]$
  K-medians (average distance):
  $E(\{\mu_k\}) = \frac{1}{N}\sum_n \min_k \left[\sqrt{(\mathbf{x}^n - \mu_k)^\top \mathbf{V}^{-1}(\mathbf{x}^n - \mu_k)}\right]$
  K-corners (average abs. error):
  $E(\{\mu_k\}) = \frac{1}{N}\sum_n \min_k \left[\sum_i |x_i^n - \mu_{ki}|\right]$
  K-centres (biggest cluster radius):
  $E(\{\mu_k\}) = \max_n \min_k \left[(\mathbf{x}^n - \mu_k)^\top \mathbf{V}^{-1}(\mathbf{x}^n - \mu_k)\right]$
- Special cases solved, e.g. K-corners: $\mu_{ki}^t = \text{median}_{c_n^t = k}[x_i^n]$

- Hierarchical clustering algorithms break the dataset into a series of nested clusters, starting with a single cluster at the top containing all the data and ending with N clusters at the bottom, one for each point. The results can be displayed as a *dendrogram*:



- Agglomerative algorithms for hierarchical clustering start with each datapoint in its own cluster and then successively merge similar clusters until a single cluster remains.
- Several methods for merging. Most based on computing cluster distances $d_{cc'}$ from pairwise distances $d_{nn'}$ between all pairs of points and then merging the two clusters with smallest $d_{cc'}$:
  Single linkage: $d_{cc'} = \min_{n\in c, n'\in c'} d_{nn'}$
  Complete linkage: $d_{cc'} = \max_{n\in c, n'\in c'} d_{nn'}$
  Average linkage: $d_{cc'} = \text{mean}_{n\in c, n'\in c'} d_{nn'}$



- Divisive algorithms for hierarchical clustering start with all the data in a single cluster and successively split clusters.
- Here's my favourite one: furthest-first traversal.

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Pick any point, mark it, and set mu(1) equal to it.
for i=2:N
  find the unmarked point furthest from {mu(1)...mu(i-1)}
  [using dist(point,{set})=min(p' in {set}) dist(point,p')]
  mark this point and set mu(i) equal to it
end
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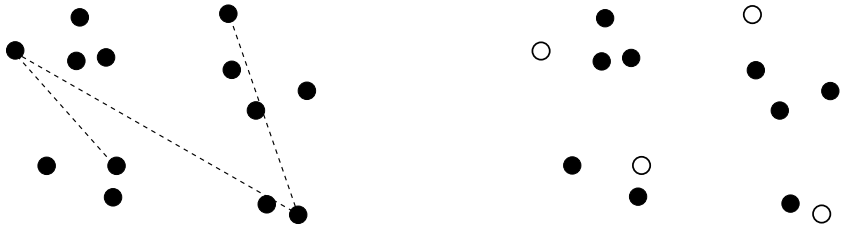
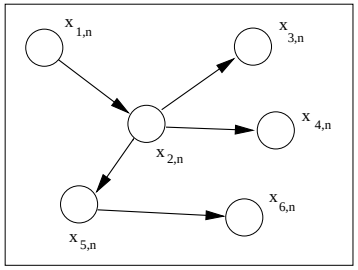


- A tree model is a unsupervised learning model in which each variable x_i has exactly one other variable as its "parent" x_{π_i}, except the "root" x_{root} which has no parents.
- The probability of a variable taking on a certain value depends only on the value of its parent:

$$p(\mathbf{x}) = p(x_{\text{root}}) \prod_{i \neq \text{root}} p(x_i | x_{\pi_i})$$

- Trees are the next step up from assuming independence. Instead of considering variables in isolation, consider them in pairs.
- WARNING: do not confuse these trees (probability model is a tree) with decision trees (algorithm proceeds in a tree structured fashion).

- If we identify each variable with a node in a graph, we can describe this model by drawing a directed arrow from each node to its children. NB: each node (except root) has exactly one parent but may have more than one child.



- This is a special case of a general way of describing statistical functions using *probabilistic graphical models*. (see CSC412/2506)

- Trees are just a special case of fully observed density models.
- For discrete data x_i with values v_i, each node stores a conditional probability table (CPT) over its values given its parent's value. The ML parameter estimates are just the empirical histograms of each node's values given its parent:

$$p^*(x_i = v_i | x_{\pi_i} = v_j) = \frac{N(x_i = v_i, x_{\pi_i} = v_j)}{\sum_{z_i} N(x_i = z_i, x_{\pi_i} = v_j)}$$

  except for the root which uses marginal counts $N(v_{root})/N$.
- For continuous data, the most common model is a two-dimensional Gaussian at each node, jointly modeling the node and its parent.
- The ML parameters are just to set the mean of $p_i(x_i, x_{\pi_i})$ to be the sample mean of $[x_i; x_{\pi_i}]$ and the covariance matrix to the sample covariance.

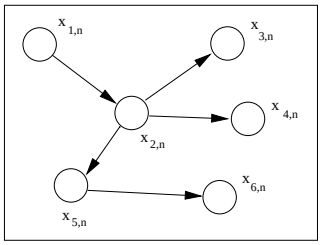
- Overall likelihood is sum of parent-conditional terms, one per node:
  $\mathbf{V}_i \equiv$ set of joint configurations of x_i and its parent x_{π_i}
  ($\mathbf{V}_{\text{root}} \equiv$ set of values of root note)

$$\begin{aligned}\ell(\theta;\mathcal{D}) &= \sum_n \log p(\mathbf{x}^n) = \sum_n \left[\log p_r(x_r^n) + \sum_{i\neq r} \log p({x_i}^n|{x_{\pi_i}}^n)\right] \\ &= \sum_n \sum_i \sum_{\mathbf{y}\in\mathbf{V}_i} [x_i, x_{\pi_i} = \mathbf{y}] \log p_i(x_i|x_{\pi_i}) \\ &= \sum_i \sum_{\mathbf{y}\in\mathbf{V}_i} N_i(\mathbf{y}) \log p_i(\mathbf{y})\end{aligned}$$

  with $p_i(\mathbf{y}_i) = p(x_i|x_{\pi_i})$ and counts $N_i(\mathbf{y}) = \sum_n [\mathbf{y}_i^n = \mathbf{y}]$.

- Trees are in the exponential family with $\mathbf{y}_i$ as sufficient statistics.

- What about the tree structure (links)?
  How do we know which nodes to make parents of which?



- Bold idea: can we also *learn* the optimal structure?
  In principle, we could search all combinatorial structures, for each compute the ML parameters, and take the best one.
- But is there a better way? Yes. It turns out that structure learning in tree models can be converted to a good old computer science problem: maximum weight spanning tree.

- Let us rewrite the overall likelihood function:

$$\begin{aligned}\ell(\theta;\mathcal{D}) &= \sum_{\mathbf{x}\in\mathbf{V}_{\text{all}}} N(\mathbf{x}) \log p(\mathbf{x}) \\ &= \sum_{\mathbf{x}} N(\mathbf{x}) \left(\log p(x_r) + \sum_{i\neq r} \log p(x_i|x_{\pi_i})\right)\end{aligned}$$

- ML parameters, are equal to the observed frequency counts $q(\cdot)$:

$$\begin{aligned}\frac{\ell^*}{M} &= \sum_{\mathbf{x}\in\mathbf{V}_{\text{all}}} q(\mathbf{x}) \left(\log q(x_r) + \sum_{i\neq r} \log q(x_i|x_{\pi_i})\right) \\ &= \sum_{\mathbf{x}} q(\mathbf{x}) \left(\log q(x_r) + \sum_{i\neq r} \log \frac{q(x_i, x_{\pi_i})}{q(x_{\pi_i})}\right) \\ &= \sum_{\mathbf{x}} q(\mathbf{x}) \sum_{i\neq r} \log \frac{q(x_i, x_{\pi_i})}{q(x_i)q(x_{\pi_i})} + \sum_{\mathbf{x}} q(\mathbf{x}) \sum_i \log q(x_i)\end{aligned}$$

- NB: second term does not depend on structure.

- Each term in sum $i \neq r$ corresponds to an edge from i to its parent.

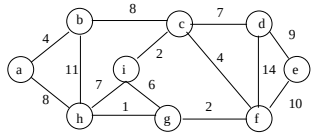
$$\begin{aligned}\frac{\ell^*}{M} &= \sum_{\mathbf{x}} q(\mathbf{x}) \sum_{i\neq r} \log \frac{q(x_i, x_{\pi_i})}{q(x_i)q(x_{\pi_i})} + C \\ &= \sum_{i\neq r} \sum_{x_i, x_{\pi_i}} q(x_i, x_{\pi_i}) \log \frac{q(x_i, x_{\pi_i})}{q(x_i)q(x_{\pi_i})} + C \\ &= \sum_{i\neq r} \sum_{y_i} q(y_i) \log \frac{q(y_i)}{q(x_i)q(x_{\pi_i})} + C \\ &= \sum_{i\neq r} W(i;\pi_i) + C\end{aligned}$$

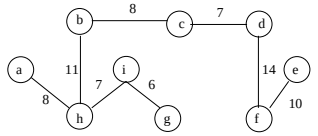
- So the overall likelihood is the sum of weights on edges that we use. We need the maximum weight spanning tree to maximize likelihood.
- The edge weights W are defined by *mutual information*:

$$W(i;j) = \sum_{x_i, x_j} q(x_i, x_j) \log \frac{q(x_i, x_j)}{q(x_i)q(x_j)}$$

Kruskal's algorithm (Greedy Search) 20

- To find the maximum weight spanning tree A on a graph with nodes U and weighted edges E:
  1. $A \leftarrow$ empty
  2. Sort edges E by nonincreasing weight: $e_1, e_2, \ldots, e_K$.
  3. for $k = 1$ to K $\{A \mathrel{+}= e_k$ unless doing so creates a cycle$\}$





Maximum Likelihood Trees 21

We can now completely solve the tree learning problem:

1. Compute the marginal counts $q(x_i)$ for each node and pairwise counts $q(x_i, x_j)$ for all pairs of nodes.
2. Set the weights to the mutual informations:

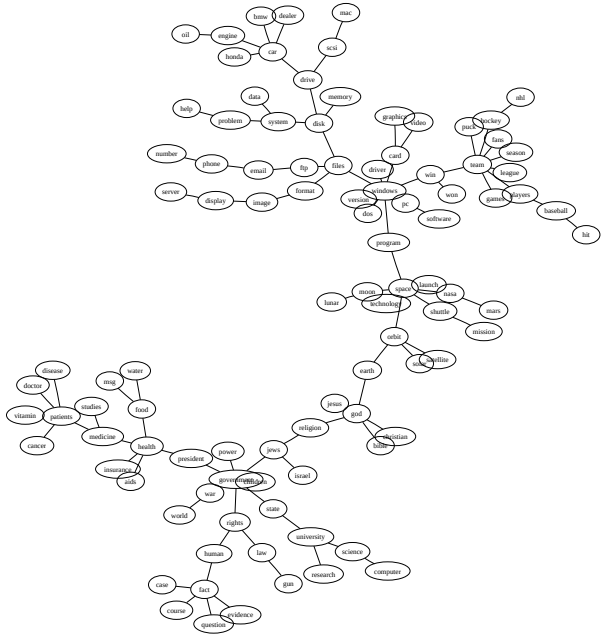
$$W(i;j) = \sum_{x_i, x_j} q(x_i, x_j) \log \frac{q(x_i, x_j)}{q(x_i) q(x_j)}$$

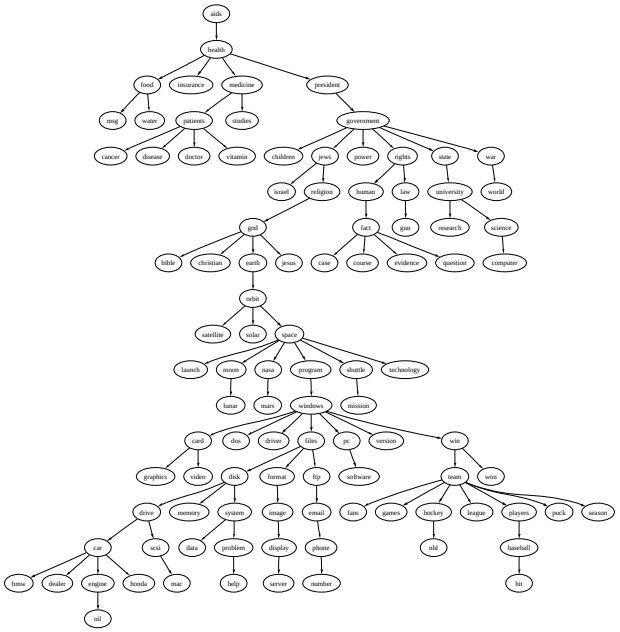
3. Find the maximum weight spanning tree A=MWST(W).
4. Using the undirected tree A chosen by MWST, pick a root arbitrarily and orient the edges away from the root. Set the conditional functions to the observed frequencies:

$$p(x_i | x_{\pi_i}) = \frac{q(x_i, x_{\pi_i})}{\sum_{x_i} q(x_i, x_{\pi_i})} = \frac{q(x_i, x_{\pi_i})}{q(x_{\pi_i})}$$

Undirected vs. Directed Trees 22

- *Any* directed tree consistent with the undirected tree found by the algorithm above will assign the same likelihood to any dataset.
- Amazingly, as far as likelihood goes, the root is arbitrary. We can just pick one node and orient the edges away from it. Or we can work with undirected models.
- For continuous nodes (e.g. Gaussian), the situation is similar, except that computing the mutual information requires an integral.
- Mutual information is the *Kullback-Leibler* divergence (cross-entropy) between a distribution and the product of its marginals. Measures how far from independent the joint distribution is.

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