In statistics, a volcano plot is a type of scatter-plot that is used to quickly identify changes in large data sets composed of replicate data. It plots significance versus fold-change on the y and x axes, respectively. These plots are increasingly common in omic experiments such as genomics, proteomics, and metabolomics where one often has a list of many thousands of replicate data points between two conditions and one wishes to quickly identify the most meaningful changes. A volcano plot combines a measure of statistical significance from a statistical test (e.g., a p value from an ANOVA model) with the magnitude of the change, enabling quick visual identification of those data-points (genes, etc.) that display large magnitude changes that are also statistically significant.

A volcano plot is constructed by plotting the negative logarithm of the p value on the y axis (usually base 10). This results in data points with low p values (highly significant) appearing toward the top of the plot. The x axis is the logarithm of the fold change between the two conditions. The logarithm of the fold change is used so that changes in both directions appear equidistant from the center. Plotting points in this way results in two regions of interest in the plot: those points that are found toward the top of the plot that are far to either the left- or right-hand sides. These represent values that display large magnitude fold changes (hence being left or right of center) as well as high statistical significance (hence being toward the top).