Steps in histogram:

1. Read the dat2.csv which has 674 genes.
2. Normalize the value of trans and proto using formula (x-min(x))/(max(x)-min(x))
3. Calculate the difference between trans and proto for the same hour points for each genes
4. Calculate Summation of all difference hour point for each genes.
5. Sorted genes according to descending order of absolute value of sum difference.