Assignment 1 Gaurav Singh, 2957104 Mice Protein Expression Data Set

The data set consists of the expression levels of 77 proteins/protein modifications that produced detectable signals in the nuclear fraction of cortex. There are 38 control mice and 34 trisomic mice (Down syndrome), for a total of 72 mice.

In the experiments, 15 measurements were registered of each protein per sample/mouse.

Therefore, for control mice, there are 38x15, or 570 measurements, and for trisomic mice, there are 34x15, or 510 measurements. The dataset contains a total of 1080 measurements per protein. Each measurement can be considered as an independent sample/mouse.

The eight classes of mice are described based on features such as genotype, behaviour and treatment. According to genotype, mice can be control or trisomic. According to behaviour, some mice have been stimulated to learn (context-shock) and others have not (shock-context) and to assess the effect of the drug memantine in recovering the ability to learn in trisomic mice, some mice have been injected with the drug and others have not.

Classes:

c-CS-s: control mice, stimulated to learn, injected with saline (9 mice)

c-CS-m: control mice, stimulated to learn, injected with memantine (10 mice)

c-SC-s: control mice, not stimulated to learn, injected with saline (9 mice)

c-SC-m: control mice, not stimulated to learn, injected with memantine (10 mice)

t-CS-s: trisomy mice, stimulated to learn, injected with saline (7 mice)

t-CS-m: trisomy mice, stimulated to learn, injected with memantine (9 mice)

t-SC-s: trisomy mice, not stimulated to learn, injected with saline (9 mice)

t-SC-m: trisomy mice, not stimulated to learn, injected with memantine (9 mice)

Objective

The aim is to identify subsets of proteins that are discriminant between the classes.

The Attribute types of the data

Mouse ID

78 Values of expression levels of 77 proteins; the names of proteins are followed by indicating that they were measured in the nuclear fraction.

79 Genotype: control (c) or trisomy (t)

80 Treatment type: memantine (m) or saline (s)

81 Behaviour: context-shock (CS) or shock-context (SC)

82 Class: c-CS-s, c-CS-m, c-SC-s, c-SC-m, t-CS-s, t-CS-m, t-SC-s, t-SC-m

Source:

Clara Higuera Department of Software Engineering and Artificial Intelligence, Faculty of Informatics and the Department of Biochemistry and Molecular Biology, Faculty of Chemistry, University Complutense, Madrid, Spain.

Email: clarahiguera@cm.es

Katheleen J. Gardiner, creator and owner of the protein expression data, is currently with the Linda Crnic Institute for Down Syndrome, Department of Pediatrics, Department of Biochemistry and Molecular Genetics, Human Medical Genetics and Genomics, and Neuroscience Programs, University of Colorado, School of Medicine, Aurora, Colorado, USA.

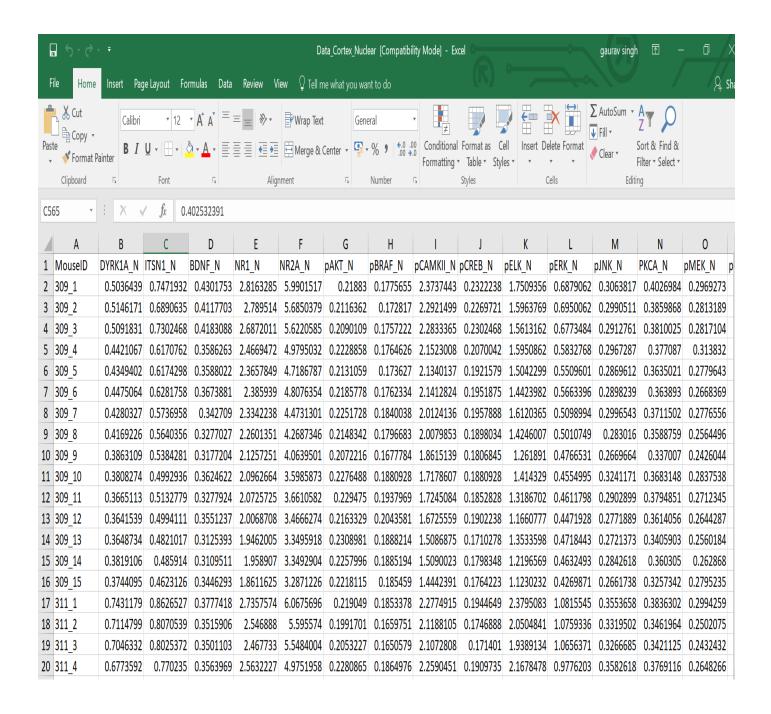
Email: katheleen.gardiner@ucdenver.edu

Krzysztof J. Cios is currently with the Department of Computer Science, Virginia Commonwealth University, Richmond, Virginia, USA, and IITiS Polish Academy of Sciences, Poland.

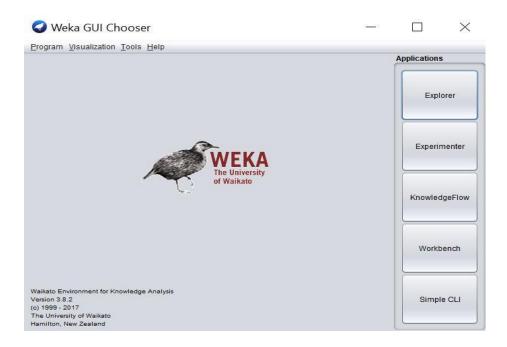
Email: kcios@vcu.edu

Relevant Papers:

- Higuera C, Gardiner KJ, Cios KJ (2015) Self-Organizing Feature Maps Identify Proteins Critical to Learning in a Mouse Model of Down Syndrome.
- Ahmed MM, Dhanasekaran AR, Block A, Tong S, Costa ACS, Stasko M, et al. (2015) Protein Dynamics Associated with Failed and Rescued Learning in the Ts65Dn Mouse Model of Down Syndrome.

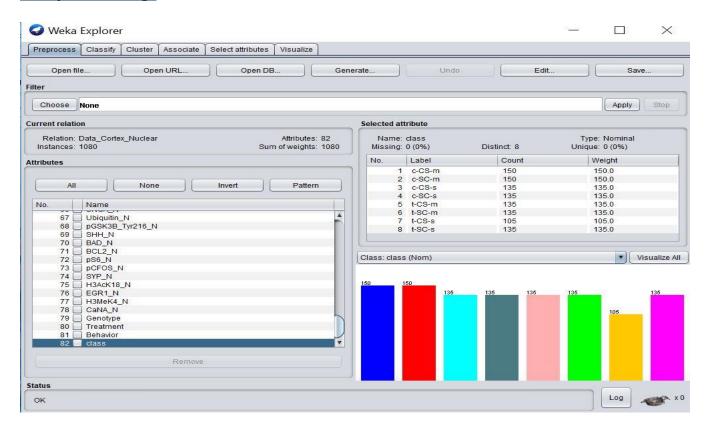


Launch WEKA application and click on the 'Explorer' button.

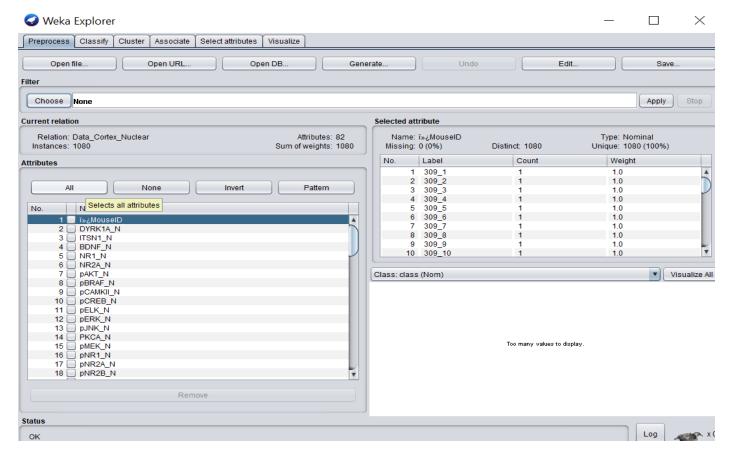


Then load the dataset into WEKA with Open file button and navigate to the directory containing the dataset file and perform the Pre-processing filters.

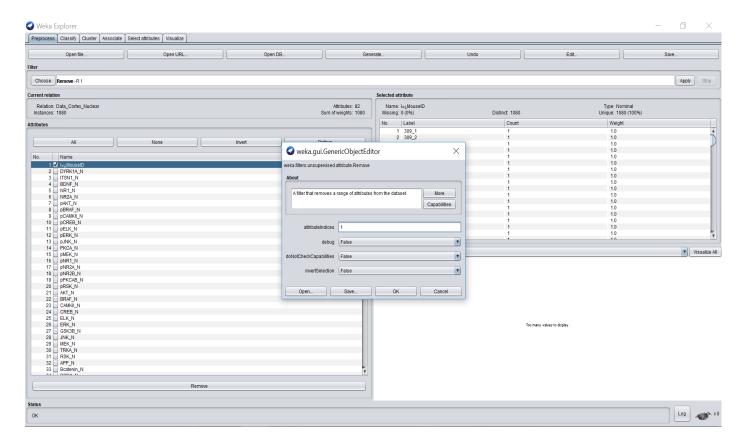
Pre-processing:

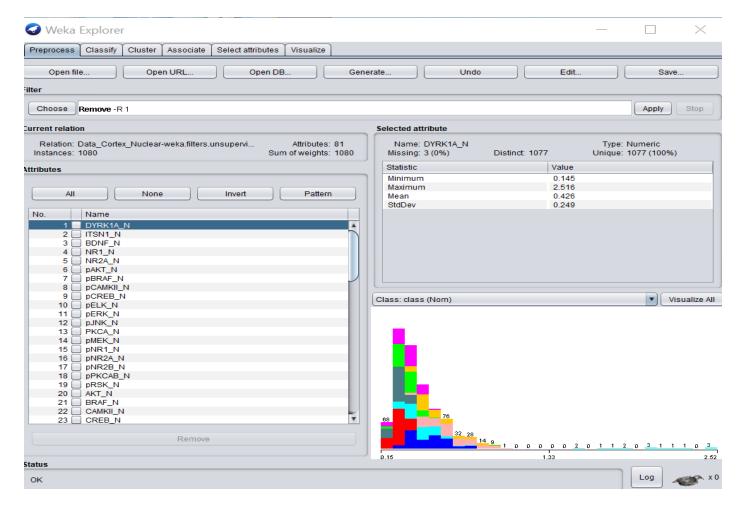


As we can see below the 1st attribute as mouseID need to remove for data mining step by using the Attribute filters in WEKA, which can be done by in the "Filter" panel, click on the "Choose" button and select "weka.filters.unsupervised.attribute.Remove" filter.

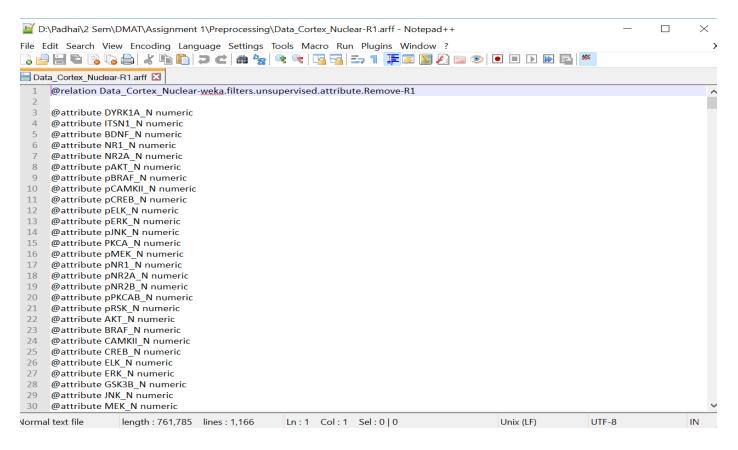


Click on text box immediately to the right of the "Choose" button. In the resulting dialog box enter the index of the attribute to be filtered out. In this case, we enter 1 which is the index of the "id" attribute. Make sure that the "invertSelection" option is set to false. Then click "OK". Now, in the filter box you will see "Remove -R 1" and then click on Apply.





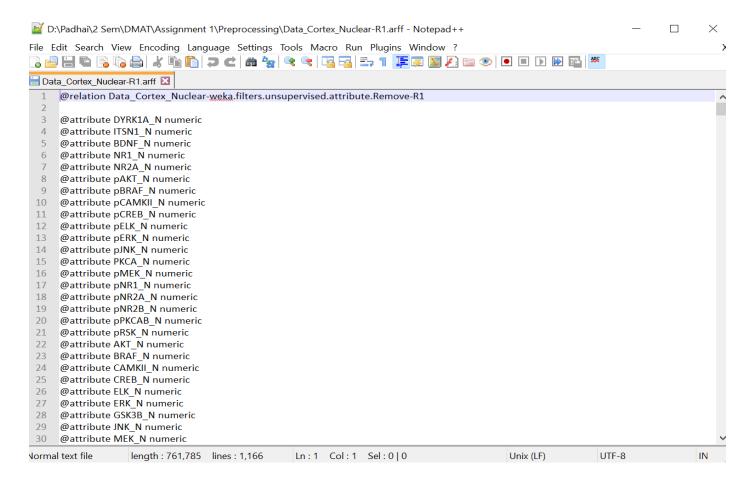
Then save as Data_Cortex_Nuclear-R1.arff and open the file in text editor.



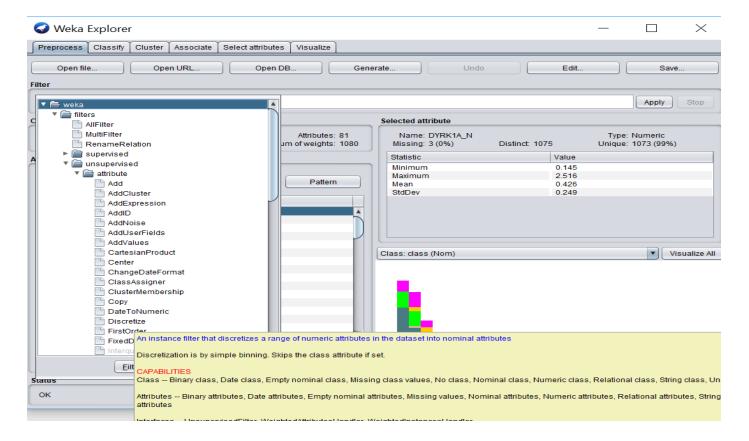
As in the new data set, the "id" attribute and all the corresponding values in the records have been removed.

Discretization

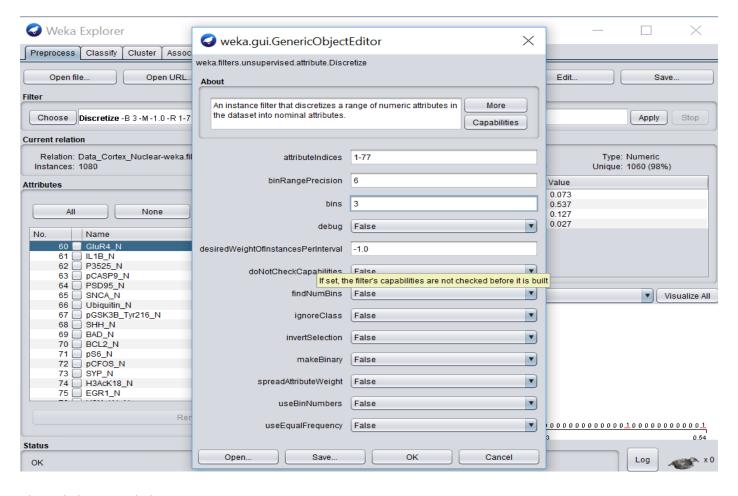
To perform advance techniques such as association rule mining data must be discretized, load the filtered data set into WEKA. There are 77 such attributes in this dataset.



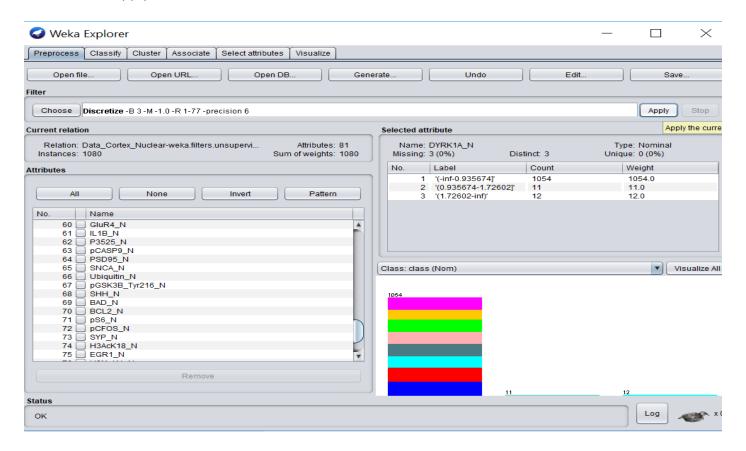
Now to perform Discretization in WEKA, open the filtered data into Weka and select Discretize in Filter.



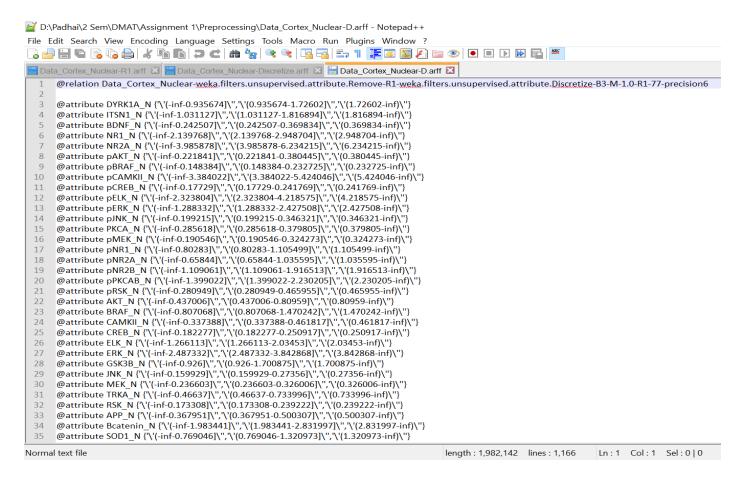
Next, click on the textbox right to the "Choose" button and add 1 to 77 and click on OK button.



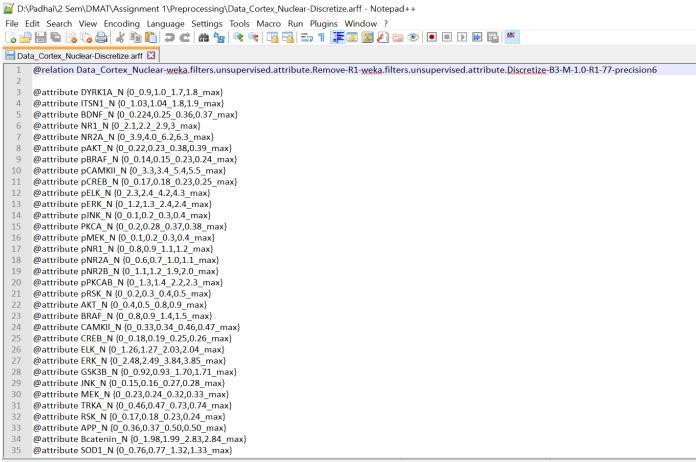
Then click on Apply button.



And then save the file and open into the text editor.



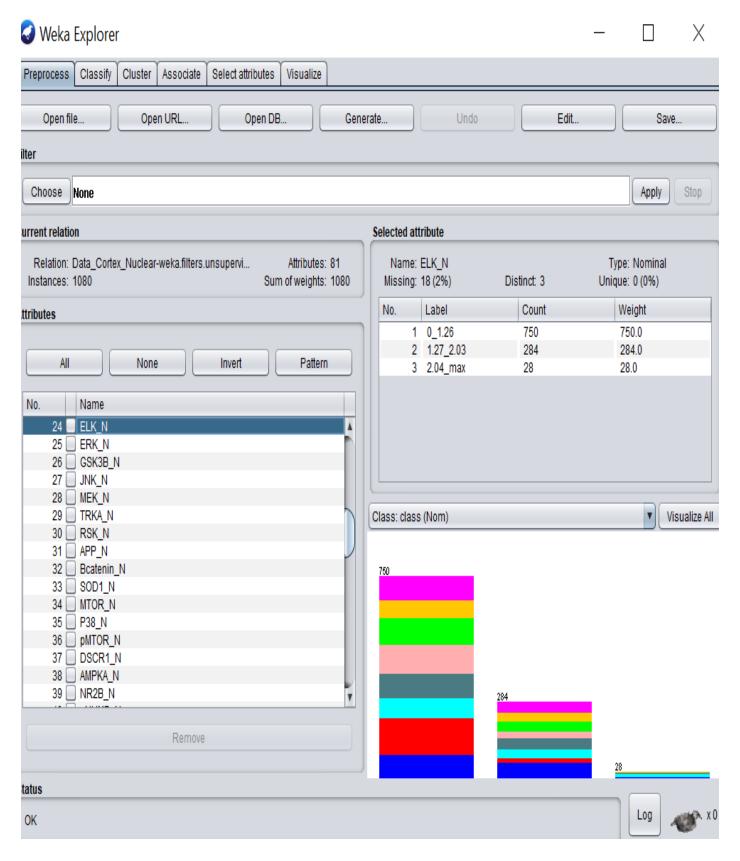
Now filter the data for example, the lower range "(-inf-0.935674)" and so on need to replace manually with more succinct and readable ones.



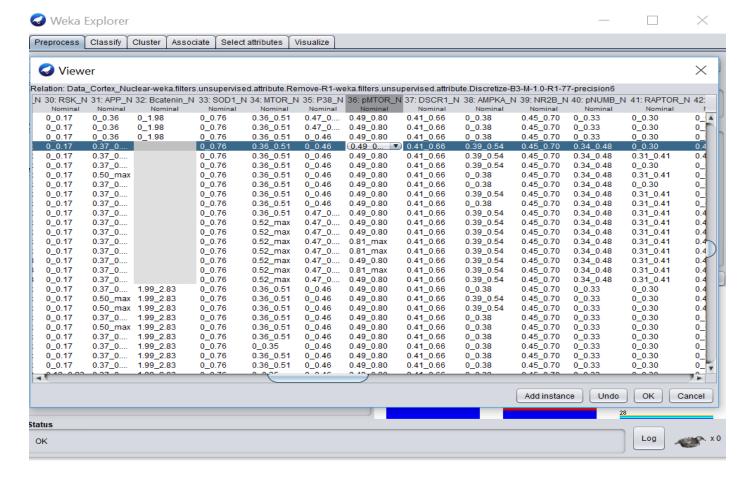
Normal text file | length: 721,282 | lines: 1,166 | Ln:1 | Col:1 | Sel:0 | 0

Missing Values

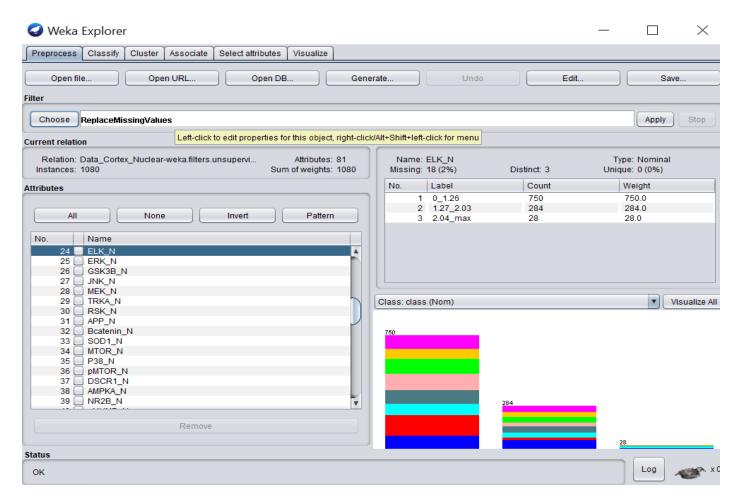
Open the filtered file into WEKA and check if any missing values in any attributes.



Edit data to make some missing values to view the missing values.



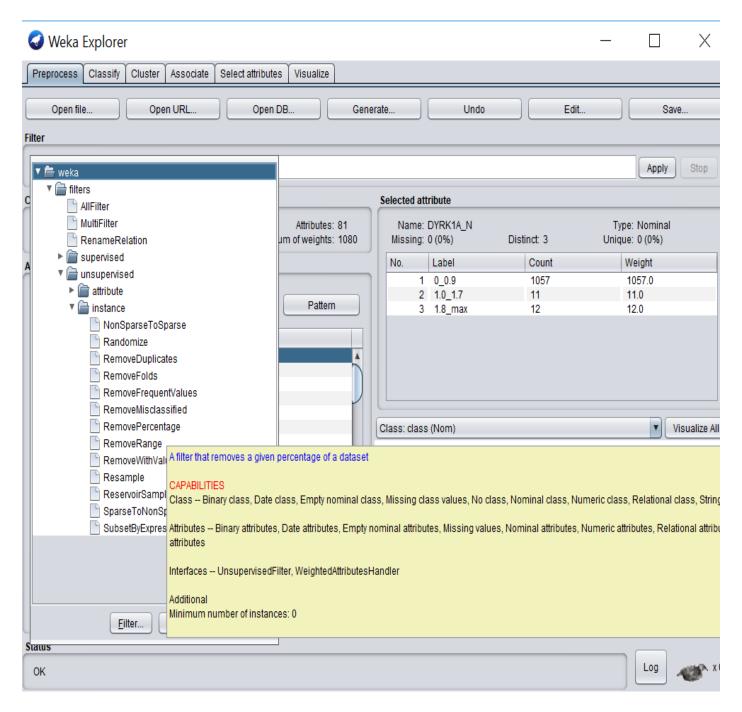
To fill the missing values, choose "ReplaceMissingValues" filter. Then click on Apply button.



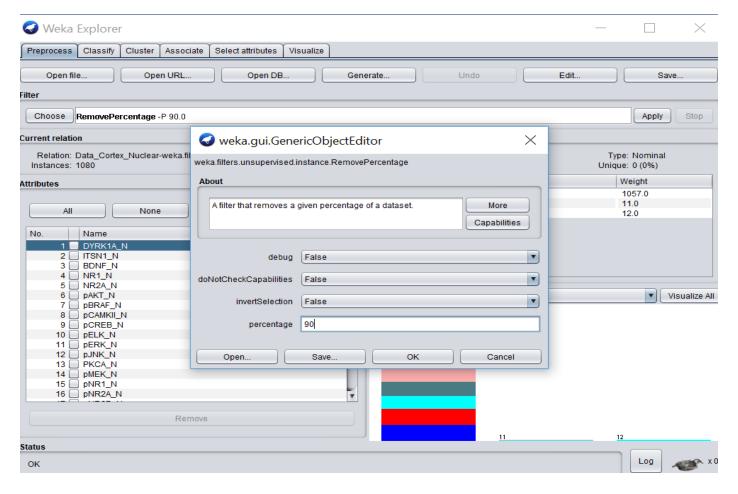
And then save the dataset into dataset.arff.

Divide the dataset into training and test set

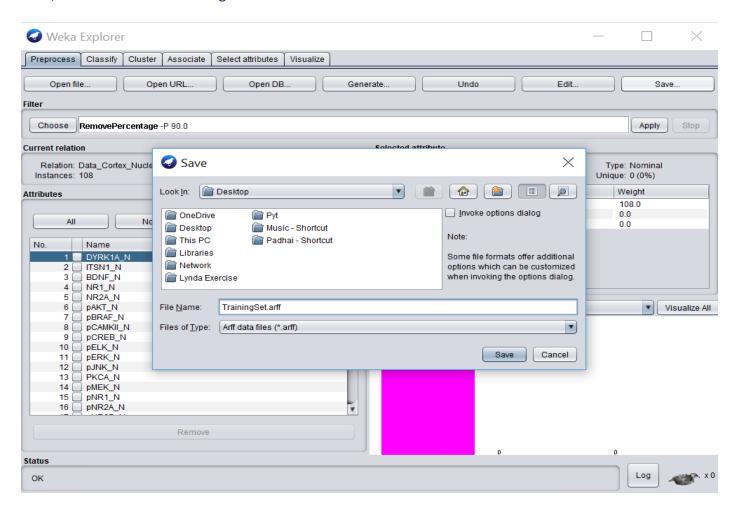
To divide the data set into training and testing, load the dataset into WEKA and choose RemovePercentage.



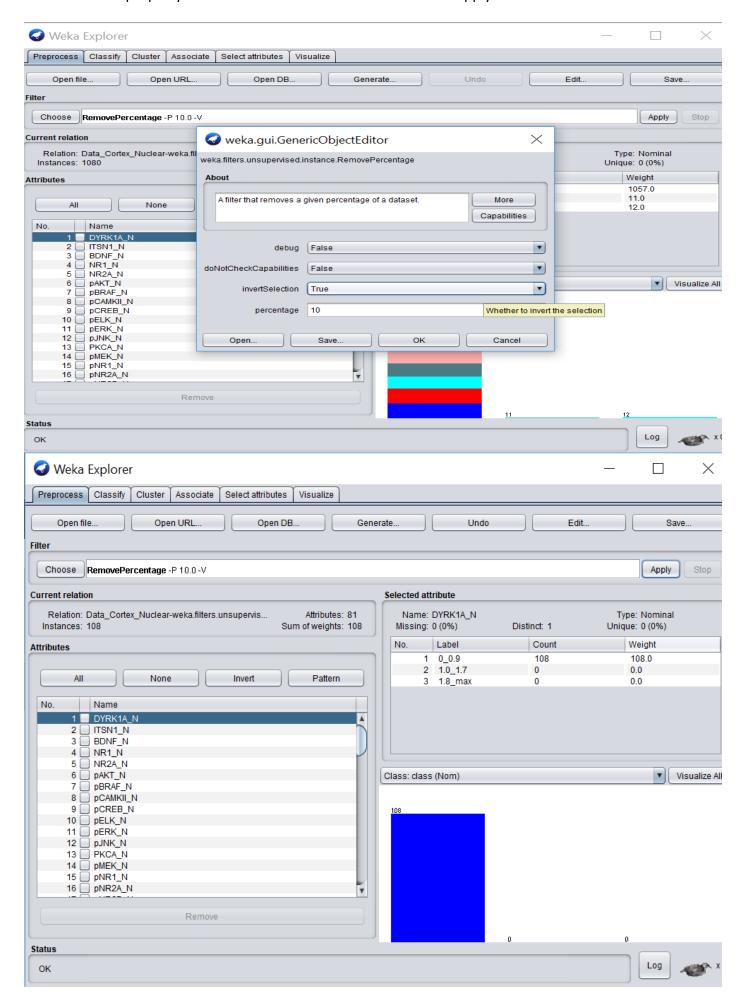
Then click on the text box next to the Choose button and set the correct percentage to 90% then click on OK button and apply.



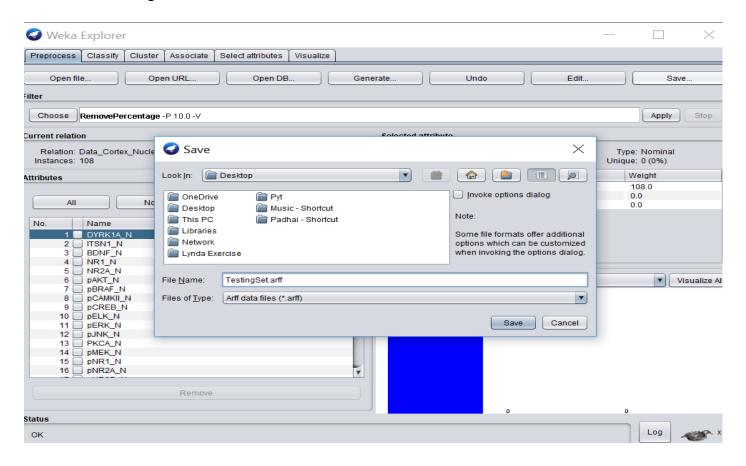
Next, save the file with TrainingSet.arff name.



Then click on Undo to revert the changes and select the RemovePercentage filter if not yet selected set the invertSelection property to true and set the 10% and then click on apply.

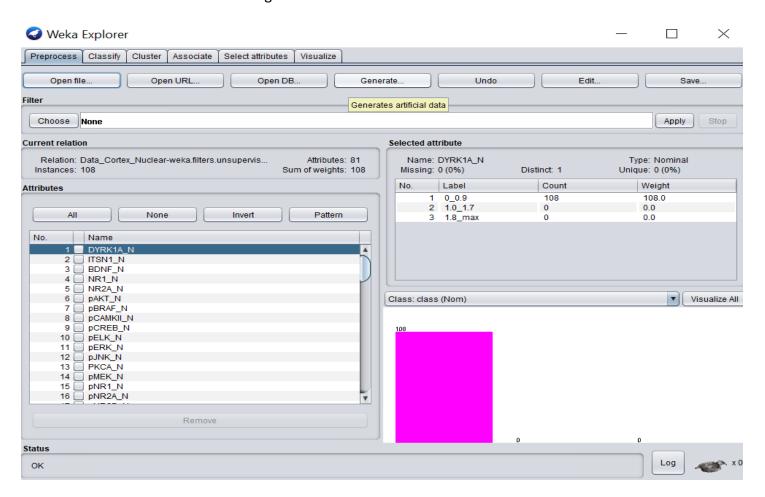


Now save as TestingSet.arff

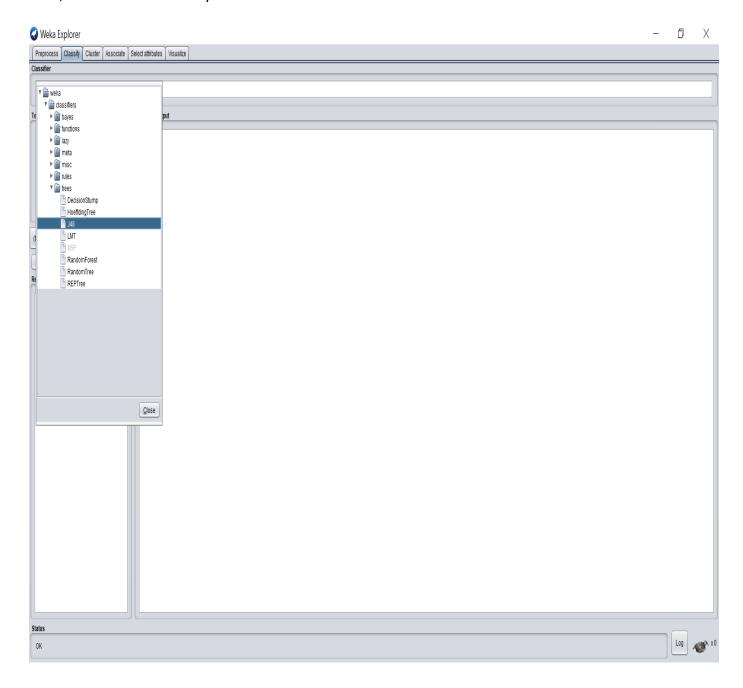


Classification

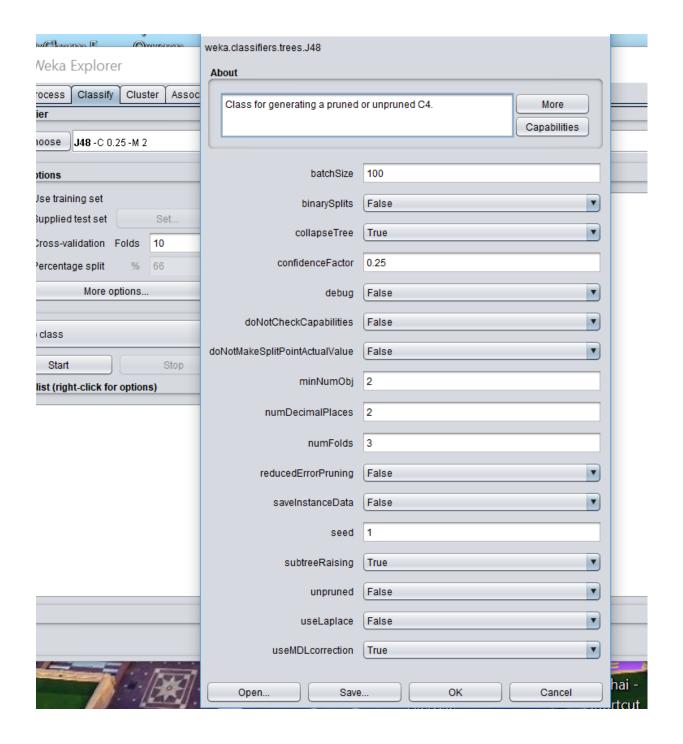
Load the data into WEKA with TrainingSet.arff



Next, we select the "Classify" tab and click the "Choose" button to select the J48 classifier.

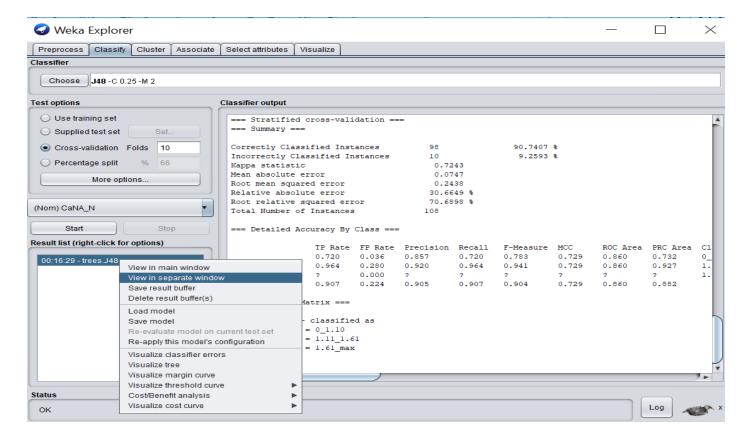


Now, we can specify the various parameters. These can be specified by clicking in the text box to the right of the "Choose" button. In this dataset we accept the default values. The default version does perform some pruning, but does not perform error pruning. Click on OK.



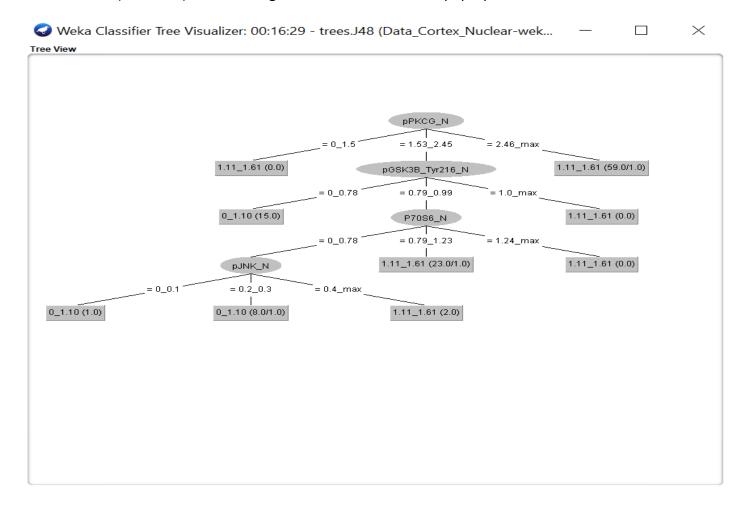
Under the "Test options" in the main panel as by default 10-fold cross-validation as our evaluation approach, then click "Start" to generate the model.

To view the result, right click on the result and select separate window.

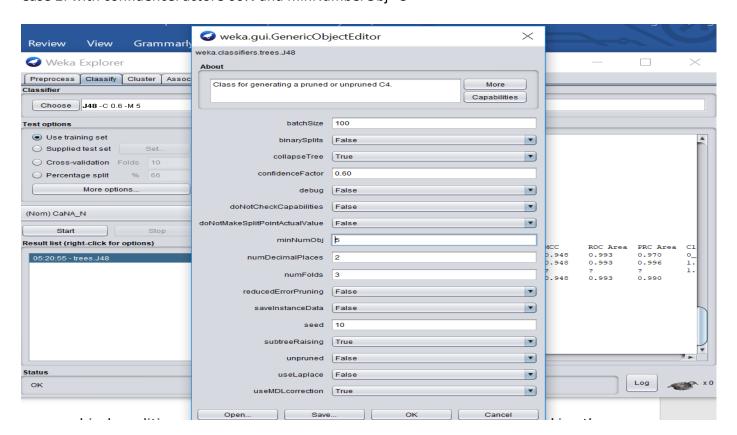


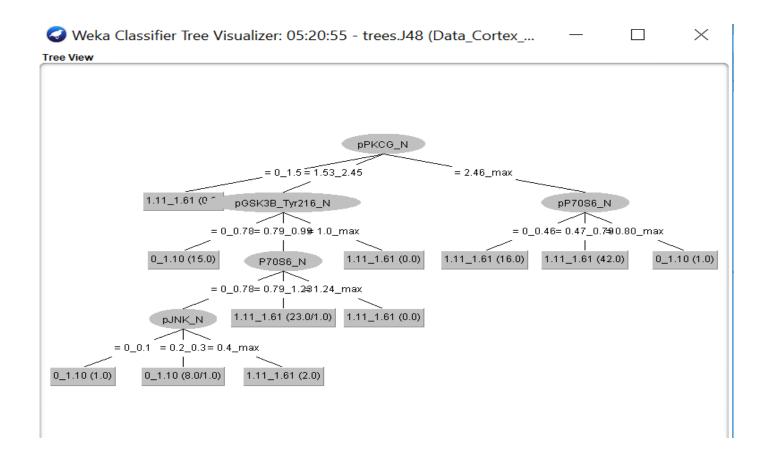
```
00:16:29 - trees.J48
                                                                                                                    \rightarrow
J48 pruned tree
pPKCG_N = 0_1.5: 1.11_1.61 (0.0)
pPKCG_N = 1.53_2.45
   pGSK3B_Tyr216_N = 0_0.78: 0_1.10 (15.0)
   pGSK3B_Tyr216_N = 0.79_0.99
    P70S6_N = 0_0.78
       | pJNK_N = 0.0.1: 0_1.10 (1.0)
| pJNK_N = 0.2_0.3: 0_1.10 (8.0/1.0)
| pJNK_N = 0.4_max: 1.11_1.61 (2.0)
       P70S6_N = 0.79_1.23: 1.11_1.61 (23.0/1.0)
       P70S6_N = 1.24_max: 1.11_1.61 (0.0)
   pGSK3B_Tyr216_N = 1.0_max: 1.11_1.61 (0.0)
pPKCG_N = 2.46_max: 1.11_1.61 (59.0/1.0)
Number of Leaves :
Size of the tree :
                       13
Time taken to build model: 0.03 seconds
 === Stratified cross-validation ===
=== Summary ===
                                                         90.7407 %
Correctly Classified Instances
Incorrectly Classified Instances
                                                          9.2593 %
                                         0.7243
Kappa statistic
Mean absolute error
                                         0.0747
Root mean squared error
                                         0.2438
Relative absolute error
                                        30.6649 %
Root relative squared error
                                        70.6898 %
Total Number of Instances
                                      108
=== Detailed Accuracy By Class ===
                TP Rate FP Rate Precision Recall F-Measure MCC
                                                                           ROC Area PRC Area Class
                 0.720 0.036 0.857
                                                       0.783
                                                                  0.729
                                                                           0.860
                                                                                     0.732
                                              0.720
                                                                                               0 1.10
                 0.964
                          0.280
                                  0.920
                                              0.964
                                                      0.941
                                                                  0.729
                                                                           0.860
                                                                                     0.927
                                                                                               1.11 1.61
                          0.000
                                                                                               1.61 max
                0.907
                                 0.905
                                            0.907
                                                     0.904
                                                                0.729
                                                                           0.860
                                                                                   0.882
Weighted Avg.
                        0.224
=== Confusion Matrix ===
           <-- classified as
  a b c
 18 7 0 | a = 0_1.10
 3 80 0 | b = 1.11_1.61
```

WEKA also lets us view a graphical rendition of the classification tree. This can be done by right clicking the last result set (as before) and selecting "Visualize tree" from the pop-up menu.

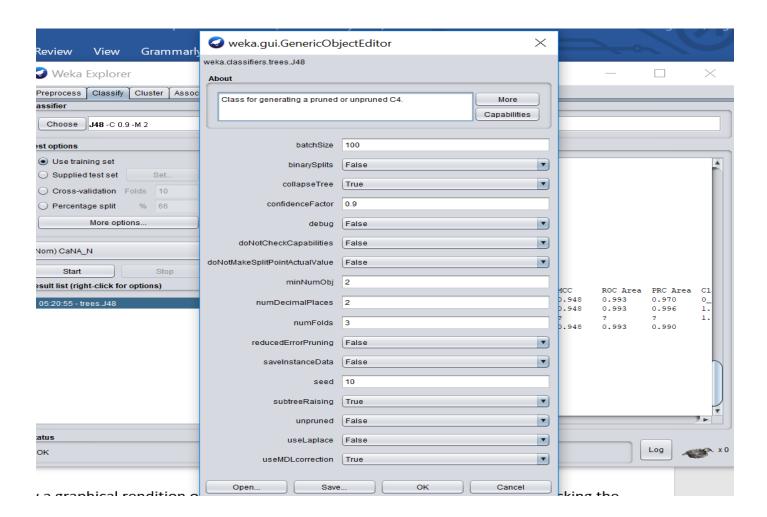


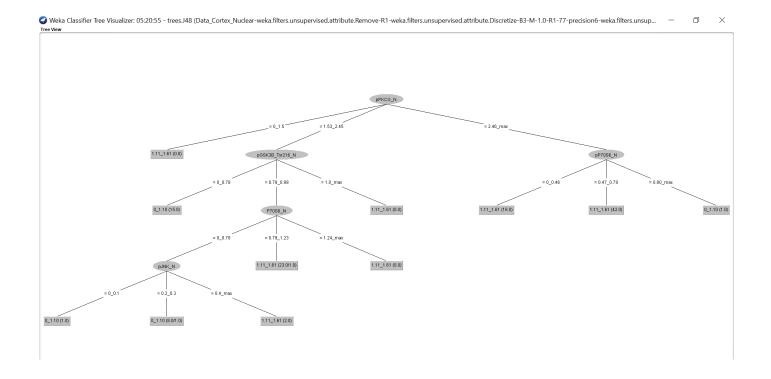
Case 2: with confidenceFactore 60% and minNumberObj =5





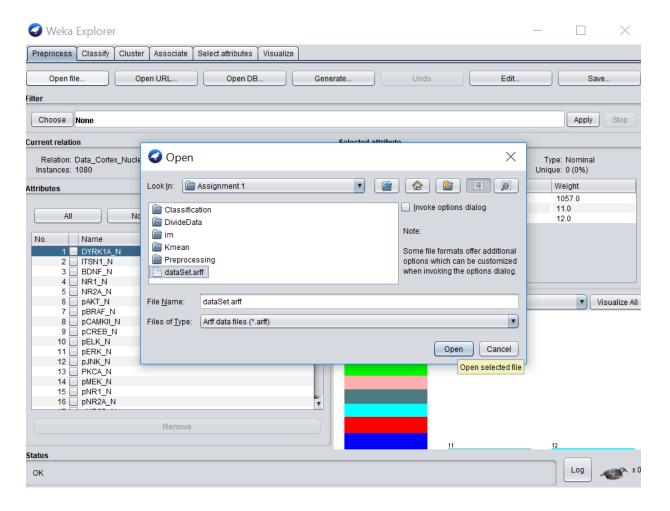
Case 3: with confidenceFactore 90% and minNumberObj =2



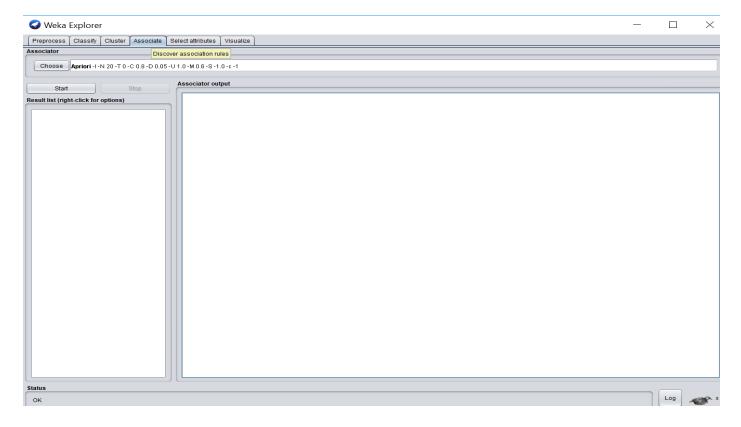


Association Rules:

Load the dataset in WEKA



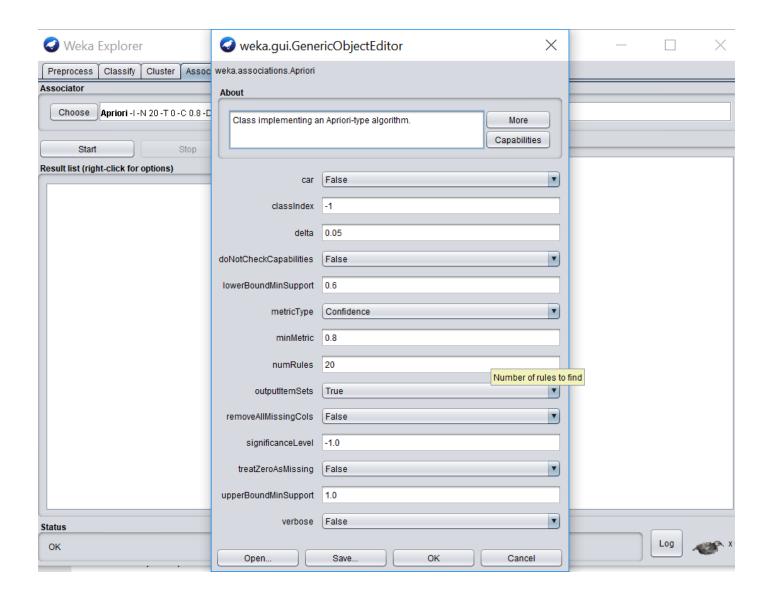
In Weka, then select Associate tab.

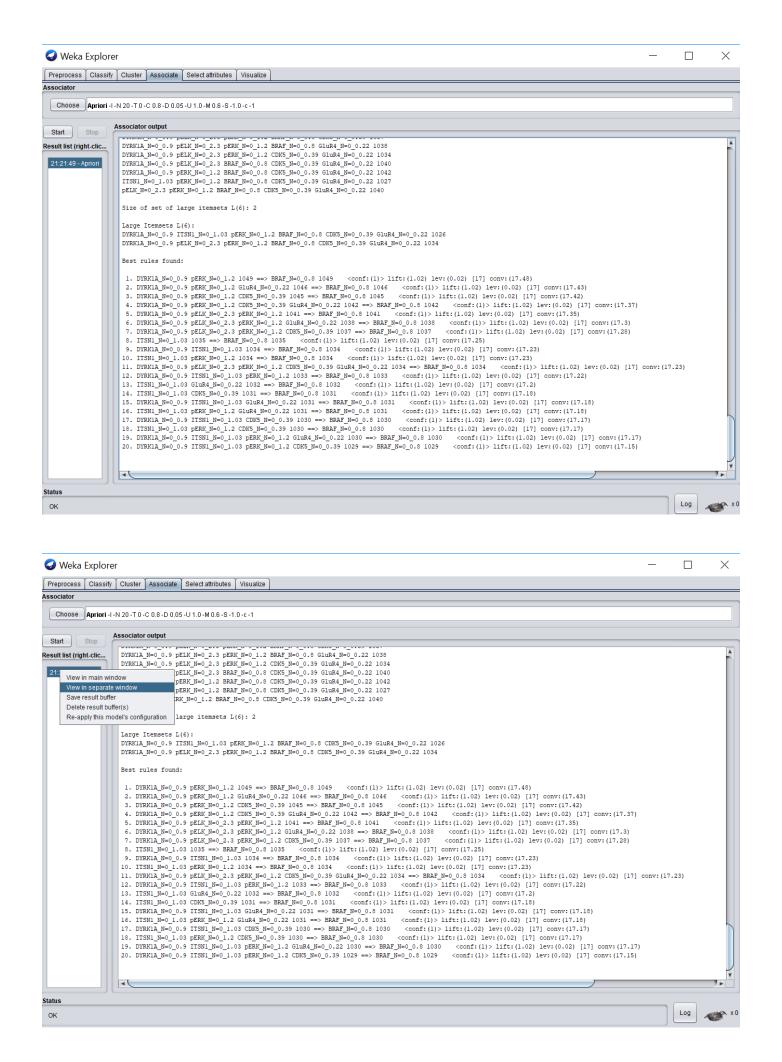


Then make sure Apriori is selected. If not then need to Choose Apriori algorithm. Then click on the text box right to the Choose button. To test the dataset with values, need to set the Apriori editor.

To test the dataset

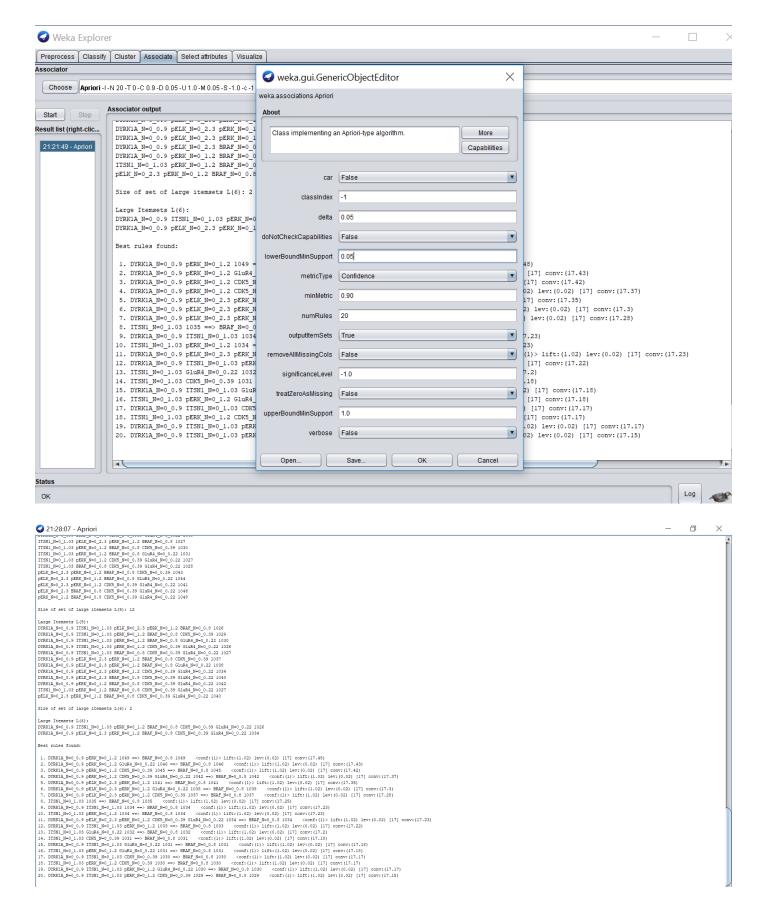
Case 1: 60% minimum support threshold and with 80% minimum confidence threshold Therefore, set the lowerBoundMinSupport: 0.6 and minMetric: 0.80 with metricType: Confidence And set the outputItemSets: True



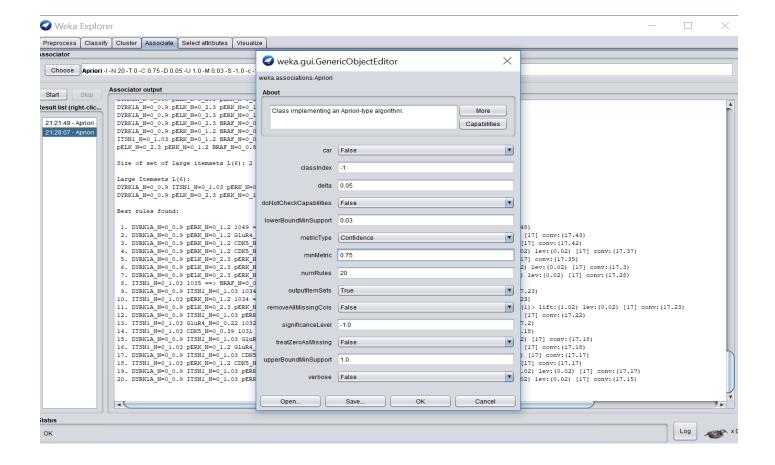


```
ITSN1_N=0_1.03 pELK_N=0_2.3 pERK_N=0_1.2 BRAF_N=0_0.8 1027
ITSN1_N=0_1.03 pERK_N=0_1.2 BRAF_N=0_0.8 CDK5_N=0_0.39 1030
ITSN1_N=0_1.03 pERK_N=0_1.2 BRAF_N=0_0.8 GluR4_N=0_0.22 1031
ITSN1_N=0_1.03 pERK_N=0_1.2 CDK5_N=0_0.39 GluR4_N=0_0.22 1027
ITSN1 N=0 1.03 BRAF N=0 0.8 CDK5 N=0 0.39 GluR4 N=0 0.22 1028
pELK_N=0_2.3 pERK_N=0_1.2 BRAF_N=0_0.8 CDK5_N=0_0.39 1043
pELK_N=0_2.3 pERK_N=0_1.2 BRAF_N=0_0.8 GluR4_N=0_0.22 1044
pELK_N=0_2.3 pERK_N=0_1.2 CDK5_N=0_0.39 GluR4_N=0_0.22 1041
pELK_N=0_2.3 BRAF_N=0_0.8 CDK5_N=0_0.39 GluR4_N=0_0.22 1046
pERK N=0 1.2 BRAF N=0 0.8 CDK5 N=0 0.39 GluR4 N=0 0.22 1048
Size of set of large itemsets L(5): 12
Large Itemsets L(5):
DYRK1A_N=0_0.9 ITSN1_N=0_1.03 pELK_N=0_2.3 pERK_N=0_1.2 BRAF_N=0_0.8 1026
DYRK1A_N=0_0.9 ITSN1_N=0_1.03 pERK_N=0_1.2 BRAF_N=0_0.8 CDK5_N=0_0.39 1029
DYRK1A_N=0_0.9 ITSN1_N=0_1.03 pERK_N=0_1.2 BRAF_N=0_0.8 GluR4_N=0_0.22 1030
DYRK1A_N=0_0.9 ITSN1_N=0_1.03 pERK_N=0_1.2 CDK5_N=0_0.39 GluR4_N=0_0.22 1026
DYRKIA_N=0_0.9 ITSN1_N=0_1.03 BRAF_N=0_0.8 CDK5_N=0_0.39 GluR4_N=0_0.22 1027
DYRK1A_N=0_0.9 pELK_N=0_2.3 pERK_N=0_1.2 BRAF_N=0_0.8 CDK5_N=0_0.39 1037
DYRK1A_N=0_0.9 pELK_N=0_2.3 pERK_N=0_1.2 BRAF_N=0_0.8 GluR4_N=0_0.22 1038
DYRKIA_N=0_0.9 pELK_N=0_2.3 pERK_N=0_1.2 CDK5_N=0_0.39 GluR4_N=0_0.22 1034
DYRK1A_N=0_0.9 pELK_N=0_2.3 BRAF_N=0_0.8 CDK5_N=0_0.39 GluR4_N=0_0.22 1040
DYRKIA N=0 0.9 pERK N=0 1.2 BRAF N=0 0.8 CDK5 N=0 0.39 GluR4 N=0 0.22 1042
ITSN1_N=0_1.03 pERK_N=0_1.2 BRAF_N=0_0.8 CDK5_N=0_0.39 GluR4_N=0_0.22 1027
pELK_N=0_2.3 pERK_N=0_1.2 BRAF_N=0_0.8 CDK5_N=0_0.39 GluR4_N=0_0.22 1040
Size of set of large itemsets L(6): 2
DYRK1A_N=0_0.9 ITSN1_N=0_1.03 pERK_N=0_1.2 BRAF_N=0_0.8 CDK5_N=0_0.39 GluR4_N=0_0.22 1026
DYRK1A_N=0_0.9 pELK_N=0_2.3 pERK_N=0_1.2 BRAF_N=0_0.8 CDK5_N=0_0.39 GluR4_N=0_0.22 1034
1. DYRKIA N=0 0.9 pERK N=0 1.2 1049 ==> BRAF N=0 0.8 1049
                                            <conf:(1)> lift:(1.02) lev:(0.02) [17] conv:(17.48)
5. DYRK1A_N=0_0.9 pELK_N=0_2.3 pERK_N=0_1.2 1041 ==> BRAF_N=0_0.8 1041 <conf:(1)> lift:(1.02) lev:(0.02) [17] conv:(17.35)
7. DYRK1A_N=0_0.9 pelk_N=0_2.3 perk_N=0_1.2 CDK5_N=0_0.39 1037 ==> BRAF_N=0_0.8 1037
8. ITSN1_N=0_1.03 1035 ==> BRAF_N=0_0.8 1035
                                   <conf:(1)> lift:(1.02) lev:(0.02) [17] conv:(17.25)
<conf:(1)> lift:(1.02) lev:(0.02) [17] conv:(17.23)
19. DYRK1A_N=0_0.9 ITSN1_N=0_1.03 pERK_N=0_1.2 GluR4_N=0_0.22 1030 ==> BRAF_N=0_0.8 1030 <conf:(1)> lift:(1.02) lev:(0.02) [17] conv:(17.17)
20. DYRK1A_N=0_0.9 ITSN1_N=0_1.03 pERK_N=0_1.2 CDK5_N=0_0.39 1029 ==> BRAF_N=0_0.8 1029
                                                                  <conf:(1)> lift:(1.02) lev:(0.02) [17] conv:(17.15)
```

Case 2: With lowerBoundMinSupport: 0.05 and minMetric: 0.90



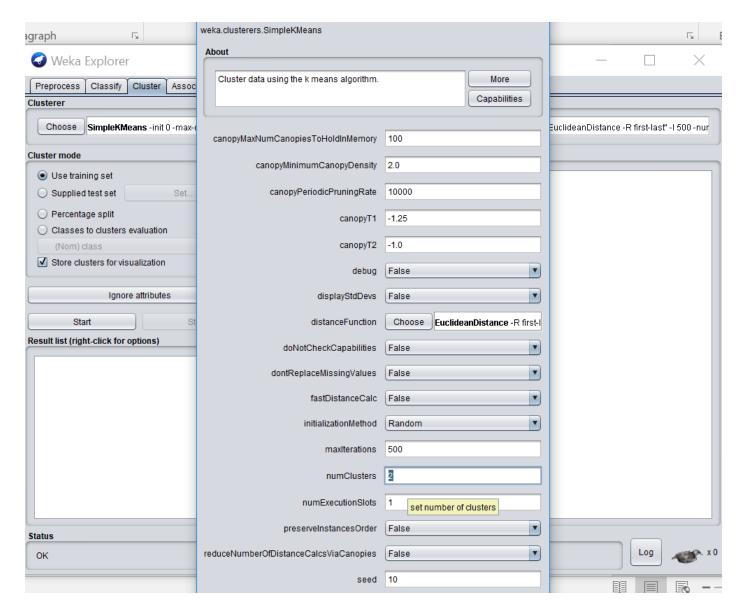
Case 3: minMetricwithConfidence: 0.75, lowerBoundMinSupport: 0.03



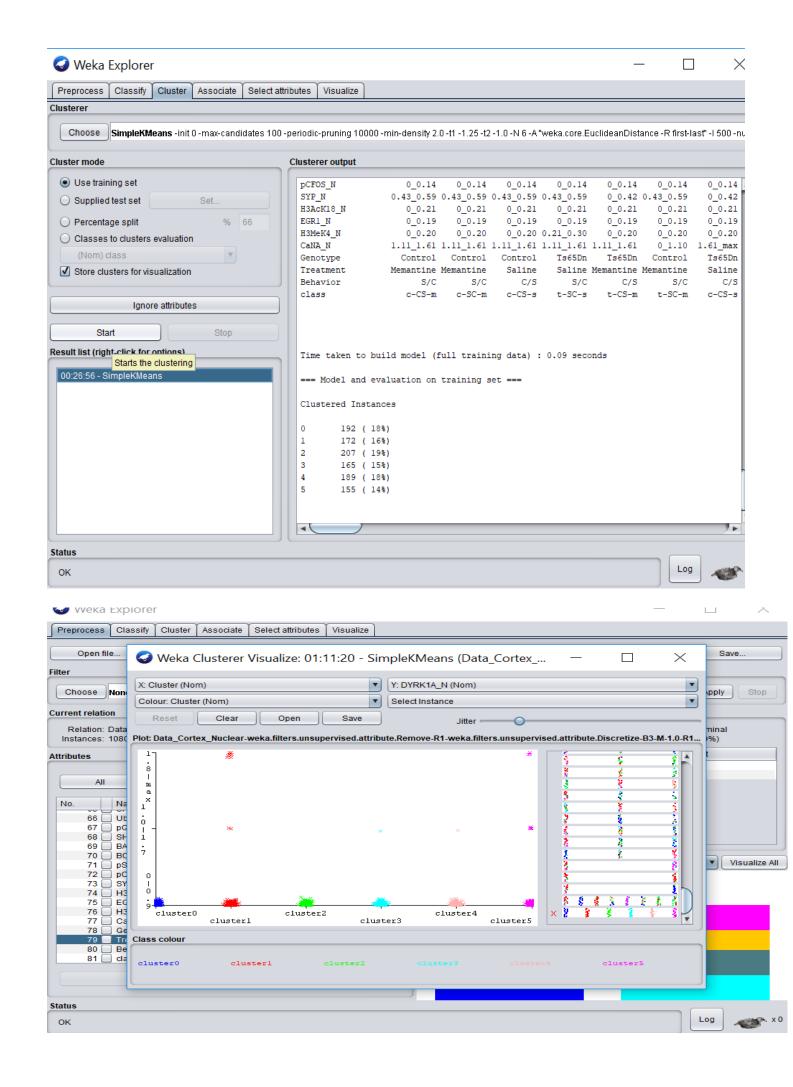
```
Behavior
              class
  == Associator model (full training set) ===
Apriori
Minimum support: 0.95 (1026 instances)
Minimum metric <confidence>: 0.75
Number of cycles performed: 1
Generated sets of large itemsets:
Size of set of large itemsets L(1): 7
Large Itemsets L(1):
DYRK1A_N=0_0.9 1057
ITSN1_N=0_1.03 1035
pELK_N=0_2.3 1056
pERK_N=0_1.2 1057
BRAF_N=0_0.8 1062
CDK5 N=0 0.39 1076
GluR4_N=0_0.22 1077
Size of set of large itemsets L(2): 21
Large Itemsets L(2):
DYRK1A_N=0_0.9 ITSN1_N=0_1.03 1034
DYRK1A_N=0_0.9 pELK_N=0_2.3 1048
DYRK1A_N=0_0.9 pERK_N=0_1.2 1049
DYRK1A_N=0_0.9 BRAF_N=0_0.8 1056
DYRK1A N=0 0.9 CDK5 N=0 0.39 1053
DYRK1A_N=0_0.9 GluR4_N=0_0.22 1054
ITSN1_N=0_1.03 pELK_N=0_2.3 1028
ITSN1_N=0_1.03 pERK_N=0_1.2 1034
ITSN1_N=0_1.03 BRAF_N=0_0.8 1035
ITSN1_N=0_1.03 CDK5_N=0_0.39 1031
ITSN1 N=0 1.03 GluR4 N=0 0.22 1032
pELK_N=0_2.3 pERK_N=0_1.2 1048
pELK_N=0_2.3 BRAF_N=0_0.8 1053
pELK_N=0_2.3 CDK5_N=0_0.39 1052
pELK_N=0_2.3 GluR4_N=0_0.22 1053
pERK_N=0_1.2 BRAF_N=0_0.8 1055
pERK_N=0_1.2 CDK5_N=0_0.39 1053
pERK_N=0_1.2 GluR4_N=0_0.22 1054
BRAF N=0 0.8 CDK5 N=0 0.39 1058
BRAF_N=0_0.8 GluR4_N=0_0.22 1059
CDK5_N=0_0.39 GluR4_N=0_0.22 1073
Size of set of large itemsets L(3): 33
Large Itemsets L(3):
DYRK1A_N=0_0.9 ITSN1_N=0_1.03 pELK_N=0_2.3 1027
DYRKIA N=0 0.9 ITSN1 N=0 1.03 pERK N=0 1.2 1033
DYRK1A_N=0_0.9 ITSN1_N=0_1.03 BRAF_N=0_0.8 1034
DYRK1A N=0 0.9 ITSN1 N=0 1.03 CDK5 N=0 0.39 1030
```

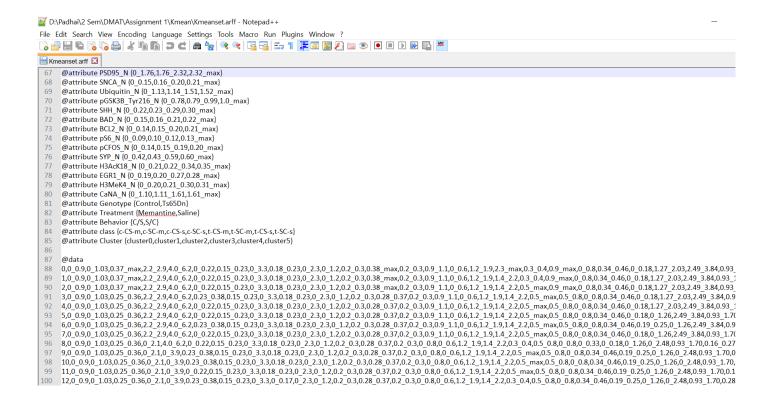
K-Mean

To perform clustering, select the "Cluster" tab in the Explorer and click on the "Choose" button. This results in a drop-down list of available clustering algorithms. In this case we select "SimpleKMeans". Next, click on the text box to the right of the "Choose" button to get the pop-up window.



In the pop-up window we enter 6 as the number of clusters (instead of the default values of 2) and we leave the value of "seed" default. Then click OK and Start the test.





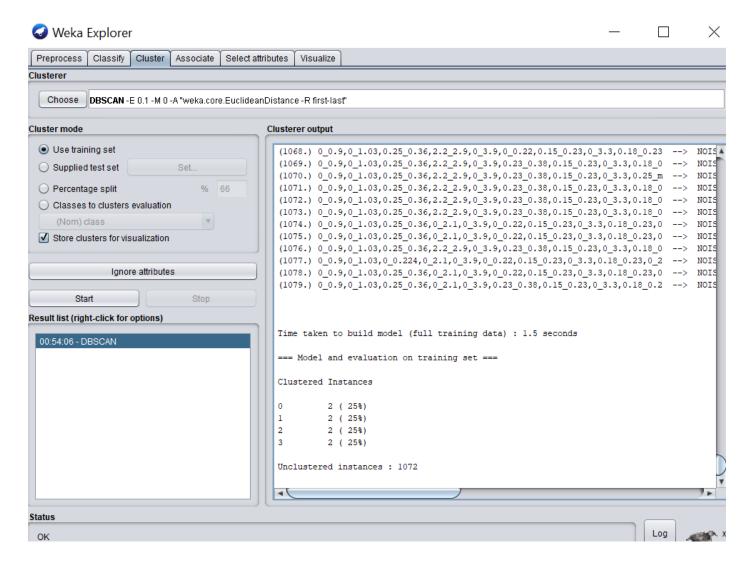
In Kmean, set the number of cluster 6 in which are very small in size, cluster 2 is the biggest among them with 19%. With visualization, it is difficult to determine graphically as they are very small in size. In the text editor, we can see that each instance have now its cluster.

6 2.32,0 0.15,0 1.13,0.79 0.99,0 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0.43 0.59,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster1 2.32,0 0.15,0 1.13,0.79 0.99,0 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0.43 0.59,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster1 4.2.0,1.76 2.32,0 0.15,0 1.13,0.79 0.99,0 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0.42 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,luster1 1.32,0 0.15,0 1.13,0.79 0.99,0 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0.42,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster1 1.32,0 0.15,0 1.13,0.79 0.99,0 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0.43 0.59,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster5 1.5,0 1.13,0.79 0.99,0 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0.43 0.59,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster5 1.2,0 0.15,0 1.13,0.79 0.99,0 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0.42,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster5 1.13,0.79 0.99,0 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0 0.42,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster5 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0 0.42,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster5 1.13,0.79 0.99,0 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0 0.42,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster5 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0.42,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster5 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0 0.42,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster5 0.22,0 0.15,0 0.14,0.10 0.12,0 0.14,0 0.42,0 0.21,0 0.19,0 0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster2 0.99,0 0.22,0.16 0.21,0 0.14,0.10 0.12,0 0.14,0.0.90,0 0.14,0.0.20,0.21,0.019,0 0.20,1.11 1.61,Control,Memantine,C/S,c-CS-m,cluster5 0.90,0 0.22,0.16 0.21,0 0.14,0.10 0.12,0 0.14,0.0.90,0 0.21,0.20 0.27,0.20,1.61 max,Control,Memantine,C/S,c-CS-m,cluster5 0.90,0 0.22,0.16 0.21,0 0.14,0.10 0.12,0 0.14,0.0.90,0 0.21,0.20 0.27,0.21,0.20 0.27,0.20,1.

DBSCAN

Epsilon: 0.02 minPoint: 2

Number of Clusters: 4 Unclustered: 1072



With DBscan the dataset generates only 4 clusters with equal size as 2. Tried with other values it generates 0 clusters.