This file (https://github.com/smart-stats/assignment-5-LuchaoQi/blob/master/expression.txt)
contains pre-normalized expression values for 100 genes over 10 time points. Most genes have
a stable background expression level, but some special genes show increased expression over
the timecourse and some show decreased expression. What can this shiny app do:

    a. Cluster the genes you upload using an algorithm of your choice. Which genes
        show increasing expression and which genes show decreasing expression? [E.g.
        K-means and hierarchical clustering are common clustering algorithms you could
        try.]
    b. Perform PCA(principal component analysis) on the data. Show the plot and color
        the points based on their cluster from part (a).
    c. Create a heatmap of the expression matrix. Order the genes by cluster, but keep
        the time points in numerical order.