Help!

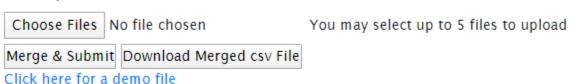
Hey, user:

We are D'Arcy Lab from university of Texas at Dallas. This website is made for analyzing and visualizing HDX data. We used DynamX to process HDX data. However, DynamX does not have many visualization functions. I crated some python code to make DynamX easy to visualize, but it is not user-friendly for general users. We decide to make an online web graphic user interface. This website can make Heapmap and volcano plot from DynamX output file, and mage two data set. The demo file can show you the file format and give you an example of output of the website.



Data

- One File
- Multiple Files



The website has two parts first is the Data upload panel. You can upload dynamX output to visualize data. Please make sure the file is *.csv format, and the title line of the file should be ['Protein', 'Start', 'End', 'Sequence', 'Modification', 'Fragment', 'MaxUptake', 'MHP', 'State', 'Exposure', 'Center', 'Center SD', 'Uptake', 'Uptake SD', 'RT', 'RT SD'

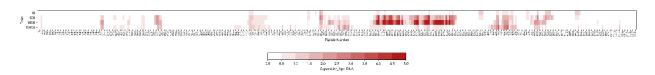
Chiclet plot:

Parameters

Plot Type
Chiclet
Volcano

Protein		Range	
	protein ▼	Max	
Comparison		Step	
State1	state ▼		
State2	state ▼	Blow 0	
Color	r 🔻	Min	
Significance Filter		Step	
Significance (p-value <)	0.01	Show	

Example:



Chiclet plot shows the HDX data in shade of color the x-axis is the list of peptides with start and end number, and the y-axis is the timepoints. The color in each box in the graph represents the difference between two states. The color bar shows the range the color represents.

Explain of Parameters for Chiclet plot:

Protein the protein you want to work on

State 1 and State2 are the two state you want to compare with

The **Range** is the different between two states, which control the shade of color in the chiclet plot.

The max represents the maxima value on the color range, and step represents how many step between 0 and maxima value is.

If you have the HDX data with negative change you can check the blow 0 box and set Min value which should be a negative value. Otherwise, the Min value is set to zero by default.

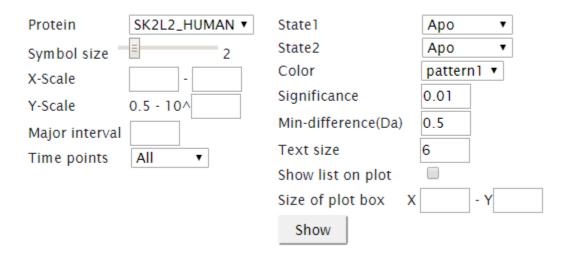
You can select a color for the color bar in the dropdown box. If you do not check the below 0 box, there will be only color. Otherwise, there will be two color to show positive and negative range.

Then you can check the Significance Filter to control if turn on the significance filter, and you can put significance level in the Significance (p-value <) box.

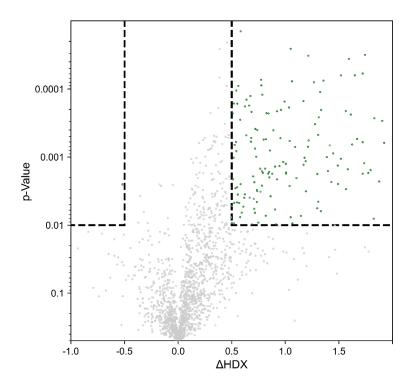
Volcano plot:

Parameters

Plot Type ○ Chiclet ● Volcano



Example:



Volcano plot show each data point on graph as a dot. The x-axis shows the different D-uptake between states and y-axis show the p-value between. The box represents significance cutoff for both D-uptake and p-value. The dots inside the box means the data points are significant.

Explain of Parameters for Volcano Plot:

You can first select the protein you want to show on the graph in the protein dropdown box. Then you can change the size of the dots by change the symbol size. You need also tell the software the boundary of the graph by putting in the X-Scale and Y-Scale. In the major interval you can put in the distance between in sticks on x-axis. In the time points dropdown box, and you can select the time point you want to show on the graph. The state1 and state2 are the two states you want to compare. In the color, you can select color series for different timepoint. If you only have one time point, the software will use the first color in the series. You can change the Significance and Min-difference (Da) to change cut-off of the dot line box. If you want to label the significant dots, you can check the show list on plot box. Then you can change the figure size by inputting the X and Y value.