GEsture Manual

Version 1.0

1 introduction

GEsture is a hand-drawn gene expression search platform, which is for describing and analyzing gene expression based on overall similarity of expression level. it can identify genes that exhibit an expression pattern similar to that of what we draw or a familiar gene and simultaneously can dig invert, shift genes. The feature of this platform including:

Based on hand-drawn expression curves to search similar genes

Search from various aspects

Display in various formats

Run quickly

2 Operation Guideline

In the home page, there are two buttons. Before you click the start menu, you can click the demo and know how to operate this tool.

2.1 Select or upload a file

If you choose the demo button first, it is not necessary to upload a file, just choose a dataset and click the next button directly.

If you choose the start button, first, a dataset file is necessary to be uploaded and the format of file is as follows: the first column in each row represents gene name and the rest columns are elements which are measurements of the expression level of corresponding gene under a specific condition. Pay attention to that do not add anything such as headline in the file. Just upload the file only with gene name and expression data. The data format is as following shows:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
1	YAL001C	-0.15	-0.15	-0.21	0.17	-0.42	-0.44	-0.15	0.24	-0.1		0.18	0.42	-0.25	-0.01	-0.13	0.77	-0.21	0.43	
2	YAL002W	-0.11	0.1	0.01	0.06	0.04	-0.26	0.04	0.19	-0.22	-0.2	0.12	0.21	-0.26	-0.3	0.22	0.58	-0.36	0.13	
3	YAL003W	-0.14	-0.71	0.1	-0.32	-0.4	-0.58	0.11	0.21	0.09	0.57	-0.14	0.29	0.01	0.04	0.05	0.55	-0.08	0.33	
4	YAL004W	-0.02	-0.48	-0.11	0.12	-0.03	0.19	0.13	0.76	0.07	0.04	-0.06	0.3	-0.47	-0.16	-0.11	0.23	-0.45	0.02	
5	YAL005C	-0.05	-0.53	-0.47	-0.06	0.11	-0.07	0.25	0.46	0.12	0.49	-0.42	0.28	-0.3	-0.18	-0.3	0.68	-0.24	0.22	
6	YAL007C	-0.6	-0.45	-0.13	0.35	-0.01	0.49	0.18	0.43	-0.23	-0.3	-0.24	0.23	0.04	0.09	0.18	0.16	-0.01	-0.21	
7	YAL008W	-0.28	-0.22	-0.06	0.22	0.25	0.13	0.34	0.44	-0.32	0.26	-0.77	0.31	-0.09	0.02	-0.45	0.47	-0.49	0.22	
8	YAL009W	-0.03	-0.27	0.17	-0.12	-0.27	0.06	0.23	0.11	0.03	-0.27	-0.24	0.36	-0.11	0	-0.27	0.46	0.23	-0.06	
9	YAL010C	-0.05	0.13	0.13	-0.21	-0.45	-0.21	0.06	0.32	0	0.26	-0.5	0.31	0.1	-0.14	-0.71	0.51	0.31	0.13	
10	YAL011W	-0.31	-0.43	-0.3	-0.23	-0.13	-0.07	0.08	0.12	-0.01	-0.13	0.12	0.47	-0.3	-0.41	1.04	0.54	-0.16	0.07	
11	YAL012W	0.02	-0.33	-0.49	-0.3	-0.15	-0.24	0.4	0.53	0.25	0.49	-0.3	0.13	-0.12	-0.35	-0.19	0.47	0.06	0.13	
12	YAL013W	-0.36	-0.19	0	-0.32	-0.27	-0.12	0.04	0.17	0.06	0.06	0.28	0.38	-0.23	-0.12	0.05	0.58	-0.25	0.24	
13	YAL014C	-0.1	-0.15	-0.01	-0.25	-0.16	-0.13	0.06	0.19	-0.06	0.05	-0.25	0.23	-0.05	-0.13	0.09	0.22	0.35	0.09	
14	YAL015C	0	-0.01	0.12	-0.23	-0.13	0.25	0.3	-0.27	0.38	-0.06	-0.18	-0.16	-0.27	-0.16	0.09	0.09	0.22	0	
15	YAL016W	0.06	0.01	0.17	-0.14	0.01	-0.24	0.15	-1.34	0.15	0.06	0.01	0.18	0.09	0.06	0.18	0.14	0.3	0.17	
16	YAL017W	-0.4	-0.22	0.19	-0.2	-0.09	0.41	0.13	-0.05	-0.29	0.06	-0.16	0.17	-0.32	0.13	0.18	0.21	0.23		
17	YAL018C	0.46	0.28	0.16	-1.72	0.33	0.05	0.22	0.3	0	0.22	-0.15	-0.06	0.11	-0.47	0.22	0.05	-0.15	0.16	

2.2 Clustering or hand-drawn

After choosing dataset or uploading profiles, you will enter into a choice page and you can choose hand-drawn button or clustering button, we provide a gif on the top of each button for you to see the general procedures.

1   If you choose the hand drawn, you will go to the main operation interface.

2   if you choose the clustering, you should complete the following steps:

(1)   Input the cluster number or use the default value 16, then search.

(2)   After calculating, choose one mode to show the result genes in the main operation interface.
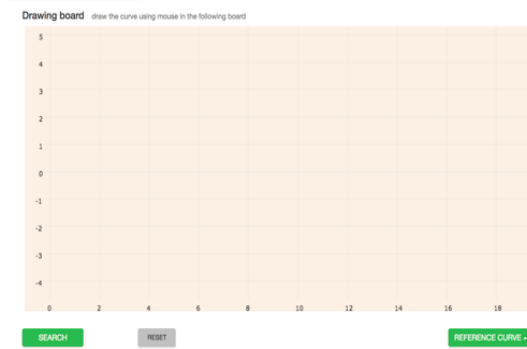
(3)   After clustering, you can just have a look at them and do not choose any one of these modes. At the bottom of the page, hand-drawn is provided again.

A:choose a operation

Step2:choose cluster or hand draw
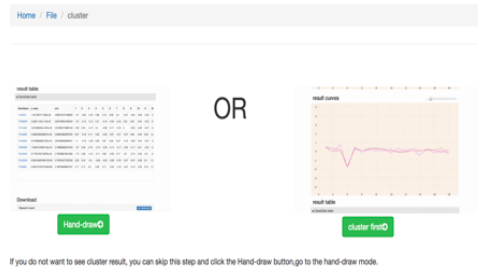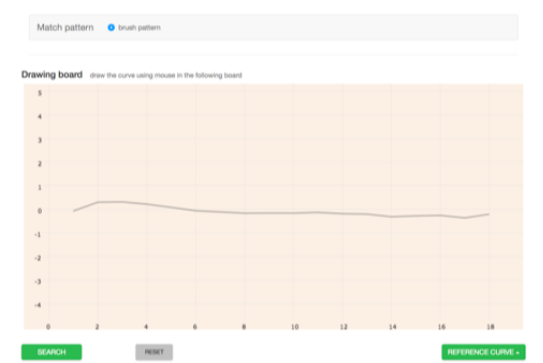
B:choose hand-draw

C:cluster result

Step4:look up search result

D: choose the second mode

2.3 Main operation interface

In the main operation interface, there is a detailed introduction about how to use it.

step1: GEsture requires a curve as an input. The curve can be obtained by drawing with mouse or randomly selecting a gene.

(1) It is suitable for you to directly draw the curve with mouse in the drawing board if you know your 'desired' curve.

(2) If you do not know how to draw the curve, Reference curve button is provided for drawing which includes 2 forms of drawing. The first form is selecting a gene, click the RANDOMLY button, then the drawing board will show one concrete gene expression curve. And you can input a gene name you expect to look for, then click the QUERY button. The second form is generating a random curve in the drawing board.

a: reference curve
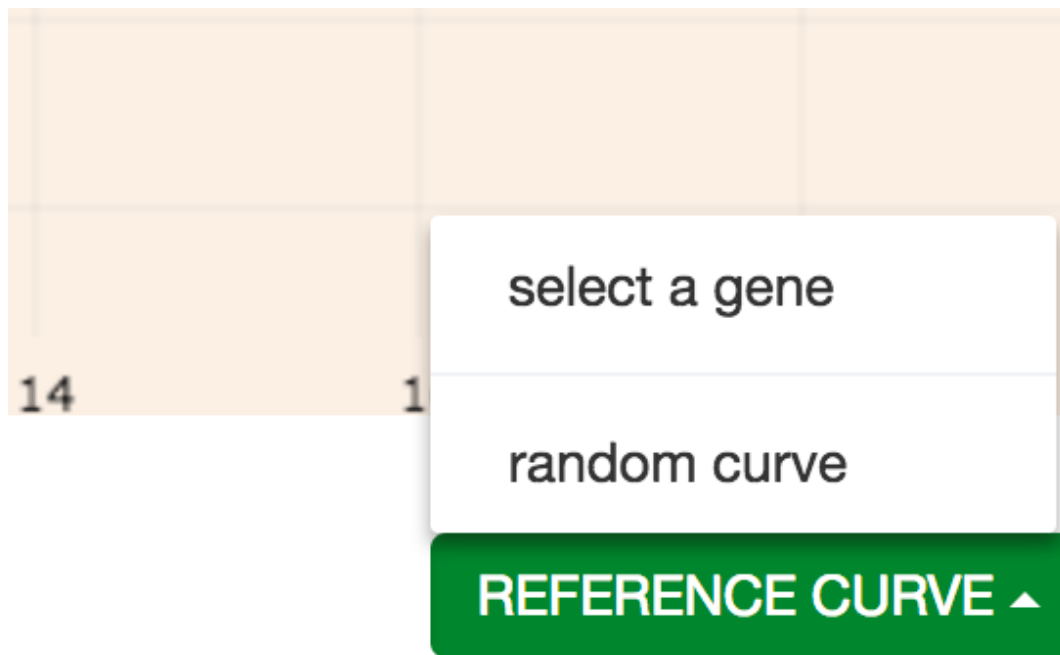

b: the form of selecting a gene
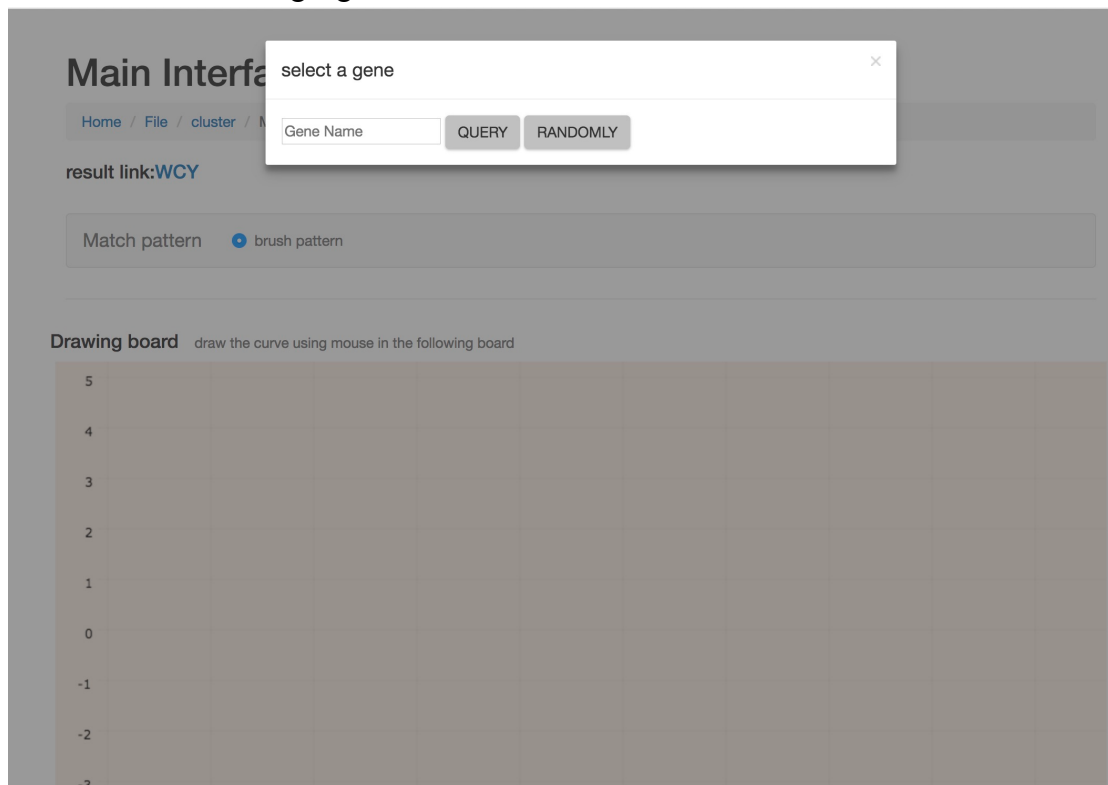
step2: After drawing the curve, click the search button, then GEsture will calculate the similarities and find the co-expression genes. It is noted that the contrast and shift

search patterns will show after searching the similar expression genes. In other words, GEsture based on the fitted curve to search the opposite and shift expression genes. So remember to use brush pattern (similar pattern) firstly and then choose contrast pattern or shift pattern directly after searching co-expression genes.
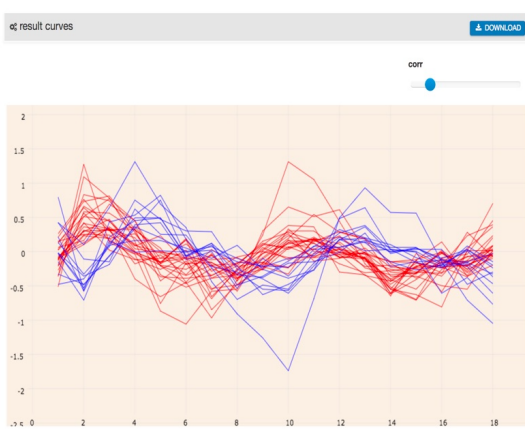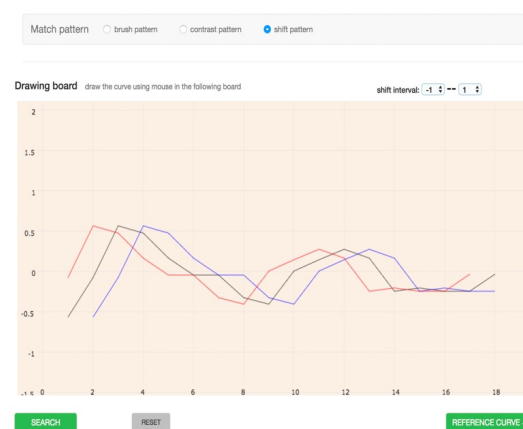

A:brush pattern
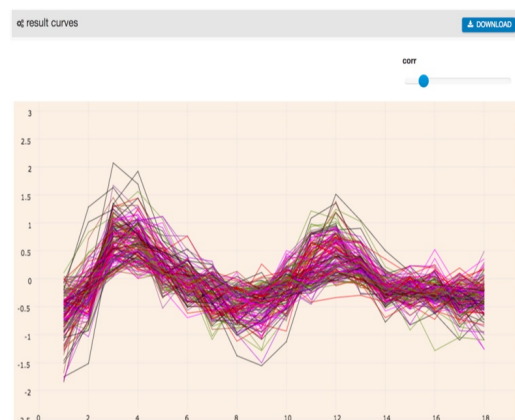
B: contrast pattern
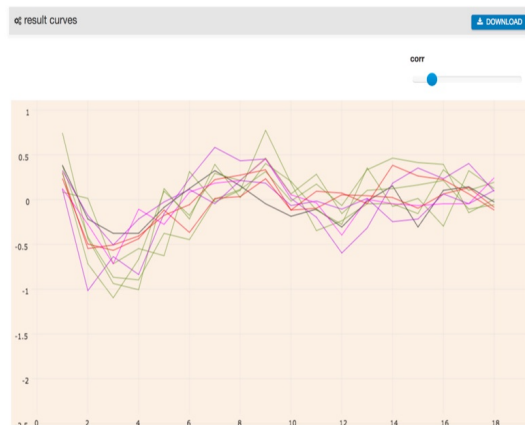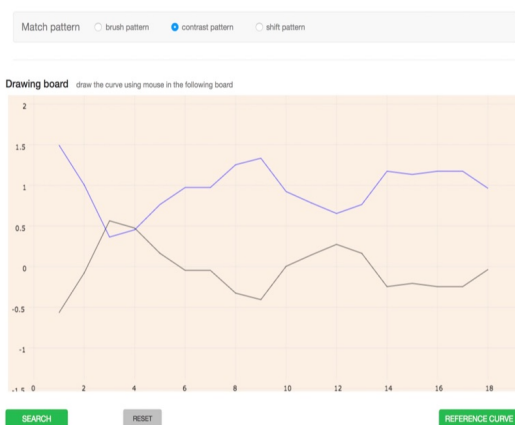
C: shift pattern

step3: Contrast pattern, GEsture will search the contrast expression gene. This

step can be overlooked if you do not expect to search its opposite expression genes.

Step4: Shift pattern. There will show a shift interval which is used to control the left and right translation of the curve. Negative represents time-ahead and positive represents time-delay.

Step5: Result filter. We provide a slider for users to change the correlation value, enable users to filter data and focus on high correlation genes. With the change of correlation value, the result curves, table content and heat map will change with it. It is particularly noted that download the table content as early as possible if you change the search pattern. For example, if you search the contrast pattern after brush pattern, the results of brush pattern will be covered by the contrast expression genes. So remember to save the result if you will do another search. The following figure shows the genes and curves which have been filtered.
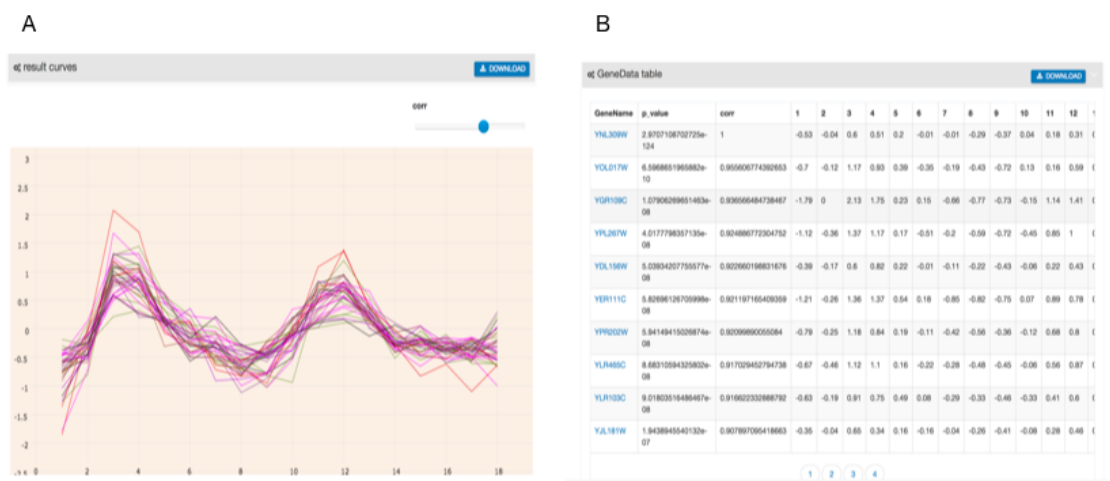
Step6: comprehensive relationship network map appears after the shift pattern. And you can use the mouse to adjust the size of the map. As following figure shows:
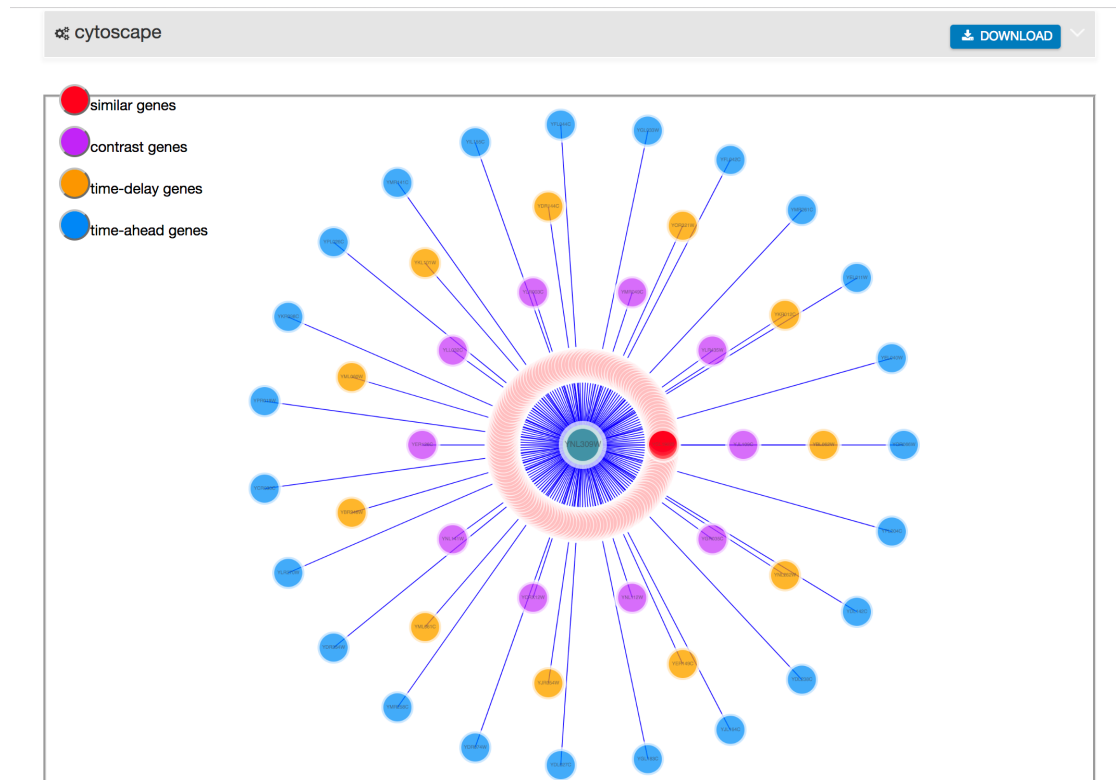
Step7: At the top of menu, a result link is provided for users next time to use without uploading the expression file again. So make sure to save this page if you need to use same gene expression data next time. The expiration date is a week after uploading.

2.4 Limitation

For the purpose of dealing with the gene expression data effectively and accurately, we set the range of time points of gene expression not to exceed 100. And in the database of GEO, we also find that the number of time points of many time series gene expression profiles is usually in the range of 4 to 100. so make sure uploading the profile whose samples should not exceed 100. Otherwise, it may cause error. Apart from that, when you draw the curve, try to include all time points. For example, if a gene has 18 time points data, you'd better draw from 1 to 18, otherwise the system will automatically help you carry out the interpolation fit, randomly generate a point which is filled in the vacancy may leading to errors and inaccuracy. Finally, make sure the file you are prepare to upload is less than 20MB, or it may fail to upload.