Data Mining Part I: "Fast Algorithms for Mining Association Rules"

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(Thanks to previous student Dan Li for many of the slide points.)

The Problem: Discovering Associated Purchases

- You have a database of customer transactions
- You want to find out which products customers buy at the same time
- Store owners might use this info to:
 - Organizing items together in catalogs/flyers
 - Figure out best arrangement of products on the shelves
 - etc.

The Problem: Notation

- You have a set of items: A, B, C, D, ….
- > You have a set of transactions:
 - 1) {A, B, D}
 - 2) {B, C, D}
 - 3) {C, D, J, R, V}
 - 4) etc.
- You want to find association rules, e.g. {A, B} => {D, R}

Support & Confidence

- ► Consider a rule $\{A, B\} => \{D, R\}$
- ▶ The <u>support</u> s is for this rule is:
 - The percentage of transactions that contain {A, B, D, R}
- ▶ The <u>confidence</u> c for this rule is:
 - The percentage of transactions containing {A, B} that also contain {D, R}
- Sets with support > s are called <u>large</u> sets

The Problem

- Given a list of transactions
- Find all rules with support > s and confidence > c

Discussion

- When generating association rules, we can set a desired support level and a desired confidence level.
- What considerations are necessary when setting values for both?
- For what applications would you choose a high confidence value? A high support value?

Important Observation about "Support"

- If a set X has support > s, then every subset of X has support > s
- ► Example:
 - Suppose there are 3 large items in the transaction list: {A}, {B}, {C}
 - Only possible sets of size 2 are {A, B}, {A, C}, {B, C}
 - Only possible set of size 3 is {A, B, C}

Problem Decomposition

- ▶ Paper breaks the problem into 2 parts:
 - Part 1:
 - Find: All sets with support > s
- Part 2:
 - ► Given solution to Part 1
 - \blacktriangleright Find all rules with support > s and confidence > c
- ► This paper solves Part 1 only.
 - But Part 2 is much easier than Part 1.





Basic outline is easy to understand. The hard part is generating "candidates" (apriori-gen)

Generating Candidate Sets: apriori-gen

insert into C_k

select $p.item_1$, $p.item_2$, ..., $p.item_{k-1}$, $q.item_{k-1}$ from L_{k-1} p, L_{k-1} qwhere $p.item_1 = q.item_1$, ..., $p.item_{k-2} = q.item_{k-2}$, $p.item_{k-1} < q.item_{k-1}$;

To make a candidate of size k, join two large sets of size (k - 1) which differ only in their last element

"But why?", you ask.

Explanation of apriori-gen

Suppose you want to generate C₃ from



 \blacktriangleright Could generate C_3 by combining each set from L_1 with each set from L_2

▶ e.g. {A, B} U {D} = {A, B, D}

▶ However, notice that in order for {A, B, D} to be large, {A, D} must also be large.

Explanation of apriori-gen

In general, suppose we have a set

 $\mathsf{a} = \{\mathsf{i}_1,\,\mathsf{i}_2,\,...,\,\mathsf{i}_{k\text{-}1}\}$

and we extend it with an item X:

a' cannot be large unless $\{i_1, i_2, ..., i_{k-2}, X\}$ is large.

Therefore, generate candidates of size k by merging all pairs $\{i_1, i_2, ..., i_{k-2}, X\}$ and $\{i_1, i_2, ..., i_{k-2}, Y\}$ from L_{k-1} .

Apriori-gen: The Prune Step

- Look at each candidate of size k generated by the join
- Check that each subset of size k-1 is large (if not, throw it away)

Apriori Algorithm: Example

Suppose the user specifies a minimum support of 20% and we have the transaction table:

TID	Itemset
1	{A, C, D, E}
2	{A, B, C}
3	{B, C, E}
4	{A, B, D, E}
5	{C, E}

Since there are 5 transactions, support of 20% means 2 or more occurrences.













Discussion

- This paper has spun off more similar algorithms in the database world than any other data mining algorithm.
- Why do you think this paper is so influential?:
 - Is it the context of association rule mining?
 - The way they approach the problem?
 - The algorithm itself?
 - Its performance?

Data Mining Part II: "BIRCH: An Efficient Data Clustering Method for Very Large Databases"

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(Thanks to previous student Joel Lanir for many of the slide points.)

What is Data Clustering?

► You are given:

- n points in d-dimensional space
- a distance function f(a,b)
- a desired number of clusters, k
- ► You want to find:
 - a partitioning that minimizes the "size" of the clusters
 - several ways to measure "size" (e.g. average distance between pairs of points in a cluster)

Clustering Application: Detecting Objects in An Image



Discussion

- The BIRCH paper gave the example of clustering 2D image features into five clusters.
- Can you think of other large datasets where discovering clusters would be useful? What constraints does this data pose on the resources required?

The Goal of the BIRCH Algorithm

- Efficient clustering of large datasets (larger than memory, that is)
- Minimize disk I/O's
- BIRCH can be seen as a "helper" algorithm enables standard clustering algorithms to run on very large datasets

Advantages of BIRCH vs. Other Clustering Algorithms

- 1) It is "local".
 - i.e. each time a new point is added, it is only compared against a subset of the other points in the dataset
- 2) There is a mechanism for removing outliers.
- BIRCH minimizes I/O costs. Also, adjusts the quality of results to the amount of available memory.
- 4) It only scans the dataset once (If phase 4 is omitted).

Clustering Feature (CF)

- Compact no need to store the individual points belonging to a cluster.
- Three parts:
 - N, the number of points in the cluster
 - LS, the sum of the points in the cluster
 - SS, the sum of the points squared
- This info is sufficient to compute the distance between two clusters
- When merging two clusters, can just add CFs

CF TREE

- ▶ The CF Tree is a hierarchy of clusters
- Each node contains a list of CFs
- T is the threshold for the <u>diameter</u> of the leaf nodes
- Data items are scanned and inserted into the CF tree, one at a time.

CF Tree Insertion

- ► To identify the appropriate leaf:
 - Starting with CF list at the root node, find the closest cluster (by using the CF values)
 - Look at all the children of this cluster, find the closest.
 - And so on, until you reach a leaf node.
- Once the point has been added, must update the CF of all ancestors
- Leaves have a max size, so they must sometimes must be split

The BIRCH Algorithm: 4 Phases

- > Phase 1: Scan all data and build an initial inmemory CF tree.
- **Phase 2**: Shrink the tree as required for Phase 3.
- > Phase 3: Run a standard ("global") clustering algorithm on the leaf clusters.
- > Phase 4: Reassign individual data points to the clusters.

BIRCH Phase 1

- Start with initial threshold T and insert points into the tree
- If we run out of memory, increase T, and rebuild Take leaf entries from original tree and re-insert into new tree This is an opportunity to remove outliers
- Methods for initializing and adjusting T are ad hoc
- Important Point:
 - After Phase 1, the data has been "shrunk" to fit in memory.
 - Subsequent phases of processing happen entirely in memory (no disk I/Os)

BIRCH Phase 2

- ► Optional.
- Number of clusters produced in Phase 1 may be larger than Phase 3 can handle.
- ▶ Shrink tree as necessary.

BIRCH Phase 3

- ► Use the leaf nodes of the CF tree as input to a standard ("global") clustering algorithm.
- ▶ Phase 1 has reduced the size of the input dataset enough so that the standard algorithm can work entirely in memory.

BIRCH Phase 4

- ▶ Optional.
- Scan through the data again, assign each data point to a cluster
 - Choose the cluster whose centroid is closest.
- This redistributes the points among clusters, in a more accurate fashion than the original CF tree

Discussion

- If you had to design a data mining algorithm for your data, which of the following criteria would you consider most important?
 - Average running time?
 - I/O cost?
 - Memory efficiency?Scalability?

 - Robustness to noise?
 - Parameter tuning?
- What are the trade-offs between your choice and the other factors? How much accuracy are you willing to sacrifice?

Applications of Data Clustering

- Helps understand the natural groupings that exist inside a dataset.
- ► Examples:
 - Market analysis: determining groups of customers with similar tastes
 - Bioinformatics: determining groups of molecules with similar functions in the cell
 - Insurance: identifying high-risk groups of policy holders