BIDEAL: DETAILED USER GUIDE

1. Download BIDEAL Package from the link provided below and unzip:

- BIDEAL Windows version
- BIDEAL Linux version

2. Prerequisites for BIDEAL

- Verify that the required MATLAB runtime version is installed in your system. If it is not installed, then run *MyAppInstaller_mcr* packaged in the BIDEAL package.

NOTE: The system needs administrator right to run *MyAppInstaller_mcr*. This will install the required MATLAB runtime complier version in the system.

3. BIDEAL Execution Steps

Step 1. Open Graphical User Interface (GUI) of BIDEAL as follows:

- For Windows: Double click on BIDEAL_GUI.exe
- For Linux: Open Linux command prompt and type ./run_BIDEAL.sh <mcr_directory>.

NOTE: <mcr_directory> is the directory where the MATLAB runtime version 9.4 is installed.
For example: ./run_BIDEAL.sh /mathworks/home/application/v94

Step 2. Load the dataset.

Step 3. Preprocess the data as required using preprocessing options available.

Step 4. Select the biclustering algorithm to be executed. If needed, change the parameters of the algorithm. However, the default values of the parameters are already provided.

Step 5. After execution, Result window will appear.

Step 6. A dialogue box will pop up to save the result in .mat file. These results can be validated and visualized if required.

4. Input /Output Details

Input:

- User can load the data in .txt/.csv/.dat/.data-numeric format. The data must consist of numerical values corresponding to the genes for different conditions.
- A sample dataset i.e. Gene Expression Data is also provided in the package.

Output:

- The results will appear in a new pop up window.
- The rows and columns indices of gene expression dataset with their corresponding bicluster number will be automatically saved in a two different .csv files. The results can be validated and visualized.

5. Visualization

User can visualize biclusters using “*Bicluster Visualization*” button from the main user interface. There are three biclusters visualization options present in the Visualization user interface as follows:

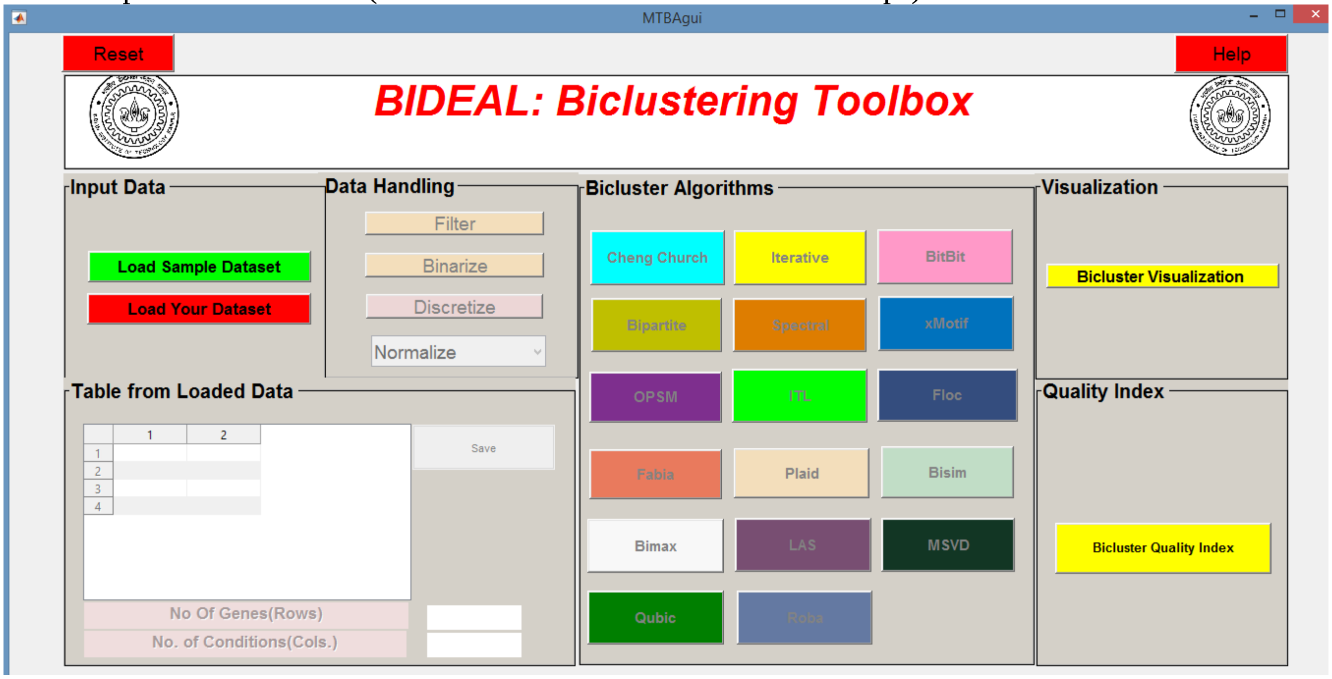
- **Plot HeatMap:** To plot HeatMap insert the desired index of bicluster in the edit box and click on “*Plot HeatMap*”.
- **Plot Cluster:** Provide the desired index of bicluster in the edit box and then click on the “*Plot Cluster*” button for plotting the mean and median values. This can also be saved as a picture.
- **Plot Gene Profile:** Gene Expression Profile can be plotted by loading a result file and giving particular bicluster index in edit box.
- **Show Bicluster:** To display bicluster as a numerical matrix, load the previously saved “*.mat”* file and provide the desired no of index of bicluster to the edit box. Then click on “Show Bicluster” button.

6. Validation

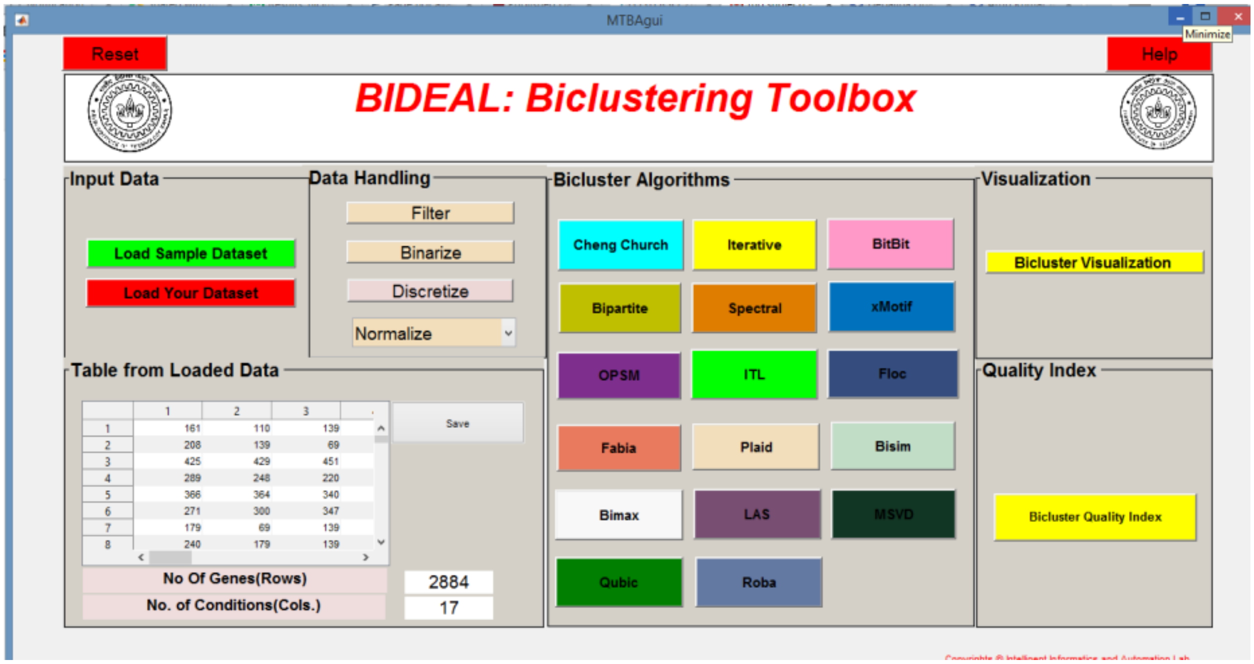
- User has six different options for measuring the quality of bicluster. Click on “*Bicluster Quality Index*” button to open validation. Then select the pre-stored result and click on “Calculate” button. Biclusterwise and overall measure value will be appeared for individual algorithm on two different panels.

7. Demo

- Open BIDEAL GUI (as mentioned in BIDEAL execution steps).



- Load sample data or insert data file of your own. Then all the pre-processing and algorithms buttons will be enabled.

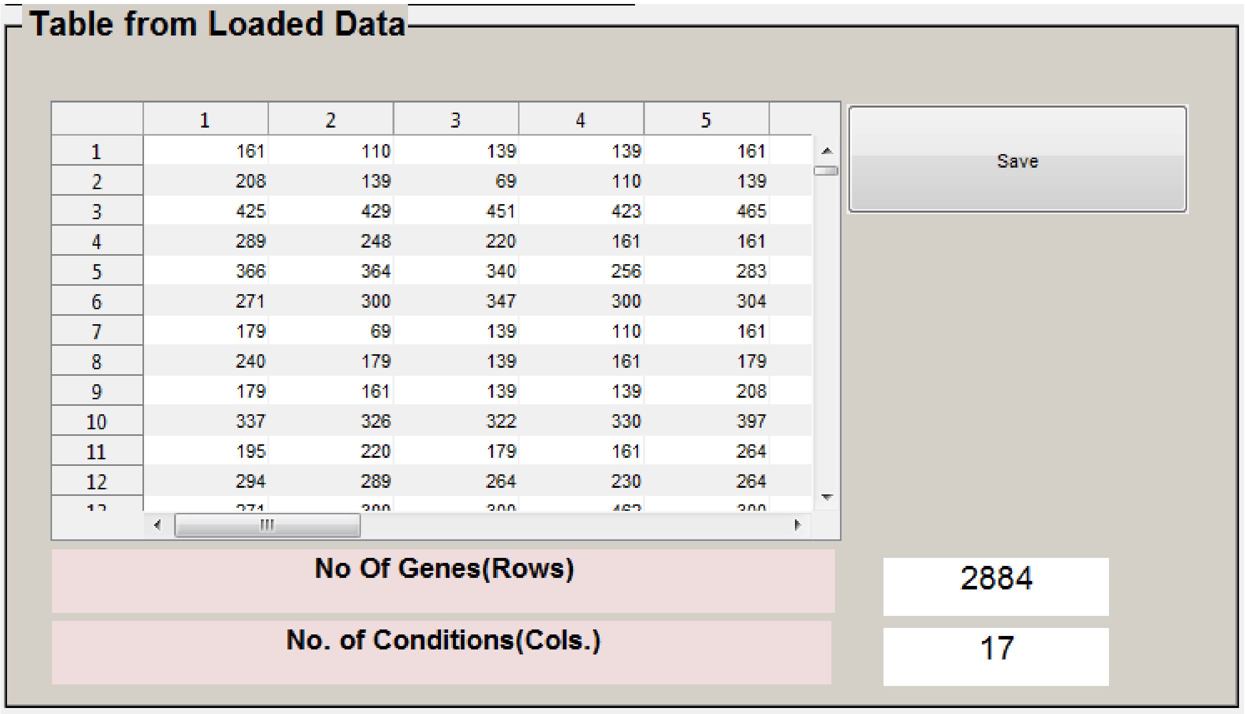


	1	2	3
1	161	110	139
2	208	139	69
3	425	429	451
4	289	248	220
5	366	364	340
6	271	300	347
7	179	69	139
8	240	179	139

No Of Genes(Rows) 2884

No. of Conditions(Cols.) 17

- Data will be shown in a table. No of genes and no of conditions will be displayed below. Here yeast dataset is loaded. No of genes is 2884 and no of conditions is 17

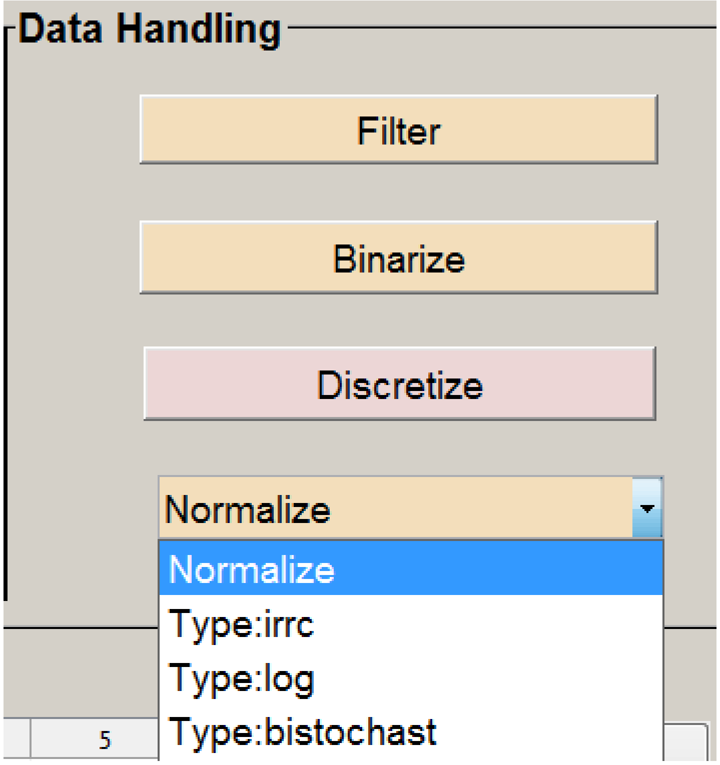


	1	2	3	4	5
1	161	110	139	139	161
2	208	139	69	110	139
3	425	429	451	423	465
4	289	248	220	161	161
5	366	364	340	256	283
6	271	300	347	300	304
7	179	69	139	110	161
8	240	179	139	161	179
9	179	161	139	139	208
10	337	326	322	330	397
11	195	220	179	161	264
12	294	289	264	230	264

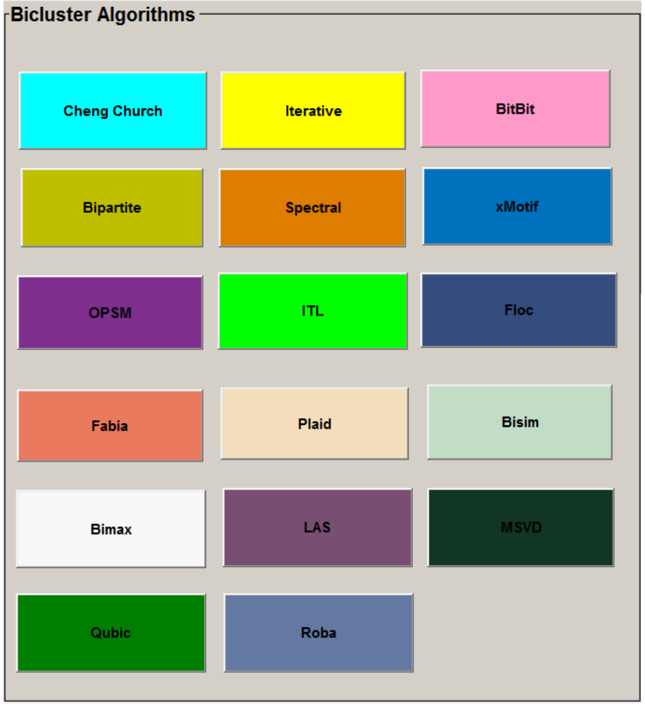
No Of Genes(Rows) 2884

No. of Conditions(Cols.) 17

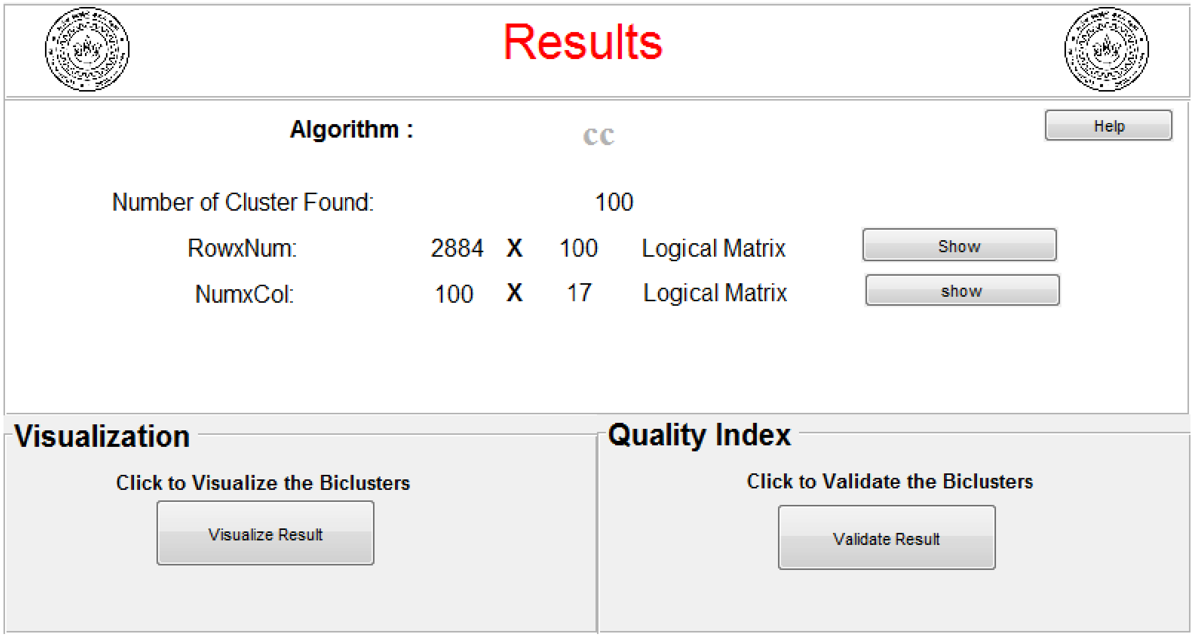
- Click on different Pre-processing steps to execute. Data after each operation will be shown in the table. Changed data can be saved by clicking on the “Save” button.



- Now click on any the bicluster algorithm for ex. here Cheng and Church Algorithm is chosen. Execution will be started. At that time other buttons are disabled.



- After execution a new window will be opened. There the summary of the result obtained will be displayed.



Results

Algorithm : cc

Number of Cluster Found: 100

RowxNum: 2884 X 100 Logical Matrix

NumxCol: 100 X 17 Logical Matrix

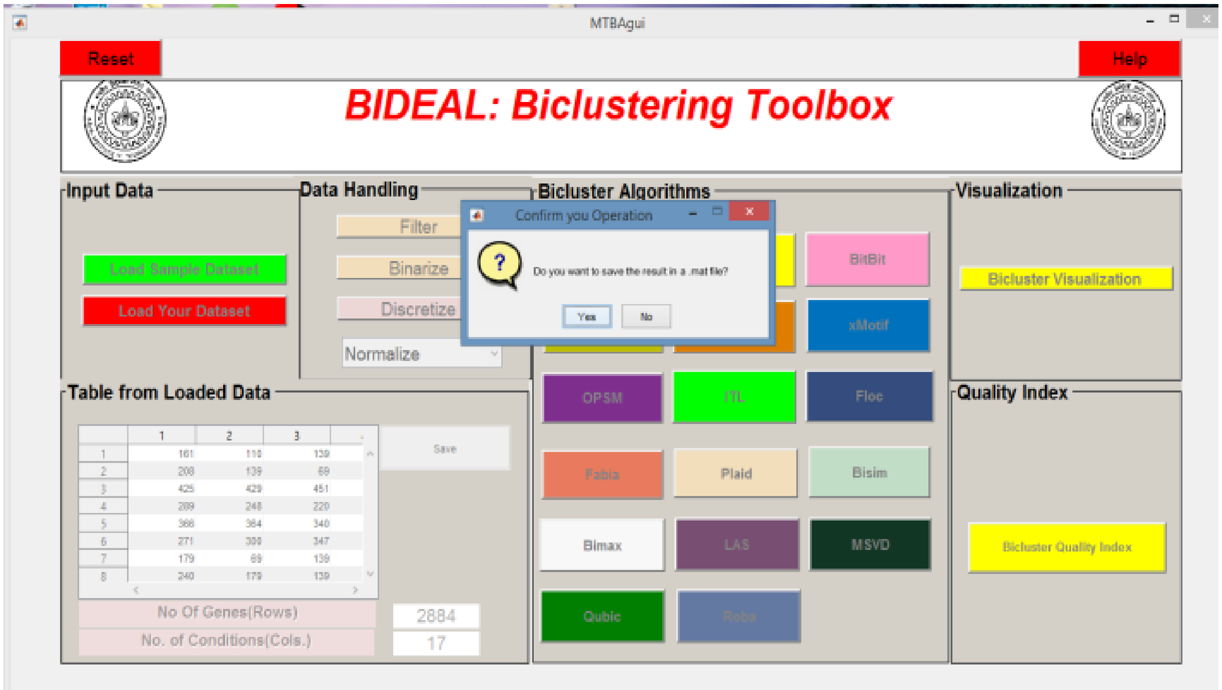
Visualization

Click to Visualize the Biclusters

Quality Index

Click to Validate the Biclusters

- Dialogue box will be opened to save the result in a ".mat "file.



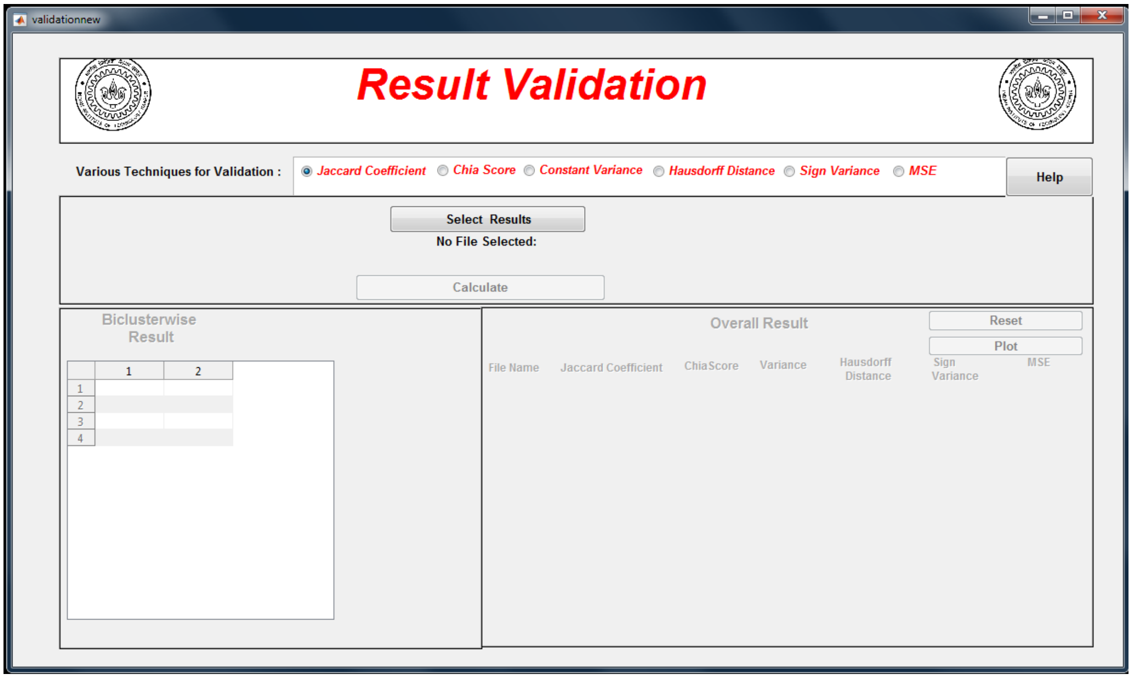
Do you want to save the result in a .mat file?

	1	2	3
1	161	110	139
2	208	139	69
3	425	429	451
4	209	248	220
5	366	364	340
6	271	303	347
7	179	69	139
8	240	179	139

No Of Genes(Rows) 2884

No. of Conditions(Cols.) 17

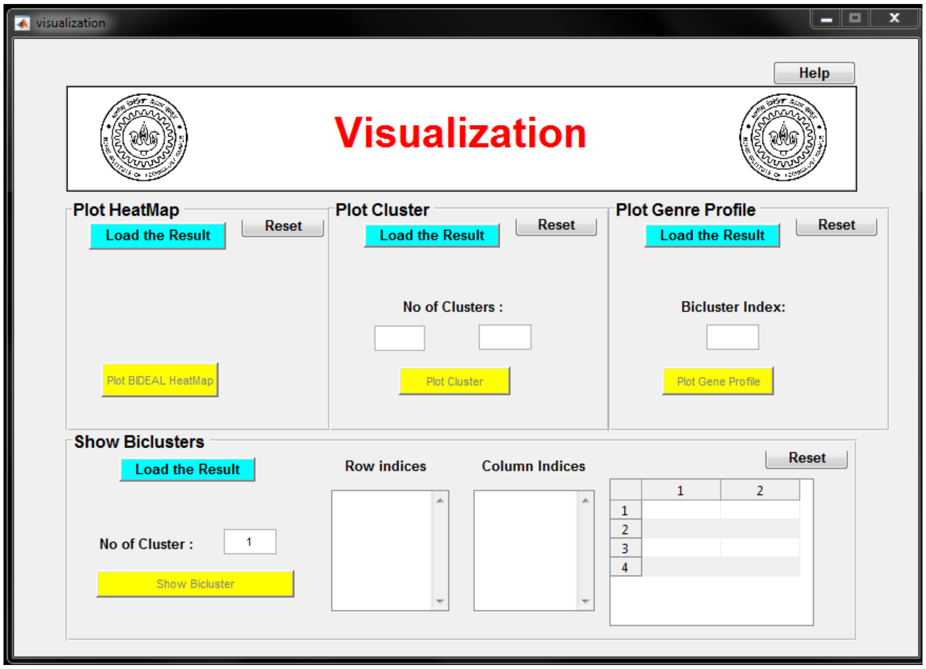
- Selected algorithm can be validated by clicking on “*Validate The Result*” button. Validation Page will be opened as shown below. Result will be loaded automatically. Click on the desired validity index and click on the “*Calculate*” button. Values will be shown in the panel. Jaccard Index can only be plotted when two results are loaded.



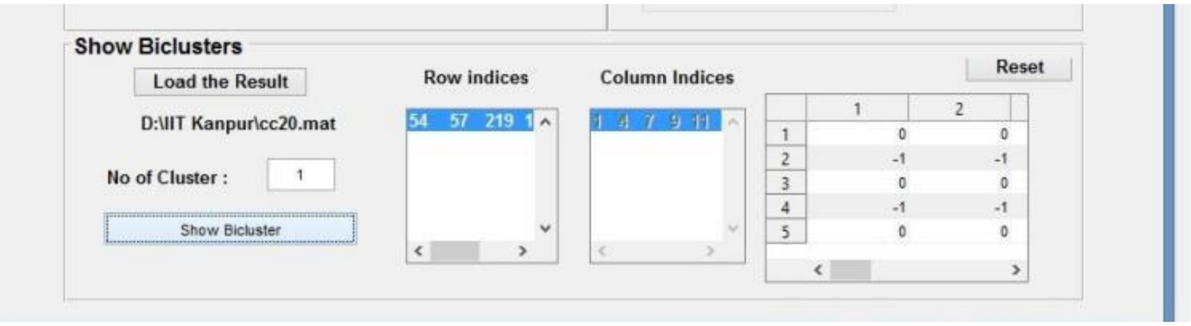
Various Techniques for Validation : ● Jaccard Coefficient ○ Chia Score ○ Constant Variance ○ Hausdorff Distance ○ Sign Variance ○ MSE

No File Selected:

- Visualization can be done this particular result by clicking on the button "*Visualize The Result*" button. Visualization Page will be opened. Result will be loaded automatically.



- For visualization of bicluster as a numerical matrix put the desired index of bicluster , The particular bicluster with row and column indices and the total matrix will be shown.



D:\IIT Kanpur\cc20.mat

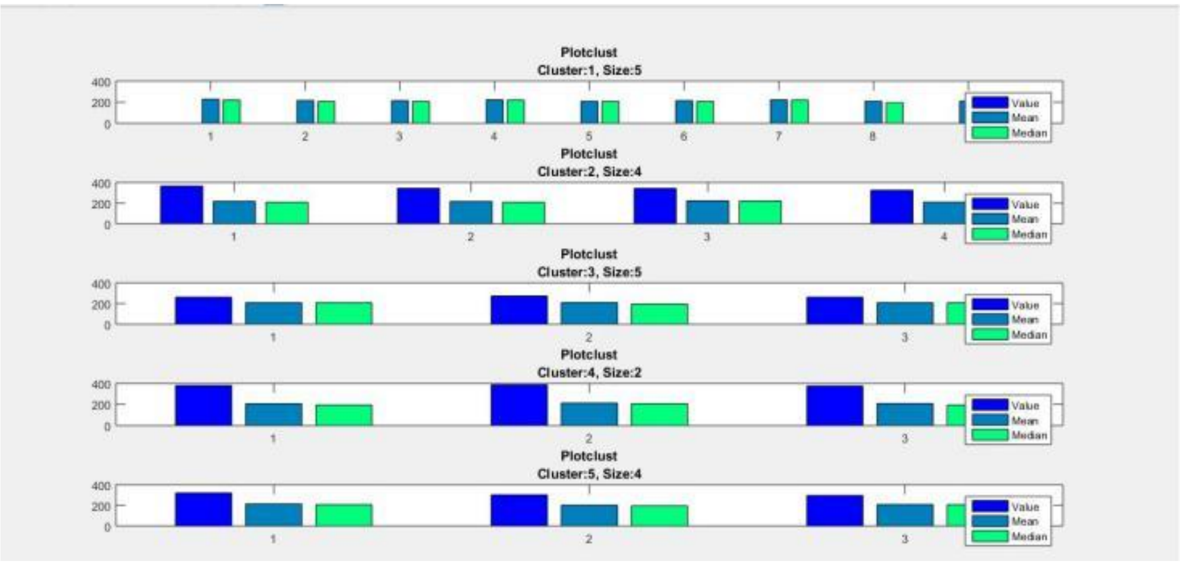
No of Cluster : 1

Row indices: 54 57 219 1

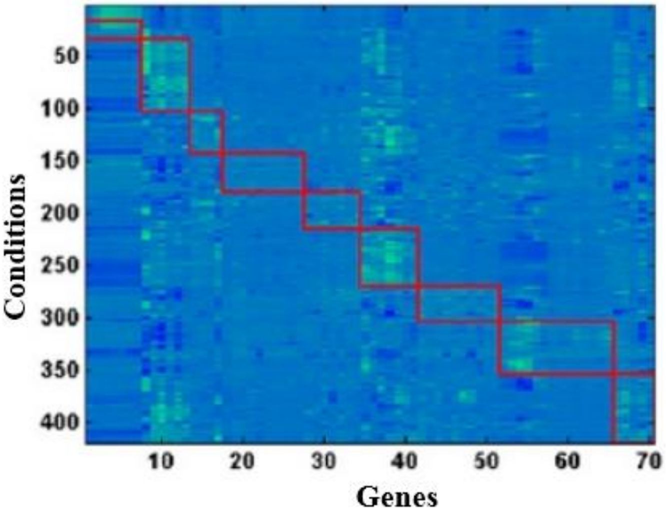
Column Indices: 1 4 7 9 11

	1	2
1	0	0
2	-1	-1
3	0	0
4	-1	-1
5	0	0

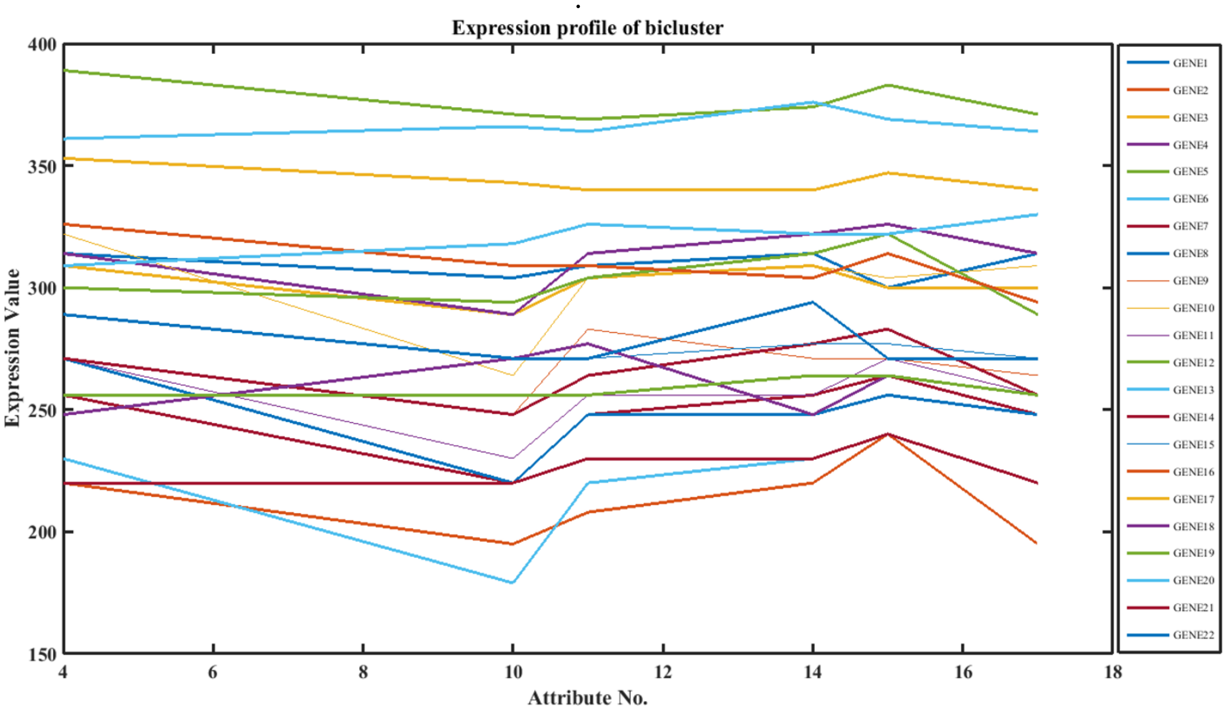
- Plot Cluster will display cluster value, Mean, Median will be plotted.



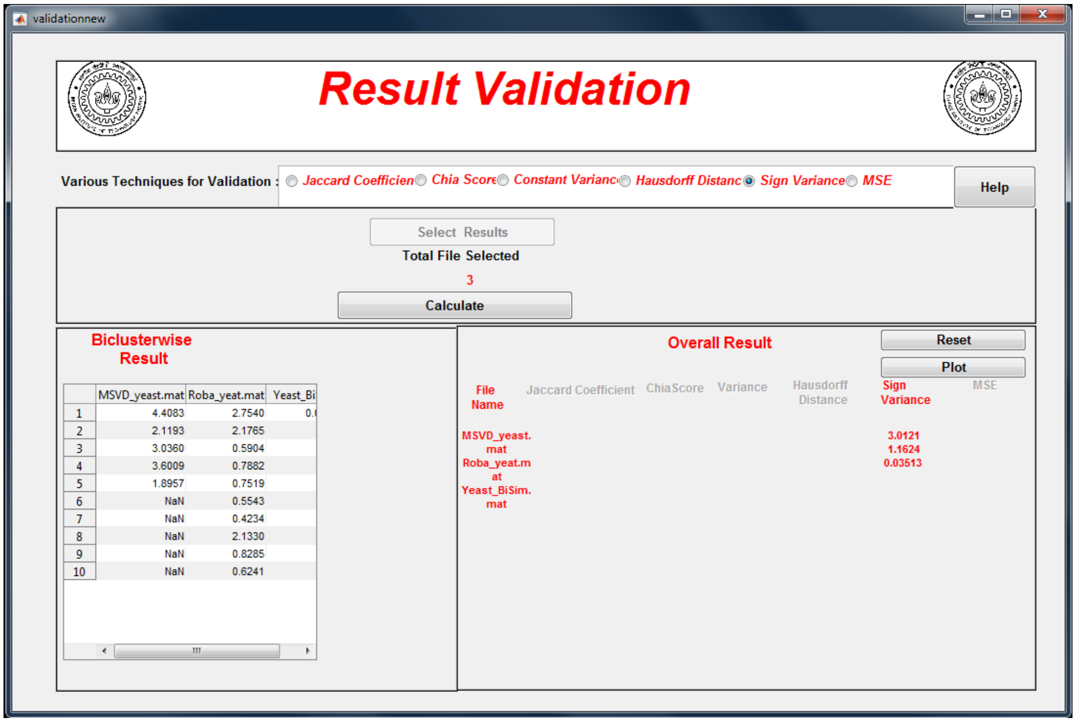
- BIDEAL HeatMap can be plotted by giving the index of bicluster in box as shown below



- Gene expression Profile of a particular bicluster can be visualized as shown below



- To validate more than one pre stored results click on the "*Bicluster Quality Index*" from the main window. In next window enter the desired index. Click on "*Select Result*" and select the desired pre stored result. No. of selected files will be shown. Now, click on the "*calculate*" button. Biclusterwise and overall result will be shown in the panel.



Various Techniques for Validation : ○ Jaccard Coefficien ○ Chia Score ○ Constant Varianc ○ Hausdorff Distanc ● Sign Variance ○ MSE

Total File Selected

3

Biclusterwise Result

	MSVD_yeast.mat	Roba_yeat.mat	Yeast_Bi
1	4.4083	2.7540	0.
2	2.1193	2.1765	
3	3.0360	0.5904	
4	3.6009	0.7882	
5	1.8957	0.7519	
6	NaN	0.5543	
7	NaN	0.4234	
8	NaN	2.1330	
9	NaN	0.8285	
10	NaN	0.6241	

Overall Result

File Name	Jaccard Coefficient	ChiaScore	Variance	Hausdorff Distance	Sign Variance	MSE
MSVD_yeast.mat					3.0121	
Roba_yeat.mat					1.1624	
Yeast_BiSim.mat					0.03513	

- Click on the "*reset*" button after one operation then load the results again.