





1. Looking over your figures, does anything surprise you? Why or why not?

There was no significant difference in PCA analysis between young and old patients. The points for most of the patients overlap. There was no significant clustering of protein data neither, especially for the k-mean clustering plot.

2. Now that you have clusters, what information would you like to know about each cluster?
How would you get this information?

I would like to know the clinical traits of patients in each cluster and perhaps the common level of expression among these genes, so that I could find the target patient and gene interested.

3. Brainstorm two ways you could combine RNA and Protein information into one figure. Provide two sketches of these figures.

The first way is the heatmap, we can examine how the level of RNA expression relates to the level of regulation of protein, just like the heatmap we constructed before.

Another way would be the scatter plot of the expression a specific protein vs. RNA among all the patients. In this way, we can figure out the trend of relationship.