IMPROVING STUDENTS ATTENTION IN HIGHER EDUCATION

R.Ashwini, S.Ancy, and B.Nasreen Fathima
Post Graduate Department of Computer Science,
Jayaraj Annapackiam College for Women (Autonomous),
Periyakulum, Theni Dist, Tamil Nadu, India

Abstract

Over the years, several statistical tools have been used to analyze students performance from different points of view. This paper presents data mining in education environment that identifies students failure patterns. The identified patterns are analyzed to offer a helpful and constructive recommendations to the academic planners in higher institutions of learning to enhance their decision making process. This will also aid in the curriculum structure and modification in order to improve the students academic performance and trim down failure rate. The software for mining student failed courses was developed and the analytical process was described.

Keywords: *Students Performance, K-Means Clustering, decision making*

1. Introduction

Attention plays a very important role in student's success in the classroom. Attention allows students to "tune out" unrelated information, background noise, visual distractions, and even their own thoughts. All students can have problems attending to their teachers from time to time. However, students with learning disabilities, processing problems, or attention deficit hyperactivity disorder (ADHD) can have more frequent and significant problems attending to their teachers. Therefore, teachers have a critical role in keeping students on task and attentive.

2. Algorithms used

2.1. Analysis

Cluster analysis is a multivariate analysis that attempts to form groups or "clusters" of objects (sample plots in our case) that are "similar" to each other but which differ among clusters. The exact definition of "similar" is variable among algorithms, but has a generic basis.

2.2. Similarity, Dissimilarity and Distance

Similarity is a characterization of the ratio of the number of attributes two objects share in common compared to the total list of attributes between them. Objects which have everything in common are identical, and have a similarity of 1.0. Objects which have nothing in common have a similarity of 0.0. Dissimilarity is the complement of similarity, and is a characterization of the number of attributes two objects have uniquely compared to the total list of attributes between them. In general, dissimilarity can be calculated as 1-similarity.

2.3. K-means Clustering

The most common partitioning method is the K-means cluster analysis. Conceptually, the K-means algorithm:

1. Selects K centroids (K rows chosen at random)
2. Assigns each data point to its closest centroid
3. Recalculates the centroids as the average of all data points in a cluster (i.e., the centroids are p-length mean vectors, where p is the number of variables)
4. Assigns data points to their closest centroids
5. Continues steps 3 and 4 until the observations are not reassigned or the maximum number of iterations (R uses 10 as a default) is reached.

R uses an efficient algorithm by Hartigan and Wong (1979) that partitions the observations into k groups such that the sum of squares of the observations to their assigned cluster centers is a minimum. This means that in steps 2 and 4, each observation is assigned to the cluster with the smallest value of:

$$SS(k) = \sum_{i=1}^{n}\sum_{i=0}^{Y}\left(x_{ij} - \bar{x}_{kj}\right)^2$$

Where k is the cluster, x_{ij} is the value of the j^{th} variable for the i^{th} observation, and x_{kj}-bar is the mean of the j^{th} variable for the k^{th} cluster.

3. Tools

3.1. The R environment

R is an integrated suite of software facilities for data manipulation, calculation and graphical display.

3.2. Cluster Analysis in R

R has an amazing variety of functions for cluster analysis. We use two of the many approaches: Partitioning, and Model based.

3.2.1. Data Preparation

Prior to clustering data, you may want to remove or estimate missing data and rescale variables for comparability.

```
# Prepare Data
mydata <- na.omit(mydata) # listwise deletion of missing
mydata <- scale(mydata) # standardize variables
```

3.2.2. Partitioning

K-means clustering is the most popular partitioning method. It requires the analyst to specify the number of clusters to extract. A plot of the within groups sum of squares by number of clusters extracted can help determine the appropriate number of clusters. The analyst looks for a bend in the plot similar to a screen test in factor analysis.

```
# Determine number of clusters
wss <- (nrow(mydata)-1)*sum(apply(mydata,2,var))
for (i in 2:15) wss[i] <- sum(kmeans(mydata, centers=i)$withinss)
plot(1:15, wss, type="b", xlab="Number of Clusters", ylab="Within
groups sum of squares")
# K-Means Cluster Analysis
fit <- kmeans(mydata, 5) # 5 cluster solution
# get cluster means
aggregate(mydata,by=list(fit$cluster),FUN=mean)
```

```
# append cluster assignment
mydata <- data.frame(mydata, fit$cluster)
```

The **pvclust( )** function in the **pvclust** package provides p-values for hierarchical clustering based on multiscale bootstrap resampling. Clusters that are highly supported by the data will have large p values. Be aware that **pvclust** clusters columns, not rows. Transpose your data before using.

```
# Ward Hierarchical Clustering with Bootstrapped p values
library(pvclust)
fit <- pvclust(mydata, method.hclust="ward",
  method.dist="euclidean")
plot(fit)
# dendogram with p values
# add rectangles around groups highly supported by the data
pvrect(fit, alpha=.95)
```

3.2.3. Model based

Model based approaches assume a variety of data models and apply maximum likelihood estimation and Bayes criteria to identify the most likely model and number of clusters. Specifically, the Mclust( ) function in the mclust package selects the optimal model according to BIC (Bayesian Information Criterion) for EM (Expectation Maximization) initialized by hierarchical clustering for parameterized Gaussian mixture models.

```
# Model Based Clustering
library(mclust)
fit <- Mclust(mydata)
plot(fit) # plot results
summary(fit) # display the best model
```

3.3. Plotting Cluster Solutions

It is always a good idea to look at the cluster results.

```
# K-Means Clustering with 5 clusters
fit <- kmeans(mydata, 5)
# Cluster Plot against 1st 2 principal components
```


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```
# vary parameters for most readable graph
library(cluster)
clusplot(mydata, fit$cluster, color=TRUE, shade=TRUE,
  labels=2, lines=0)
# Centroid Plot against 1st 2 discriminant functions
library(fpc)
plotcluster(mydata, fit$cluster)
```

3.4. Validating Cluster Solutions

The function cluster.stats() in the fpc package provides a mechanism for comparing the similarity of two cluster solutions using a variety of validation criteria.

```
# comparing 2 cluster solutions
library(fpc)
cluster.stats(d, fit1$cluster, fit2$cluster)
```

where **d** is a distance matrix among objects, and **fit1$cluster** and **fit$cluster** are integer vectors containing classification results from two different clustering of the same data.

4. Findings, Interpretations

4.1. Findings and Interpretations

- **Gender based improvement of student's attention**

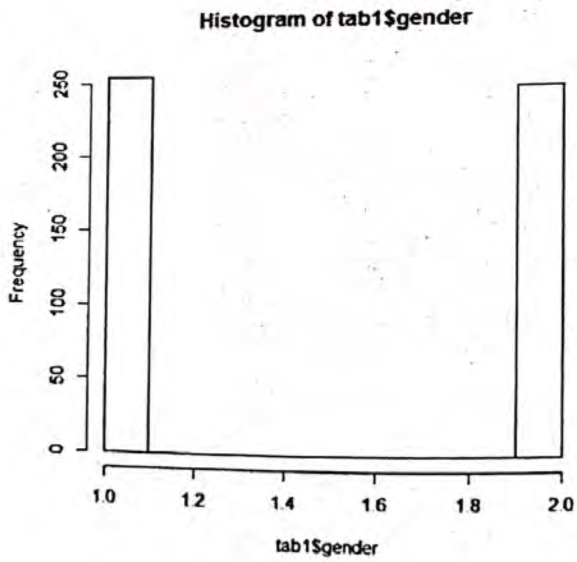

Figure 4.1

- Place based improvement of student's attention

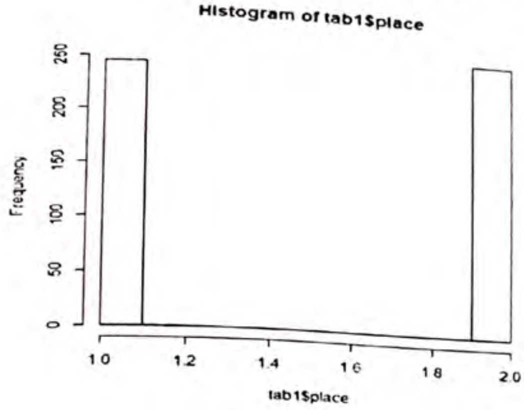

Figure 4.2

Total members of family:

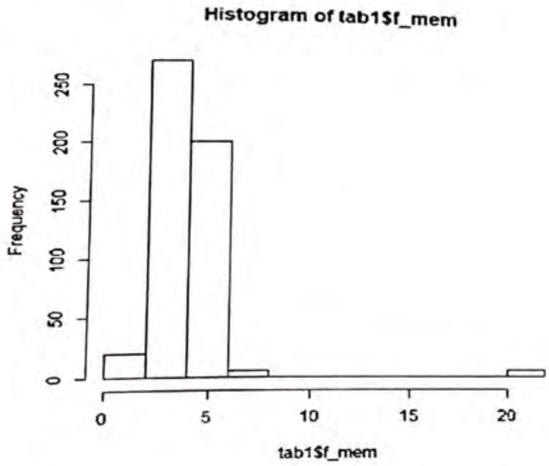

Figure 4.3

fit <- kmeans(mydata, 5)

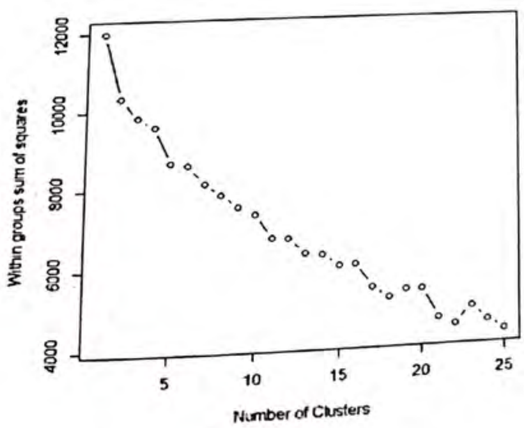

Figure 4.4 K-means

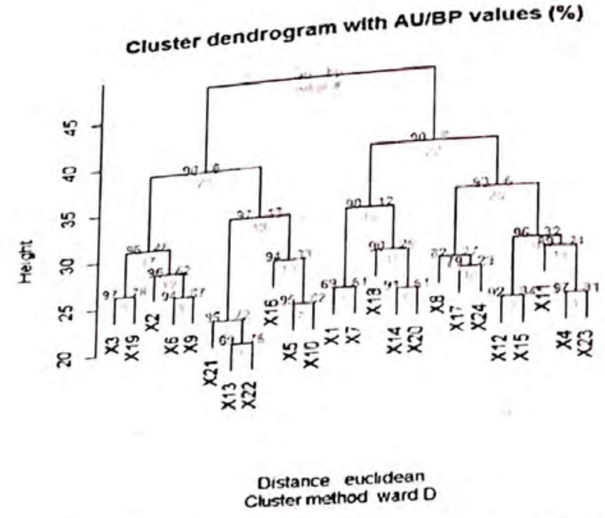

Figure 4.5 Using Plot Function

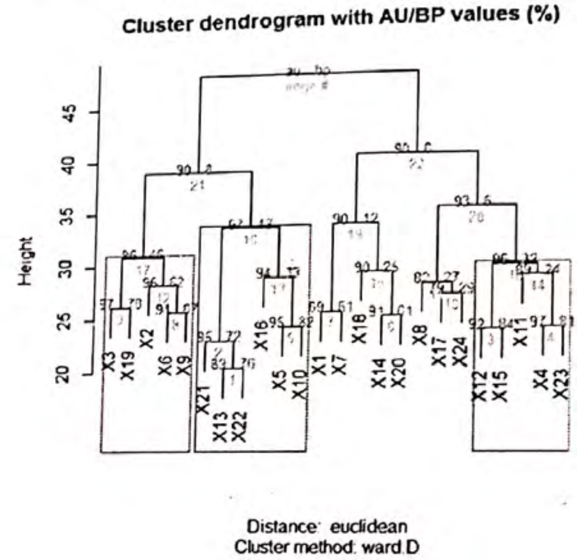

Figure 4.6 Using Pvert Function

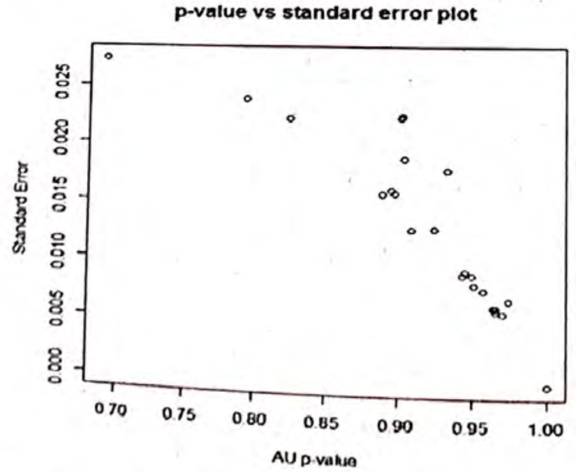

Figure 5.7 Using seplot Function

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Plot Model-based Clustering Results: BIC, classification, uncertainty and (for one- and two-dimensional data) density.

Model-based clustering plots:

1: BIC 2: classification

3: uncertainty 4: density

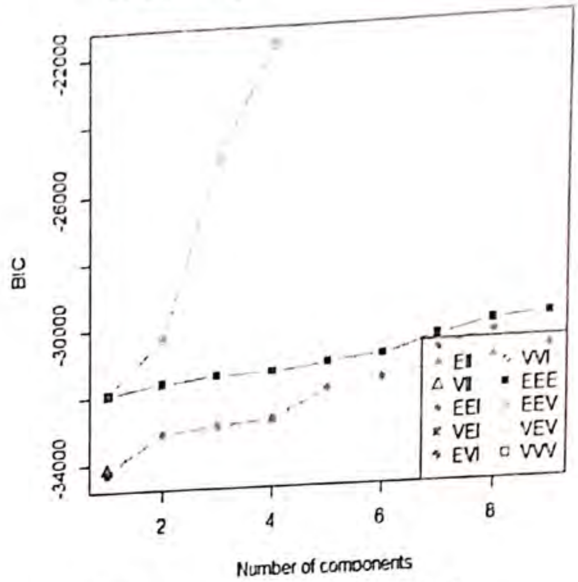

Figure 4.8 Selection 1

Model-based clustering plots:

1: BIC 2: classification

3: uncertainty 4: density

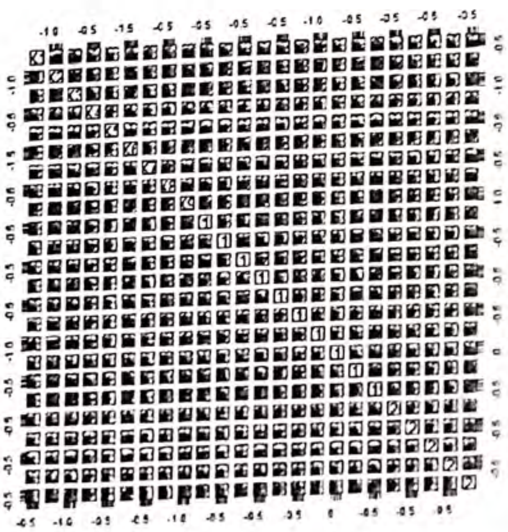

Figure 4.9 Selection: 2

Model-based clustering plots:

1: BIC 2: classification

3: uncertainty 4: density

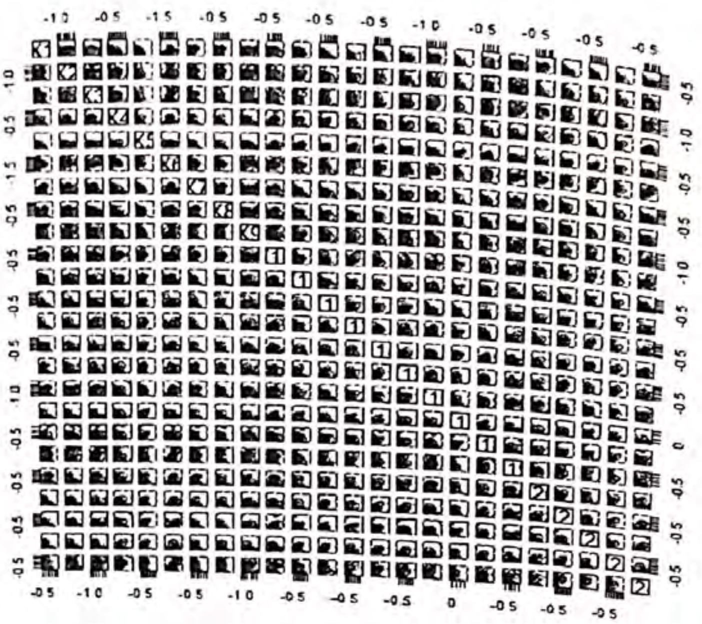

Figure 4.10 Selection: 3

Model-based clustering plots:

1: BIC 2: classification

3: uncertainty 4: density

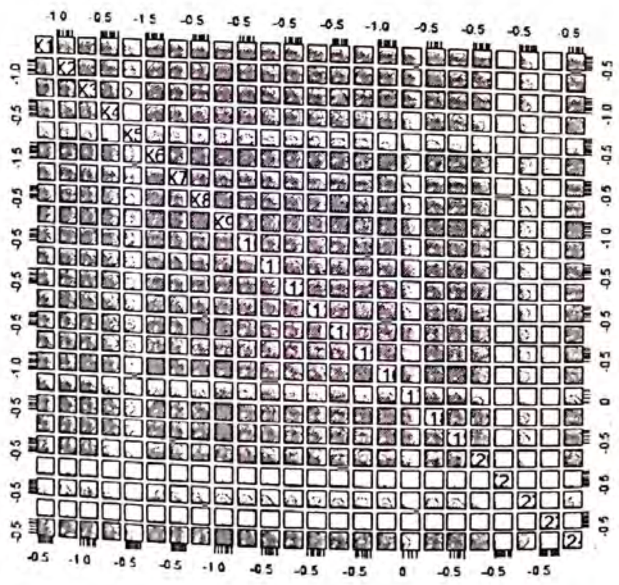

Figure 4.11 Selection: 4

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Bivariate Cluster Plot:

```
>clusplot(mydata, fit$cluster, color=TRUE, shade=TRUE, labels=2,
lines=0)
```

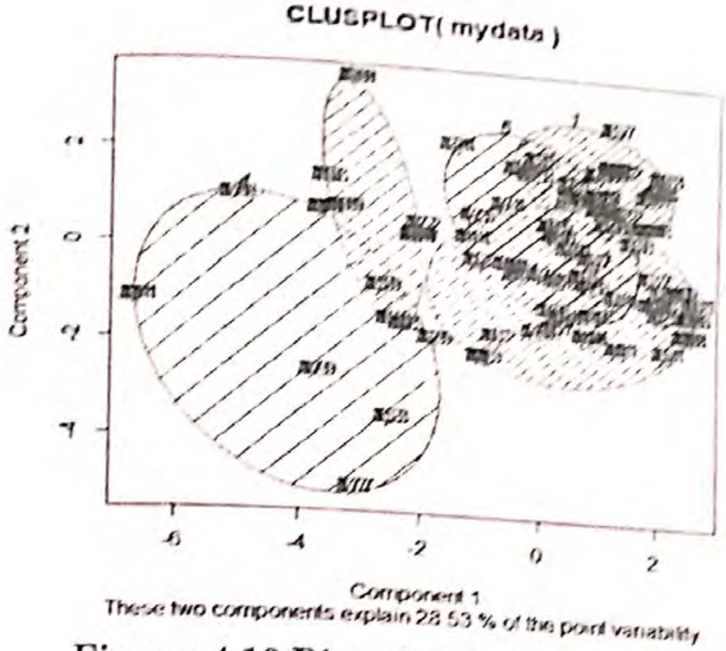

Figure 4.12 Bivariate Cluster Plot

Plot Cluster

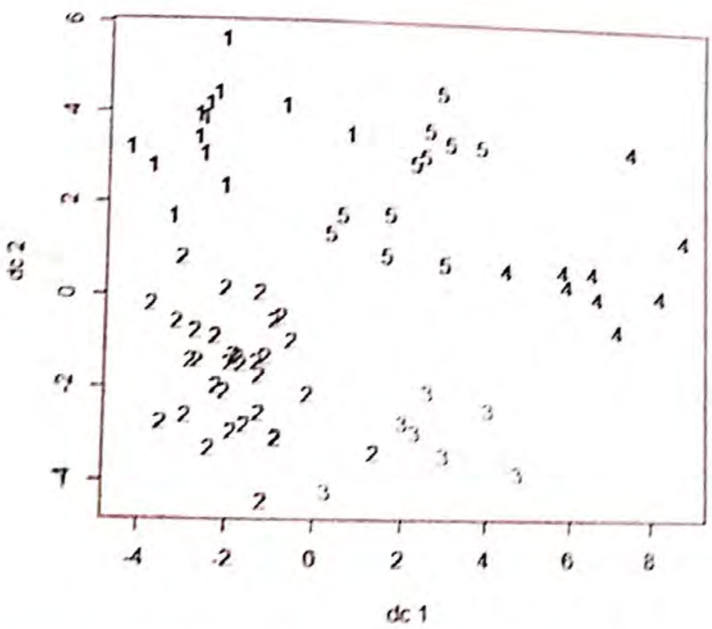

Figure 4.13 plotcluster(mydata,fit$cluster)

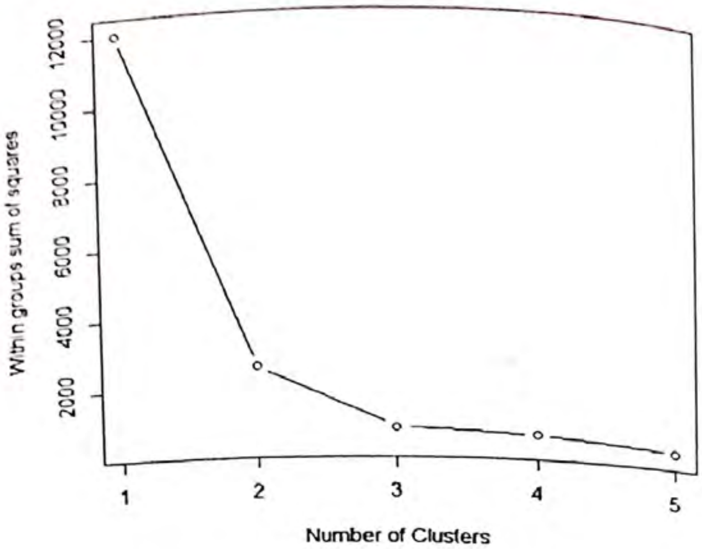

Figure 4.14 wssplot(df)

Barplot

> barplot(table(nc$Best.n[1,]), xlab="Numer of Clusters", ylab="Number of Criteria", main="Number of Clusters Chosen by 5 Criteria")

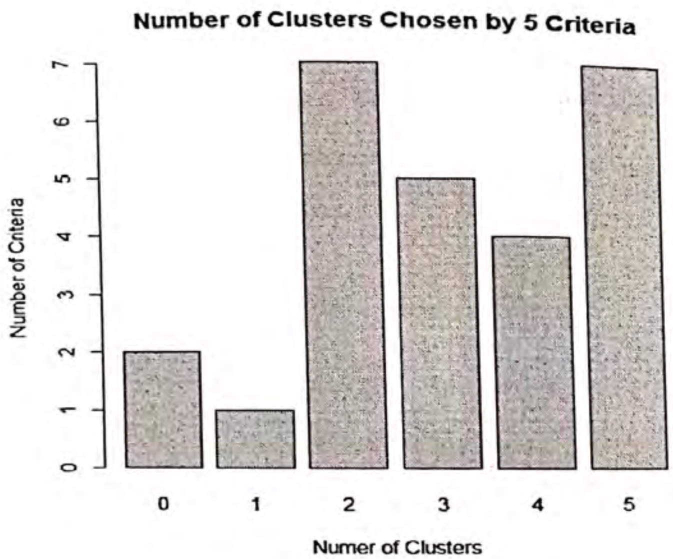

Figure 4.15 Barplot

5. Conclusion

This paper has bridge the gap in educational data analysis and shows the potential of the association rule mining algorithm for enhancing the effectiveness of academic planners and level advisers in higher institutions of leaning. Here we analysed undergraduate students. The data collected from total number of 30 courses. The analysis reveals that there are more students fail even they have the ability to study. It also reveals some hidden patterns of courses which students fail. This will help for academic planners while making academic decisions and an aid in the curriculum re-structuring and modification with a view to improve the students attention and reducing failure rate.

To adopt this approach a larger number of students should be considered from the first year to the final year. In future, in order to improve the comprehensibility and applicability of the association rules, it will be very useful to provide an ontology that would describe the content of the courses which will allow the academic planners to understand the rules.

6. References

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