Algorithms/Process for Data Mining Lab

Algorithm: Apriori. Find frequent itemsets using an iterative level-wise approach based on candidate generation.

Input:

- D, a database of transactions;
- *min_sup*, the minimum support count threshold.

Output: L, frequent itemsets in D.

Method:

```
(1)   L1 = find_frequent_1-itemsets(D);
(2)   for (k = 2; Lk−1 ≠ φ; k++) {
(3)       Ck = apriori_gen(Lk−1);
(4)       for each transaction t ∈ D { // scan D for counts
(5)           Ct = subset(Ck, t); // get the subsets of t that are candidates
(6)           for each candidate c ∈ Ct
(7)               c.count++;
(8)       }
(9)       Lk = {c ∈ Ck | c.count ≥ min_sup}
(10)  }
(11)  return L = ∪k Lk;
```

```
procedure apriori_gen(Lk−1:frequent (k − 1)-itemsets)
(1)   for each itemset l1 ∈ Lk−1
(2)       for each itemset l2 ∈ Lk−1
(3)           if (l1[1] = l2[1]) ∧ (l1[2] = l2[2])
                  ∧ ... ∧ (l1[k − 2] = l2[k − 2]) ∧ (l1[k − 1] < l2[k − 1]) then {
(4)               c = l1 ⋈ l2; // join step: generate candidates
(5)               if has_infrequent_subset(c, Lk−1) then
(6)                   delete c; // prune step: remove unfruitful candidate
(7)               else add c to Ck;
(8)           }
(9)   return Ck;
```

```
procedure has_infrequent_subset(c: candidate k-itemset;
          Lk−1: frequent (k − 1)-itemsets); // use prior knowledge
(1)   for each (k − 1)-subset s of c
(2)       if s ∉ Lk−1 then
(3)           return TRUE;
(4)   return FALSE;
```

Apriori algorithm for discovering frequent itemsets for mining Boolean association rules.

Algorithms/Process for Data Mining Lab

Generating Association Rules from Frequent Itemsets

Once the frequent itemsets from transactions in a database D have been found, it is straightforward to generate strong association rules from them (where *strong* association rules satisfy both minimum support and minimum confidence). This can be done using Eq. (6.4) for confidence, which we show again here for completeness:

$$confidence(A \Rightarrow B) = P(B|A) = \frac{support\_count(A \cup B)}{support\_count(A)}.$$

The conditional probability is expressed in terms of itemset support count, where $support\_count(A \cup B)$ is the number of transactions containing the itemsets $A \cup B$, and $support\_count(A)$ is the number of transactions containing the itemset A. Based on this equation, association rules can be generated as follows:

- For each frequent itemset l, generate all nonempty subsets of l.
- For every nonempty subset s of l, output the rule "$s \Rightarrow (l - s)$" if $\frac{support\_count(l)}{support\_count(s)} \geq min\_conf$, where min_conf is the minimum confidence threshold.

Because the rules are generated from frequent itemsets, each one automatically satisfies the minimum support. Frequent itemsets can be stored ahead of time in hash tables along with their counts so that they can be accessed quickly.

Algorithms/Process for Data Mining Lab

Algorithm: **FP_growth.** Mine frequent itemsets using an FP-tree by pattern fragment growth.

Input:

- D, a transaction database;
- *min_sup*, the minimum support count threshold.

Output: The complete set of frequent patterns.

Method:

1. The FP-tree is constructed in the following steps:
   (a) Scan the transaction database D once. Collect F, the set of frequent items, and their support counts. Sort F in support count descending order as L, the *list* of frequent items.
   (b) Create the root of an FP-tree, and label it as "null." For each transaction *Trans* in D do the following.
   Select and sort the frequent items in *Trans* according to the order of L. Let the sorted frequent item list in *Trans* be $[p|P]$, where p is the first element and P is the remaining list. Call insert_tree($[p|P]$, T), which is performed as follows. If T has a child N such that $N.item\text{-}name = p.item\text{-}name$, then increment N's count by 1; else create a new node N, and let its count be 1, its parent link be linked to T, and its node-link to the nodes with the same *item-name* via the node-link structure. If P is nonempty, call insert_tree(P, N) recursively.
2. The FP-tree is mined by calling FP_growth(*FP_tree*, *null*), which is implemented as follows.

```
procedure FP_growth(Tree, α)
(1)  if Tree contains a single path P then
(2)     for each combination (denoted as β) of the nodes in the path P
(3)        generate pattern β ∪ α with support_count = minimum support count of nodes in β;
(4)  else for each a_i in the header of Tree {
(5)     generate pattern β = a_i ∪ α with support_count = a_i.support_count;
(6)     construct β's conditional pattern base and then β's conditional FP_tree Tree_β;
(7)     if Tree_β ≠ ∅ then
(8)        call FP_growth(Tree_β, β); }
```

FP-growth algorithm for discovering frequent itemsets without candidate generation.

Algorithms/Process for Data Mining Lab

Mining Frequent Itemsets Using the Vertical Data Format

ECLAT (Equivalence Class Transformation) algorithm

- Both the Apriori and FP-growth methods mine frequent patterns from a set of transactions in *TID-itemset* format (i.e., f*TID* : *itemset*g), where *TID* is a transaction ID and *itemset* is the set of items bought in transaction *TID*. This is known as the **horizontal data format**.
- Alternatively, data can be presented in *item-TID set* format (i.e., f*item* : *TID set*g, where *item* is an item name, and *TID set* is the set of transaction identifiers containing the item. This is known as the **vertical data format**.
- Consider the horizontal data format of the transaction database, *D*, of Table 6.1 in Example 6.3.
- This can be transformed into the vertical data format shown in Table 6.3 by scanning the data set once.
- Mining can be performed on this data set by intersecting the TID sets of every pair of frequent single items. The minimum support count is 2.
- Because every single item is frequent in Table 6.3, there are 10 intersections performed in total, which lead to eight nonempty 2-itemsets, as shown in Table 6.4.
- Notice that because the itemsets {I1, I4} and {I3, I5} each contain only one transaction, they do not belong to the set of frequent 2-itemsets.
- Based on the Apriori property, a given 3-itemset is a candidate 3-itemset only if every one of its 2-itemset subsets is frequent.
- The candidate generation process here will generate only two 3-itemsets: {I1, I2, I3} and {I1, I2, I5}.
- By intersecting the TID sets of any two corresponding 2-itemsets of these candidate 3-itemsets, it derives Table 6.5, where there are only two frequent 3-itemsets: {I1, I2, I3: 2} and {I1, I2, I5: 2}.

Table 6.3 The Vertical Data Format of the Transaction Data Set *D* of Table 6.1

itemset	*TID_set*
I1	{T100, T400, T500, T700, T800, T900}
I2	{T100, T200, T300, T400, T600, T800, T900}
I3	{T300, T500, T600, T700, T800, T900}
I4	{T200, T400}
I5	{T100, T800}

Table 6.4 2-Itemsets in Vertical Data Format

itemset	*TID_set*
{I1, I2}	{T100, T400, T800, T900}
{I1, I3}	{T500, T700, T800, T900}
{I1, I4}	{T400}
{I1, I5}	{T100, T800}
{I2, I3}	{T300, T600, T800, T900}
{I2, I4}	{T200, T400}
{I2, I5}	{T100, T800}
{I3, I5}	{T800}

Table 6.5 3-Itemsets in Vertical Data Format

itemset	*TID_set*
{I1, I2, I3}	{T800, T900}
{I1, I2, I5}	{T100, T800}

Algorithms/Process for Data Mining Lab

Algorithm: Generate_decision_tree. Generate a decision tree from the training tuples of data partition, *D*.

Input:

- Data partition, *D*, which is a set of training tuples and their associated class labels;
- *attribute_list*, the set of candidate attributes;
- *Attribute_selection_method*, a procedure to determine the splitting criterion that "best" partitions the data tuples into individual classes. This criterion consists of a *splitting_attribute* and, possibly, either a *split-point* or *splitting subset*.

Output: A decision tree.

Method:

```
(1)  create a node N;
(2)  if tuples in D are all of the same class, C, then
(3)      return N as a leaf node labeled with the class C;
(4)  if attribute_list is empty then
(5)      return N as a leaf node labeled with the majority class in D; // majority voting
(6)  apply Attribute_selection_method(D, attribute_list) to find the "best" splitting_criterion;
(7)  label node N with splitting_criterion;
(8)  if splitting_attribute is discrete-valued and
         multiway splits allowed then // not restricted to binary trees
(9)      attribute_list ← attribute_list − splitting_attribute; // remove splitting_attribute
(10) for each outcome j of splitting_criterion
     // partition the tuples and grow subtrees for each partition
(11)     let Dj be the set of data tuples in D satisfying outcome j; // a partition
(12)     if Dj is empty then
(13)         attach a leaf labeled with the majority class in D to node N;
(14)     else attach the node returned by Generate_decision_tree(Dj, attribute_list) to node N;
     endfor
(15) return N;
```

Basic algorithm for inducing a decision tree from training tuples.

Algorithms/Process for Data Mining Lab

Naïve Bayesian Classification

The **naïve Bayesian** classifier, or **simple Bayesian** classifier, works as follows:

1. Let D be a training set of tuples and their associated class labels. As usual, each tuple is represented by an n-dimensional attribute vector, $\boldsymbol{X} = (x_1, x_2, \ldots, x_n)$, depicting n measurements made on the tuple from n attributes, respectively, $A_1, A_2, \ldots, A_n$.

2. Suppose that there are m classes, $C_1, C_2, \ldots, C_m$. Given a tuple, $\boldsymbol{X}$, the classifier will predict that $\boldsymbol{X}$ belongs to the class having the highest posterior probability, conditioned on $\boldsymbol{X}$. That is, the naïve Bayesian classifier predicts that tuple $\boldsymbol{X}$ belongs to the class C_i if and only if

$$P(C_i|\boldsymbol{X}) > P(C_j|\boldsymbol{X}) \quad \text{for } 1 \leq j \leq m, j \neq i.$$

   Thus, we maximize $P(C_i|\boldsymbol{X})$. The class C_i for which $P(C_i|\boldsymbol{X})$ is maximized is called the *maximum posteriori hypothesis*. By Bayes' theorem (Eq. 8.10),

$$P(C_i|\boldsymbol{X}) = \frac{P(\boldsymbol{X}|C_i)P(C_i)}{P(\boldsymbol{X})}. \tag{8.11}$$

3. As $P(\boldsymbol{X})$ is constant for all classes, only $P(\boldsymbol{X}|C_i)P(C_i)$ needs to be maximized. If the class prior probabilities are not known, then it is commonly assumed that the classes are equally likely, that is, $P(C_1) = P(C_2) = \cdots = P(C_m)$, and we would therefore maximize $P(\boldsymbol{X}|C_i)$. Otherwise, we maximize $P(\boldsymbol{X}|C_i)P(C_i)$. Note that the class prior probabilities may be estimated by $P(C_i) = |C_{i,D}|/|D|$, where $|C_{i,D}|$ is the number of training tuples of class C_i in D.

4. Given data sets with many attributes, it would be extremely computationally expensive to compute $P(\boldsymbol{X}|C_i)$. To reduce computation in evaluating $P(\boldsymbol{X}|C_i)$, the naïve assumption of **class-conditional independence** is made. This presumes that the attributes' values are conditionally independent of one another, given the class label of the tuple (i.e., that there are no dependence relationships among the attributes). Thus,

$$\begin{aligned} P(\boldsymbol{X}|C_i) &= \prod_{k=1}^{n} P(x_k|C_i) \qquad (8.12) \\ &= P(x_1|C_i) \times P(x_2|C_i) \times \cdots \times P(x_n|C_i). \end{aligned}$$

   We can easily estimate the probabilities $P(x_1|C_i), P(x_2|C_i), \ldots, P(x_n|C_i)$ from the training tuples. Recall that here x_k refers to the value of attribute A_k for tuple $\boldsymbol{X}$. For each attribute, we look at whether the attribute is categorical or continuous-valued. For instance, to compute $P(\boldsymbol{X}|C_i)$, we consider the following:

(a) If A_k is categorical, then $P(x_k|C_i)$ is the number of tuples of class C_i in D having the value x_k for A_k, divided by $|C_{i,D}|$, the number of tuples of class C_i in D.

(b) If A_k is continuous-valued, then we need to do a bit more work, but the calculation is pretty straightforward. A continuous-valued attribute is typically assumed to have a Gaussian distribution with a mean μ and standard deviation σ, defined by

$$g(x, \mu, \sigma) = \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{(x-\mu)^2}{2\sigma^2}}, \tag{8.13}$$

so that

$$P(x_k|C_i) = g(x_k, \mu_{C_i}, \sigma_{C_i}). \tag{8.14}$$

These equations may appear daunting, but hold on! We need to compute μ_{C_i} and σ_{C_i}, which are the mean (i.e., average) and standard deviation, respectively, of the values of attribute A_k for training tuples of class C_i. We then plug these two quantities into Eq. (8.13), together with x_k, to estimate $P(x_k|C_i)$.

For example, let $\boldsymbol{X} = (35, \$40{,}000)$, where A_1 and A_2 are the attributes *age* and *income*, respectively. Let the class label attribute be *buys_computer*. The associated class label for $\boldsymbol{X}$ is *yes* (i.e., *buys_computer* = *yes*). Let's suppose that *age* has not been discretized and therefore exists as a continuous-valued attribute. Suppose that from the training set, we find that customers in D who buy a computer are

38 ± 12 years of age. In other words, for attribute *age* and this class, we have $\mu = 38$ years and $\sigma = 12$. We can plug these quantities, along with $x_1 = 35$ for our tuple $\boldsymbol{X}$, into Eq. (8.13) to estimate $P(age = 35|buys\_computer = yes)$. For a quick review of mean and standard deviation calculations, please see Section 2.2.

5. To predict the class label of $\boldsymbol{X}$, $P(\boldsymbol{X}|C_i)P(C_i)$ is evaluated for each class C_i. The classifier predicts that the class label of tuple $\boldsymbol{X}$ is the class C_i if and only if

$$P(\boldsymbol{X}|C_i)P(C_i) > P(\boldsymbol{X}|C_j)P(C_j) \quad \text{for } 1 \le j \le m, j \ne i. \tag{8.15}$$

In other words, the predicted class label is the class C_i for which $P(\boldsymbol{X}|C_i)P(C_i)$ is the maximum.

Algorithms/Process for Data Mining Lab

Algorithm: Sequential covering. Learn a set of IF-THEN rules for classification.

Input:

- *D*, a data set of class-labeled tuples;
- *Att_vals*, the set of all attributes and their possible values.

Output: A set of IF-THEN rules.

Method:

```
(1)  Rule_set = {}; // initial set of rules learned is empty
(2)  for each class c do
(3)      repeat
(4)          Rule = Learn_One_Rule(D, Att_vals, c);
(5)          remove tuples covered by Rule from D;
(6)          Rule_set = Rule_set + Rule; // add new rule to rule set
(7)      until terminating condition;
(8)  endfor
(9)  return Rule_Set;
```

Basic sequential covering algorithm.

Algorithms/Process for Data Mining Lab

Algorithm: Bagging. The bagging algorithm—create an ensemble of classification models for a learning scheme where each model gives an equally weighted prediction.

Input:

- D, a set of d training tuples;
- k, the number of models in the ensemble;
- a classification learning scheme (decision tree algorithm, naïve Bayesian, etc.).

Output: The ensemble—a composite model, $M*$.

Method:

(1) **for** $i = 1$ to k **do** // create k models:
(2) create bootstrap sample, D_i, by sampling D with replacement;
(3) use D_i and the learning scheme to derive a model, M_i;
(4) **endfor**

To use the ensemble to classify a tuple, X:

let each of the k models classify X and return the majority vote;

Bagging.

Algorithms/Process for Data Mining Lab

Algorithm: AdaBoost. A boosting algorithm—create an ensemble of classifiers. Each one gives a weighted vote.

Input:

- D, a set of d class-labeled training tuples;
- k, the number of rounds (one classifier is generated per round);
- a classification learning scheme.

Output: A composite model.

Method:

(1) initialize the weight of each tuple in D to $1/d$;
(2) **for** $i = 1$ to k **do** // for each round:
(3) sample D with replacement according to the tuple weights to obtain D_i;
(4) use training set D_i to derive a model, M_i;
(5) compute $error(M_i)$, the error rate of M_i (Eq. 8.34)
(6) **if** $error(M_i) > 0.5$ **then**
(7) go back to step 3 and try again;
(8) **endif**
(9) **for** each tuple in D_i that was correctly classified **do**
(10) multiply the weight of the tuple by $error(M_i)/(1 - error(M_i))$; // update weights
(11) normalize the weight of each tuple;
(12) **endfor**

To use the ensemble to classify tuple, X:

(1) initialize weight of each class to 0;
(2) **for** $i = 1$ to k **do** // for each classifier:
(3) $w_i = log\frac{1-error(M_i)}{error(M_i)}$; // weight of the classifier's vote
(4) $c = M_i(\boldsymbol{X})$; // get class prediction for $\boldsymbol{X}$ from M_i
(5) add w_i to weight for class c
(6) **endfor**
(7) return the class with the largest weight;

AdaBoost, a boosting algorithm.

Algorithms/Process for Data Mining Lab

Random Forest

Forest-RI

- A training set, *D*, of *d* tuples is given.
- The general procedure to generate *k* decision trees for the ensemble is as follows. For each iteration, *i* .*i* D 1, 2, : : : , *k*), a training set, *Di* , of *d* tuples is sampled with replacement from *D*.
- That is, each *Di* is a bootstrap sample of *D*, so that some tuples may occur more than once in *Di* , while others may be excluded.
- Let *F* be the number of attributes to be used to determine the split at each node, where *F* is much smaller than the number of available attributes.
- To construct a decision tree classifier, *Mi* , randomly select, at each node, *F* attributes as candidates for the split at the node. The CART methodology is used to grow the trees.
- The trees are grown to maximum size and are not pruned.
- Random forests formed this way, with *random input selection*, are called Forest-RI.

Forest-RC

- Another form of random forest, called Forest-RC, uses *random linear combinations* of the input attributes.
- Instead of randomly selecting a subset of the attributes, it creates new attributes (or features) that are a linear combination of the existing attributes.
- That is, an attribute is generated by specifying *L*, the number of original attributes to be combined.
- At a given node, *L* attributes are randomly selected and added together with coefficients that are uniform random numbers on [-1, 1].
- *F* linear combinations are generated, and a search is made over these for the best split. This form of random forest is useful when there are only a few attributes available, so as to reduce the correlation between individual classifiers.

Algorithms/Process for Data Mining Lab

K-NN

- The training tuples are described by *n* attributes.
- Each tuple represents a point in an *n*-dimensional space.
- In this way, all the training tuples are stored in an *n*-dimensional pattern space.
- When given an unknown tuple, a ***k*-nearest-neighbor classifier** searches the pattern space for the *k* training tuples that are closest to the unknown tuple.
- These *k* training tuples are the *k* "nearest neighbors" of the unknown tuple.
- "Closeness" is defined in terms of a distance metric, such as Euclidean distance

  Euclidean distance between two points or tuples, say, $X_1 = (x_{11}, x_{12}, \ldots, x_{1n})$ and $X_2 = (x_{21}, x_{22}, \ldots, x_{2n})$, is

$$dist(X_1, X_2) = \sqrt{\sum_{i=1}^{n} (x_{1i} - x_{2i})^2}. \qquad (9.22)$$

- For nominal attributes, a simple method is to compare the corresponding value of the attribute in tuple ***X***1 with that in tuple ***X***2.
- If the two are identical (e.g., tuples ***X***1 and ***X***2 both have the color blue), then the difference between the two is taken as 0.
- If the two are different (e.g., tuple ***X***1 is blue but tuple ***X***2 is red), then the difference is considered to be 1.
- *Good value for k,* can be determined experimentally. Starting with *k* D 1, we use a test set to estimate the error rate of the classifier.
- This process can be repeated each time by incrementing *k* to allow for one more neighbor. The *k* value that gives the minimum error rate may be selected

Algorithms/Process for Data Mining Lab

Algorithm: *k*-means. The *k*-means algorithm for partitioning, where each cluster's center is represented by the mean value of the objects in the cluster.

Input:

- *k*: the number of clusters,
- *D*: a data set containing *n* objects.

Output: A set of *k* clusters.

Method:

(1) arbitrarily choose *k* objects from *D* as the initial cluster centers;
(2) **repeat**
(3) (re)assign each object to the cluster to which the object is the most similar, based on the mean value of the objects in the cluster;
(4) update the cluster means, that is, calculate the mean value of the objects for each cluster;
(5) **until** no change;

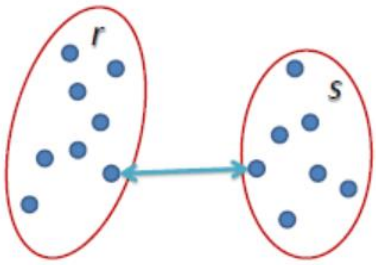
The *k*-means partitioning algorithm.

Hierarchical Clustering

- A **hierarchical clustering method** works by grouping data objects into a hierarchy or "tree" of clusters.
- Representing data objects in the form of a hierarchy is useful for data summarization and visualization.
- A hierarchical clustering method can be either *agglomerative* or *divisive*, depending on whether the hierarchical decomposition is formed in a bottom-up (merging) or topdown (splitting) fashion.
- An **agglomerative hierarchical clustering method** uses a bottom-up strategy.
- It typically starts by letting each object form its own cluster and iteratively merges clusters into larger and larger clusters, until all the objects are in a single cluster or certain termination conditions are satisfied.
- The single cluster becomes the hierarchy's root.
- For the merging step, it finds the two clusters that are closest to each other (according to some similarity measure), and combines the two to form one cluster.
- Because two clusters are merged per iteration, where each cluster contains at least one object, an agglomerative method requires at most *n* iterations.
- A **divisive hierarchical clustering method** employs a top-down strategy.

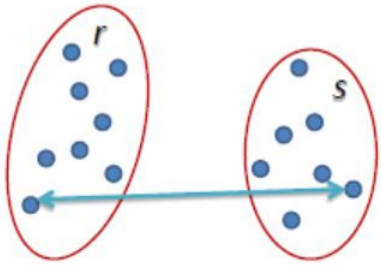
Algorithms/Process for Data Mining Lab

- It starts by placing all objects in one cluster, which is the hierarchy's root.
- It then divides the root cluster into several smaller subclusters, and recursively partitions those clusters into smaller ones.
- The partitioning process continues until each cluster at the lowest level is coherent enough—either containing only one object, or the objects within a cluster are sufficiently similar to each other.
- The following three methods differ in how the distance between each cluster is measured.
- Single Linkage: In single linkage hierarchical clustering, the distance between two clusters is defined as the shortest distance between two points in each cluster. For example, the distance between clusters "r" and "s" to the left is equal to the length of the arrow between their two closest points



$$L(r,s) = \min(D(x_{ri}, x_{sj}))$$

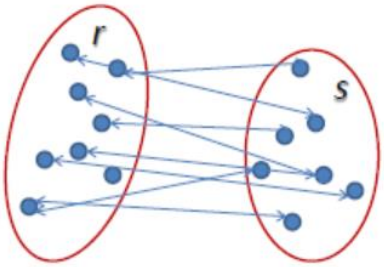
- Complete Linkage: In complete linkage hierarchical clustering, the distance between two clusters is defined as the longest distance between two points in each cluster. For example, the distance between clusters "r" and "s" to the left is equal to the length of the arrow between their two furthest points.



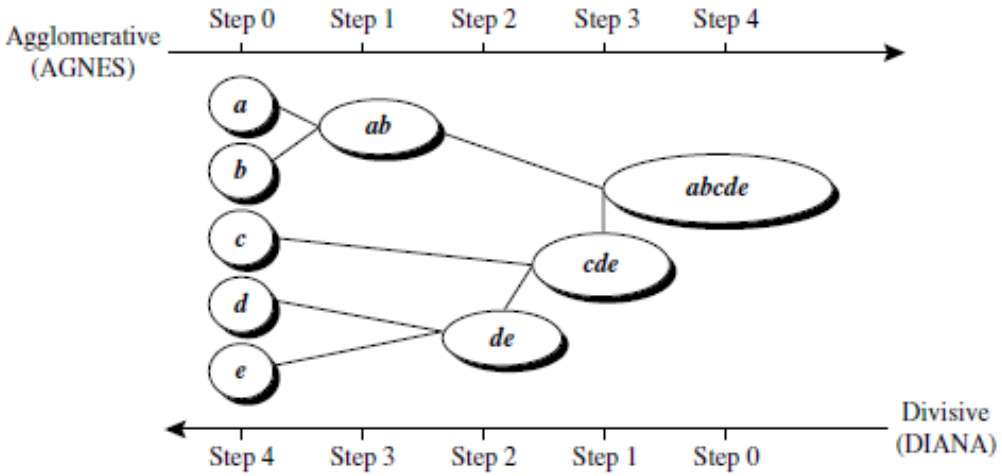
$$L(r,s) = \max(D(x_{ri}, x_{sj}))$$

- Average Linkage: In average linkage hierarchical clustering, the distance between two clusters is defined as the average distance between each point in one cluster to every point in the other cluster. For example, the distance between clusters "r" and "s" to the left is equal to the average length each arrow between connecting the points of one cluster to the other.

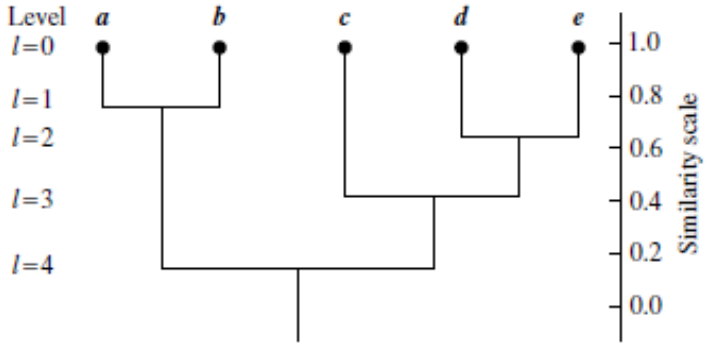
Algorithms/Process for Data Mining Lab



$$L(r,s) = \frac{1}{n_r n_s} \sum_{i=1}^{n_r} \sum_{j=1}^{n_s} D(x_{ri}, x_{sj})$$



Agglomerative and divisive hierarchical clustering on data objects $\{a, b, c, d, e\}$.



Dendrogram representation for hierarchical clustering of data objects $\{a, b, c, d, e\}$.

Algorithms/Process for Data Mining Lab

Algorithm: DBSCAN: a density-based clustering algorithm.

Input:

- *D*: a data set containing *n* objects,
- ϵ: the radius parameter, and
- *MinPts*: the neighborhood density threshold.

Output: A set of density-based clusters.

Method:

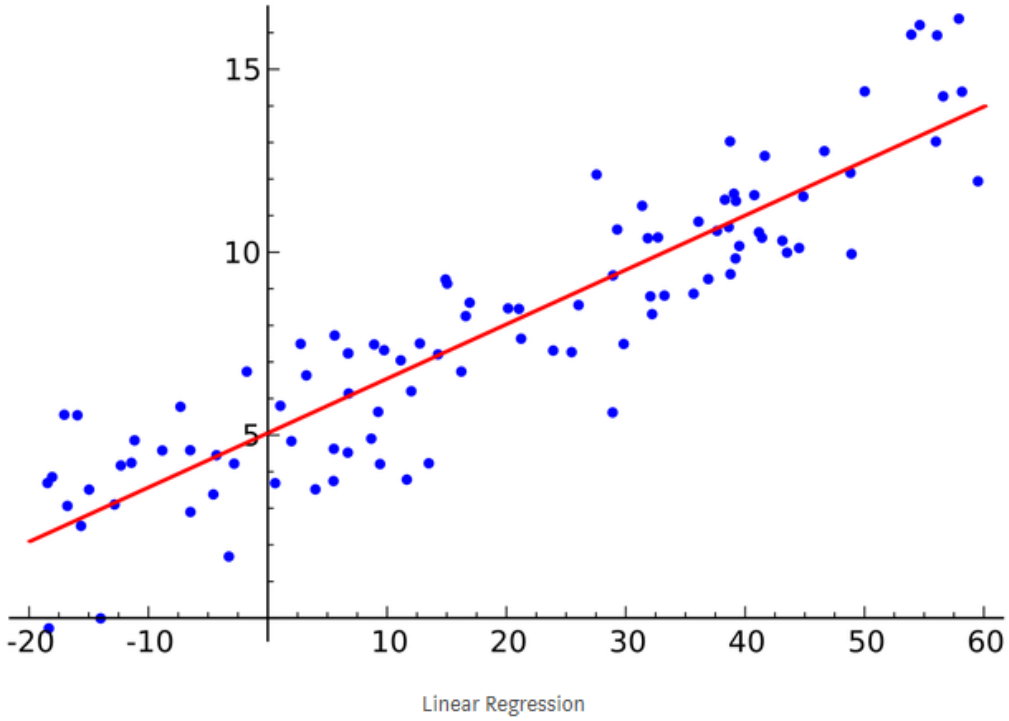
```
(1)  mark all objects as unvisited;
(2)  do
(3)      randomly select an unvisited object p;
(4)      mark p as visited;
(5)      if the ε-neighborhood of p has at least MinPts objects
(6)          create a new cluster C, and add p to C;
(7)          let N be the set of objects in the ε-neighborhood of p;
(8)          for each point p' in N
(9)              if p' is unvisited
(10)                 mark p' as visited;
(11)                 if the ε-neighborhood of p' has at least MinPts points,
                     add those points to N;
(12)             if p' is not yet a member of any cluster, add p' to C;
(13)         end for
(14)         output C;
(15)     else mark p as noise;
(16) until no object is unvisited;
```

DBSCAN algorithm.

Algorithms/Process for Data Mining Lab

Linear Regression

Regression is a method of modelling a target value based on independent predictors. This method is mostly used for forecasting and finding out cause and effect relationship between variables. Regression techniques mostly differ based on the number of independent variables and the type of relationship between the independent and dependent variables.



Linear Regression

Simple linear regression is a type of regression analysis where the number of independent variables is one and there is a linear relationship between the independent(x) and dependent(y) variable. The red line in the above graph is referred to as the best fit straight line. Based on the given data points, we try to plot a line that models the points the best. The line can be modelled based on the linear equation shown below.

y = a_0 + a_1 * x ## Linear Equation

The motive of the linear regression algorithm is to find the best values for a_0 and a_1. Before moving on to the algorithm, let's have a look at two important concepts you must know to better understand linear regression.

Cost Function

The cost function helps us to figure out the best possible values for a_0 and a_1 which would provide the best fit line for the data points. Since we want the best values for a_0 and a_1, we convert this search problem into a minimization problem where we would like to minimize the error between the predicted value and the actual value.

$$minimize \frac{1}{n} \sum_{i=1}^{n} (pred_i - y_i)^2$$

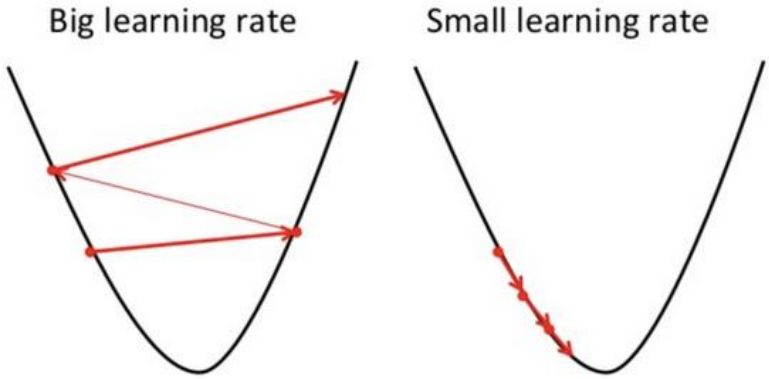
$$J = \frac{1}{n} \sum_{i=1}^{n} (pred_i - y_i)^2$$

Minimization and Cost Function

We choose the above function to minimize. The difference between the predicted values and ground truth measures the error difference. We square the error difference and sum over all data points and divide that value by the total number of data points. This provides the average squared error over all the data points. Therefore, this cost function is also known as the Mean Squared Error(MSE) function. Now, using this MSE function we are going to change the values of a_0 and a_1 such that the MSE value settles at the minima.

Gradient Descent

The next important concept needed to understand linear regression is gradient descent. Gradient descent is a method of updating a_0 and a_1 to reduce the cost function(MSE). The idea is that we start with some values for a_0 and a_1 and then we change these values iteratively to reduce the cost. Gradient descent helps us on how to change the values.



Gradient Descent

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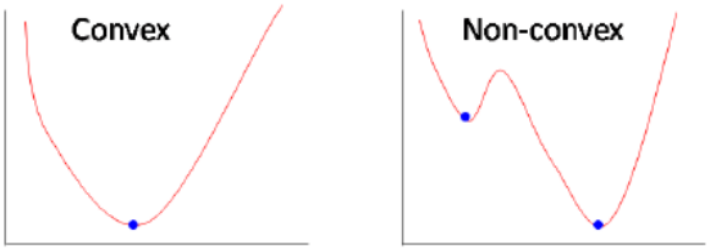
To draw an analogy, imagine a pit in the shape of U and you are standing at the topmost point in the pit and your objective is to reach the bottom of the pit. There is a catch, you can only take a discrete number of steps to reach the bottom. If you decide to take one step at a time you would

eventually reach the bottom of the pit but this would take a longer time. If you choose to take longer steps each time, you would reach sooner but, there is a chance that you could overshoot the bottom of the pit and not exactly at the bottom. In the gradient descent algorithm, the number of steps you take is the learning rate. This decides on how fast the algorithm converges to the minima.



Convex vs Non-convex function

Sometimes the cost function can be a non-convex function where you could settle at a local minima but for linear regression, it is always a convex function.

You may be wondering how to use gradient descent to update a_0 and a_1. To update a_0 and a_1, we take gradients from the cost function. To find these gradients, we take partial derivatives with respect to a_0 and a_1. Now, to understand how the partial derivatives are found below you would require some calculus but if you don't, it is alright. You can take it as it is.

$$J = \frac{1}{n}\sum_{i=1}^{n}(pred_i - y_i)^2$$

$$J = \frac{1}{n}\sum_{i=1}^{n}(a_0 + a_1 \cdot x_i - y_i)^2$$

$$\frac{\partial J}{\partial a_0} = \frac{2}{n}\sum_{i=1}^{n}(a_0 + a_1 \cdot x_i - y_i) \implies \frac{\partial J}{\partial a_0} = \frac{2}{n}\sum_{i=1}^{n}(pred_i - y_i)$$

$$\frac{\partial J}{\partial a_1} = \frac{2}{n}\sum_{i=1}^{n}(a_0 + a_1 \cdot x_i - y_i) \cdot x_i \implies \frac{\partial J}{\partial a_1} = \frac{2}{n}\sum_{i=1}^{n}(pred_i - y_i) \cdot x_i$$

$$a_0 = a_0 - \alpha \cdot \frac{2}{n}\sum_{i=1}^{n}(pred_i - y_i)$$

$$a_1 = a_1 - \alpha \cdot \frac{2}{n}\sum_{i=1}^{n}(pred_i - y_i) \cdot x_i$$

The partial derivates are the gradients and they are used to update the values of a_0 and a_1. Alpha is the learning rate which is a hyper parameter that you must specify. A smaller learning rate could get you closer to the minima but takes more time to reach the minima, a larger learning rate converges sooner but there is a chance that you could overshoot the minima.