VASAVI COLLEGE OF ENGINEERING (AUTONOMOUS)

IBRAHIMBAGH, HYDERABAD – 31

Department of computer Science and Engineering

Innovative Teaching Methods

Course: Data Mining **Faculty:** Dr.T.Adilakshmi

Topic: Data Clustering **Class:** B.E. VIII

Innovative Teaching Aid: Mahout

Description: Apache Mahout is a highly scalable machine learning library that enables developers to use optimized algorithms. Mahout implements popular machine learning techniques such as recommendation, classification, and clustering.

Clustering is used to form groups or clusters of similar data based on common characteristics. Clustering is a form of unsupervised learning.

- Search engines such as Google and Yahoo! use clustering techniques to group data with similar characteristics.
- Newsgroups use clustering techniques to group various articles based on related topics.

The clustering engine goes through the input data completely and based on the characteristics of the data, it will decide under which cluster it should be grouped.

URL: https://mahout.apache.org/

Procedure of Clustering

To cluster the given data you need to -

- Start the Hadoop server. Create required directories for storing files in Hadoop File System. (Create directories for input file, sequence file, and clustered output in case of canopy).
- Copy the input file to the Hadoop File system from Unix file system.
- Prepare the sequence file from the input data.
- Run any of the available clustering algorithms.
- Get the clustered data.

1. **Starting Hadoop**

Mahout works with Hadoop, hence make sure that the Hadoop server is up and running.

```
$ cd HADOOP_HOME/bin
$ start-all.sh
```

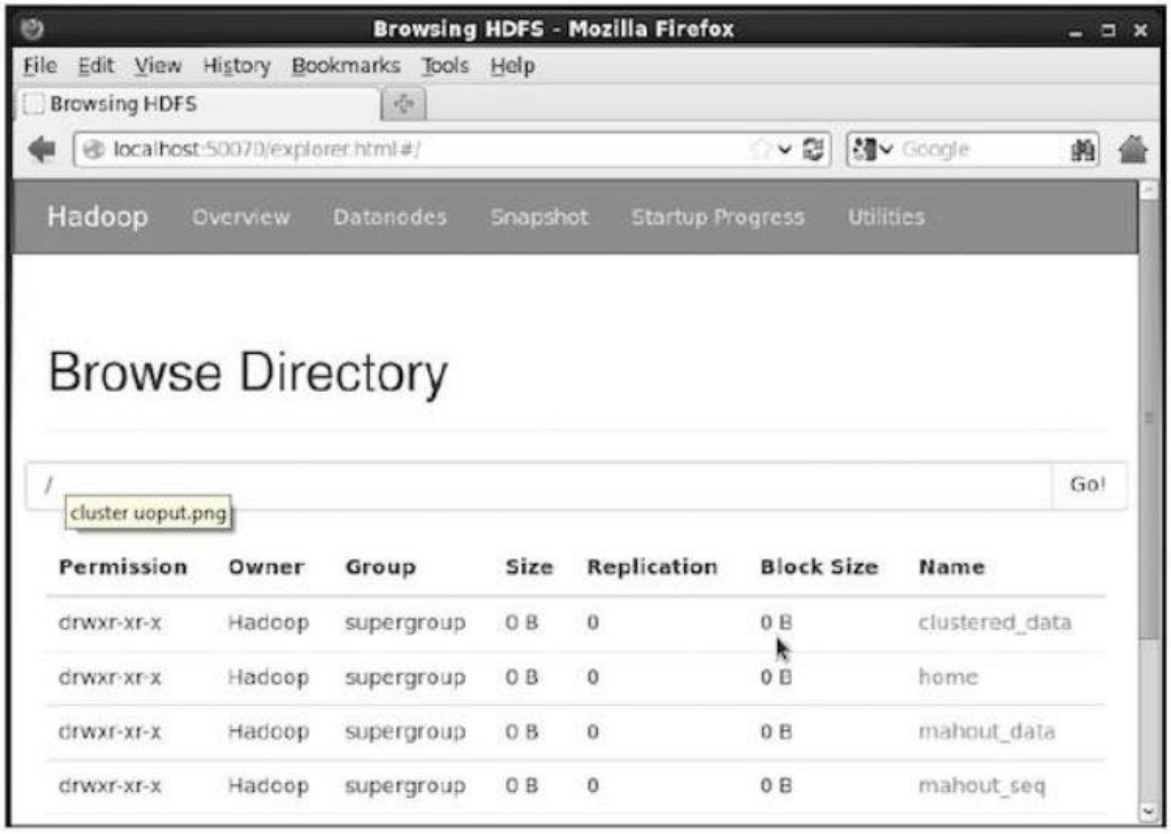
2. **Preparing Input File Directories**

Create directories in the Hadoop file system to store the input file, sequence files, and clustered data using the following command:

$ hadoop fs -p mkdir /mahout_data
$ hadoop fs -p mkdir /clustered_data
$ hadoop fs -p mkdir /mahout_seq

You can verify whether the directory is created using the hadoop web interface in the following URL - **http://localhost:50070/**

It gives you the output as shown below:



3. Copying Input File to HDFS

Now, copy the input data file from the Linux file system to mahout_data directory in the Hadoop File System as shown below. Assume your input file is mydata.txt and it is in the /home/Hadoop/data/ directory.

$ hadoop fs -put /home/Hadoop/data/mydata.txt /mahout_data/

4. Preparing the Sequence File

Mahout provides you a utility to convert the given input file in to a sequence file format. This utility requires two parameters.

- The input file directory where the original data resides.
- The output file directory where the clustered data is to be stored.

Given below is the help prompt of mahout **seqdirectory** utility.

Step 1: Browse to the Mahout home directory. You can get help of the utility as shown below:

[Hadoop@localhost bin]$ ./mahout seqdirectory --help
Job-Specific Options:
--input (-i) input Path to job input directory.
--output (-o) output The directory pathname for output.
--overwrite (-ow) If present, overwrite the output directory

Generate the sequence file using the utility using the following syntax:

mahout seqdirectory -i <input file path> -o <output directory>

Example

mahout seqdirectory
-i hdfs://localhost:9000/mahout_seq/
-o hdfs://localhost:9000/clustered_data/

5. Clustering Algorithms

Mahout supports two main algorithms for clustering namely:

- Canopy clustering
- K-means clustering

Canopy Clustering

Canopy clustering is a simple and fast technique used by Mahout for clustering purpose. The objects will be treated as points in a plain space. This technique is often used as an initial step in other clustering techniques such as k-means clustering. You can run a Canopy job using the following syntax:

mahout canopy -i <input vectors directory>
-o <output directory>
-t1 <threshold value 1>
-t2 <threshold value 2>

Canopy job requires an input file directory with the sequence file and an output directory where the clustered data is to be stored.

Example

mahout canopy -i hdfs://localhost:9000/mahout_seq/mydata.seq
-o hdfs://localhost:9000/clustered_data
-t1 20
-t2 30

You will get the clustered data generated in the given output directory.

K-means Clustering

K-means clustering is an important clustering algorithm. The k in k-means clustering algorithm represents the number of clusters the data is to be divided into. For example, the k value specified to this algorithm is selected as 3, the algorithm is going to divide the data into 3 clusters.

Each object will be represented as vector in space. Initially k points will be chosen by the algorithm randomly and treated as centers, every object closest to each center are clustered. There are several algorithms for the distance measure and the user should choose the required one.

Creating Vector Files

- Unlike Canopy algorithm, the k-means algorithm requires vector files as input, therefore you have to create vector files.
- To generate vector files from sequence file format, Mahout provides the **seq2parse** utility.

Given below are some of the options of **seq2parse** utility. Create vector files using these options.

```
$MAHOUT_HOME/bin/mahout seq2sparse
--analyzerName (-a) analyzerName  The class name of the analyzer
--chunkSize (-chunk) chunkSize    The chunkSize in MegaBytes.
--output (-o) output              The directory pathname for o/p
--input (-i) input                Path to job input directory.
```

After creating vectors, proceed with k-means algorithm. The syntax to run k-means job is as follows:

```
mahout kmeans -i <input vectors directory>
-c  <input clusters directory>
-o  <output working directory>
-dm <Distance Measure technique>
-x  <maximum number of iterations>
-k  <number of initial clusters>
```

K-means clustering job requires input vector directory, output clusters directory, distance measure, maximum number of iterations to be carried out, and an integer value representing the number of clusters the input data is to be divided into.