IMPROVEMENT OF CLUSTERING ON HIGH DIMENSIONAL DATASETS USING PCA

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Abstract: The last decade has seen an explosive growth in the generation and collection of data. In the field of data mining there are various techniques used to extract useful information from the data set. There are various estimation techniques are used in clustering methods out of these, Euclidean distance and density is used for estimation. Out of these estimation techniques one another technique mass is also used. Mass based clustering gives better performance when apply with PCA technique in multidimensional and high dimensional data set. On the basis of run time behaviour the DEMassDBSCAN algorithm is better than DBSCAN clustering algorithm is discussed.

Keywords: KDD, PCA, CLI.

INTRODUCTION

In the emerging field of knowledge discovery in databases (KDD) and data mining there are various techniques are used to find useful information from large amount of data. The term “KDD” is an overall process of discovering useful knowledge from data. A new generation of computational techniques and tools is required to support the extraction of useful knowledge from the rapidly growing volumes of data [1]. In KDD there are various steps are used for extraction useful knowledge of large amount of data are selection, preprocessing, transformation, data mining and evaluation. Data mining is a step in KDD [2]. In the data mining there are various techniques are used out of which clustering is mostly used. In clustering there are methods like partitioning, density based, hierarchical, grid and model based clustering. These methods are used in clustering but a new technique is introduced here is mass based clustering.

CLUSTERING

In Field of data mining there are various techniques are used like association, information retrieval, classification, clustering, regression, prediction and frequent pattern mining. Clustering is an important unsupervised learning technique. In partitioning method the popular algorithm k-means is used and in the density based algorithm the DBSCAN algorithm is used [3]. In clustering there are various clusters are formed based on the data sets i.e. distance, density and mass. Now a days in clustering mass estimation technique is used it is alternate of density based clustering. The distance estimation is applied on partitioning method of clustering the algorithm which is used to implement is k-means clustering algorithm. The DBSCAN clustering algorithm is applied on arbitrary shaped spatial data with noise. In the DBSCAN algorithm the points are grouped are dense and forms cluster. In DBSCAN algorithm is based on various parameters like core points, min pts, border points and noise. The points are not belonging to cluster are called noise [4]. In the DEMassDBSCAN algorithm there are also core regions and noise points are used as a parameter.

RELATED WORK

Mass based clustering:

In the clustering approach there is various estimation techniques are used to form clusters. The mass estimation is another technique to find clusters in arbitrary shape data. In the clustering the mass estimation is unique because in this estimation there is no use of distance or density [6]. In the DBSCAN clustering algorithm hyper spheres are used to show points but in DEMassDBSCAN clustering algorithm rectangular regions are used for showing the points [7]. What is Mass?

Number of points in a given region is called mass of that region. Each region in a given data space having rectangular shape and for estimation of mass a function that called rectangular function [5].

One- Dimensional Mass Estimation: The estimation of mass in data space is depends on levels (h). If value of level h=1 the shape of function is concave. For multidimensional mass estimation the value of h is >1.

\[
\operatorname{mass}(x, h) = \begin{cases} 
\sum_{i=1}^{n-1} \operatorname{mass}(x, h-1)p(s_i), & h > 1 \\
\sum_{i=1}^{n} m_i(x)p(s_i), & h = 1 
\end{cases}
\]

Eq-1 [6]

In the one dimensional mass estimation the value of \( p(s_i) \) is equals to:

\[
p(s_i) = \frac{x_i+1-x_i}{x_n-x_i}
\]

For one-dimensional mass estimation the value of h is equals to 1.

\[
\sum_{i=1}^{n-1} m_i(x)p(s_i), \\
\sum_{i=1}^{n} m_i(x)p(s_i), & h = 1
\]

In the above equation the \( m_i(x) \) mass base function.
\[
\text{mass}(x,h) = \frac{1}{t} \sum_{k=1}^{t} \text{mass}(x,h/D_k) \quad \text{Eq. 2}
\]

Combining these two equations:
\[
\sum_{i=1}^{n} m_i(x)p(S_i) \approx \frac{1}{t} \sum_{i=1}^{t} m(T_i(x))
\]
\[
\text{mass}(x,h) \approx \frac{1}{t} \sum_{i=1}^{t} m(T_i^h(x))
\]
\[
\text{mass}(x,h) \approx \frac{1}{t} \sum_{i=1}^{t} m(T_i^h(x)/D_i) \quad [6]
\]

For large data bases the values of \( t \) is 1000 and \( \Psi \) 256. For small data sets the value of \( h \) and \( \Psi \) is varies.

**Multi-dimensional mass estimation:**

In multidimensional mass estimation there is value of \( h \) > 1. In multidimensional mass estimation there are two functions mass and random spaces generator in data space.

\[
\text{gmass}(x) \approx \frac{1}{t} \sum_{i=1}^{t} m(T_i^h(x)/D_i) \quad [6]
\]

Mass Based Clustering:
\[
h: d Tree(x) = m_j = m(T_i^h(x)/D)) \quad [6]
\]

Multidimensional mass estimation using h: d Trees:
\[
\text{gmass}(x) \approx \frac{1}{t} \sum_{i=1}^{t} h: d (x) Tree_i(X) \quad [6]
\]

The multi dimensional data set the value of \( h \) (level) is greater than 1 and is similar to one dimensional mass estimation. In this equation the value of \( x \) is replaced by \( X \).

**MassTER Algorithm:** In the masTER algorithm the mass will estimate using h:d trees. In the h:d trees the h stands for no of times attribute appears and d stands for no of dimensions. The height of tree is calculated as \( l= h x d \).

**Algorithm**

1. Step 1 Build trees \( t_i \).
2. Step 2 Assign a cluster seed for every instance.
3. Step 3 Join two seed based clusters.
4. Step 4 Clustering having instances less than \( \Gamma \) are called noise instances.
5. Step 5: return clusters \( c_{i,j}=1,2,3,-------k \). And E.(noise instances)

**Data input:**
- \( D= \) Input Data.
- \( T= \) No of trees.
- \( \Psi= \) Sampling size.
- \( h= \) how many times attribute come in a path.
- \( \Gamma= \) minimum instances in a cluster.

In this algorithm firstly h:d trees are made of instance in a region. The cluster seed is assigned for each region in data space. The cluster seed are joined and make pair with neighbour cluster seed. The instances having value less than \( \Gamma \) are defined noise [6].

**Proposed Work:** in the proposed work the principle component analysis is applied on the pre-processed data sets then clustering is applied on numeric data sets.

**PCF (principle component analysis):**

PCA is a powerful tool for analyzing data and patterns are identified in data. For high dimensional data sets the reduction in the dimensions without loses of information. In the PCA first of all take data set and then subtract the means from each of dimensions. In next step covariance matrix is computed from mean subtracted data. For information about data the eigenvectors and eigen values are calculated from covariance matrix. The eigenvector having high eigen value is called principle component of the dataset. In the final step we will take transpose of vector and multiply from original data set [10]. In the generalized PCA there is constructive algebra-geometric solution of subspace if no. of subspaces is known. In the generalized PCA algebraic and geometric interpretations are done in probabilistic manner [11].

**TOOL**

In the implementation of data mining algorithms mostly weka toolkit is used. Weka is developed by University of Waikato in New Zealand weka . Weka is popular open source machine learning software and it provides Graphical user interface. Weka is mainly consists of four interfaces like Explorar, Experimentor, Knowledge flow and Simple CLI [8]. In the implementation of any algorithm arff file format data is used. Weka’s main user interface is the explorer, but essentially the same functionality can be accessed through the component based Knowledge Flow interface and from the command line. By using weka we can implement all standard algorithms [9].

**EXPERIMENTAL RESULT**

In this paper there is K-means and DBSCAN clustering algorithm is used for benchmark. The clustering result is
analyzed in terms of CPU run time (in nano seconds), clustered instances, unclustered instances. In the implementation of masTER the two data sets are used. The experimental result will described in following subsections. In the implementation of DEMassDBSCAN and DBSCAN algorithm there are only one parameter is used at one time h for DEMassDBSCAN and ε for DBSCAN. For implementation of DEMassDBSCAN and DBSCAN algorithm we take following data sets that are shown below:

**Pollution Data set:** The Iris data set contains 60 instances and 16 attributes. In the clustering result the run time is better than DBSCAN algorithm that is shown in table 1.

<table>
<thead>
<tr>
<th>Run Time</th>
<th>Cluster</th>
<th>Unassigned</th>
</tr>
</thead>
<tbody>
<tr>
<td>DEMassDBSCAN</td>
<td>0.03</td>
<td>1</td>
</tr>
<tr>
<td>DBSCAN</td>
<td>0.05</td>
<td>6</td>
</tr>
</tbody>
</table>

**Segment Data set:** The Segment Data set contains 2310 instances and 20 attributes. In the clustering result the run time is better than DBSCAN algorithm that is shown in table 2.

<table>
<thead>
<tr>
<th>Run Time</th>
<th>Cluster</th>
<th>Unassigned</th>
</tr>
</thead>
<tbody>
<tr>
<td>DEMassDBSCAN</td>
<td>0.48</td>
<td>3</td>
</tr>
<tr>
<td>DBSCAN</td>
<td>7</td>
<td>1</td>
</tr>
</tbody>
</table>

**Waveform 5000 Data set:** The Pollution Data set contains 5000 instances and 41 attributes. In the clustering result the run time is better than DBSCAN algorithm that is shown in table 3.

<table>
<thead>
<tr>
<th>Run Time</th>
<th>Cluster</th>
<th>Unassigned</th>
</tr>
</thead>
<tbody>
<tr>
<td>DEMassDBSCAN</td>
<td>0.01</td>
<td>13</td>
</tr>
<tr>
<td>DBSCAN</td>
<td>61.08</td>
<td>53</td>
</tr>
</tbody>
</table>

**Mfeat-factors:** The Diabetes data set contains 2000 instances and 217 attributes. In the clustering result the run time is better than DBSCAN algorithm that is shown in table 4.

<table>
<thead>
<tr>
<th>Run Time</th>
<th>Cluster</th>
<th>Unassigned</th>
</tr>
</thead>
<tbody>
<tr>
<td>DEMassDBSCAN</td>
<td>0.6</td>
<td>1</td>
</tr>
<tr>
<td>DBSCAN</td>
<td>8.57</td>
<td>19</td>
</tr>
</tbody>
</table>

On the basis of run time behaviour the DEMass DBSCAN clustering algorithm is better than DBSCAN clustering algorithm. It gives better result when applied on large datasets. The result is shown in Table 5.

<table>
<thead>
<tr>
<th>Run time behaviour</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pollution</td>
</tr>
<tr>
<td>DEMassDBSCAN</td>
</tr>
<tr>
<td>DEMassDBSCAN without PCA</td>
</tr>
<tr>
<td>DBSCAN</td>
</tr>
<tr>
<td>DBSCAN without PCA</td>
</tr>
</tbody>
</table>

The comparison between DEMassDBSCAN And DBSCAN Clustering algorithm is based on their run time is shown below.

**CONCLUSION**

In this paper the runtime behaviour of the DEMassDBSCAN algorithm is better than DBSCAN clustering algorithm. It will give better results on the large data sets. The un-assigned clusters are less than the DBSAN clustering algorithm. The result of the DEMassDBSCAN is efficient and having less noise points out of whole data set. In future mass estimation is applied on other tasks.

**REFERENCES**


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