Name: Jannatul Shoma

Title:

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

Research Questions:

1. What is the Frequency Distribution of nuclear area per tissue section of the pancreatic cancer patient samples?
2. How do the Protein1 and Protein2 staining correlate within the Tumor cell compartments of the Pancreatic Cancer patient samples?
3. Is there a significant Difference in their correlation between the expression levels of these proteins in Normal vs Pancreatic Cancer Cells?

Objectives:

1. I propose to begin by constructing a frequency distribution graph to analyze the nuclear area of pancreatic cancer patient samples. This step will provide an estimate of the area occupied by tumor cells within the samples. Subsequently, I intend to isolate these tumor cells and conduct Spearman r correlation analysis to explore the expression patterns of my proteins of interests localized outside the nucleus across all tumor cells.

Approach:

I will be using R packages such as ggplot2, dplyr, tidy verse etc. and various functions such as hist(), cor(), etc.

Selected References:

1. Aquino AF, Runa F, Shoma JF, Todd A, Wallace M, de Barros NR, Kelber JA. Multidimensional screening of pancreatic cancer spheroids reveals vulnerabilities in mitotic and cell-matrix adhesion signaling that associate with metastatic progression and decreased patient survival. Biochem Biophys Res Commun. 2024 Apr 9;703:149575. doi: 10.1016/j.bbrc.2024.149575. Epub 2024 Feb 6. PMID: 38382357.
2. R for Data Science (2e) by Hadley Wickham, Mine Çetinkaya-Rundel, and Garrett Grolemund. https://r4ds.hadley.nz/