

1. How reproducible is the data? Plot and quantify.

a-e.

First start by plotting the data as a scatter plot.

Start in linear scale but you will almost always end up in log scale.

Instead of a scatter plot now try plotting the difference of the log levels on the x axis.

How is this better worse?

Now using the sort function (look in the matlab help) try sort the log difference based on the average exon counts (this is called a MA plot).

k.

Think loops, random number generator, and conditional statements

2.

First normalize counts per sequencing.

Next, because gene length is different, normalize counts by length.

3.

Think histograms.

Think sort. Be careful when you index back the names from the textdata file because of the header line.