**Co-expression Study Analysis of two potential Biomarkers in Pancreatic Cancer Patient samples using R coding language.**

Biomarkers are some sort of proteins that are found in Blood samples or tissue samples, and these are an indicative sign of any normal or abnormal process is going on in the human body. I study those potential Biomarkers in the context of Pancreatic Ductal Adenocarcinoma (PDAC) with the focus of finding any novel biomarker to treat this disease.

For this project, I used Immunofluorescence staining data and R language to look for co-expression pattern for my proteins of interests. I used one Experimental data which is PDAC tissue sample, a section named G5 and one Control data which is a normal pancreas tissue sample named J7 from the tissue microarray slide. I used R packages (“readxl”), (“dplyr”) and (“ggplot2”) to perform my analysis.

I started by constructing a frequency distribution graph to analyze the nuclear area of PDAC patient samples. This step provided me with an estimate of the area occupied by tumor cells within the samples. Next, I isolated these tumor cells and performed Spearman r correlation analysis to explore the expression patterns of my proteins of interests localized outside the nucleus across all tumor cells for both the Control and Experimental data.

Lastly, I found that there is more correlation of the expression of my target proteins in the Experimental data compared to my control data. These are the preliminary findings which could be used in my future following experiments in hoping for developing PDAC treatment.