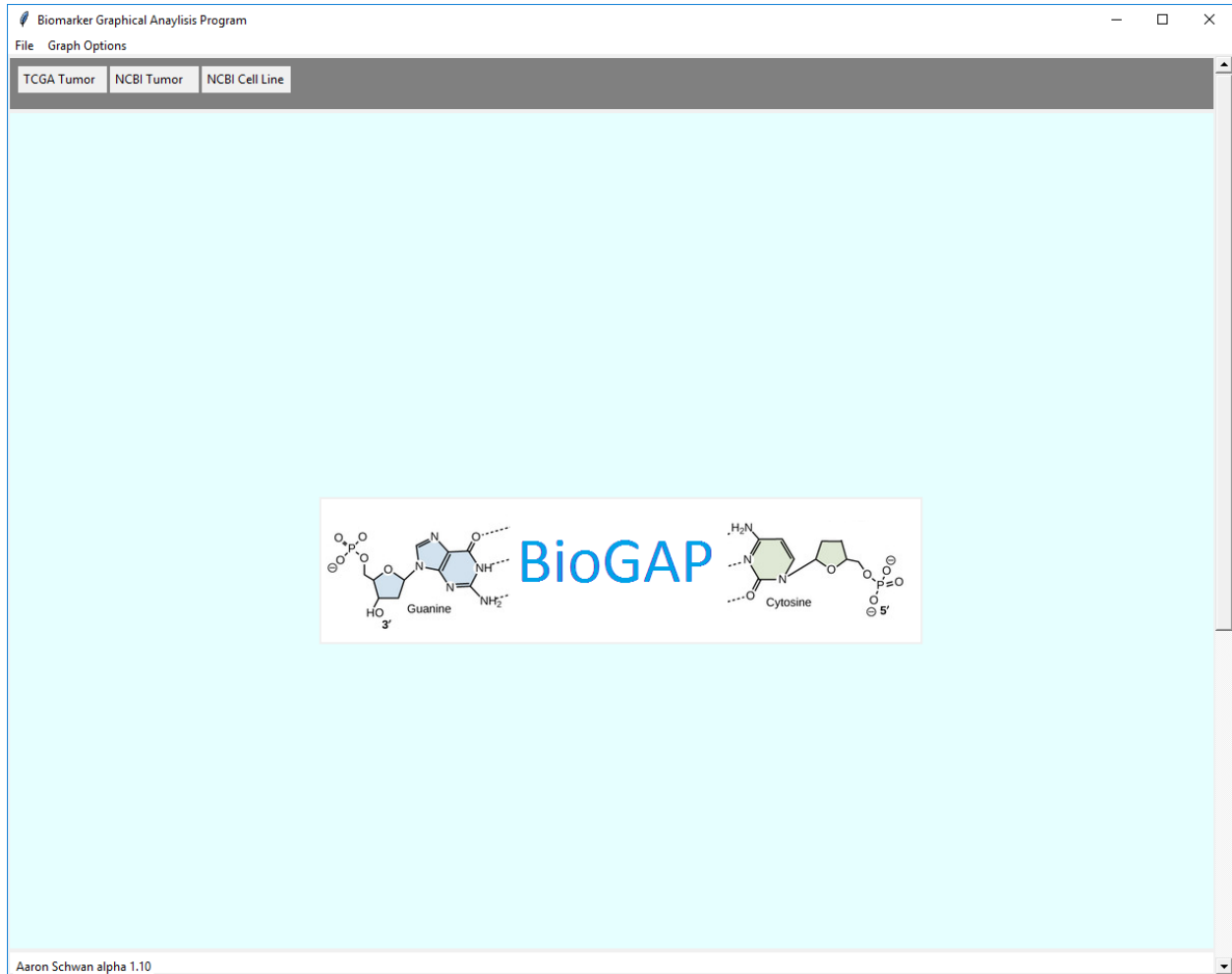


## Choose the Database you want access to

- [TCGA](#)
- [NCBI Tumor](#)
- [NCBI Cell Lines](#)



## TCGA Database Usage:

- Search Gene
  - Normal Search
  - Advanced Search
- Correlations
  - Normal
  - Heat map
- Kaplan Meier
  - Normal Kaplan
  - Retrieving p-value
  - Automated Kaplan Meier's
- Stage Graph
- Expression Graph

Biomarker Graphical Analysis Program

File Graph Options

TCGA Tumor NCBI Tumor NCBI Cell Line

Data Source: Include Outliers Search Gene Search More Options

Standard Statistics:

Average:	
Standard Deviation:	
Interquartile Range:	
Range:	
Minimum:	
First Quartile Median:	
Median:	
Third Quartile Median:	
Maximum:	

Correlations:

Correlate to Gene Correlate to Gene Heat Map Genes

R Squared: t-test: Start Heat Map

☐ Graph Regression Line

Kaplan Meiers:

	Low Value	High Value	
First Line:			<input type="checkbox"/>
Second Line:			<input type="checkbox"/>
Third Line:			<input type="checkbox"/>
Fourth Line:			<input type="checkbox"/>
Fifth Line:			<input type="checkbox"/>
Sixth Line:			<input type="checkbox"/>
Seventh Line:			<input type="checkbox"/>
Eighth Line:			<input type="checkbox"/>
Ninth Line:			<input type="checkbox"/>
Tenth Line:			<input type="checkbox"/>

Graph Kaplan Mieres

Line: Line: p-value

Auto Kaplan Meier Graphs:

2 Line Best Kaplan Mieres Graph ☐ Include All Patients

Stage Graphs:

Graph Stage Data ☐ Show Medians

Expression Graphs:

Aaron Schwan alpha 1.10

## Search Gene:

### Normal gene Search:

The image shows a horizontal search bar with four main components. From left to right: a 'Data Source:' dropdown menu, an 'Include Outliers' dropdown menu, a 'Search Gene' text input field, and a 'Search' button. To the right of the 'Search' button is a link that says 'More Options' with a double arrow icon. Four orange arrows with black numbers 1, 2, 3, and 4 point upwards to each of these four components respectively.

1. Choose Data Source

2. Decide to include or exclude outliers a. Exclude Outliers works on a standard statistical measure that says anything 1.5 times the Interquartile away from the median of the third and first quartile is an outlier.

3. Type gene into text box (if the gene doesn't work try it under a different name and hit Search Gene.)

4. Hit "Search" button.

### Advanced gene Search:

This image shows the same search bar as the normal search interface. However, an orange arrow with the number 1 points upwards to the 'More Options' link, which is located to the right of the 'Search' button.

1. Select "More Options"

The image shows the search bar with the 'More Options' link expanded into a dropdown menu. The menu contains several filter options, each with a checkbox: 'Sex' (Male, Female), 'Stages' (Stage 1, Stage 2, Stage 3, Stage 4), 'Races' (White, Black or African American, Asian, Not Reported), and 'Age Range (years):' with two input fields labeled 'TO'. The entire dropdown menu is enclosed in a red rectangular border. To the right of the dropdown menu, the 'Search' button and a 'Less Options' link are visible.

2. Select all requirements you want the individuals to have (sex, stage, race, age).

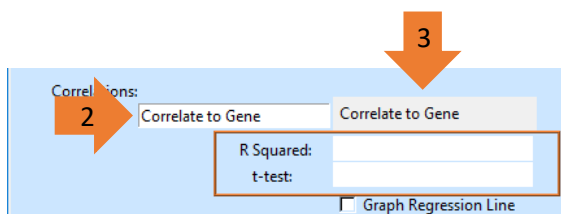
\*One of each field must be selected or else no data will fit the requirements.

\*\* if no data comes through with all fields having a selection there is no individual meeting all requirements.

\*\*\* when “Less Options” is selected the requirements are reset to allow all patient data with expression data to be used.

## Correlations:

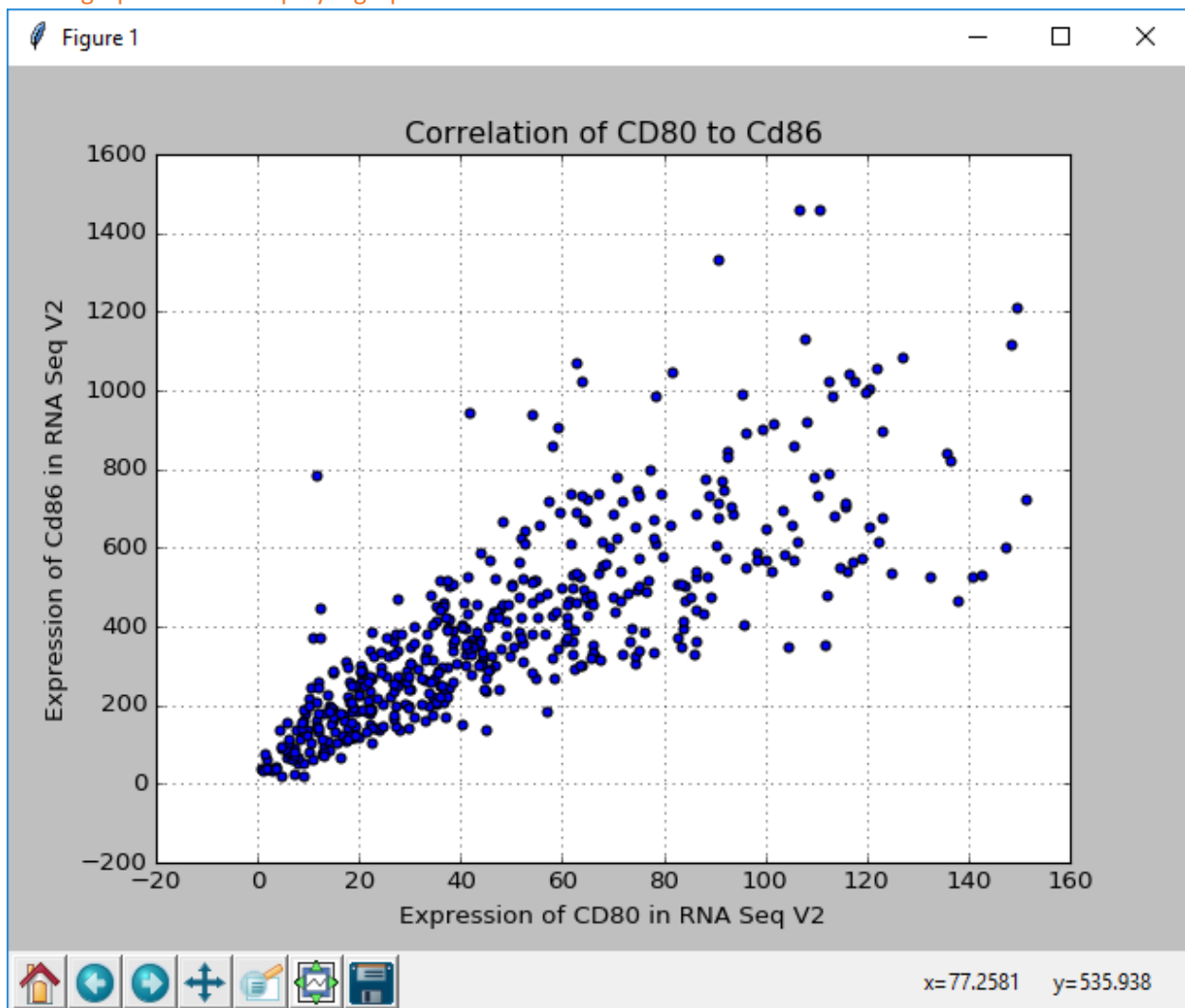
### Normal:



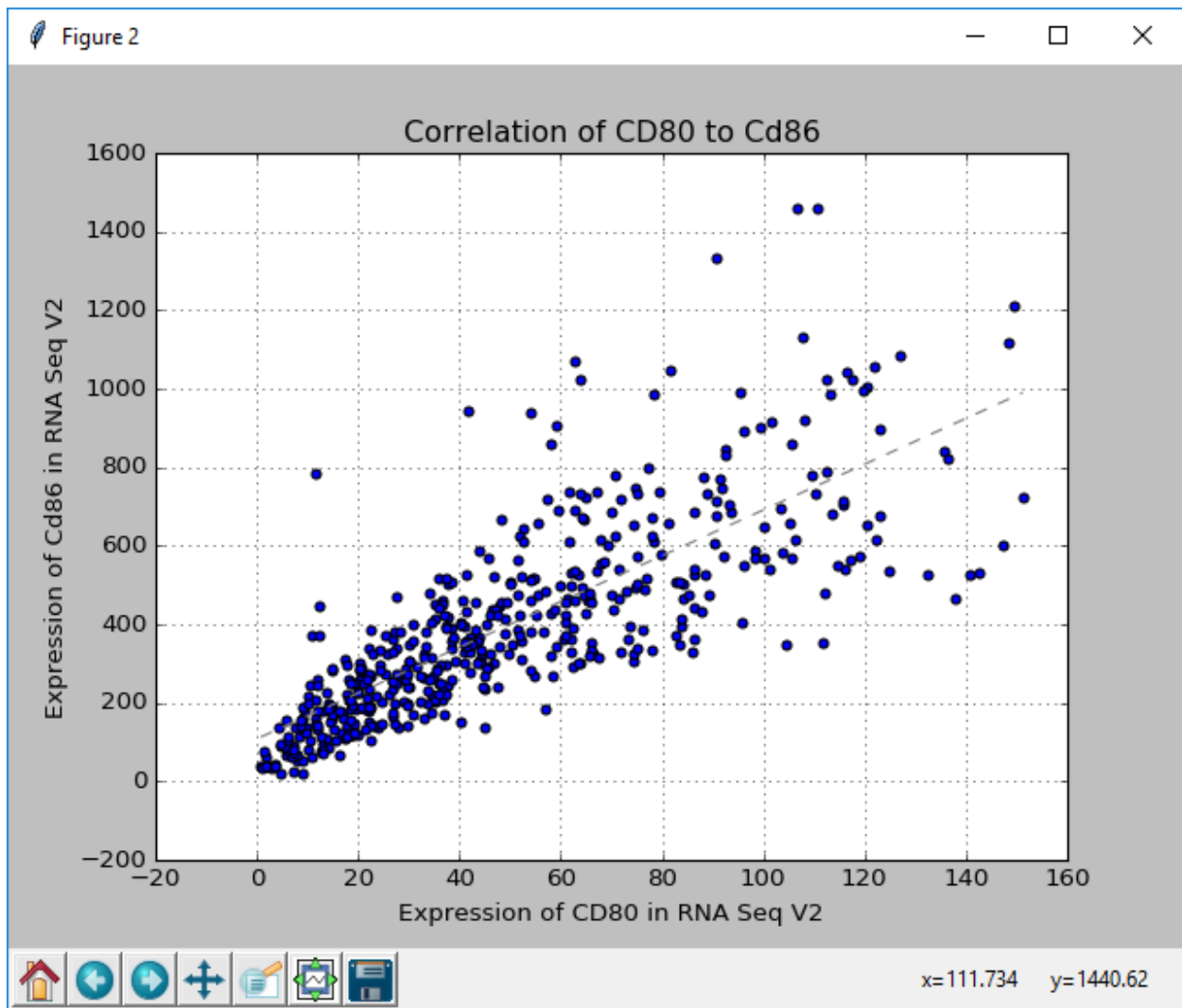
The screenshot shows a software interface for correlations. On the left, a blue box contains the text "Correlations:". An orange arrow with the number "2" points to a text input field labeled "Correlate to Gene". To the right of this field is a grey button also labeled "Correlate to Gene". An orange arrow with the number "3" points down to this button. Below the input field and button is a box containing two labels, "R Squared:" and "t-test:", each followed by a white text input field. At the bottom of the interface is a checkbox labeled "Graph Regression Line".

1. Select a gene with gene search function.
2. Choose a gene to correlate this uses all requirements set up in your initial gene search.
3. Press correlate button to have graph made.
  - a. If a linear regression line is wanted select the check box “Graph Regression Line”
4. The box shows where the linear regression coefficient and t-test values are displayed automatically once graphed.

When graphed it will display a graph like these:

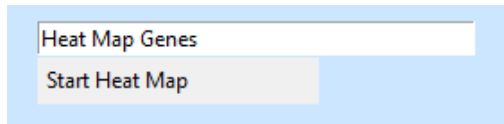


\*Without linear regression line



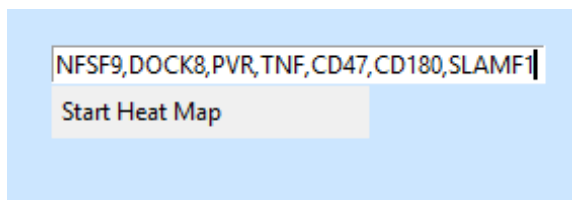
\*With linear regression line

## Heat map:



A screenshot of a web interface showing a text input box labeled "Heat Map Genes" and a button labeled "Start Heat Map". The input box is empty.

\*As with normal correlation graphs the heat map function uses the requirements set by gene search in the initial search unlike correlations it doesn't use the gene search box only genes typed into the "Heat Map Genes" entry box.



A screenshot of the same web interface, but the "Heat Map Genes" input box now contains the text "NFSF9,DOCK8,PVR,TNF,CD47,CD180,SLAMF1". The "Start Heat Map" button is still visible below the input box.

Once genes are typed into "Heat Map Genes" entry box when you hit the "Start Heat Map" button it begins to make the heat map.

\*this may take several minutes

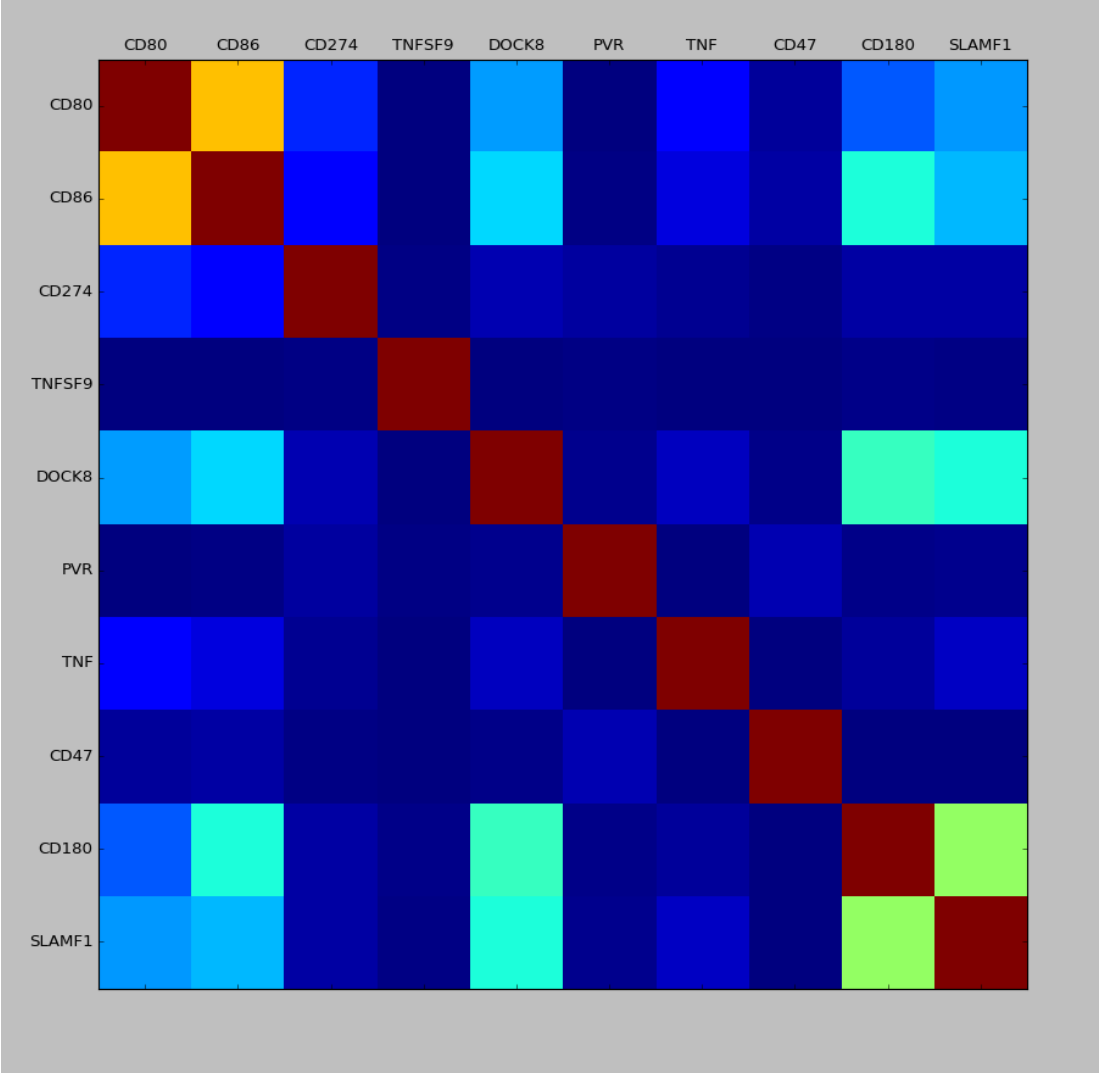
When done it graphs the data in a normal matrix.

Red = good correlation above .8

Yellow = correlation above .7

Green = correlation above .5

Blue = correlation below .5





## Kaplan Meier Graphs:

### Normal Kaplan:

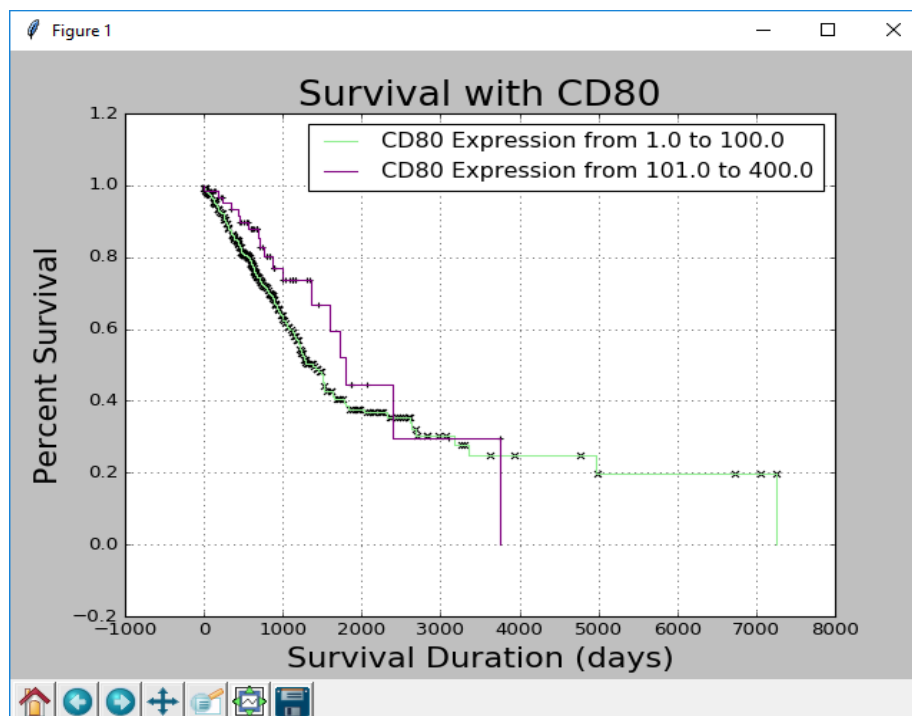
1 2 3

	Low Value	High Value	
First Line:	1	100	<input checked="" type="checkbox"/>
Second Line:			<input type="checkbox"/>
Third Line:			<input type="checkbox"/>
Fourth Line:			<input type="checkbox"/>
Fifth Line:	101	400	<input checked="" type="checkbox"/>
Sixth Line:			<input type="checkbox"/>
Seventh Line:			<input type="checkbox"/>
Eighth Line:			<input type="checkbox"/>
Ninth Line:			<input type="checkbox"/>
Tenth Line:			<input type="checkbox"/>

Graph Kaplan Mieres

Line:  Line:  p-value

1. Type in low values you want to graph in "Low Value" column.
2. Type in High values you want to graph in "High Value" column.
3. Choose what expressions you want to graph with the check boxes.



## Retrieving p-value:

	Low Value	High Value	
First Line:	1	100	<input checked="" type="checkbox"/>
Second Line:			<input type="checkbox"/>
Third Line:			<input type="checkbox"/>
Fourth Line:			<input type="checkbox"/>
Fifth Line:	101	400	<input checked="" type="checkbox"/>
Sixth Line:			<input type="checkbox"/>
Seventh Line:			<input type="checkbox"/>
Eighth Line:			<input type="checkbox"/>
Ninth Line:			<input type="checkbox"/>
Tenth Line:			<input type="checkbox"/>

Graph Kaplan Mieres

Line:  Line:  p-value

2 3 4 5

1. Graph a Normal Kaplan Meier with at least two lines.
2. Select first line.
3. Select second line to compare using the log rank test.
4. Hit the “p-value” button.
5. p-value displayed in box next to “p-value” button.

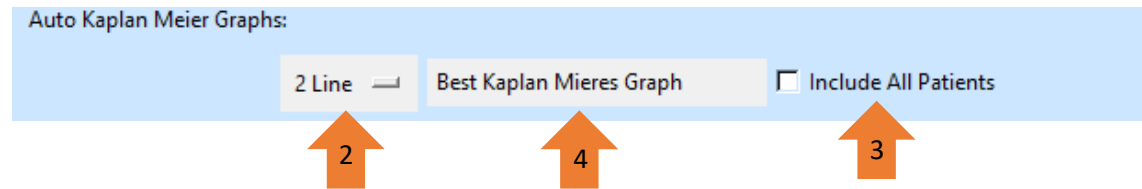
It should end up looking something like this:

	Low Value	High Value	
First Line:	1	100	<input checked="" type="checkbox"/>
Second Line:			<input type="checkbox"/>
Third Line:			<input type="checkbox"/>
Fourth Line:			<input type="checkbox"/>
Fifth Line:	101	400	<input checked="" type="checkbox"/>
Sixth Line:			<input type="checkbox"/>
Seventh Line:			<input type="checkbox"/>
Eighth Line:			<input type="checkbox"/>
Ninth Line:			<input type="checkbox"/>
Tenth Line:			<input type="checkbox"/>

Graph Kaplan Mieres

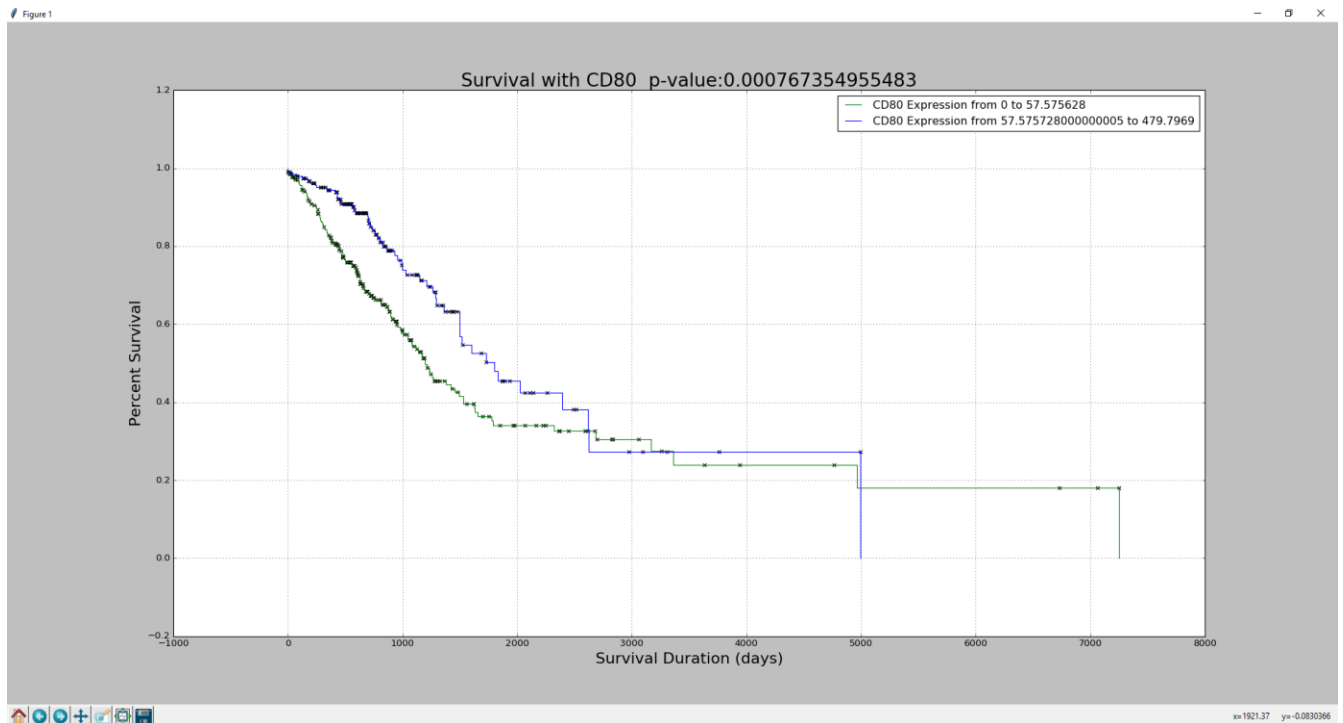
1  5  p-value 0.09054097708800216

## Auto Kaplan Graphs:

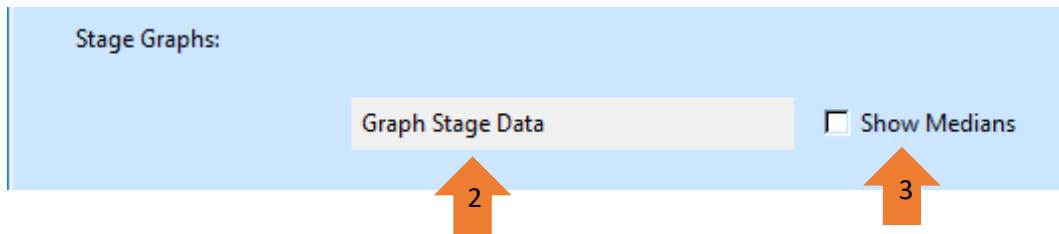


1. Search a gene.
2. Select amount of lines wanted (default 2).
3. Include all patients or not
  - a. What this does is if you include all patients the graph will contain all people that the found by the program but if not checked it goes by the best p-value it can find.
4. Hit "Best Kaplan Meier's Graph" button to begin graph.

It will return a graph similar to this:

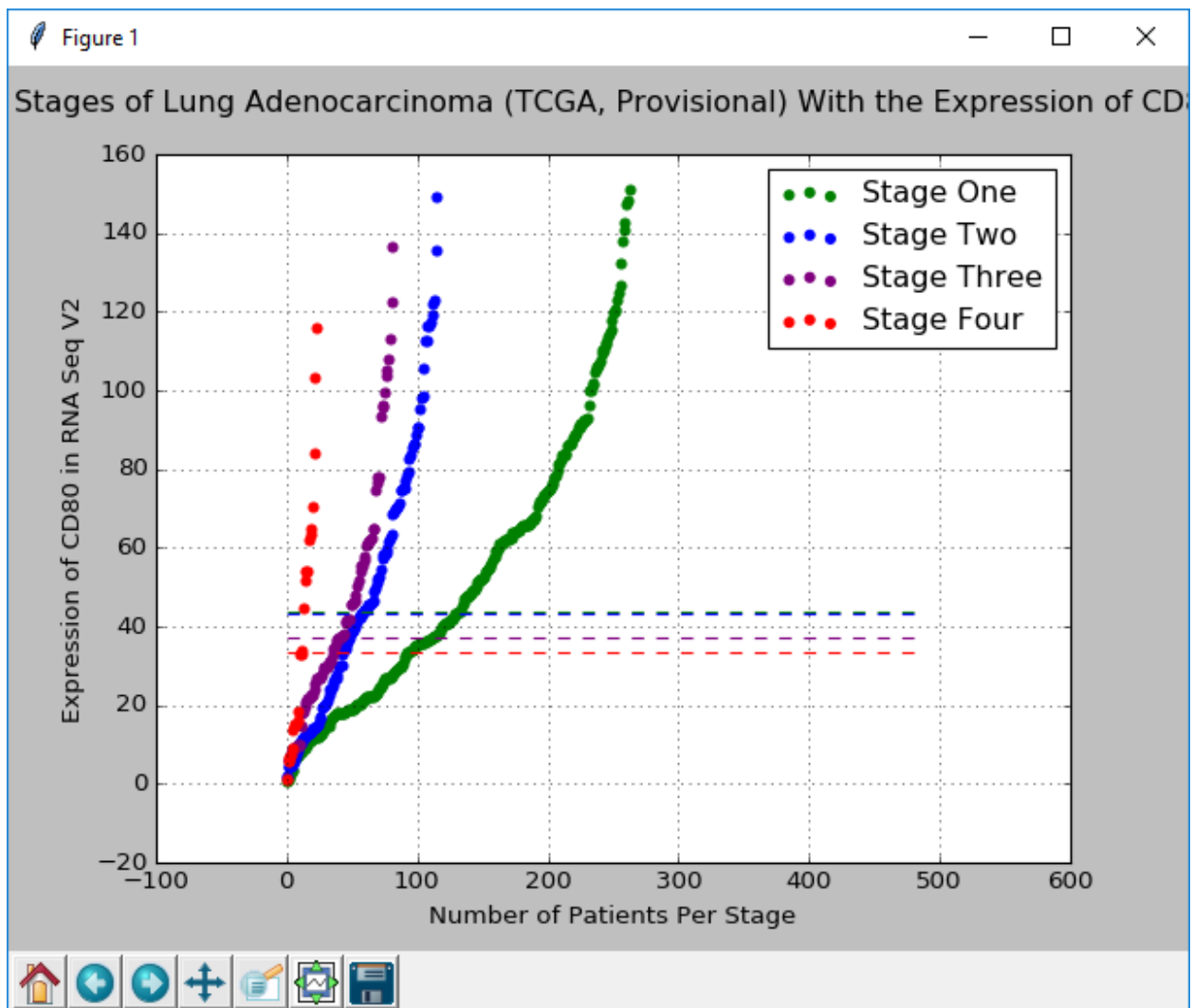


## Stage Graph:

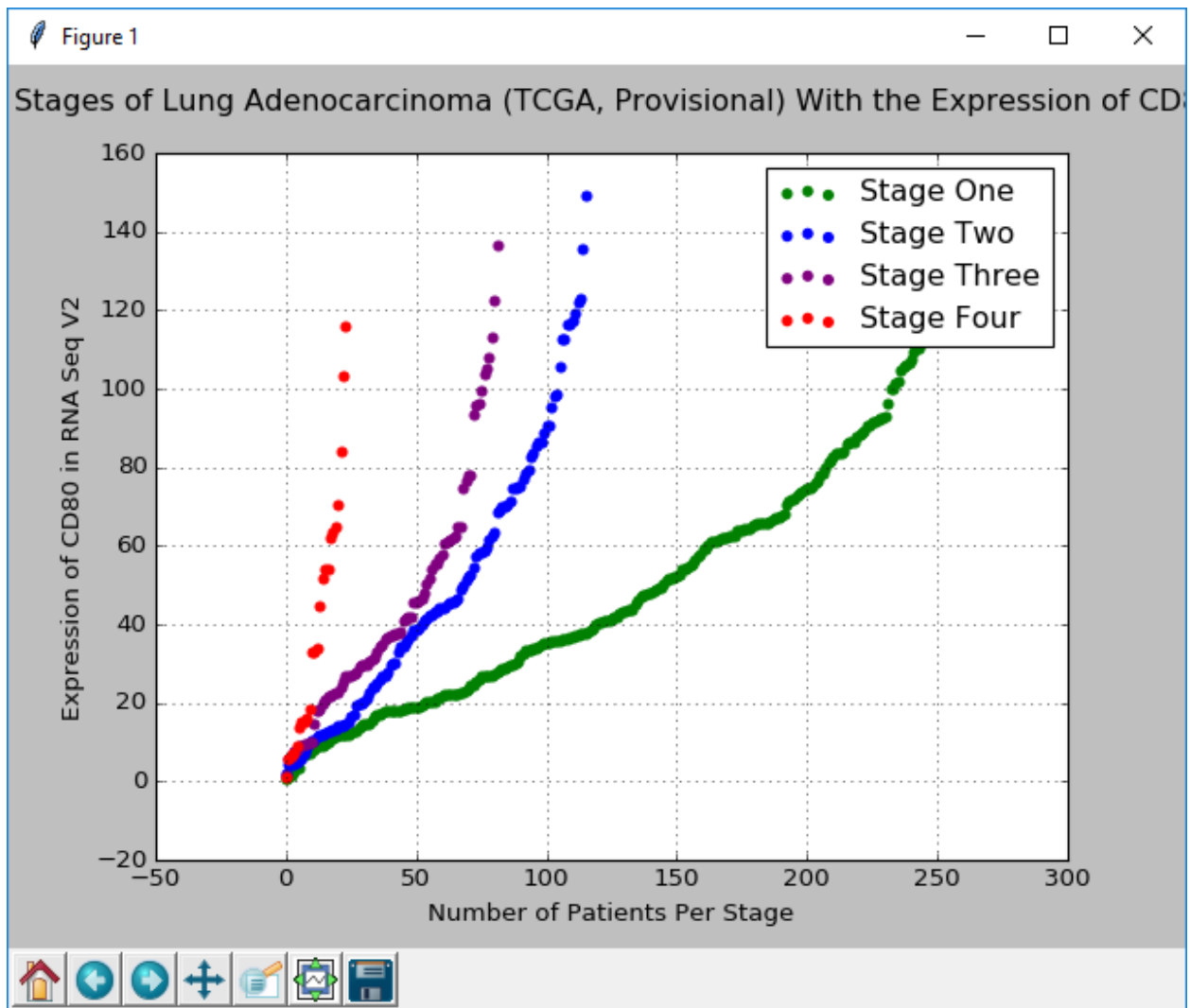


1. [Search a gene.](#)
2. Choose "Show Medians" or not.
3. Hit "Graph Stage Data"

The graph should look similar to this:



\*With median lines



\*Without median lines.

## Expression Graph:

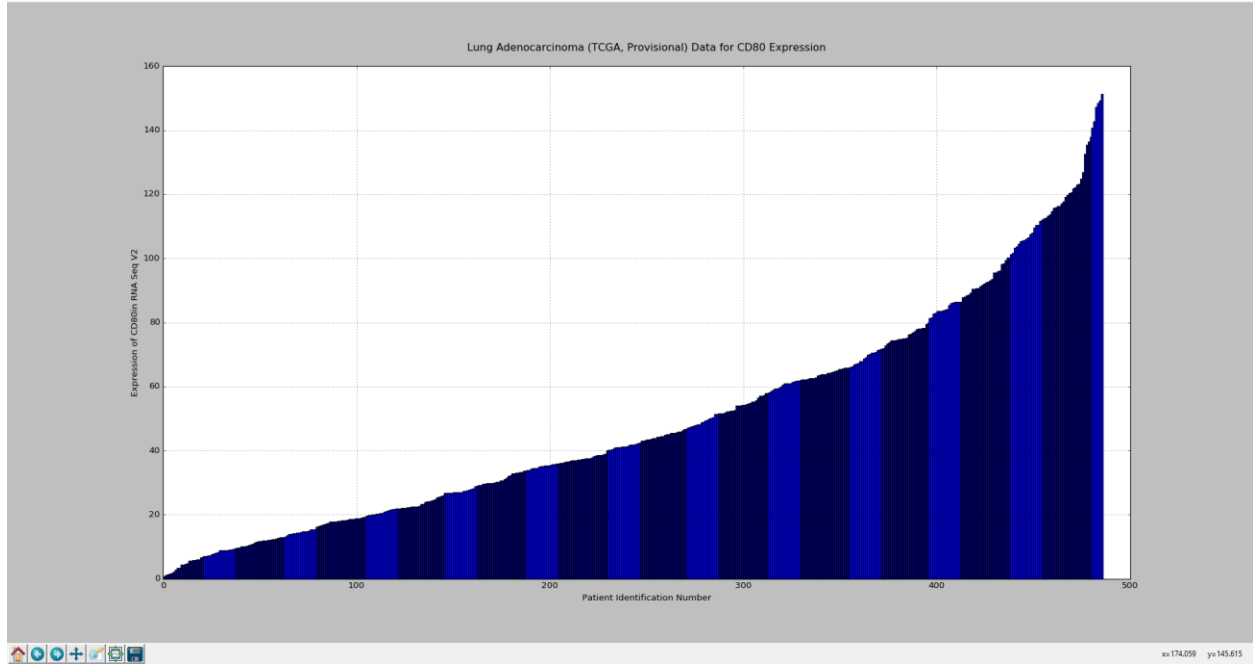
Expression Graphs:

Expression Graph

1. Search a gene.
2. Hit "Expression Graph"

The graph will look similar to this:

Figure 1



## NCBI Tumor Usage:

- Search Gene
- Correlations
  - Normal
  - Heat map
- Expression Graph

Biomarker Graphical Analysis Program

File

TCGA Tumor NCBI Tumor NCBI Cell Line

Data Source: Include Outliers: Search Prob Number Search

Standard Statistics:

Average:	
Standard Deviation:	
Interquartile Range:	
Range:	
Minimum:	
First Quartile Median:	
Median:	
Third Quartile Median:	
Maximum:	

Correlations:

Correlate to Prob	Correlate to Gene	Heat Map Probes
R Squared:		Start Heat Map
t-test:		
<input type="checkbox"/> Graph Regression Line		

Expression Graphs:

Expression Graph

Aaron Schwan alpha 1.10

## Search Probe:

The image shows a horizontal toolbar with four elements. From left to right: a dropdown menu labeled 'Data Source:', a dropdown menu labeled 'Include Outliers', a text input field labeled 'Search Prob Number', and a button labeled 'Search'. Below each element is an orange arrow pointing upwards, numbered 1 through 4 respectively.

1. Choose Data Source

2. Decide to include or exclude outliers a. Exclude Outliers works on a standard statistical measure that says anything 1.5 times the Interquartile away from the median of the third and first quartile is an outlier.

3. Type gene into text box (if the gene doesn't work try it under a different name and hit Search Gene.)

4. Hit "Search" button.

## Correlations:

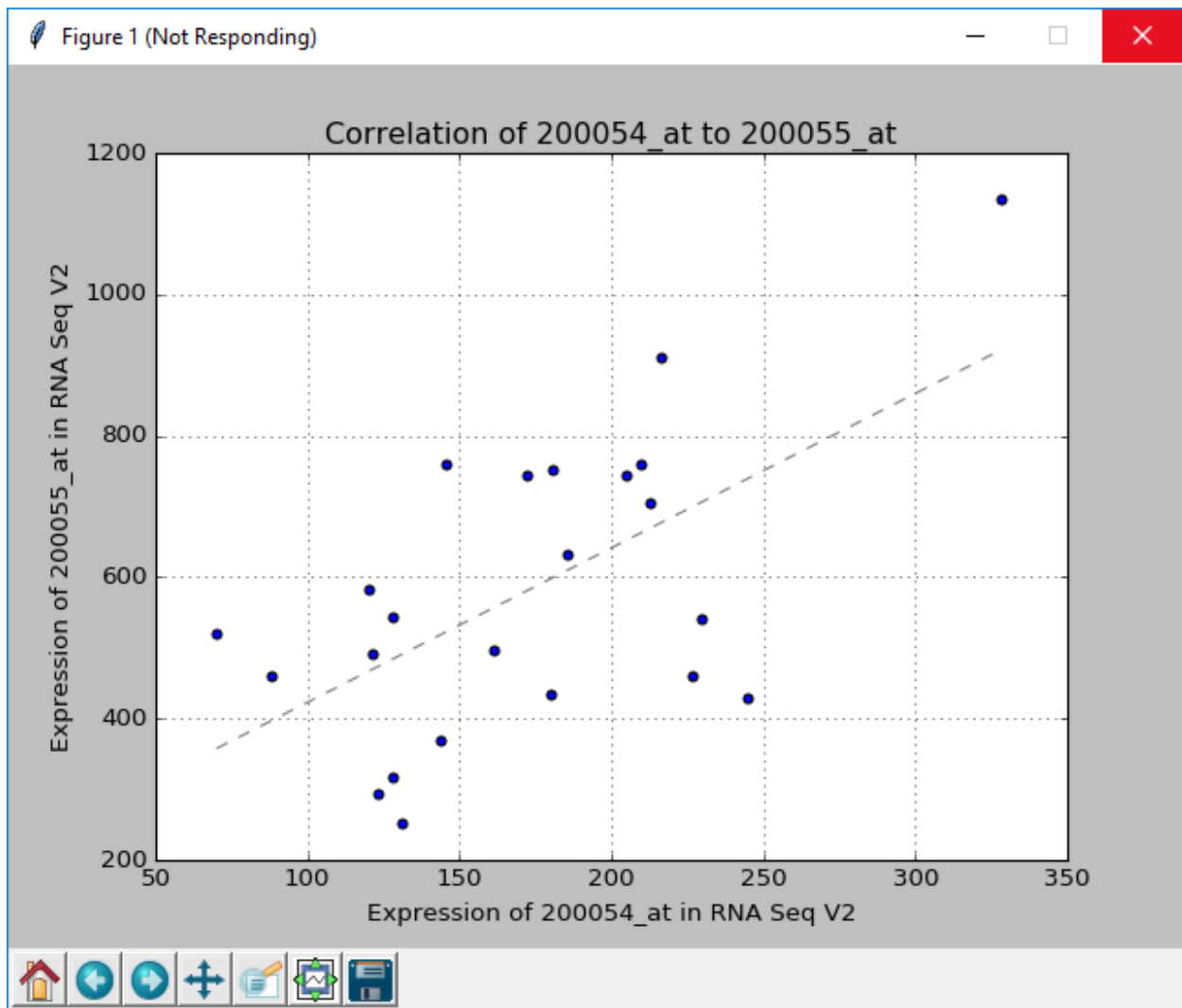
### Normal:

The image shows a section titled 'Correlations:'. Below the title are two buttons: 'Correlate to Prob' and 'Correlate to Gene'. Below these buttons is a box containing two input fields: 'R Squared:' and 't-test:'. Below the box is a checkbox labeled 'Graph Regression Line'. An orange arrow labeled '2' points to the 'Correlate to Prob' button. Another orange arrow labeled '3' points to the 'Correlate to Gene' button.

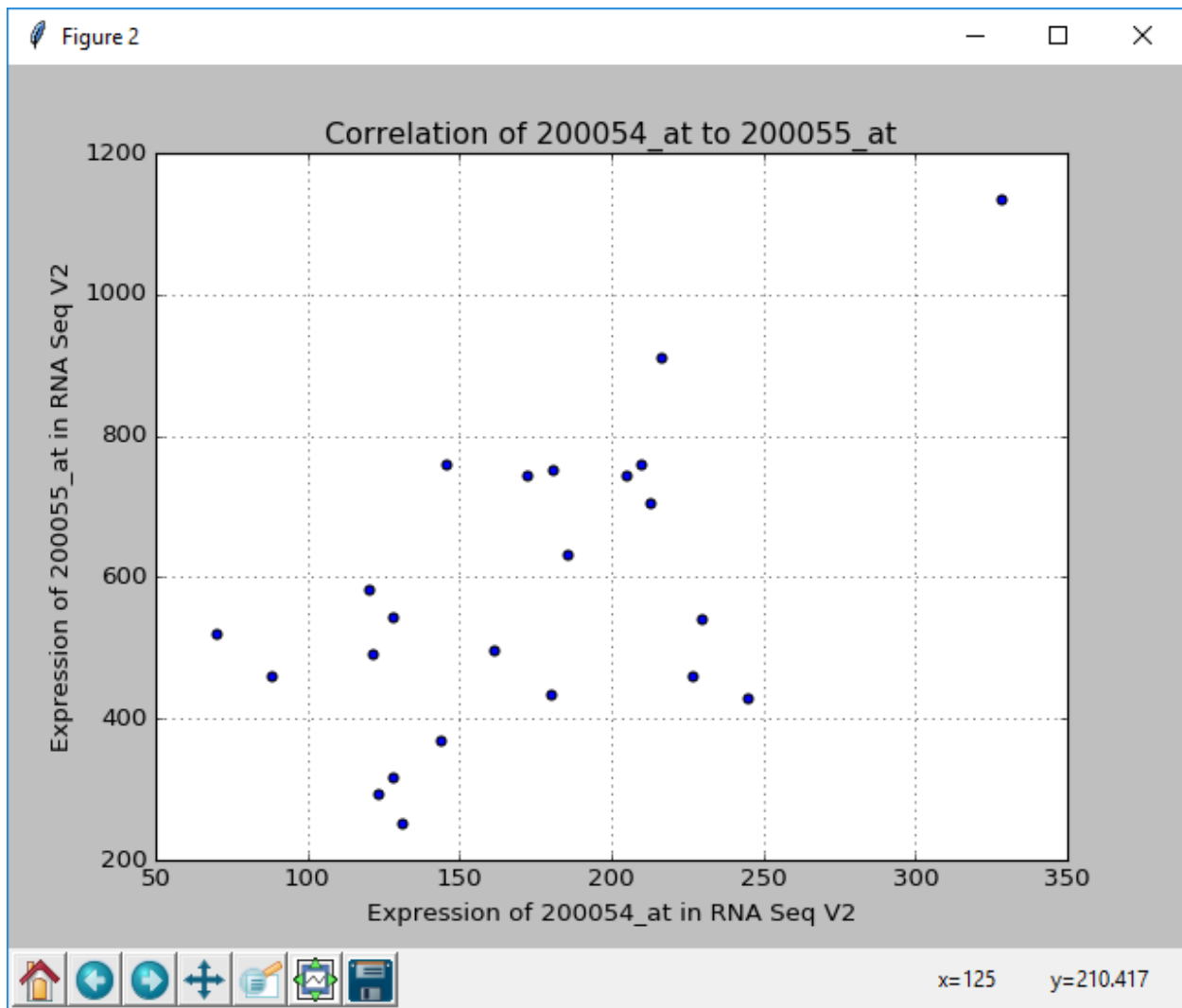
1. Select a gene with Probe search function.
2. Choose a gene to correlate this uses all requirements set up in your initial Probe search.
3. Press correlate button to have graph made.
  - a. If a linear regression line is wanted select the check box "Graph Regression Line"
4. The box shows where the linear regression coefficient and t-test values are displayed automatically once graphed.

The Graph should look similar to these:





With linear regression line



Without linear regression line.

## Heat Map:

A screenshot of a web interface for generating a heat map. It features a light green background. On the left, there is a white rectangular input box with the text "Heat Map Probes" inside. To the right of this box is a grey rectangular button with the text "Start Heat Map".

Once genes are typed into “Heat Map Genes” entry box when you hit the “Start Heat Map” button it begins to make the heat map.

\*this may take several minutes

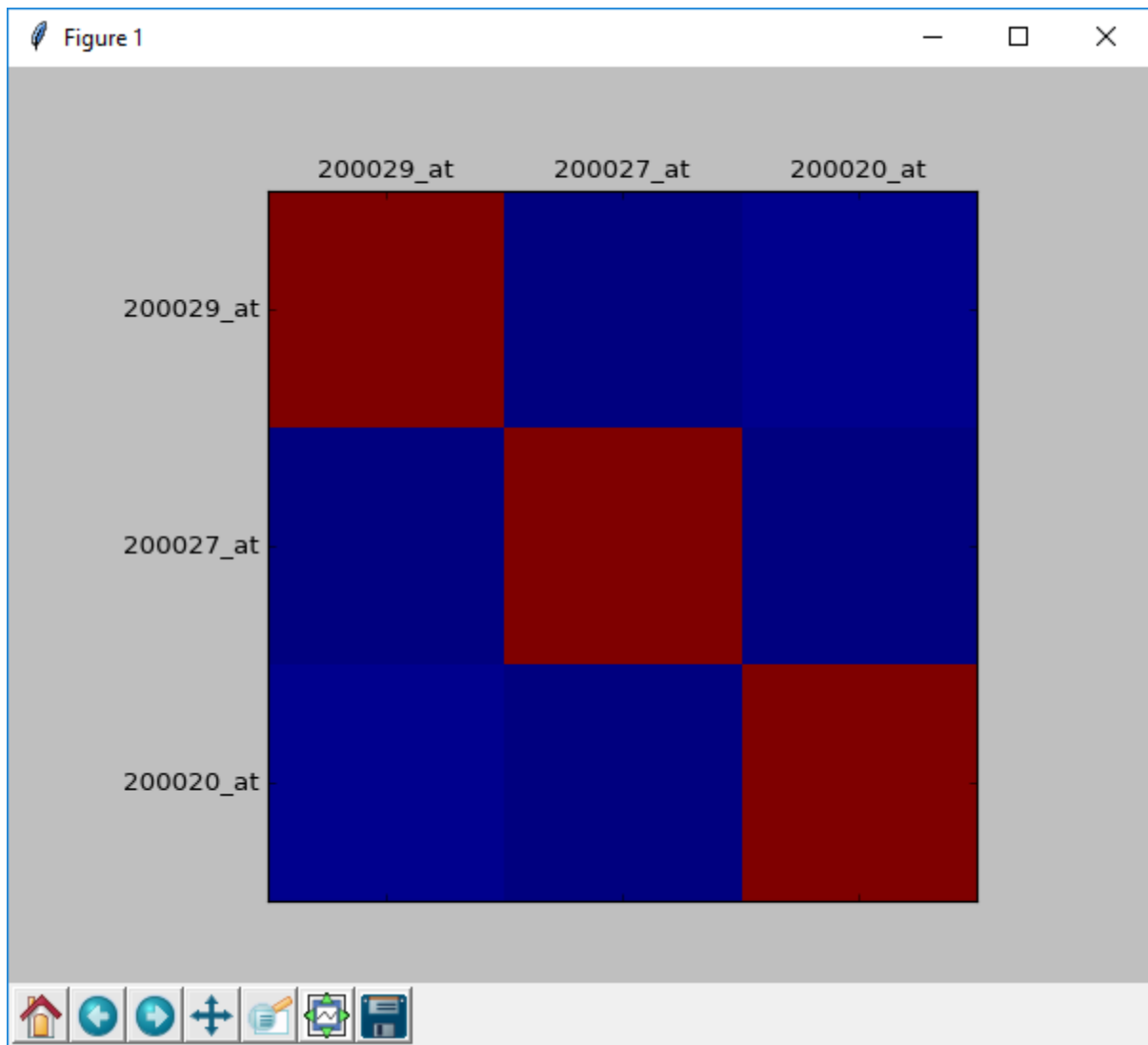
When done it graphs the data in a normal matrix.

Red = good correlation above .8

Yellow = correlation above .7

Green = correlation above .5

Blue = correlation below .5



## Expression Graph:

Expression Graphs:

Expression Graph

1. Search Probe
2. Hit Expression Graph

## NCBI Cell Line Usage:

- [Search Cell Line](#)
- [Search Probe](#)
- [Expression Graph](#)
- [Heat Map](#)

Biomarker Graphical Analysis Program

File

TCGA Tumor NCBI Tumor **NCBI Cell Line**

Cell Line Search Cell Line

Include Outliers Prob Number Search Prob

Standard Statistics:

Average:	
Standard Deviation:	
Interquartile Range:	
Range:	
Minimum:	
First Quartile Median:	
Median:	
Third Quartile Median:	
Maximum:	

Expression Graphs:

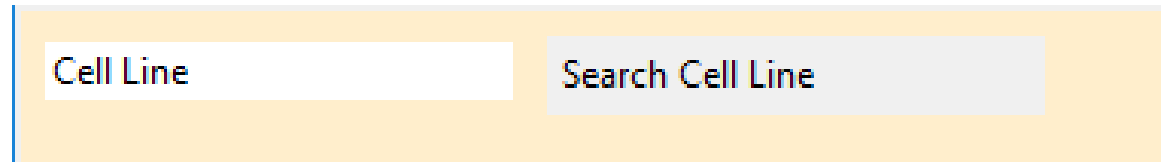
Expression Graph

Heat Map Graph:

Heat Map Prob Number Start Heat Map

Aaron Schwan alpha 2.45

## Search Cell Line:

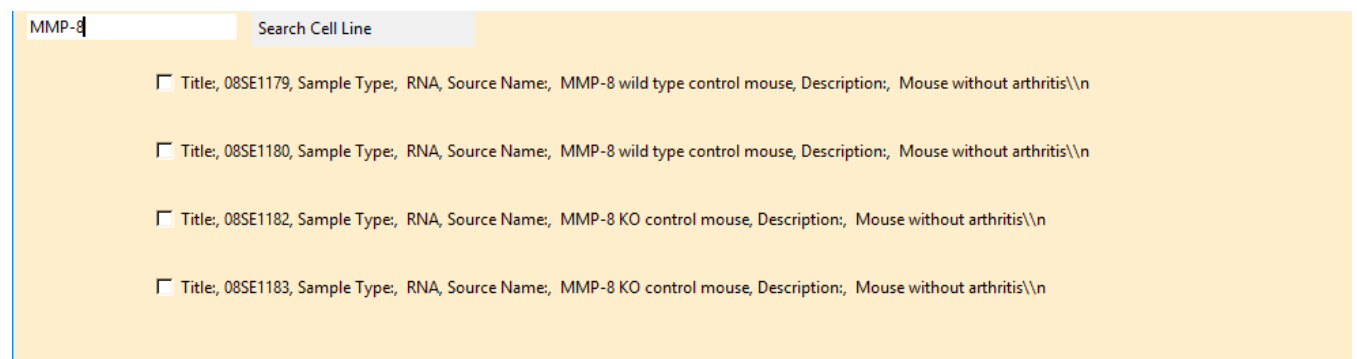
A screenshot of a web interface for searching cell lines. It features a light orange background. On the left, there is a white text input field labeled "Cell Line". To its right is a grey button with the text "Search Cell Line".

Cell Line

Search Cell Line

1. Type in cell line
2. Hit Search the program automatically finds any controls

It should return between 0 and 4 results:

A screenshot of the search results page. At the top, there is a search bar with "MMP-8" entered and a "Search Cell Line" button. Below the search bar, there are four search results, each preceded by a checkbox. The results are: 1. Title: 08SE1179, Sample Type: RNA, Source Name: MMP-8 wild type control mouse, Description: Mouse without arthritis\\n. 2. Title: 08SE1180, Sample Type: RNA, Source Name: MMP-8 wild type control mouse, Description: Mouse without arthritis\\n. 3. Title: 08SE1182, Sample Type: RNA, Source Name: MMP-8 KO control mouse, Description: Mouse without arthritis\\n. 4. Title: 08SE1183, Sample Type: RNA, Source Name: MMP-8 KO control mouse, Description: Mouse without arthritis\\n.

MMP-8

Search Cell Line

☐ Title: 08SE1179, Sample Type: RNA, Source Name: MMP-8 wild type control mouse, Description: Mouse without arthritis\\n

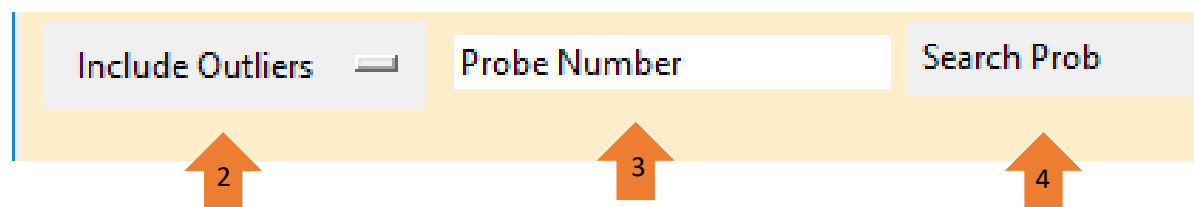
☐ Title: 08SE1180, Sample Type: RNA, Source Name: MMP-8 wild type control mouse, Description: Mouse without arthritis\\n

☐ Title: 08SE1182, Sample Type: RNA, Source Name: MMP-8 KO control mouse, Description: Mouse without arthritis\\n

☐ Title: 08SE1183, Sample Type: RNA, Source Name: MMP-8 KO control mouse, Description: Mouse without arthritis\\n

3. Select all choices that are appropriate for what you intend to look for

## Search Probe:

A screenshot of a web interface for searching probes. It features a light orange background. There are three main components: a grey button labeled "Include Outliers" with a small icon, a white text input field labeled "Probe Number", and a grey button labeled "Search Prob". Below each of these three components is an orange arrow pointing upwards, with the numbers 2, 3, and 4 respectively. The "Include Outliers" button is on the left, "Probe Number" is in the center, and "Search Prob" is on the right.

Include Outliers

Probe Number

Search Prob

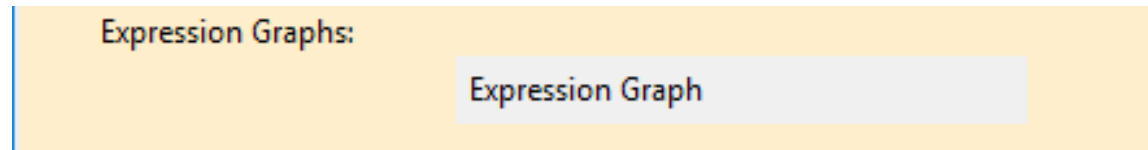
2

3

4

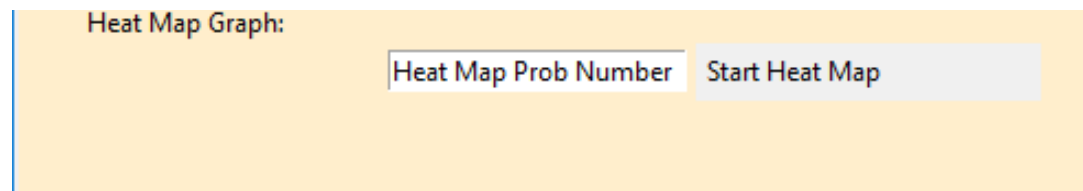
1. Search Cell line
2. Include/Exclude outliers
3. Choose probe
4. Hit "Search Probe"

## Expression Graph

A screenshot of a web interface for 'Expression Graphs'. It features a light orange background. On the left, the text 'Expression Graphs:' is displayed. To its right is a grey rectangular button with the text 'Expression Graph' in black.

1. Search Cell Line/ Search Probe
2. Hit "Expression Graph"

## Heat Map:

A screenshot of a web interface for 'Heat Map Graph'. It features a light orange background. On the left, the text 'Heat Map Graph:' is displayed. To its right are two elements: a white text input field with the placeholder text 'Heat Map Prob Number' and a grey rectangular button with the text 'Start Heat Map' in black.

1. Choose a probe number and enter it into the "Heat Map Probe Number"
2. Hit "Start Heat Map"

\*This is not a correlation heat map it is used to find which cell line will work best for research it automatically adds to itself the more it is used.

The graph should look similar to this:



Figure 1

