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Association Rules Patterns Discovery From Mixed Data

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ASSOCIATION RULES PATTERNS DISCOVERY FROM MIXED DATA

by

WELENDAWA ACHARIGE CHARITH AKANANKA ELSON

(Under the Direction of Ionut Iacob)

ABSTRACT

Finding Association Rules has been a popular unsupervised learning technique for discovering interesting patterns in commercial data for well over two decades. The method seeks groups of data attributes and their values where their probability density of these attributes at the respective values is maximized. There are currently well-established methods for tackling this problem for data with categorical (discrete) attributes. However, for the cases of data with continuous variables, the techniques are largely focusing on categorizing continuous variables into intervals of interest and then relying on the categorical data methods to address the problem. We address the problem of finding association rules patterns in mixed data by using another unsupervised learning technique, clustering. The data attributes are organized into categorical and continuous attributes groups, and then we find the association rules patterns among attributes in each group that would satisfy the required probability density thresholds. We have implemented and tested our method, which produces very good results when used on real, mixed data.

INDEX WORDS: Frequent itemsets, Association rules, Clustering 2009 Mathematics Subject Classification: 15A15, 41A10, 68W99,62H30

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DEDICATION

This thesis is dedicated to my beautiful wife Ama Waidyarathna "The Love of my life" and my loving parents and brother.

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- ∩ Intersection
- ∪ Union
- ∈ An element of a set
- ⊂ A subset of a set
- $\|\|$ Norm
- || Cardinality

CHAPTER 1

INTRODUCTION

Association rules, a popular unsupervised learning method that has been around for almost two decades, is utilized in determining patterns in sales transactions in most salesbased databases. In these databases, you find the transactions with some values under different variables with high probabilities. For two sets of values, A and B, an association rule is defined as $A \Rightarrow B$. A is called the "antecedent" and B is called the "consequent" of the association rule. The probability calculations are done using two definitions named "support" and "confidence." The "support" for the given rule $A \Rightarrow B$, is the probability of the union of A or B, $P(A \cup B)$ and the "confidence" is the conditional probability of $P(A|B)$.

Clustering is another unsupervised learning method used to cluster data items with similar attributes. There are several popular methods for clustering such as K-means and hierarchical clustering. ClustOfVar, in Chavent et al, [5], is a package in R introduced for clustering variables instead of the data items.

In this study, we have proposed a novel method in which variable clustering is used to determine the association rules for both qualitative and quantitative variables. We started from the clustering with qualitative data, subsequently, we have extended the method for quantitative data as well. We have managed to establish an unbelievable relationship between distance measure in clusters and the confidence of the association rules, and the result was used to determine whether association rules have the desired confidence.

Since we could not identify an appropriate distance function for all types of variables, which relates to the confidence measure of the association rules, our method cannot find all possible association rules that include continuous variables since there could be a very large set of data to choose from. We believe addressing the above issue would be a good direction to further this study.

Our method will be a great contribution to the field of data mining, which is also known as the knowledge discovery of databases in which they look for useful patterns in databases to improve the efficiency and the effectiveness of the operation. Some of the fields that use data mining are banking, medicine, and entertainment such as Netflix.

CHAPTER 2

ASSOCIATION RULES

2.1 ASSOCIATION RULE MINING

Association rules have been a popular tool used in businesses. Association rules can provide valuable information such as 60% of people who buy comprehensive motor insurance also buy health insurance; 80% of those who buy music online, also buy books online. There is a diverse number of areas that employ association rules. A few of them are credit card transactions to study the transactions and predict what customer is likely to purchase; medical patient histories to detect increased risks of further complications using their past medical data.

Customer	Purchases
	Tiling Cement; Tiles
	Paint; White Spirit
3	Paint; Wallpaper; Plaster
	Paint; Plaster; Tiling Cement; Tiles

Table 2.1: Purchase data for some customers

The basic objective of the association rules is to find the variables, $X = (X_1, X_2, X_3, \ldots, X_p)$, appearing mostly in the database. This is often used in a binary sense where the presence or absence of the variable is considered, that is $X_j \in \{0, 1\}$. This is known as "market" basket analysis," since the observations are supermarket sales. x_{ij} , j^{th} item of the i^{th} transaction, is assigned 1 or 0 based on whether it was in the sale or not. Table 2.1 consists of items purchased by a customer at a supermarket. The original data in Table 2.1 can be transformed into binary format to do further analysis as showing in Table 2.2 .

The idea of association rules is to find a collection of values, $v_1, v_2, ...v_L$ for X, whose probability of occurring, $P(v_l)$ for $l = 1, 2,...L$ is relatively high. But this probability will

Customer $ $	Tiling Cement Tiles Paint White Spirit Wallpaper Plaster			
		Ω		
		Ω		

Table 2.2: Binary converted data of Table 2.1

nearly be too small for a reliable estimation when there are many variables and many values under each variable are present.

Therefore instead of finding single values with high probabilities, it makes more sense to find regions of X-space with high probabilities. Let S_j be the set of all possible values of the j^{th} variable (its support, which will be defined later), let $s_j \subset S_j$, a subset of all possible values. Now, finding association rules can be stated as finding subsets of variable values $s_1, \ldots s_p$ such that probability of each variable taking the values of its respective subset at the same time,

$$
P\left[\bigcap_{i=1}^{p} (X_j \in s_j)\right] \tag{2.1}
$$

is relatively higher, Friedman et al, [9]. The intersection of subsets \bigcap p $i=1$ $(X_j \in s_j)$ is referred to as a conjunctive rule. For qualitative variables, the subsets are a list of nominal values and for quantitative variables, subsets are contiguous intervals. If the subset happens to be the whole set of values ($s_j = S_j$), X_j won't appear in the rule.

2.2 MARKET BASKET ANALYSIS

The probability calculated in (2.1) is not feasible for very large databases. Therefore to simplify (2.1) further, only two types of subsets are considered. Either s_j is a single

value of X_j , v_{0j} , or the entire set of values of S_j . Hence (2.1) is simplified as

$$
P\left[\bigcap_{j\in J} (X_j = v_{0j})\right]
$$
\n(2.2)

Let K be the number of all the values in all j variables. Therefore

$$
K = \sum_{j=1}^{p} |S_j|
$$
 (2.3)

where $|S_j|$ is the number of distinct values in X_j . To indicate whether a certain value was present or not in a transaction, new K binary variables, $Z_1, Z_2,...Z_K$ are introduced. This transforms (2.2) into finding a subset of integers $\kappa \subset 1, 2, ..., K$, making the probability,

$$
P\left[\bigcap_{k\in\kappa}(Z_k=1)\right] = P\left[\prod_{k\in\kappa}(Z_k=1)\right]
$$
\n(2.4)

high, Friedman et al, [9]. (2.4) gives the standard formulation of the market basket problem. From the items in \bigcup p $i=1$ S_j , a set of items that κ refers to, is called an "item set." The number of dummy variables in the item set is called its "size." (This is supposed to be less than p). (2.4) can be estimated by taking the proportion of observations that satisfy (2.5).

$$
\hat{P}\left[\prod_{k\in\kappa}(Z_k=1)\right] = \frac{1}{N}\sum_{i=1}^N\prod_{k\in\kappa}(Z_k=1)
$$
\n(2.5)

 Z_{ik} is the value of Z_k for the i^{th} case.

This is referred to as "Support" (a proper definition is provided later in the chapter), $T(\kappa)$ of the item set κ . An observation i is said to contain the item set K if z_{ik} is 1 for all k in κ .

In the mining of association rules, a bound for support is specified and all items sets K_l that can be formed from the dummy variables Z_1, Z_2, \ldots, Z_k is sought.

$$
\{K_l|T(K_l)>t\}\tag{2.6}
$$

2.3 ALGORITHMS

The threshold t is adjusted so that (2.6) consists of only a small number of a fraction of all 2^K possible item sets. Agrawal et al, [2] introduce the "Apriori" algorithm to address (2.6). The algorithm computes the supports for all single item sets and removes the ones with support less than the threshold, t. The second pass takes the items of two with the ones that are already chosen in the previous pass and ones with the supports less than the threshold are removed. This process continues until the highest number of items with a support less than the threshold are selected.

Definition 2.1. *To speed up the process and the convergence, the set of items with higher support,* κ*, returned by the Apriori algorithm is selected into two disjoint subsets, A and B. Therefore,* κ *can be written as* $\kappa = A \cup B$ *, and defined as an "association rule" and indicated as* $A \Rightarrow B$ *. The items on left, A is called "antecedent" and the items on right, B is called "consequent."*

Definition 2.2. *The proportion of observations that are the union of A and B is defined to be the "support" of the association rule* $A \Rightarrow B$ *.* $T(A \Rightarrow B)$ *is used for the support of* $A \Rightarrow B$.

This is as same as the support derived from the item set κ . In other words, it is the probability of observing $A \cup B$ in data items.

Definition 2.3. *The "confidence" of the association rule* $A \Rightarrow B$, $C(A \Rightarrow B)$ *is defined by the ratio between the support of* $A \Rightarrow B$, $T(A \Rightarrow B)$ *, and the support of* A, $T(A)$ *.*

$$
C(A \Rightarrow B) = \frac{T(A \Rightarrow B)}{T(A)}
$$
\n(2.7)

This can also be interpreted as $P(B|A)$. "Expected Confidence" is defined as the support of the consequent $T(B)$, which can be estimated with $P(B)$.

For an example, consider the rule $\{Paint\} \Rightarrow \{White \, Spirit\}$ for item set $\kappa =$ {P aint, T iling Cement, T iles, W hite Spirit, W allpaper, Plaster}. Support is calculated to be .25, suggesting $\{ Paint, White Spirit\}$ appears in 25% of the observations. The confidence is calculated to be .67, suggesting when $Paint$ was purchased, 67% of the time $White$ Spirit was purchased as well.

In association rules finding, the goal is to find the rules with supports and confidences with their corresponding thresholds, t, and c. Eventually, there will be association rules that satisfy the conditions $T(A \Rightarrow B) > t$ and $C(A \Rightarrow B) > c$.

So far, association rule mining was for qualitative variables, transformed into boolean dummy variables, that is, it only indicated whether an item was present or not in a transaction. Databases could have qualitative and quantitative attributes in other domains. In Srikant et al, [21] addressed the problem of quantitative association rule by fine partitioning the quantitative attribute and combining adjacent partitions as needed. In this, they introduced a measure of partial completeness to measure the information lost due to partitioning. This measure helps the user decide whether or not to partition. The possibility of this method generating too many similar rules is addressed by using an interesting measure "greater-than-expected-value" to identify the interesting rules in the output.

In Aumann et al, [3], an approach was introduced with algorithms involving two specific types, which are qualitative to quantitative and vice versa with a single attribute on the left-hand side. The right-hand side has the distribution properties of the quantitative variable. Yoda et al, [25] introduced some optimization-based approach in which a new measure named "gain" was introduced. Extensions to the method in Yoda et al, [25] were introduced in Brin et al, [4], but the rules were limited to one or two attributes. Mata et al, [18] proposed an algorithm to optimize the support of item sets on uninstantiated intervals on numeric attributes.

In Salleb-Aouissi, [19], QuantMiner, an algorithm capable of handling both qualitative

and quantitative algorithms while optimizing the quantitative attributes to mine association rule, was introduced. QuantMiner is focused on maximizing the gain of an association rule and it penalizes the variables with large intervals.

2.4 CURRENT WORK

In this work, we establish a surprising connection between the confidence of association rules and Jaccard similarity, a popular similarity/dissimilarity measure, to be used on the clustered variables (unlike the traditional observations clustering) to determine association rules of data with mixed variables. Firstly, we develop our method for binary and categorical variables and then extend it to mixed variables.

CHAPTER 3

CLUSTERING

Cluster analysis is the process of separating a collection of observations into groups called "clusters" in such a way that objects in the cluster are related to one another than the objects in different clusters. For this, values of the variables of the objects are used as characteristics and these characteristics are used to cluster the variables.

Cluster analysis is used to determine whether or not objects can be placed into subgroups that have substantially different properties. The second objective needs an assessment of the degree difference between the objects assigned to respective clusters.

There are two ways data can be grouped into clusters as hard and soft clustering.

Definition 3.1. *In hard clustering, each data point either belongs to a cluster completely or not.*

Definition 3.2. *In soft clustering, instead of putting a data point into a separate cluster, a data point is assigned to a distribution over all clusters. This way a data point has a fractional membership in several clusters.*

An important measure with cluster analysis is the degree of similarity between the objects in clusters. Any clustering method uses some definition of similarity to figure out what clusters the objects belong to. Similarities or dissimilarities (lack of similarity) can be represented in a form of $N*N$ matrix with (i, i') entry giving the similarity/dissimilarity between i^{th} and i'^{th} observations, where $i, i' \in \{1, 2, \dots N\}$.

3.1 MEASURE THE DISTANCE BETWEEN TWO CLUSTERS

There are a few strategies to measure the distance between clusters.

• Single

This method takes the shortest distance between an item in one cluster and an item

in the other cluster. This tends to produce elongated clusters or chains (similar items because of their similarity with intermediate items)

• Complete

In this, the minimum longest distance between an item in one cluster and an item in the other cluster is considered. The method tends to join clusters with the approximately same diameter, producing compact clusters.

• Average

This method uses the shortest average of distances between all pairs of items in two clusters. This is very sensitive to outliers and it tends to join clusters with small variances.

• Centroid

The mean of all data items in each cluster is computed and called the centroid. Then the minimum distances between centroids are used. This is relatively easy to understand and to be used.

• Ward

The minimum sum of squares of differences between the items in the two clusters is calculated for this. This puts together clusters with a roughly equal number of components and this method is sensitive to outliers.

3.2 K-MEANS CLUSTERING

K-means algorithm is one of the most popular clustering methods. It is used for all quantitative variables scenarios. Let x_{ij} be a data point from j^{th} variable (attribute) and i^{th} observation, where $i = 1, 2,...N$ and $j = 1, 2..., p$. A dissimilarity measure used is the Euclidean distance between i^{th} and i'^{th} observations is given by

$$
d(x_i, x_{i'}) = \sum_{j=1}^{p} (x_{ij} - x_{i'j})^2 = ||x_i - x_{i'}||^2
$$
\n(3.1)

At the beginning of the algorithm, assign each observation to the cluster with the nearest centroid mean, which is with the least squared Euclidean distance. In the next step, recalculate the centroid means for a cluster of observations in each cluster. The process will continue until the assignments won't change.

K- means algorithm was used on the data in Table 3.1.

Table 3.1: Sample dataset

The distance matrix for the sample data was calculated.

K was specified to be three and the cluster diagram in Figure 3.1 was generated.

3.3 HIERARCHICAL CLUSTERING

The initial configuration assignment and the number of clusters specified for the Kmeans clustering algorithm affects the results of the K-means algorithm, whereas hierarchical clustering only requires the user to specify a measure of dissimilarity between groups of observations, that is based on pairwise dissimilarities among the observations in the two groups. The clusters at a lower level merge themselves to create a cluster at a higher level, hence it has the name hierarchical clustering.

				Alex Bruce Chris Don Emil Fred		
Alex 0						
	Bruce .83333 0					
	Chris .83333 .8	$\overline{0}$				
		Don .4 .83333 .6	\sim 0			
			Emil .33333 .5 .71428 .33333 0			
Fred .6	$\overline{8}$		$\overline{5}$.83333 .83333 0	

Table 3.2: Sample distance matrix for the sample data

There are two main types of hierarchical clustering, Agglomerative (bottom-up) and Divisive (top-down). Agglomerative strategies begin from the bottom at every level some two clusters with the smallest dissimilarity are merged to form one cluster. As it gets to a higher level, the number of clusters reduces by one. The agglomerative method starts by considering all the observations as one big cluster and that splits into two clusters with the largest dissimilarity between those two groups. Eventually, there will be $N - 1$ level in the hierarchy.

A dendrogram is a graphical diagram that provides a highly interpret-able description of hierarchical clustering and this is one of the reasons hierarchical clustering is popular.

The data in Table 3.1 were clustered using hierarchical clustering. The dendrogram is shown in Figure 3.3.

3.4 CLUSTERING OF VARIABLES

Principal Component Analysis (PCA) and Multiple Correspondence Analysis (MCA) are two statistical tools used in multivariate data analysis for quantitative and qualitative variables respectively. As an alternative to PCA and MCA, the clustering of variables, even though cluster analysis was originally meant for clustering objects, can also be used to

Component 1 These two components explain 73.74 % of the point variability.

Figure 3.1: K-means clustering when K=3 for the data in Table 3.1

cluster variables into groups so that the meaningful structures can be derived. Variables that cluster together can be assumed to be strongly related to each other in a general perspective. Therefore when the variables are clustered together, selecting one variable from each group may be sufficient for carrying out the analysis. Perhaps one variable selected from each group could be synthetic for certain cases.

For clustering a set of variables, a common approach is to calculate the dissimilarity matrix between the variables and to apply a classical cluster analysis method used for clustering observations to the dissimilarity matrix. The functions in R to facilitate this are *hclust* from the package stats, introduced by Takeuchi et al, [22] and *agnes* from the package cluster, introduced by Maecheler et al, [17]. The type of dissimilarity matrix changes depending upon the fact whether variables are qualitative or quantitative. For qualitative variables, many measures can be used such as correlation coefficients (parametric or nonparametric) and as for qualitative variables measures such as Chi-squared, Rand, Belson, etc can be used. There are strategies to be used if the practitioner is not sure what measure

Figure 3.2: Hierarchical clustering for the data in 3.1

is to be used.

In the above methods, classical methods of clustering observations were transformed into the clustering of variables. There are also methods for directly clustering variables. VARCLUS in Sarle, W, S, [20] is such a tool developed by the SAS institute. Clustering around latent variables (CLV), a method based on PCA, and Diametrical clustering were introduced in Vigneau et al, [23], and Dhillon et al, [7] respectively. These methods are not implemented in other platforms than in R and they only work for quantitative variables.

A package for clustering of a mixture of both qualitative and quantitative variables has been introduced in R named ClustOfVar by Chavent et al, [5]. This also works excursively on qualitative or quantitative variables. In the package, two methods are proposed for clustering variables, a hierarchical clustering based algorithm and K-means based algorithm, which are used in functions *hclustvar* and *kmeansvar* respectively. These methods use PCAMIX, a PCA-based method for a mixture of qualitative and quantitative variables in Kiers et al, [13]. The ordinary PCA and MCA are two special cases that fall under

PCAMIX. A Singular Value Decomposition was performed on PCAMIX in Chavent et al, [6]. The clustering criterion they used is that variables were considered to be homogeneous when they have a strong relationship with a quantitative synthetic variable. The squared Pearson correlation and correlation ratio were used for quantitative and qualitative variables respectively.

Let $\{X_1, X_2,...X_{p_1}\}$ be a set of p_1 quantitative variables and $\{Y_1, Y_2,...Y_{p_2}\}$ a set of p_2 qualitative variables. Let X and Y be the corresponding quantitative and qualitative matrices of dimensions $n * p_1$ and $n * p_2$, where n is the number of observations. Let's denote $x_j \in R^n$ the j^{th} column of X and $y_j \in M^n$ the j^{th} column of Y with M the set of categories of y_j . Let $P_k = (C_1, \ldots C_K)$ be a partition into K clusters of the $p = p_1 + p_2$ variables.

The synthetic variable of a cluster C_k is $c_k \in \mathbb{R}^n$ is defined to be the "most linked" to all the variables in C_k .

$$
c_k = \arg \max_{u \in R^n} \left\{ \sum_{x_j \in C_k} r_{u,x_j}^2 + \sum_{y_j \in C_k} \eta_{u|y_j} \right\}
$$
(3.2)

where r^2 denotes the squared Pearson correlation and $\eta_{u|y_j}^2 \in [0,1]$ measures the part of the variance measured by the categories of y_j

$$
\eta_{u|y_j} = \frac{\sum_{s \in M_j} n_s(\bar{u}_s - \bar{u})}{\sum_{i=1}^n (u_i - \bar{u})^2}
$$
(3.3)

where n_s is the frequency of category s, \bar{u}_s is the mean values of u calculated on the observations belonging to category s and \bar{u} is the mean of u.

The qualitative synthetic variable of a cluster is that when the first principal component when PCAMIX applied to all the variables in the cluster. These central synthetic variables are helpful in terms of reducing the dimension of the data. Further to clustering variables, the method is capable of evaluating the stability of the partition of variables and determining the number of clusters using the stability function.

CHAPTER 4

FINDING ASSOCIATION RULES OF MIXED TYPE DATA USING CLUSTERING OF VARIABLES

In this chapter, we present our association rule mining method of mixed data, based on the clustering of data variables and subsequently inferring interesting association rulesbased on the clusters, we find and their proximities. Our main contribution is twofold: we perform data clustering on the dataset variables (rather than the traditional dataset samples), and we establish a relationship between the clustering distance and the association rules' confidence. This relationship allows us to find association rules from clusters of the dataset variables.

The chapter is organized as follows. We give some background on the association rules mining and clustering that are strictly specific for our work, as well as some notation in Section 4.1. In the rest of the section, we discuss the specifics of finding the association rules using clustering for binary data (Section 4.2), categorical data (Section 4.3), and continuous data (Section 4.4).

4.1 PRELIMINARIES

Let us start by establishing some notations. If D is a dataset of N samples of p dimensional data, we denote by x_i the sample $i = 1...N$ in D , hence a vector of dimension $1 \times p$. We denote by $X_1, ..., X_p$ the variables in D , which are also vectors of dimensions $N \times$ 1. Consequently, a (scalar) data entry of D can be identified as both x_{ij} or x_{ji} . The dataset variables $X_1, ..., X_p$ can be binary (with two possible values, 0 and 1 or True and False), categorical (or qualitative, with a finite number of values), or continuous (or quantitative, when a continuous set of values is possible).

To establish the connection between data clustering and finding the association rules, let us consider a classic "shopping basket" dataset example, which is a classical application

#Items/Customers $A \ B \ C \ D \ E \ F \ G$					
Alex	5°		$0 \t 0 \t 0 \t 2 \t 1 \t 2$		
Bruce	$\mathcal{D}_{\mathcal{L}}$		$1\quad 2\quad 0\quad 0\quad 0$		$\overline{0}$
Chris	Ω		$0 \t1 \t4 \t0 \t0$		$\overline{1}$
Don	Ω		$0 \t2 \t0 \t1 \t1 \t2$		
Emil	6		$2 \t2 \t0 \t1 \t1 \t2$		
Fred	$\overline{4}$	Ω	$0 \t2 \t0 \t0 \t2$		

Table 4.1: Shopping basket data example

of association rule mining. Table 4.1 shows such a dataset example, with six customers (Alex, Bruce, Chris, Don, Emil, and Fred) and seven products (A, B, C, D, E, F, and G). While the entries of each customer's shopping basket contain quantities, these quantities are irrelevant for the association rule mining. Rather, only the presence or absence of a product matters for the purpose of the association rule. However, for clustering one may consider these quantities as relevant to measure the similarities between different shopping baskets (depending on the distance measure being considered).

Let us next recall the definitions of the two main measures for association rules (ARs): support and confidence.

Definition 4.1 (AR support). Let $X \Rightarrow Y$ be an association rule, where X and Y are *disjoint sets of data variables in a dataset* D . The support *of the rule* $X \Rightarrow Y$ *is:*

$$
sup(X \Rightarrow Y) = \frac{|X \cap Y|}{|\mathcal{D}|} \tag{4.1}
$$

Definition 4.2 (AR confidence). Let $X \Rightarrow Y$ be an association rule, where X and Y are *disjoint sets of data variables in a dataset D. The confidence of the rule* $X \Rightarrow Y$ *is:*

$$
conf(X \Rightarrow Y) = \frac{|X \cap Y|}{|X|}
$$
\n(4.2)

Shopping basket clusters

Figure 4.1: Clustering example for the shopping baskets data

For example, for the dataset in Table 4.1, the rule $\{A, B\} \Rightarrow C$ has the following support and confidence:

where the cardinalities union and intersection were computed as counts of the presence of one or the other, and presence of both products, respectively. An example of clustering of the dataset in Table 4.1 (using the Euclidian distance) is shown in Figure 4.1. We can immediately notice a discrepancy between finding the association rules and the clustering of the same data: while the former works with the data variables (columns), the latter computes similarities between the data customers (rows). To establish a connection between the two data analysis methods we need to address this discrepancy. Consequently, we will perform clustering of the data variables (columns), instead of the traditional data rows. Other significant differences between finding the association rules and clustering consist of the different measures (support, confidence, and distance) used for these analyses. We will need to find a connection between these different measures.

Figure 4.2: Mining Mixed Variables Association Rules using Clustering

The architecture we propose is illustrated in Figure 4.2. We first perform clustering on the binary and categorical variables using a similarity/distance measure as appropriate to determine the confidence of potential association rules (as described in the next section). Then we perform a linear search through the continuous variables set and include all continuous variables that satisfy the minimum required thresholds for support and confidence of the association rules. Additional clustering might be performed to find multiple continuous variables that can be included in the association rules.

4.2 THE CASE OF BINARY VARIABLES

We show that in the case of binary variables there is a close connection between a distance measure that can be used for clustering and the association rules' confidence.

The similarity measure defined below is widely used in many applications, such as

data mining and information retrieval (some references can be found in Kosub et al, [14]), or even similarities of DNA sequences, Vorontsov et al, [24].

Definition 4.3 (Jaccard similarity, Jaccard, P, [12]). *The Jaccard similarity coefficient of two sets* A *and* B *(not both empty) is defined as:*

$$
J_{sim}(A,B) = \frac{|A \cap B|}{|A \cup B|} \tag{4.3}
$$

Clearly, the higher the coefficient value (between 0 and 1) the more similar the two sets are. For two binary variables X and Y , the Jaccard similarity between them can be quickly computed by using one norm and/or corresponding probabilities:

$$
J_{sim}(X,Y) = \frac{||X \wedge Y||_1}{||X \vee Y||_1} = \frac{P(X \wedge Y)}{P(X \vee Y)}
$$

For the corresponding Jaccard distance the following result is well-known:

Theorem 4.4 (Jaccard distance, Levandowsky el at, [15], Gilbert, G, [10], Lipkus, A, H, [16], Kosub, S, [14], Grygorian et al, [11]). *For the non-empty sets* A *and* B*, the function:*

$$
J_{dist}(A, B) = 1 - J_{sim}(A, B) = 1 - \frac{|A \cap B|}{|A \cup B|}
$$
(4.4)

represents a distance function.

The following result establishes a relationship between the Jaccard similarity/distance between two binary variables X and Y (or sets of binary variables) and the confidence of the corresponding association rule $X \Rightarrow Y$.

Theorem 4.5 (Relationship between Jaccard distance and confidence). *Let* X, Y *be disjoint subsets of the dataset* D *set of variables,* $X, Y \subset \{X_1, ..., X_p\}$, $X \cap Y = \emptyset$ *. Then:*

$$
conf(X \Rightarrow Y) \ge J_{sim}(X, Y) = 1 - J_{dist}(X, Y)
$$
\n(4.5)

$$
conf(X \Rightarrow Y) = P(Y | X) = \frac{P(X \land Y)}{P(X)}
$$

$$
= \frac{|X \cap Y|}{|X|} = \frac{|X \cap Y|}{|X \cup Y|} \cdot \frac{|X \cup Y|}{|X|}
$$

Since:

$$
\frac{|X \cup Y|}{|X|} \ge 1
$$

it follows that:

$$
conf(X \Rightarrow Y) = \frac{|X \cap Y|}{|X \cup Y|} \cdot \frac{|X \cup Y|}{|X|} = J_{sim}(X, Y) \cdot \frac{|X \cup Y|}{|X|} \ge J_{sim}(X, Y)
$$

The theorem states that for two binary variables X and Y for which $J_{dist}(X, Y) < d$ we have that $1 - J_{dist}(X, Y) > 1 - d$ and hence $conf(X \Rightarrow Y) > 1 - d$. This guarantees that if the two variables X and Y are in a cluster with a diameter no larger than d then the association rule $X \Rightarrow Y$ has confidence larger than $1 - d$. Closer (more similar) two variables are, higher confidence is in their corresponding association rule.

For instance, for the variables A and C in the dataset in Table 4.1, we have:

$$
J_{dist}(A, C) = \frac{|A \cap C|}{|A \cup C|} = \frac{2}{4} = .5
$$

$$
conf(A \Rightarrow C) = \frac{P(A \cap C)}{P(A)} = \frac{2}{4} = .5
$$

$$
conf(C \Rightarrow A) = \frac{P(C \cap A)}{P(C)} = \frac{2}{2} = 1
$$

The result of Theorem 4.5 holds for the confidence of both rules $A \Rightarrow C$ and $C \Rightarrow A$.

The following result represents the fundament of our association rules mining using the clustering of binary variables (which is the first part of the diagram in Figure 4.2).

Theorem 4.6. Let $X_1, ..., X_k$ be a cluster of k binary variables with diameter d: $max(J_{dist}(X_i, X_j) =$ d, $i, j = 1, ..., k$ *. Then for any rule of the form* $X \Rightarrow Y$ *with* $X, Y \subset \{X_1, ..., X_k\}$ *,* $X \cap Y = \emptyset$ *we have that:*

$$
conf(X \Rightarrow Y) \ge 1 - d
$$

Proof. The proof relies on the fact that for some $X_i \in X$, $Y_j \in Y$ we have that

$$
J_{dist}(X_i, Y_i) \ge J_{dist}(X, Y)
$$

hence

$$
1 - J_{dist}(X_i, Y_i) \le 1 - J_{dist}(X, Y)
$$

Then by Theorem 4.5:

$$
conf(X \Rightarrow Y) \ge 1 - J_{dist}(X, Y) \ge 1 - J_{dist}(X_i, Y_j) \ge 1 - d
$$

Since $J_{dist}(X_i, Y_j) \le d$, it follows that $1 - J_{dist}(X_i, Y_j) \ge 1 - d$ and therefore:

$$
conf(X \Rightarrow Y) \ge 1 - d
$$

An immediate consequence of Theorem 4.6 is that any association rule with variables from clusters of diameter at most $1 - \alpha$ will have a confidence of at least α . We, therefore, perform clustering of variables for a given dataset (using, for instance, compact hierarchical clustering), cut the hierarchy at a given distance $1 - \alpha$ (for a given parameter α), and all association rules from the resulting clusters have at least confidence α .

Two key observations are worth noting:

1. Some association rules may not have the desired support. The support threshold for each rule must be separately verified.

2. Some rules may not be discovered. Because (4.5) represents an inequality, rules with given confidence may be discovered if the diameter of a cluster less than $1 - \alpha$ is being considered. If this is important, in practice one can start at a fraction of the distance $1 - \alpha$ and subsequently verify if all confidences will pass the threshold α .

In the subsequent sections, we will explain how we deal with the cases of categorical and continuous variables.

4.3 THE CASE OF CATEGORICAL VARIABLES

Categorical variables can be considered an extension of binary variables by expanding each categorical variable into several binary variables, one binary variable for each category value. For instance, let us assume that an 8th categorical variable $\vec{H} = (a, b, a, a, c, d)$ is appended to the shopping basket dataset in Table 4.1 (as a column). We assume that the new categorical variable can take one of the discrete values $\{a, b, c, d\}$. Then H can be expanded in 4 binary variables as follows:

> $\vec{H}_a = (1, 0, 1, 1, 0, 0)$ $\vec{H}_b = (0, 1, 0, 0, 0, 0)$ $\vec{H}_c=(0,0,0,0,1,0)$ $\vec{H}_d = (0, 0, 0, 0, 0, 1)$

where a 1 or a 0 denotes the presence or absence of the respective category at the respective position. This approach is intuitive and easy to implement, however, an explicit expansion can considerably enlarge a dataset (especially if there are many categories) and consequently make computations significantly more expensive. In practice, however, the expansion needs not to be performed explicitly. The new binary variables \vec{H}_a , \vec{H}_b , \vec{H}_c , and \vec{H}_d can be considered for computing desired cardinalities of unions and intersections

based on the values in \vec{H} , without explicitly creating their content. For instance, computing $||A \vee \vec{H}_a||$ amounts to counting rows where A is non-zero and \vec{H} holds value a.

4.4 THE CASE OF CONTINUOUS VARIABLES

The case of continuous variables is difficult to address in practice and many solutions have been proposed in the literature (discretization and model as categorical/binary variables, heuristic methods, etc.). Typically, choosing one approach or another greatly depends on the data being analyzed and the practical application being considered. There is no "measure fits all" solution and no "best method" among the proposed solutions. In this section, we describe our approach, which adds to the multitude of the proposed solutions.

Let us consider the set of continuous variables $\{\vec{W}_1, ..., \vec{W}_p\}$. Given a desired confidence α , our method consists of the following three steps.

- 1. Find all binary variables clusters of diameter at most 1α .
- 2. For each continuous variable $\vec{W}_i = (w_{i1}, ..., w_{iN})$ and binary cluster $X_1, ..., X_k$
	- compute a range $(minW_i, maxW_i]$, where $minW_i$ and $maxW_i$
	- create a corresponding binary vector $\vec{b}W_i = (bw_{i1}, ..., bw_{iN})$, where

$$
bw_{ij} = \begin{cases} 1 & \text{if } w_{ij} \in [minW_i, maxW_i] \\ 0 & \text{otherwise} \end{cases}
$$

3. For each binary cluster, append the corresponding binary variables obtained from the continuous variables, then perform clustering again. Note that each continuous variable \vec{W}_i must appear in each rule together with the range $[minW_i, maxW_i]$ found in the previous step.

For instance, let us consider an additional continuous variable for the dataset in Table 4.1: $\vec{W} = (1.2, -2.3, 1.1, 2.2, 2.0, 2.3)$. For the cluster $\{\vec{A}, \vec{C}\}$ with diameter .5 we considered
in Section 4.2, we compute $\vec{A} \wedge \vec{C} = (0, 1, 0, 0, 1, 0)$ and subsequently compute a $minW =$ -2.3 and $maxW = 2.0$ (only among the second and fifth positions in \vec{W}). We then create the binary vector $\vec{b}W = (1, 1, 1, 0, 1, 0)$, with zeros for entries outside the range [−2.3, 2.0] and ones otherwise. Next, we cluster (find the association rules) among the variables \vec{A}, \vec{C} , and $\vec{b}W$.

CHAPTER 5

EXPERIMENTAL RESULTS

5.1 THE CENSUS DATA

We have used the USCensus1990 dataset [8] for experiments and testing our method. The USCensus1990 dataset is a discretized version of the USCensus1990raw dataset. Many of the less useful attributes in the original dataset have been dropped, the few continuous variables have been discretized and the few discrete variables that have a large number of possible values have been collapsed to have fewer possible values.¹

The USCensus1990raw dataset was obtained from the U.S. Department of Commerce Census Bureau website using the Data Extraction System. This system can be found at http://www.census.gov/DES/www/des.html.

The USCensus1990raw dataset contains a one percent sample of the Public Use Microdata Samples (PUMS) person records drawn from the full 1990 census sample (all fifty states and the District of Columbia but not including "PUMA Cross State Lines One Percent Persons Records"). A description of the fields and the coding of the values can be found in the Appendix. Additional information can be found at the Census Bureau website described above.

5.2 VARIABLE CLUSTERING AND FINDING ASSOCIATION RULES FOR THE CENSUS DATA

For all the experimental results we present here we used a PC equipped with an Intel Core i7-4770 CPU @3.40GH. The R code listing for producing our results are included in the Appendix.

We have randomly selected 20% of the Census data rows (about half a million rows)

¹Unlike the USCensus1990raw dataset, the order of the cases in the USCensus HAS been randomized.

for our experiments. The dendrogram of complete hierarchical clustering is displayed in Figure 4.2.

Census clusters

Figure 5.1: Clustering for a fragment of Census data (binary variables)

Association Rule	Cluster	Confidence
$\{DISABL10, MARKITAL4\} \Rightarrow \{ OCCUPCLASS\}$		0.5615501
$\{DISABL10\} \Rightarrow \{ OCCUPCLASS, MARITAL4\}$	1	0.9995998
$\{DISABL12\} \Rightarrow \{ENGLISH0, SEX1\}$	3	0.4515397
$\{ENGLISH0, SEX1\} \Rightarrow \{DISABL12\}$	3	0.3201189
$\{DISABL10, DISABL12\} \Rightarrow \{ OCCUPCLASS, ENGLISH0, SEX1\}$	1 and 3	-0

Table 5.1: ARs confidences for Census data

We used a hierarchy cut at distance 0.7 and the resulting list of clusters of variables is given in Table 5.2. From the dendrogram, in Figure 5.1 we can determine that clusters 1 and 3 (for instance) are both below the cutting line, hence all pairwise distances are not larger than $d = 0.7$. It follows that the result of Theorem 4.6 will apply to all association rules constructed with combinations of variables within each cluster, or between the two clusters. That is each such rule $X \Rightarrow Y$ must satisfy:

$$
conf(X \Rightarrow Y) \ge 1 - d = 0.3
$$

The results of the experiments are summarized in Table 5.1. All rules consisting of variables from the same cluster satisfy the result of Theorem 4.6. The last association rule in the table is composed of variables from different clusters, 1 and 3, which are joined into their super cluster above the height at $d = 0.7$. Hence it comes as no surprise that the confidence of such a rule is not greater than $1 - d = 0.3$, as it does not satisfy the requirements of the theorem.

	Variable	Cluster
1	DISABL10	$\mathbf{1}$
$\overline{2}$	MARITAL4	1
3	OCCUPCLASS	1
$\overline{4}$	DISABL11	2
5	DISABL12	3
6	ENGLISHO	3
7	SEX1	3
8	ENGLISH1	$\overline{4}$
9	ENGLISH2	5
10	ENGLISH3	6
11	ENGLISH4	7
12	MARITAL0	8
13	SEX ₀	8
14	MARITAL1	9
15	MARITAL2	10
16	MARITAL3	11
17	OCCUPCLASS1	12
18	OCCUPCLASS2	13
19	OCCUPCLASS3	14
20	OCCUPCLASS4	15
21	OCCUPCLASS5	16
22	OCCUPCLASS6	17
23	OCCUPCLASS7	18
24	OCCUPCLASS8	19

Table 5.2: Clusters of variables from the Census data

CHAPTER 6

CONCLUSION

Mining the association rules was initially introduced in the early nineties by Agrawal et al, [1], and it has been intensively studied ever since. Originally introduced for binary data, association rules mining for continuous data was capturing the attention of the data science research community shortly thereafter. However, while many approaches and algorithms were proposed, there is no measure fits all for finding the association rules for continuous data. It comes as no surprise that the subject is still of interest nowadays.

In this work, we proposed a novel method for the association rules mining for mixed data case: data that contains binary, categorical, and continuous variables. Our method relies on performing clustering of data variables, then inferring the association rules based on the clusters we find and the proximities between these clusters.

Our main contributions can be summarized as follows:

- We establish a surprising connection between one of the association rules' main analysis measure (confidence) and a popular similarity/distance measure (Jaccard similarity/distance) used for discrete (categorical) data.
- We perform clustering of data variables (columns), instead of the traditional approach where rows are used.
- We introduce a novel method of finding association rules based on the clustering of data variables. First, we develop our method for binary and categorical data and subsequently extend it to data with mixed variables (discrete and continuous).

Like all the methods for finding the association rules of data that include continuous variables, our method cannot find all possible association rules that include continuous variables, as there might be a very large set of possibilities to choose from. One shortcoming of

the method we propose is its inability to perform clustering of all variables (binary, categorical, and continuous) and then determine association rules from these mixed clusters. This shortcoming stems from the fact that we could not identify an appropriate distance function on all types of variables that can be directly connected to the confidence parameter of the association rules (like we did with the Jaccard similarity/distance for the binary variables). We believe that finding such a distance function is a direction worth investigating in future work.

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APPENDIX A

THE USCENSUS1990 DATASET ATTRIBUTES DESCRIPTION

U.S. DEPARTMENT OF COMMERCE

BUREAU OF CENSUS

*** DATA EXTRACTION SYSTEM ***

DOCUMENTATION OF: FILE CONTENTS

FOR DATA COLLECTION: 'pums901p' - 1990 Decenial Census 1% PUMS - Persons Records

VAR: TYP: DES: LEN: CAT: VARIABLE/CATEGORY LABEL:

1 Yes

__

090001 \$90, 001 or More State Median of Topcode

12 Other Method

VAR: TYP: DES: LEN: CAT: VARIABLE/CATEGORY LABEL:

1 Yes, Has a Personal Care Limitation

2 No, Does Not Have a Personal Care Limita

- 221 Laos
-
- 222 Lebanon

338 Dominica

- 339 Dominican Repub.
- 340 Grenada
- 341 Guadeloupe
- 342 Haiti
- 343 Jamaica 344 Martinique 345 Montserrat 346 Netherlands Antilles 347 St. Barthelemy 348 St. Kitts Nevis 349 St. Lucia 350 St. Vincent and the Grenadines 351 Trinidad and Tobago 352 Turks and Caicos Islands 353 Caribbean, Not Specified 354 Antilles, Not Specified 355 British West Indies, Not Specified 356 Latin America, Not Specified 357 Leeward Islands, Not Specified 358 West Indies, Not Specified 359 Windward Islands, Not Specified 375 Argentina 376 Bolivia 377 Brazil 378 Chile 379 Colombia 380 Ecuador 381 Falkland Islands 382 French Guiana 383 Guyana 384 Paraguay 385 Peru 386 Suriname 387 Uruguay 388 Venezuela 389 South America, Not Specified 400 Algeria 401 Angola 402 Bassas Da India 403 Benin 404 Botswana 405 British Indian Ocean Territory 406 Burkina Faso 407 Burundi 408 Cameroon 409 Cape Verde 410 Central African Repub. 411 Chad

412 Comoros

- 428 Lesotho
- 429 Liberia
- 430 Libya
	-
- 431 Madagascar
- 432 Malawi
- 433 Mali
- 434 Mauritania
- 435 Mayotte
- 436 Morocco
- 437 Mozambique
- 438 Namibia
- 439 Niger
- 440 Nigeria
- 441 Reunion
- 442 Rwanda
- 443 Sao Tome and Principe
- 444 Senegal
- 445 Mauritius
- 446 Seychelles
- 447 Sierra Leone
- 448 Somalia
- 449 South Africa
- 450 St. Helena
- 451 Sudan
- 452 Swaziland
- 453 Tanzania
- 454 Togo
- 455 Tromelin Island
- 456 Tunisia
- 457 Uganda
- 458 Western Sahara
- 459 Zaire
- 460 Zambia
- 461 Zimbabwe
- 462 Africa, Not Specified
- 463 Central Africa, Not Specified
- 464 Eastern Africa, Not Specified

465 Equatorial Africa, Not Specified

00000 N/a Not a Worker Not in the Labor Force,

13 Other Pers. in Grp. Qtrs.

VAR: TYP: DES: LEN: CAT: VARIABLE/CATEGORY LABEL:

0 N/a Less Than 16 Yrs. Old

1 Worked Last Year

2 Did Not Work Last Year

APPENDIX B

R CODE

B.1 EXPERIMENT 1

 $\frac{1}{2}$ # Multiclass Experiment 1: comparison of 1vs1 and DCSVM for various data sets # using linear SVM. \pm library (e1071) library(igraph) #load functions $source("utils.R")$ #generate data: run with one option for a specific data set #DATA_GEN <- "artificial1" #DATA_GEN <- "iris" #DATA_GEN <- "segmentation" #DATA_GEN <- "letter" #DATA GEN <- "heart" #DATA_GEN <- "wine" DATA_GEN <- "wine-quality" #DATA_GEN <- "glass" #DATA_GEN <- "covertype" #DATA GEN <- "svmquide4" #DATA_GEN <- "vowel" source("datagen.R") #create a list of all classes pairs in the training data set #store in a list $cls.al1 \leftarrow list()$ cls.levels <- levels (factor(df.train\$class)) cls.n <- length(cls.levels) $idx \leftarrow 1$ for $(i \text{ in } 1; (cls.n-1))$ { for $(j \in (i+1):cls.n)$ { c1 <- cls.levels[i] $c2 \leftarrow c1s. levels[j]$ cls.all[[idx]] <- df.train[df.train\$class == c1 | df.train\$class == c2,] cls.all[[idx]]\$class <- factor(cls.all[[idx]]\$class) $idx \leftarrow idx + 1$ $\,$ $\,$ $\bar{\mathrm{t}}$ #create linear svm models for all pairs of classes svmkernel <- 'linear' #svmkernel <- 'radial'

```
cls.sum \leftarrow list()idx \leftarrow 1for (i \text{ in } 1; (cls.n-1)) {
  for (j in (i+1):cls.n) {
    c1 \leftarrow cls. levels[i]c2 <- cls.levels[j]
    #compute weights
    wts <- 100 / table(cls.all[[idx]]$class)
    cls.svml[[idx]] <- svm(class"., data=cls.all[[idx]], kernel=svmkernel, class.weights = wts)
    idx \leftarrow idx + 1\, \, \,\bar{\mathrm{t}}
```
print ('All SVMs created:') print (Sys.time())

1vs1 prediction sample <- df.test

plvs1 <- onevsone(cls.svml, cls.levels, sample)

print (paste ('1vs1 prediction results for: "', DATA_GEN,'"', sep = "")) ans \leq table(sample\$class == p1vs1) print (ans)

print (Sys.time()) # DCSVM prediction

#initialize $info \leftarrow intSWMDC(df.train, cls.n, cls. levels, cls.suml, cls.suml)$ allpredict <- info\$allpredict svmdc.plan <- createSVMDCplan(cls.n, cls.levels, info\$pnodes, astree = T)

print ('DCSVM initialization completed:') print (Sys.time())

 $#s$ vmdc.plan = make_tree(0,2) #vertex.id <- 1 #svmdc.plan <- createSVMDCplan(svmdc.plan, NULL, rep(T, cls.n), pnodes, cls.n, cls.levels)

OPTIONAL: let's print it using a tree-specific layout # (N.B. you must specify the root node) co <- layout.reingold.tilford(svmdc.plan, params=list(root=1)) plot.igraph(svmdc.plan, layout=co)

#library(qgraph) #qgraph(svmdc.plan,edge.labels=T)

#predict and print

```
psvmdc \leftarrow 0for (i \text{ in } 1;\text{nrow}(\text{sample}))# Pick a single observation for the one-vs-one classifiers to vote on
  candidate = sample[i, ]vote <- svmdc.predict(svmdc.plan, cls.levels, candidate)
  psymdc[i] <- vote
\}print (paste ('SVMDC prediction results for: "', DATA GEN,'"', sep = ""))
ans \leftarrow table(sample\{class} == pswmdc)
print (ans)
print(Sys.time() )#compute errors per each class and how classes were mis-classified (the confusion table)
res <- data.frame(orig = sample$class, p1vs1 = p1vs1, psvmdc = psvmdc)
print ('Confusion Table 1vs1')
table(res$orig, res$p1vs1, dnn = c("Original", "1vs1"))
print ('Confusion Table DCSVM')
{\tt table}({\tt res}\verb|5orig, {\tt res}\verb|5pswmdc, {\tt dnn = c("Original", "DCSWM"))|}
```
B.2 THE R CODE FOR COMPUTING CLUSTERING AND ARS

```
\#\ddot{\phantom{1}}#set memory limit
memory.limit(6410241024*1024)
dsd <- '../data/census/' #data source directory
dsf <- 'USCensus1990raw.data2.csv' #data source file
#dsf <- 'Census_income_clustD59500Q993.csv' #data source file
dsfa <- 'census-varinfo2.csv' #data attributes file
\# load data
dfa <- read.csv(paste0(dsd, dsfa), header= T, sep=",")
#df <- read.table(paste0(dsd, dsf), sep = "", header = F, nrows = 100,
              na.strings ="", stringsAsFactors= T)
\#numvars \leq c (13, 56, 63, 64, 66: 73, 91, 105)
ccl <- rep('factor', 127)
ccl[numvars] <- 'numeric'
\text{ccl}[97] \leftarrow 'character'df <- read.csv(paste0(dsd, dsf), header= F, sep=",", #nrows = 100,
                           na.strings =NA, stringsAsFactors= F,
         colClasses = ccl\rightarrow#make REARNING numeric (cannot read numeric from file)
indx \leftarrow 97
df[index] \leftarrow \text{lapply}(df[index], function(x) as. numeric(as. character(x)))
```
#remove caseid (first column) toremove <- c(1:12,14:35,38:47,49:53) df <- df[,-toremove] header <- c(as.character(dfa[,1]))[-toremove] colnames(df) <- header

#count missing sum(is.na(df))

####################################

#select some categorical vars cvarsnames <- c(#"Avail", #"Citizen", #"Class", "Disabl1", "ENGLISH", #"Immigr", #"LANG1", #"Looking", "Marital", #"RACE", "Sex",

#"Vietnam", #"INDUSTRYCLASS", #"WWII", "OCCUPCLASS"

 \rangle

set.seed(2020)

dfx <- df[sample(nrow(df), as.integer(nrow(df)*.2)),which(colnames(df) %in% toupper(cvarsnames))]

#convert to binary #install.packages("dummies") library(dummies) dfxb <- dummy.data.frame(dfx)

sum(is.null(dfxb))

#install.packages('proxy') library(proxy)

#compute all distances between these vectors d <- dist(t(as.matrix(dfxb)), method = "jaccard")

#hierarchical clustering using Jaccard groups <- hclust(d,method="complete") #try method = "ward.D", "complete", "single", "average" #plot dendogram, use hang to ensure that labels fall below tree plot(groups, hang=-1, main = 'Census clusters', sub = '', xlab = 'Variables')

#####################################

```
clusters <- sort(cutree(groups, h = 0.7))
cdf <- data.frame(Variable = names(clusters), Cluster = clusters)
rownames(cdf) <- NULL
library(xtable)
xtable(cdf)
names(clusters[clusters == 1])
names(clusters[clusters == 3])
confidence <- function(df, left, right) {
 rule <- paste0('{', left[1])
 if (length(left) > 1) {
   for (i in 2:length(left)) {
     rule <- paste0(rule, ', ', left[i])
   }
  }
  rule \leftarrow paste0(rule, '} => {', right[1])
  if (length(right) > 1) {
   for (i in 2:length(right)) {
      rule <- paste0(rule, ',', right[i])
   \rightarrow}
  rule <- paste0(rule, '}')
  print(rule)
  a = rep(T, nrow(df))for (i in 1:length(left)) {
   a = a \& df[[left[i]]]\lambdafor (i in 1:length(right)) {
   a = a \& df[[right[i]]]}
  a = sum(a)b = rep(F, nrow(df))for (i in 1:length(left)) {
   b = b | df[[left[i]]]
  }
  b = sum(b)return (a/b)
}
confidence(dfxb, c("DISABL10","MARITAL4"), c("OCCUPCLASS"))
confidence(dfxb, c("DISABL10"), c("OCCUPCLASS","MARITAL4"))
```
confidence(dfxb, c("DISABL12"), c("ENGLISH0","SEX1")) confidence(dfxb, c("ENGLISH0","SEX1"), c("DISABL12"))

confidence(dfxb, c("DISABL10","DISABL12"), c("OCCUPCLASS", "ENGLISH0","SEX1"))