Histograms

A histogram is a plot that summarizes the underlying frequency of a set of data with the variable of interest on one axis and the frequency distribution of that variable in the other axis. In Partek Flow, histogram can be invoked on continuous or categorical variable.

From a data viewer session, click on New plot > Bar chart (Figure 1).

Point Point<
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Figure 1. Select the Bar chart option from the New plot menu.

Upon clinking on the *Bar chart* menu, a dialogue opens up with the different data sources that can be displayed on the histogram. Select your data node of interest and the content data (Figure 2).

Set plot axes				
Content data A1BG 🔹 🔵				
Add Cancel				

Figure 2. Select the appropriate data node and content data to display on the histogram plot

The first row in the data will be displayed by default in the histogram and in this case, it is the histogram of the expression values for the gene A1BG (Figure 3).



Figure 3. Histogram showing the distribution of AIBG expression (red)

Change the data displayed on the histogram by using the *Configure > Axes* menu and selecting the desired variable to display. Here the data displayed was switched to "Expressed genes" which is a continuous variable (Figure 4).

⊞ Axes						D ×
Content Data	A1BG -	X axis Show title	Value	Y axis Show title Title	Frequency]
Transpose	All Attributes Data Samples # Cells Sample name 4_CellTypes Garnett annotation Expressed genes Total count Data Data A1BG A2M-AS1 AAED1 AAGAB AAK1 AAMDC AAMP AARSD1 AARSD1	Title font Show axis Show labels Label font Rotate labels Value override	12 px 10 px Min 0 Max 11.0374	Title font Show axis Show labels Label font Rotate labels Frequency override	12 px 12 px 10 px Min 0 Max 5413	36
		X grid Axis ticks 5 Sorting Sort by Defau Binning Bin by () Bin count Smoothing ()	It ▼ © Count ○ Size 20 0	Y grid Show lines Axis ticks 5		



Figure 4. Histogram showing the distribution of expressed genes variable (red rectangle)

Use the "Sort by" function to sort the plot. The default sorting is by Value on the x-axis and this default setting is sorted in ascending order. Users have the option to change that by changing the Default to value or frequency in the sort option (Figure 5)



Figure 5. Sort by function can be by Value or Frequency (red)

Users can color the histograms by a categorical attribute using the Color by function (in red below). The bars were colored by the graph-based classifications in the example below (Figure 6).



Figure 6. Histogram annotated by automatic classifications

The bars in the histogram above were stacked. They can be unstacked using the Sty/e menu as seen below in red (Figure 7).



Figure 7. Unstacked bars in the histogram plot

Users also have the option to bin by either Count or Size. When binned by Count, the user specifies the number of bins for the data and the distribution is fit into the specified number of bins. Data below is binned by Count (Figure 8).



Figure 8. Histogram of expressed genes with number of bins specified as 10

When binned by Size, the user specifies the number of items in the bin (size of a bin). This is used to calculate the number of bins required for the data. Data below is binned by Size (Figure 10).



Figure 9. Histogram of expressed genes with size of bin specified as 75

Click the **Save image** button to save a PNG or SVG image to your computer.

Click the **Send to notebook** button by to send the image to a page in the Notebook.

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.