DDS document:

This package will only accept Ct values in .csv files. Example datasets can be found in the /data folder of this repository. Please convert your Ct values to the appropriate format and note for polysome profiling and pfaffl analysis both technical and experimental replicates are required for input. This is to ensure rigor and reproducibility of science. Pfaffl method also requires a primer efficiency calculation to ensure accuracy of data.

Updates:

Will continue to work on the design by incorporating the ability to perform statistics. These include ANOVAs and t-tests on the data. Also will incorporate the ability to save your csv files. Hojae added functionality to save plots, so I will update the tutorial to show that. Finally will try to improve data importing by allowing for more input by the users

Updates for HW4: -- including biological dataset
The primary goal of this analysis is to see how the gene ATF4 is expressed during acute arsenite stress. The approach will be to monitor mRNA levels of ATF4 in the cell and in polysomes in stressed and unstressed conditions. To do this, we will use this qPCR analysis package which can calculate primer efficiency of qPCR primers, the gene expression ration compared to GAPDH of a gene of interest, and the percent mRNA in a fraction of a polysome. This dataset will go over the main functionalities of the qPCR analysis package which include primer effieciency calculation, which inputs a dilution series of Ct values and calculates a slope and primer efficiency. Using this primer efficiency calculation, you can then perform the pfaffl method of qPCR analysis, which takes into account a gene of interest and a control gene followed by a gene expression ration calculation. Finally, we will use previously established methods to quantify the percent mRNA in polysome fractions.