# **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).

Input Data	Data Handling	Bicluster Algorithm	ns ———		Visualization —
Load Sample Data	Aset Binarize	Cheng Church	Iterative	BitBit	
Load Your Datas	Discretize	Bipartite	Spectral	xMotif	
Table from Loaded	Data	OPSM	m.	Floc	Quality Index
1 2 1 2 3 4	Save	Fabia	Plaid	Bisim	
4		Bimax	LAS	MSVD	Bicluster Quality Index

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

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	Reset									Help
					Bl	DEAL:	: Bicluster	ing To	olbox	
In	put Da	ata ———		Data	Han	dling ———	Bicluster Algorit	hms ———		Visualization ———
						Filter				
	Loa	id Sample [	Dataset			Binarize	Cheng Church	Iterative	BitBit	Bicluster Visualization
	L	oad Your Da	ataset		Norn	Discretize	Bipartite	Spectral	xMotif	
Т	able fr	om Loade	ed Data ·				OPSM	ιπ	Floc	Quality Index
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Т		om Loade	2 110	3 139		Save	OPSM	m.	Floc	Quality Index
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T	1 2 3 4 5 6	om Loade	2 110 139 429 248 364 300	3 139 69 451 220 340 347		Save	Fabia Bimax	ITL Plaid LAS	Floc Bisim MSVD	Quality Index

• 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		^	Save
2	208	139	69	110	139	C		
3	425	429	451	423	465			
1	289	248	220	161	161			
5	366	364	340	256	283			
5	271	300	347	300	304			
7	179	69	139	110	161			
8	240	179	139	161	179			
9	179	161	139	139	208			
0	337	326	322	330	397			
1	195	220	179	161	264			
.2	294	289	264	230	264			
<b>1</b>	274	200	200	400	200	•		
_				1			_	
		NO OF G	enes(Row	(S)				2884
	N	lo. of Con	ditions(C	ols.)				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.

-Bicluster Algorithms —		
Cheng Church	Iterative	BitBit
Bipartite	Spectral	xMotif
OPSM	m	Floc
Fabia	Plaid	Bisim
Bimax	LAS	MSVD
Qubic	Roba	

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

		R	esu	lts	
Algorithm :			сс		Help
Number of Cluster Found:			10	0	
RowxNum:	2884	х	100	Logical Matrix	Show
NumxCol:	100	X	17	Logical Matrix	show
Visualization				Quality Index —	
Click to Visualize the Biclusters				Click to	Validate the Biclusters

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

	Reset						MTBAgui		Help
Γ					Bl	DEAL	: Biclustering T	oolbox	
In	nput Dat	a ———		Data	Hand	dling	Bicluster Algorithms		Visualization
	Load	Sample (	Dataset	ſ		Binarize	Do you want to save the result in a .mat file?	BitBit	Bicluster Visualization
	Loa	d Your Da	ataset			Discretize	Yes No		
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T	able fro	m Loade	ed Data –		Norm	nalize	OPSM HTL	Floc	Quality Index
Т	able fro	m Loade	ed Data –	3	Norm	nalize	OPSM 17k	Floc	Quality Index
Т	able from	m Loade	ed Data -	3 139	Norm	nalize <sub>Save</sub>	OPSM WE	Floc	Quality Index
Т		m Loade	ed Data	3 139	Norm	nalize Save	OPSM III.	Floc	Quality Index ————
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-T	able from	m Loade	2 110 139 429 245 944	3 139 69 451 220 340	Norm	nalize Save	V OPSM Hill	Floc	Quality Index
Т	Table from           1           2           3           4           5           6	1 181 208 425 209 288 271	2 110 139 429 248 384 200	3 139 69 451 220 340 347	Norm	nalize Save	OPSM FIT:     Plaid	Floc	Quality Index ————
T	Table from           1           2           3           4           5           6           7	1 181 208 425 209 288 271 179	ed Data	3 139 69 451 220 340 347 139	Norm	Save	V OPSM Plaid Bimax UAS	Floc Bisim MSVD	Quality Index
Т	able from           1           2           3           4           5           6           7           8	T Loade	ed Data	3 139 69 451 220 340 347 139 139	Norm	nalize Save	V OPSM BL. Zzos Plaid Bimax LAS	Floc Bisim MSVD	Quality Index ————————————————————————————————————
-T	able froi	m Loade	ed Data	3 129 69 451 220 340 340 340 340 340 340 35)	Norm	save	V OPSM Fatter Plaid Bimax LAS	Floc	Quality Index

• 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.

Jaccard Coefficient   Chia	Score  Constant Variance	Hausdorff Distance 🔘 S		
C - 1			lign Variance 🛛 🔘 I	WSE Help
No File	t Results Selected:			
Calc	ulate			
		Overall Resul	t	Reset
	File Name Jaccard Coefficient	ChiaScore Variance	Hausdorff Distance	Sign MSE Variance
	Calc	Calculate File Name Jaccard Coefficient	Calculate Overall Result File Name Jaccard Coefficient ChiaScore Variance	Calculate Overall Result File Name Jaccard Coefficient ChiaScore Variance Hausdorff Distance

• 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.

	Help
Visualization	
Plot Cluster Reset	Plot Genre Profile  Load the Result
No of Clusters :	Bicluster Index:
Plot Cluster	Plot Gene Profile
Pow indices Column Indices	Reset
v v	4
	Visualization Plot Cluster  Plot Clusters:  Plot Clusters:  Plot Cluster  Row indices Column Indices

• 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.

Load the Result	Row indices	Column Indices			Reset
DUIT IL DO	54 57 340 4			1	2
D:\III Kanpur\cc20.mat	34 37 213 I A		1	0	0
			2	-1	-1
No of Cluster : 1			3	0	0
provide the second seco			4	-1	-1
Show Bicluster	×	×.	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.

			F	Result	Valio	datic	on	_		(	
Various	Techniques for	Validation :	Jaccar	d Coefficien⊚ Chia	Score Constant	Varianco Ha	usdorff Dis	stanc    Sig	n Variance 🔿	MSE	Help
			ſ	Select Total File Calcu	Results Selected 3 Ilate	]					
Bio	lusterwise						Overa	ll Result		R	eset
	Result									F	Plot
M	SVD veast.mat Rob	a veat.mat Y	east Bi		File Jaccar	d Coefficient C	hiaScore	Variance	Hausdorff	Sign	MSE
1	4.4083	2.7540	0.0		Name				Distance	variatice	
2	2.1193	2.1765			MSVD veast.					3.0121	
3	3.0360	0.5904			mat					1.1624	
4	3.6009	0.7882			Roba_yeat.m					0.03513	
5	1.8957	0.7519	_		Yeast_BiSim.						
6	NaN	0.5543			mat						
/	NaN	0.4234									
0	NaN	0.8285									
10	NaN	0.6241									
			4								

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