

FIGS USER'S MANUAL

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1.0 GENERAL INFORMATION

1.1 System Overview

Fuzzy inference of gene sets (FIGS) is a Matlab-based standalone executable package that uses dendritic cell and A549 epithelial cell influenza response to represent data driven fuzzy gene-sets. This interactive graphic user interface (GUI) package comes with several control parameters to probe fuzzy gene-sets where you can also perform enrichment analysis by providing your own gene set. The results of overlapping gene-sets are presented as circular graph that can be inspected interactively.

1.2 Authorized Use Permission

FIGS is developed solely for the research purpose to benefit immunologist and broader bioinformatics community. FIGS is freely available for the personal use. However, unauthorized or commercial redistribution of FIGS is highly prohibited.

The use of FIGS package is subject to the following conditions:

- (1) The package and portions thereof may not be sold. Users may modify the software for their own use, but may not redistribute any version of the package other than the original version without the express permission of the authors.
- (2) This package is provided on an "as is" basis. The authors in no way warrant either this package or results it may produce.
- (3) The authors are under no obligation to provide any services by way of maintenance, updates or corrections for this package.
- (4) Reports or publications resulting from use of this package must contain an acknowledgment in the form commonly used in academic research.

By downloading this package, you agree to the above conditions.

1.3 Points of Contact

For further information regarding development of FIGS, assistance in using FIGS or potential collaborative opportunities please contact:

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juilee_thakar@urmc.rochester.edu

1.4 Citing FIGS

Thank you for using FIGS. Please cite the FIGS package as:

- Atif Khan, Dejan Katanic and Juilee Thakar, “FIGS: Fuzzy Inference of Gene-Sets: A data driven clustering approach”, PLOS Computational Biology, **(Under Review, To be updated later)**.

FIGS is an advanced tool developed subsequently after PathCellNet that can be accessed at <http://www.bio-networks.com/>. Please cite PathCellNet as:

- Dejan Katanic, Atif Khan and Juilee Thakar. "PathCellNet: Cell-type specific pathogen-response network explorer." Journal of Immunological Methods (2016).

1.5 Acronyms and Abbreviations

FIGS: Fuzzy inference of gene-sets

PathCellNet: Pathogen specific cell type network

DC: Dendritic cells

EC: Epithelial cells

FCM: Fuzzy c-means clustering

ISGs: Interferon stimulated genes

KEGG: Kyoto encyclopedia of genes and genomes

U: Unified distance matrix

MV: fuzzy membership value

GUI: Graphic user interface

2.0 INSTALLATION AND SYSTEM REQUIREMENTS

FIGS is a computational package that allows user to identify groups of gene signatures in human monocyte derived dendritic cell (DC) and A549 epithelial cells (EC) responsive to influenza infection.

2.1 System Requirements

FIGS is developed in Matlab R2016a environment and deployed as installable package. FIGS package does not explicitly require Matlab but it requires ‘Matlab Runtime’ during the installation process (in case you haven’t installed it previously).

The ‘Matlab Runtime’ is a freely available standalone set of shared libraries that enables the execution of compiled Matlab applications or components on computers that do not have Matlab installed.

2.2 Installation Procedure

FIGS can be downloaded from <https://github.com/Thakar-Lab/FIGS>

Please make sure you downloaded FIGS.exe file (~20 Mb) from GitHub. Double click FIGS.exe to install FIGS package on the desired directory.

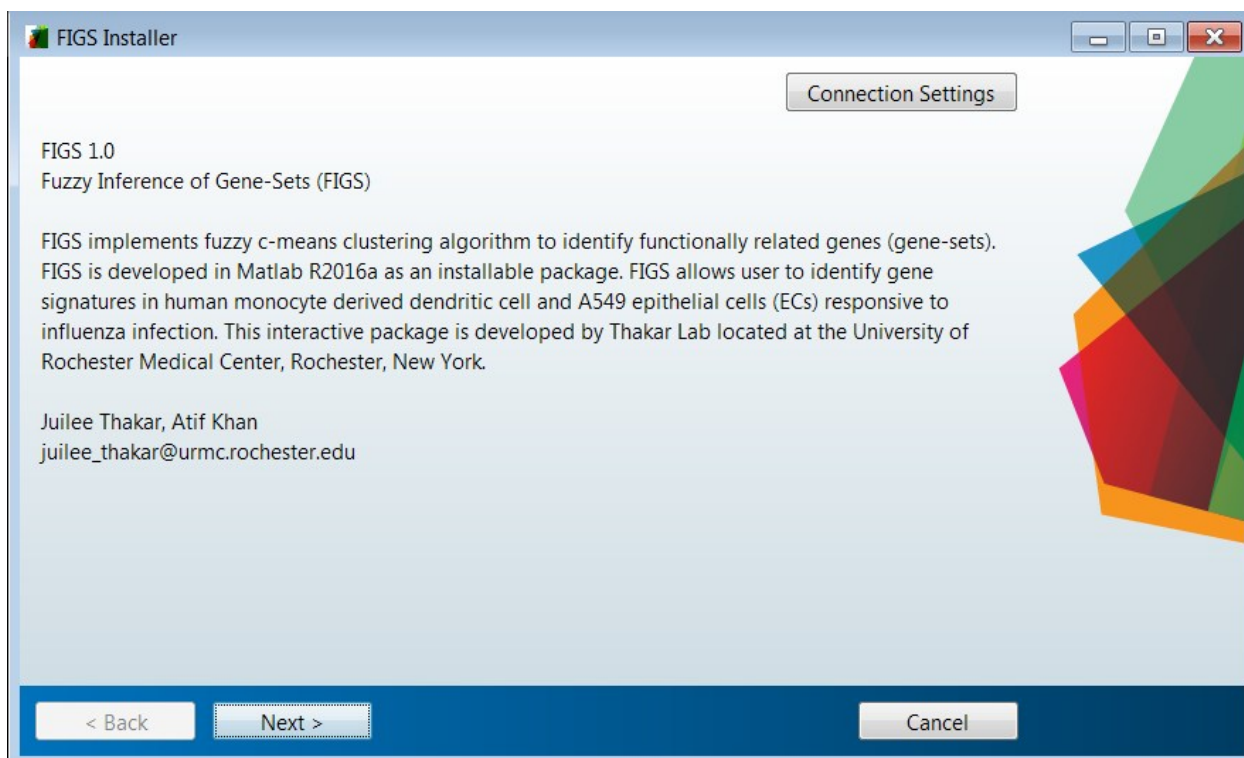


Figure 1: Installation of FIGS Package

If the FIGS installer finds the appropriate version of 'Matlab Runtime' already installed on your PC, the following information will be displayed (Figure 2) and you will no longer be required to install it again.



Figure 2: Detection of Previously Installed Matlab Runtime

In case the 'Matlab Runtime' is not found on your PC, the following information will be displayed (Figure 3). For the ease of use, 'Matlab Runtime' compiler installation is packaged with FIGS.exe. You will be automatically redirected to the Matlab website for downloading and installation of Matlab compiler (Figure 4).

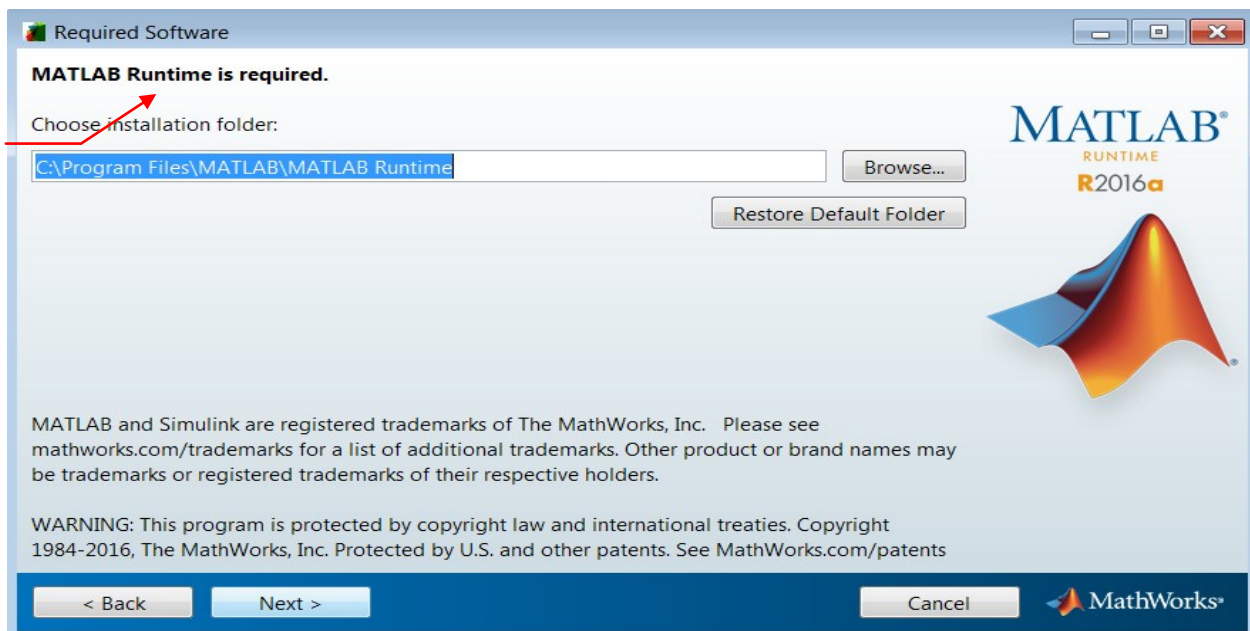


Figure 3: Matlab Runtime Installation Requirement

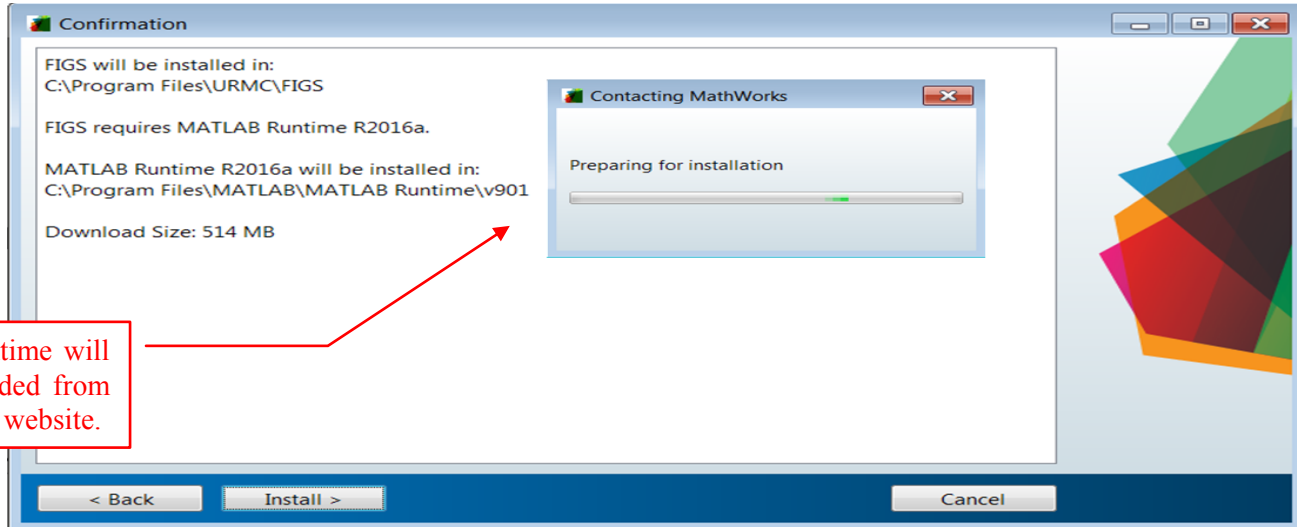


Figure 4: Automatic Downloading of Matlab Runtime

Please beware that Matlab Runtime (size ~500 Mb) will be downloaded from Matlab website (www.MathWorks.com). Downloading and installation (Figure 5) might take some time depending on your connection and internet speed.

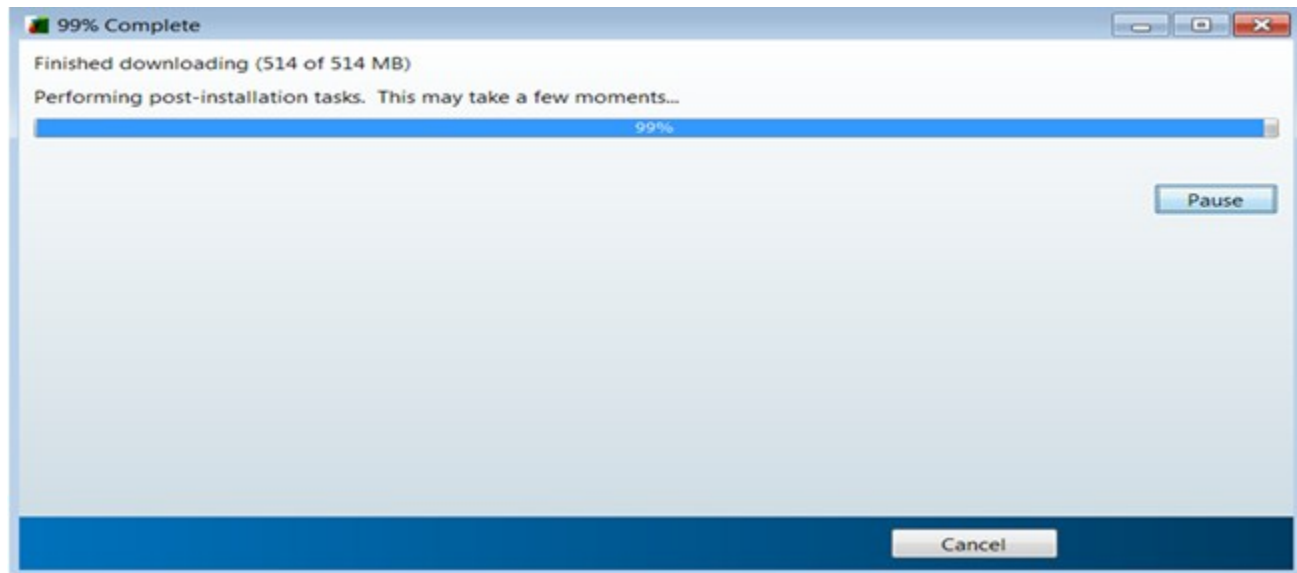


Figure 5: Automatic Installation of Matlab Runtime

2.3 Getting Started

Once the installation is finished, FIGS package can be accessed by running FIGS application from the program list (in case you have not created a desktop shortcut).

3.0 MAIN SYSTEM MENU

This section provides a general overview of the FIGS package with the help of screen shots.

3.1 Graphic User Interface

Run FIGS from the program list (in case you have not created a desktop shortcut). The main menu will appear with several control parameters as shown and described in figure 6.

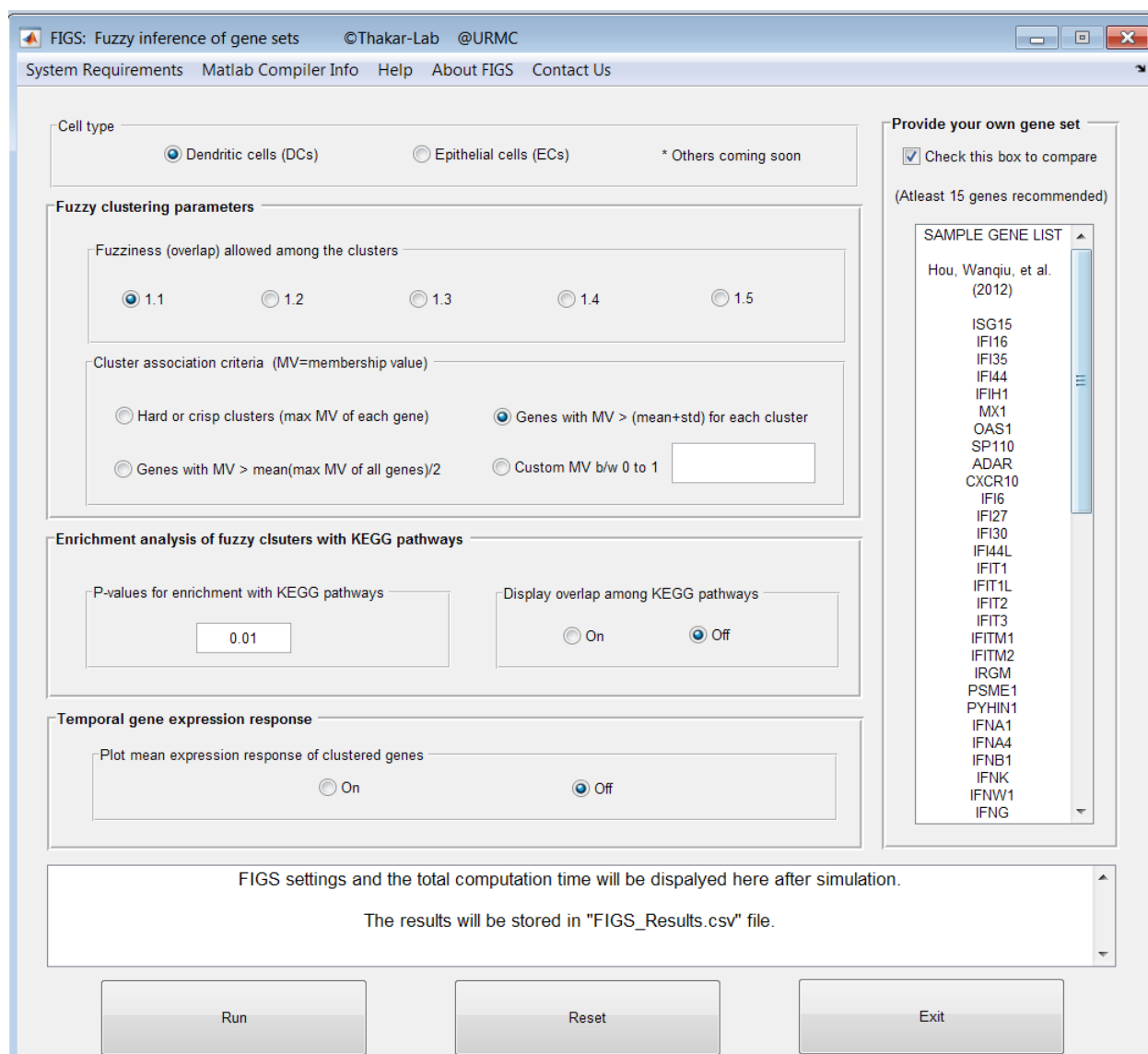


Figure 6: Main GUI of the FIGS Package

3.2 Menu Tabs

The main menu of FIGS that has several navigation tabs and menu bars. The description of tabs and the menu bars (figure 7) are self-explanatory.

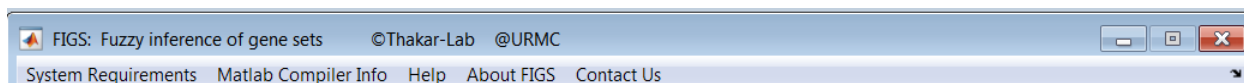


Figure 7: Main Menu Tabs

3.3 Cell Type Selection

Currently, FIGS package database includes Dendritic Cells (DCs) and Epithelial Cells (ECs). The results of FCM clustering for these datasets are stored in database to save computational time and facilitate quick retrieval. In future, more cell types will be added to the database and FIGS package will be updated accordingly.

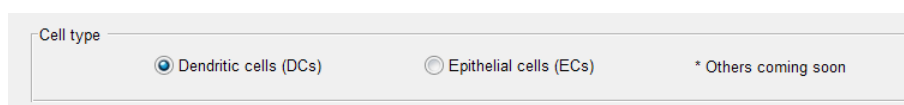
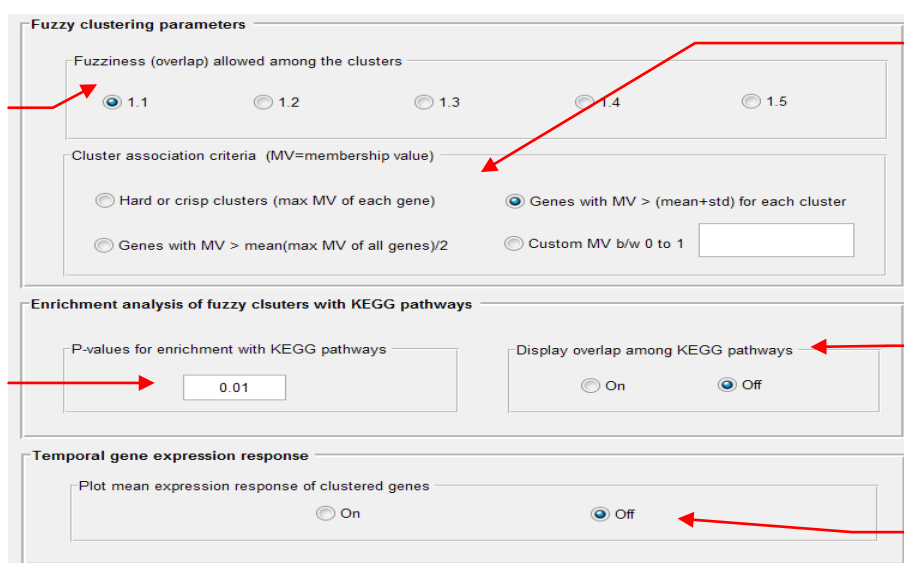


Figure 8: Cell Type Selection Tabs

3.4 Panel of Controllable Parameters

FIGS package comes with several user defined control parameters. We recommend using the default parameters but for the exploratory purposes, parameters can be modified depending on your requirement.



The extent of overlap allowed between the clusters. (A high value means more overlap).

Four different criteria for associating genes to the clusters, 1: Hard clusters 2: The distribution based assignment. 3: Mean-Max ($\sum_{i=1}^n \max(U_i)/2n$) and 4. User defined threshold.

Provides an additional output to represent overlap among ISGs and KEGG pathways.

Provides an additional output plot to represent temporal expression of the clustered genes.

Figure 9: Controllable Parameters of FIGS Package

3.5 Upload User Gene-Sets

There is an option to provide your own gene-sets for enrichment with FCM produced gene-sets. Gene names can be manually entered or can be copy-pasted in the panel shown below (Figure 10). To do the enrichment of your own gene-sets, please check the box “Check this box to compare”.

Provide your own gene set

☒ Check this box to compare
(Atleast 15 genes are recommended)

SAMPLE GENE LIST

Hou, Wanqiu, et al.
(2012)

ISG15
IFI16
IFI35
IFI44
IFIH1
MX1
OAS1
SP110
ADAR
CXCR10
IFI6
IFI27
IFI30
IFI44L
IFIT1
IFIT1L
IFIT2
IFIT3
IFITM1
IFITM2
IRGM
PSME1
PYHIN1
IFNA1
IFNA4
IFNB1
IFNK
IFNW1
IFNG
IFNA14
IFNA21
IFNA6
IFNE
IL15
IFRD1
IL28A
IL29
IRF1

Check this box in order to do enrichment of your own gene-sets with FCM gene-sets.

Copy-paste your gene-sets here or type/enter one per line for the enrichment with FCM gene-sets.

Figure 10: User Provided Gene-Sets for Enrichment with FCM Gene-Sets

3.6 Run, Reset and Exit

Pressing the run tab will start computation and exit tab will quit the package. Pressing reset tab will clear the setting of all the parameters to the default state.

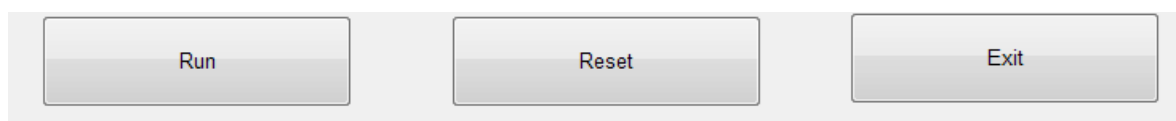


Figure 11: Control Tabs for Computation

3.7 Error Dialogs

The package will show an error dialog if the cell type, cluster association criteria and/or fuzziness values are not selected. Additionally, there will be an error message if the value of the user provided membership value threshold is not between 0 and 1.

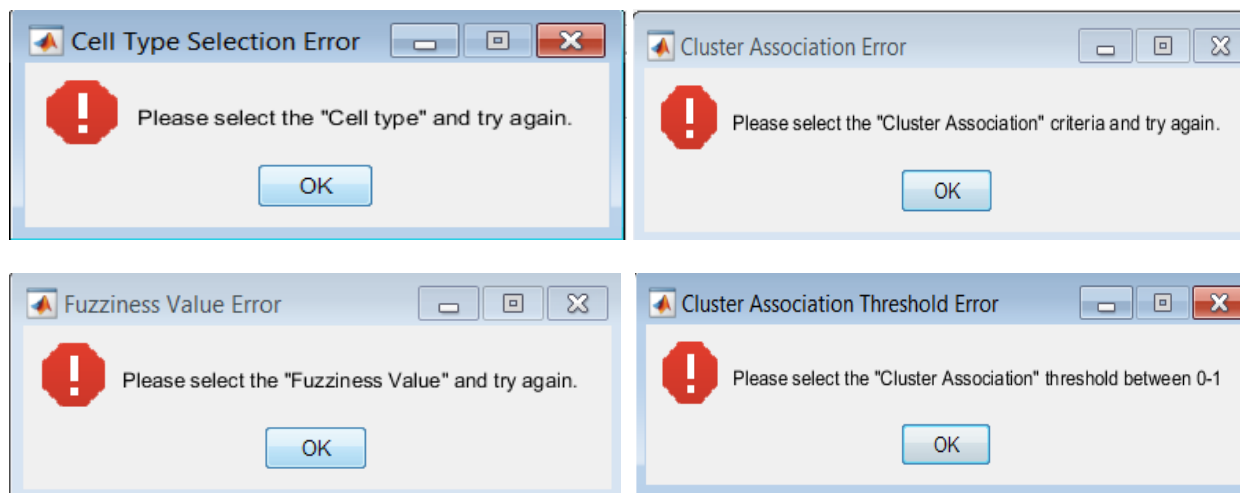


Figure 12: Error Dialogs for FIGS Parameter Settings

3.8 Progress Bars

The package computes output in three steps as shown in Figure 13. The progress at each step will be shown by the green color progress bar.

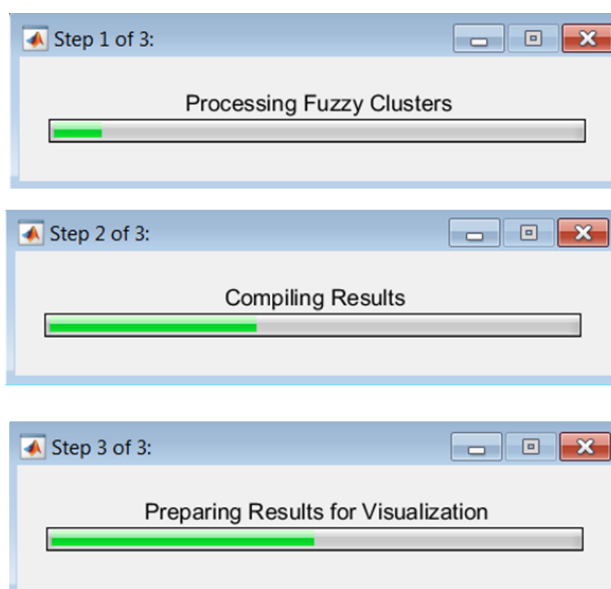


Figure 13: Automatic Installation of Matlab Runtime

4.0 USING THE SYSTEM

This section provides a descriptive usage of the FIGS package.

4.1 Fuzzy Gene-Sets

The results of FCM gene-sets are displayed in tabular as well as interactive circular graphs. Figure 14 shows the composition of FCM gene-sets and their enrichment with KEGG pathways (where red color shows significant overlap based on user selected p-value).

The screenshot shows the FIGS Genesets interface. The top table lists 44 immunologically relevant KEGG pathways and ISGs. The bottom table shows the enrichment (P-Value) of FIGS gene-sets in user-defined genes, sorted by their belongingness (membership-value) with that cluster.

Table 1: KEGG Pathways and Enrichment

Pathway	C35	C36	C37	C38	C39	C40	C41	C42	C43	C44	C45	C46	C47	C48	C49
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.15986	0.20181	0.094257	0.70654	0.61489	0.6358	0.085645	0.16337	0.67694	0.79738	0.47505	0.025991	0.25362	0.69698	0.072629
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.22917	0.02059	0.00040081	0.78873	0.70179	0.72217	0.46568	0.0017766	0.76134	0.58434	1.3193e-05	0.0029213	0.12451	0.060583	0.60252
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.11124	0.1424	0.055336	0.6247	0.53063	0.55398	0.32641	9.7232e-05	0.59473	0.12795	0.091665	0.0126	0.04037	0.0022174	0.13218
KEGG_RIG_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.38234	0.0001937	0.0006741	0.55792	0.47023	0.48956	0.28043	0.064969	0.52871	0.65453	3.0293e-06	0.0053884	0.13621	0.042237	0.28563
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	0.37231	0.015825	0.031968	0.5457	0.12218	0.13394	0.27247	0.00021753	0.15596	0.26676	4.5863e-05	0.0056454	0.46885	0.038732	0.27241
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	0.6547	0.0071803	0.2137	0.83495	0.75392	0.7733	0.51631	4.687e-06	0.48845	0.19548	0.066355	0.23175	0.4192	0.5176	0.027948
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	0.042237	0.22908	0.11434	0.14275	0.27322	0.6672	0.41633	0.1946	0.34235	0.24131	0.1525	0.0074425	0.65841	0.72762	0.51993
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.0268	0.53587	0.26103	0.30072	0.21103	0.60146	0.3625	0.72737	0.26897	0.41932	0.019039	0.019078	0.59267	0.66292	0.1744
KEGG_FC_EPSILON_RL_SIGNALING_PATHWAY	0.36213	0.093781	0.029165	0.53314	0.44725	0.46609	0.26443	0.58792	0.50441	0.25373	0.32994	0.51175	0.48809	0.52374	0.63465
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	0.58067	0.01719	0.37707	0.17513	0.68208	0.33627	0.44768	0.50455	0.38712	0.28868	0.17782	0.15466	0.69403	0.76162	0.29639
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_ISA_PRODUCTION	0.29748	0.0073219	0.097951	0.45019	0.37222	0.36909	0.21429	0.004628	0.42379	0.54108	0.0034739	0.10513	0.38191	0.11122	0.54648
INTERFERON_STIMULATED_GENES_SCHOGGINS	0.87416	5.3628e-29	0.088163	0.94137	0.68872	0.87527	0.70263	5.1182e-05	0.91745	0.99967	1.7225e-60	0.023966	0.95646	0.35888	0.95783

Table 2: Enrichment (P-Value) of FIGS gene-sets in user-defined genes

Cluster	C37	C38	C39	C40	C41	C42	C43	C44	C45	C46	C47	C48	C49
Enrichment (P-Value) of FIGS gene-sets in user-defined genes	5.0207079	0.614315	0.523609	0.543834	0.318949	0.0223177	0.584004	0.710774	3.9640e-16	0.00167989	0.53527	0.0620247	0.351105
Total genes found in fuzzy clusters	1	0	0	0	0	3	0	0	12	4	0	2	1

Table 3: Composition of each cluster where the genes are sorted based on their belongingness (membership-value) with that cluster.

Cluster	C26	C27	C28	C29	C30	C31	C32	C33	C34	C35	C36	C37	C38	C39	C40	C41	C42	C43	C44	C45	C46	C47	C48	C49
1	ZORF28	C10RF77	FCER1	DMIT1L	LOC1	RAPH1	HMB5	COG2	C3ORF34	TPMT	DDI60	TMEM206	HSD17B12	ADIPOR1	HIF1	HSD17B7	LOC728830	CCNC	PH6	MT2A	LOC729501	LOC646483	LOC651202	PRDM14
2	TM2P2	FCER1	LOC100128104	LOC100128104	C3ORF156	C12ORF47	BNO2	KCNH6	TACC1	UBE2L6	TCF12	COMMD1	CNPY2	DBNDD2	CRCP	LTA	CYBBR4	EXOSC7	IFITM2	KLHL28	LOC644039	LOC389787	VRK3	
3	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1	FCER1
4	NO6	SMAD4	LSM14A	PELP1	PGK1	MAP3K11	LOC100133484	C14ORF15	TGFB	SP110	TP53L2	SUPT4H1	ERH	NHP2	BLZF1	COL20	LOC100131104	LOC100132210	ITIM3	DUSP6	BTIF3	LOC646785	PAK2A	
5	OTUD4	CD1E	WDR6	ACOX3	HMOCS1	PMM1	MTMR12	SEMA3E	TORG1	MICB	TCF1	COL1A	GLTSCR2	MCEE	MCM8	PMM1	LOC387791	PMP1	USP41	NFKB1	SF3B14	LOC100125109	YFP6	
6	ADAM17	LOC650215	TTG16	COQ10B	MED30	DCTPP1	PREX1	CO3E1	TKT	EPF2A2	THEM2	ARPC2	SULT1A4	PTPMT1	LOC1001335AT1	ARPC5	CNTM8	MI2	LGAM	RPSA11	PTMA	ZNF142		
7	BALGAT1	HACL1	C2ORF29	LOC209F51	PURB	C7ORF49	LOC731314	ZNF682	TMED9	LBA1	TBPL1	LOC653225	C14ORF112	LOC100131720	F549	LOC387763	LOC1001316	GPD1L	C19ORF66	SNX16	POLE4	LOC1001319	REBM14	
8	PPTC7	UBE4B	MTF2	BCAP31	ARNTL	CLEC4A	ZNF275	LOC1001267	TMEM101	SERPINC1	CD163	RAB31	DUSP23	MRPS15	LOC731542	COL3L1	PABPN1	SLC3A3R1	IL15RA	PLRA	OSTC	LOC388621	FAM105E	
9	ZC3H4	IK	CD1E	LOC1001335AT1	ZNF382	RRS1	CCDC125	NGRN	OAS3	TFOP2	FUC42	EIF3E	TPM1	MG28336	CD89	LOC728823	PTGFRN	INTS3	GTZE1	PPR2	FLJ43681	RAVIGAP		
10	PTGER4	PDHB	GSA2	DNAJB11	PAPSS2	PRAM1	FKBP4	LOC729090	TRIM4	DTL3L	NOUFAF3	PSMB4	ZNF428	GLR15	LRR337B2	COL2	C10RF43	ARAP3	HES4	EWSR1	HCF1R1	LGAL3	CTN15	
11	SAP30L	LOC654191	MAVBA	FAM174A	RAP1GAP	LOC728431	COX15	LOC1001253	MEU1	LOC728200	C6ORF108	REI102	LOC644250	MGC10997	LOC729992	MFSD6	OAS2	LRRIC2	LOC646688	LOC100125701	MYC1H			
12	PSCDBP	FADS1	LARS	LOC1001307	FBR5	MAP7	FARSA	LOC730313	TMEM19	DYLL1T1	SASH1	SOD1	LOC844877	C10ORF91	ZNF738	SOD2	COX8B1	EBNA1BP2	IGS15	PPP1R10	LSM5	FTH1	FBI011	
13	ZNF22	ANAPC5	HEATR2	LDHA	PAFAH1B1	CEHPB	KIAA0319L	ARL16	NOSP	CCNA1	MTX	PAPOLA	ATP50	ZNF311	CREB1	HST2H2A4	LOC644131	C10ORF54	APOL3	YEATS2	LOC644863	LOC1001325	SLC11A2	
14	RAPGEF2	LTV1	DDI18	OXB	PTGER2	CEGR5	WDFY2	LOC36586	TBIAS1	IFH1	INSIG2	CLYBL	SPIN4	POLR2G	MSH3	THFAP3	SSBP1	GALK1	CMPK2	DDIT3	LOC285900	C6ORF160	LHFPL2	
15	ACTR1A	CCR1	FDT1	TYW1B	BID	COX5C	POCDA	FAM106A	LOC1001281	NA4A	MASTL	TM6SF1	HNR1P0	C10ORF17	TTCC3C	MCART1	THCRV4	ZFAND2A	RAB23	CICL10	MEF2A	GTF2H5	LOC653688	DTX2
16	AT2	FLJ10081	KIAA0494	ACSL3	LAPTM5	AKAP13	RAB34	SNAPC2	LOC728993	NHLRC3	DDI60L	TOR3A	MFSD1	LOC728969	MRPL21	POFUT1	SERPINE2	LOC1001284	ARHGAP9	IFT1	ZC3H12C	SRP4P1	LOC728973	LOC7308
17	PRH2	TYH2	DKC1	HNRPL2	LOC644774	LOC729608	VINT5B	RPK3	LOC1001252	TDG	STAP1	TMEM69	HSD17B11	CHCHD10	POPS	ZNF486	TM6SF19	DNAJC15	TUSC4	IF35	ACTR10	LY96	LOC645157	PTPRP
18	MAP7D1	EXOSC5	ATM	CCDC37	USP34	FAM143A	CEBPA	BCYRN1	TEC	OAS1	HLA-DRA1	SEH1	UIT	CANLG	LOC1001300	LOC642956	C10ORF32	TTL	IF44	PLEK	ACINB	LOC387934	SLC7A8	

P-values from hypergeometric test to represent significant overlap between FCM gene-sets and KEGG/ISGs pathways. The p-values that are less than the user defined p-value threshold are highlighted with red color.

Figure 14: Tabular Representation of FCM Gene-Sets and Their Enrichment with KEGG Pathways

4.2 Enrichment of User Provided Genes

If there is a user provided gene set, the results for the enrichment of user genes with FCM gene-sets will be displayed as shown in the Figure 15 below.

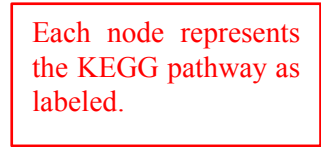
	C35	C36	C37	C38	C39	C40	C41	C42	C43	C44	C45	C46	C47	C48	C49
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.15986	0.20181	0.094257	0.70654	0.61489	0.6358	0.085645	0.16337	0.67694	0.79738	0.47505	0.029991	0.25362	0.69698	0.072629
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.22917	0.02059	0.00040081	0.78873	0.70179	0.72217	0.46568	0.0017766	0.76134	0.59434	1.3193e-05	0.0029213	0.12451	0.060583	0.60252
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.11124	0.1424	0.055336	0.6247	0.53363	0.55398	0.32641	9.7232e-05	0.59473	0.12795	0.091665	0.06126	0.54537	0.0022174	0.13215
KEGG_IL1_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.38234	0.0001937	0.0006741	0.55792	0.47023	0.48956	0.28043	0.064969	0.52871	0.65453	3.0293e-06	0.0063884	0.13621	0.042237	0.28663
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	0.37231	0.015825	0.031968	0.5457	0.12218	0.13394	0.27247	0.00021753	0.15996	0.26576	4.5863e-05	0.0056454	0.46985	0.038732	0.27241
KEGG_JAK_STAT_SIGNALING_PATHWAY	0.6547	0.0071083	0.2137	0.83495	0.75392	0.7733	0.51631	4.6867e-06	0.48845	0.19548	0.066355	0.23175	0.4192	0.5176	0.027948
KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.096069	0.0029883	0.007779	0.59267	0.15076	0.52285	0.30379	0.081685	0.56296	0.68946	0.37631	0.0089988	0.51441	0.21232	0.32509
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	0.040184	0.011503	0.10918	0.36968	0.26542	0.65961	0.40996	0.44292	0.33327	0.50087	0.030004	0.70805	0.2778	0.35761	0.82257
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	0.042327	0.22908	0.11434	0.14275	0.27322	0.6672	0.41633	0.1946	0.34235	0.24131	0.1525	0.0074425	0.45841	0.72762	0.51993
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.0268	0.53587	0.25103	0.30072	0.21103	0.60146	0.3625	0.72737	0.26897	0.41932	0.019839	0.018018	0.59267	0.66292	0.1744
KEGG_FC_EPSILON_RL_SIGNALING_PATHWAY	0.36213	0.093781	0.029165	0.53314	0.44725	0.46609	0.26443	0.58792	0.50441	0.25373	0.32951	0.51175	0.45809	0.52374	0.63465
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	0.58067	0.01719	0.37707	0.17513	0.68208	0.33627	0.44768	0.50455	0.38712	0.28868	3.1776e-05	0.15466	0.69403	0.76162	0.29639
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IL12_PRODUCTION	0.29748	0.0073219	0.097951	0.45019	0.37222	0.38909	0.21429	0.0042628	0.42379	0.547108	0.0034739	0.10513	0.38191	0.11122	0.54648
INTERFERON_STIMULATED_GENES_SCHOGGINS	0.87416	5.3629e-29	0.088163	0.94137	0.68872	0.87527	0.70263	5.1182e-05	0.91745	0.99967	1.7225e-60	0.023966	0.56646	0.35888	0.95783
Enrichment (P-Value) of Figs gene-sets in user-defined genes	5.0207079	0.614315	0.523609	0.543834	0.318949	0.0223177	0.584004	0.710774	3.9648e-16	0.00167989	0.53527	0.0620247	0.351105		
Total genes found in fuzzy clusters	1	0	0	0	0	3	0	0	12	4	0	2	1		

P-values from hypergeometric test to represent significant overlap between FCM gene-sets and the user provided gene-sets. The p-values that are less than the user defined p-value threshold are highlighted with red color.

Figure 15: Enrichment of User Genes with FCM Gene-Sets

4.3 Overlap among KEGG Pathways

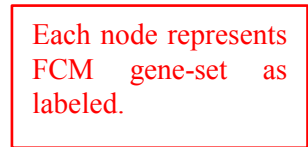
There overlap found among the KEGG pathways are displayed as interactive circular graph (Figure 16). Each node of the circular graph represents KEGG pathway as labelled where a line or an arc between the two nodes shows the existence of common genes between the two pathways. The width of the line/arc corresponds to the number of common genes between the two pathways.



The width of the arc is directly proportional to the number of common genes between the two pathways.

4.4 Overlap between Fuzzy Gene-Sets

The overlap among FCM gene-sets are displayed a separate interactive circular graph (Figure 17). In addition to the representation of an overlap, each cluster is labelled with the KEGG that was most significantly enriched by that cluster.



Each FCM gene-set is additionally labelled by the most significant KEGG/ISG pathway it enriched.

4.5 Interactive Circular Graphs

The overlap among KEGG pathways and among FCM gene-sets are represented by interactive circular graphs (Figure 18). User can select/hide the nodes by mouse clicks. A single mouse click on a node will change its state from 'show connection' to 'hide connections' and vice versa.

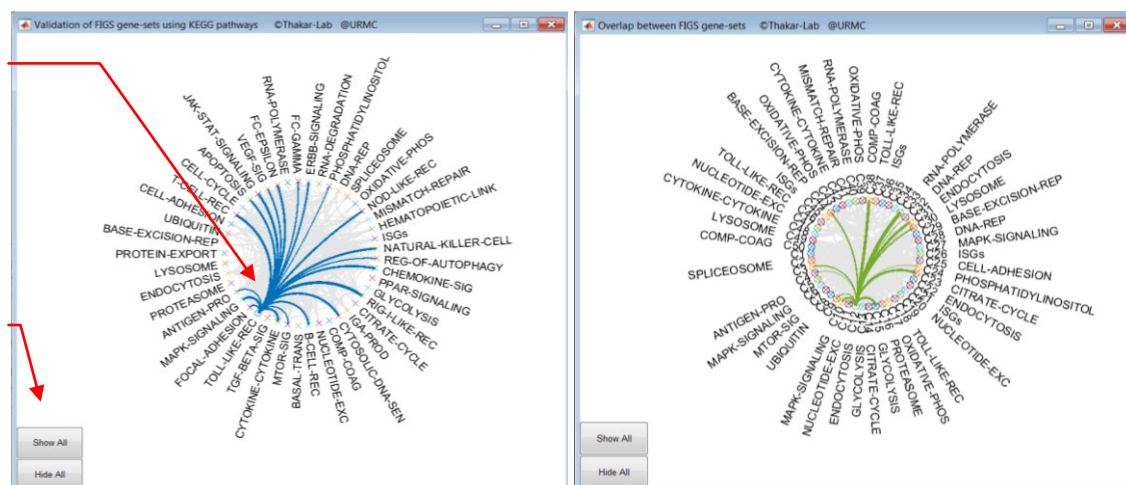


Figure 18: Overlap among FCM Gene-Sets

4.6 Temporal Expression Profile of Gene-Sets

From the drop down menu, the temporal expression of any two clusters can be compared at a time.

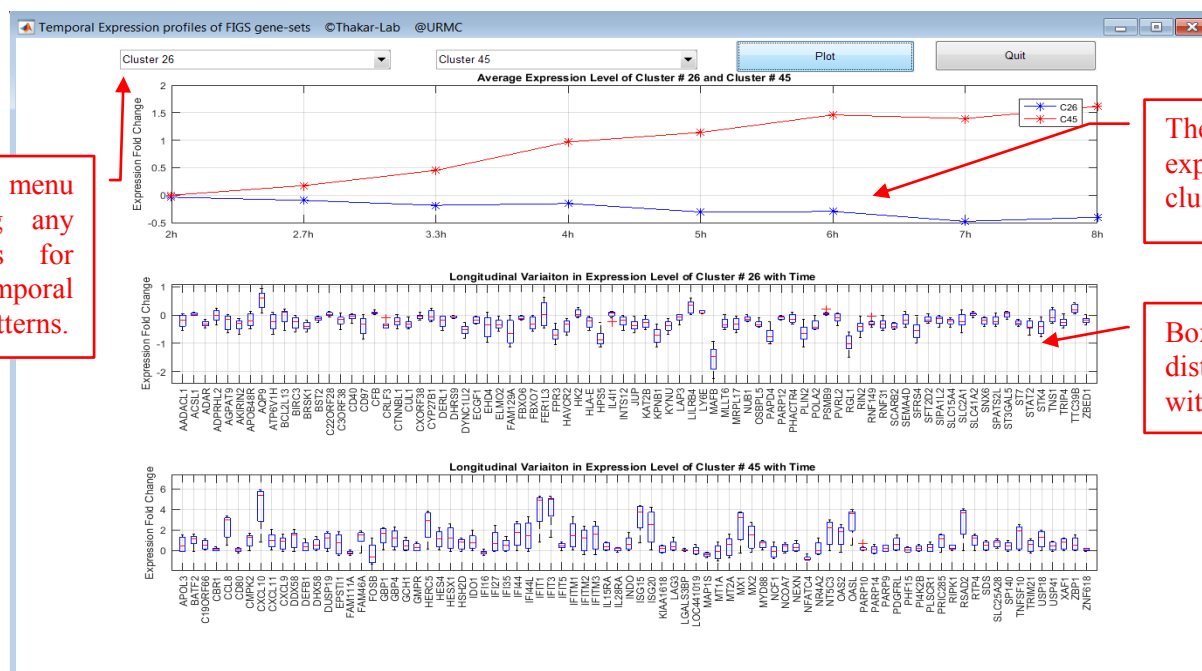


Figure 19: Temporal Expression Pattern of FCM Gene-Sets

4.7 Saving the Results

The detailed results are displayed in the tabular form (see section 4.1). A copy of the data-driven FCM gene-sets will be generated and saved as “FIGS_Results.csv”. This results file can be found in the installation folder of FIGS.

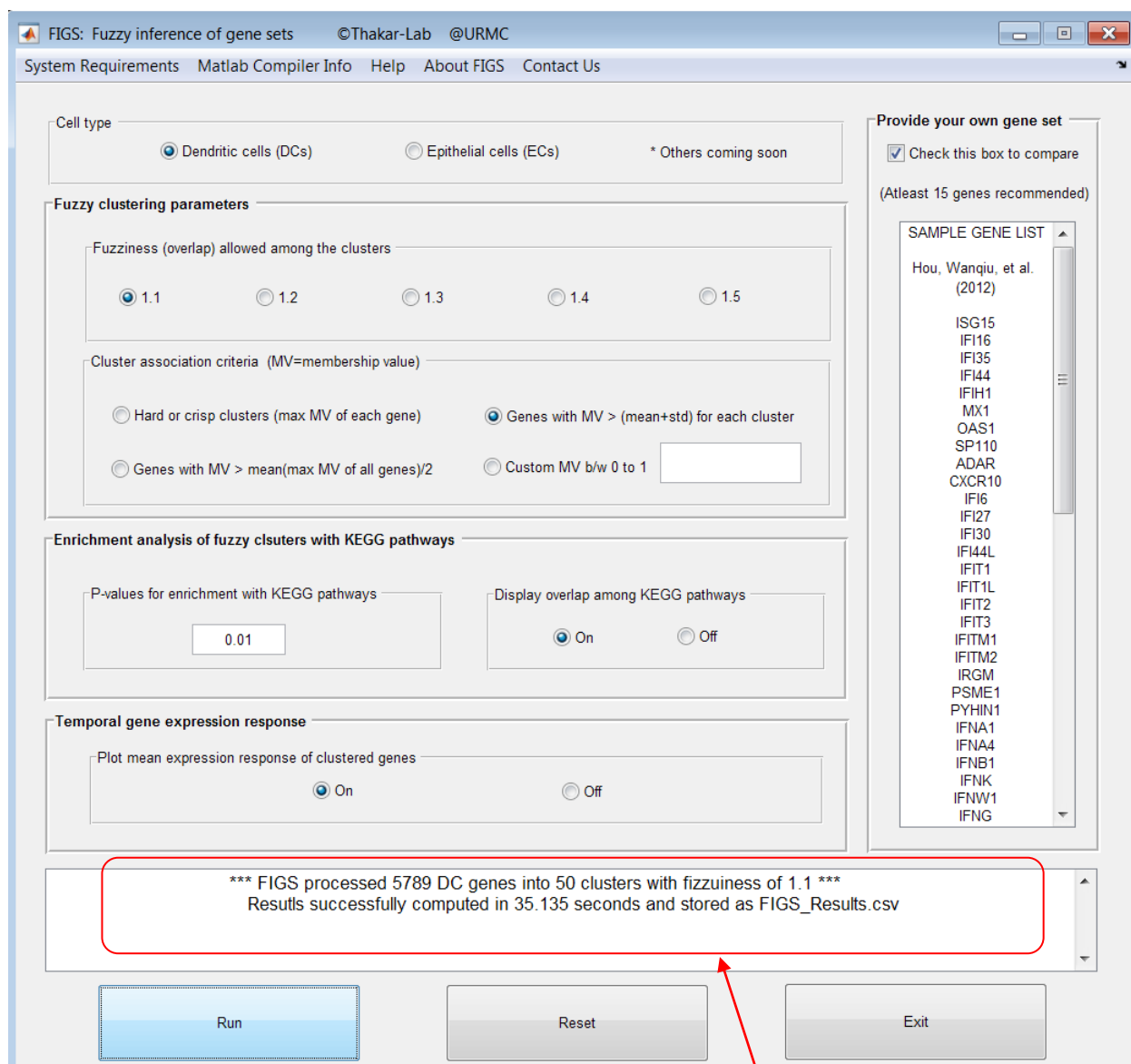


Figure 20: FIGS Results

The gene-sets produced by FIGS will be stored as FIGS_Results.csv file.