1. Title:

Frequency distribution analysis of nuclear area of ITGA1 and PLK1 proteins in pancreatic cancer patient samples using AI tools and R.

1. Research question:

How are the ITGA1 and PLK1 proteins co-expressed within the tumor cell compartment of pancreatic cancer patient samples.

1. Objective(s):
2. An attempt to generate a frequency distribution graph of the nuclear area of a pancreatic cancer patient sample to estimate the area for the tumor cells. Then, taking those tumor cells we will create a correlation graph showing the expression pattern of ITGA1 and PLK1 proteins outside the nucleus of all those tumor cells.
3. Document and understand which kinds of prompts lead ChatGPT to produce useful code vs. not useful code.
4. Approach

We will be prompting ChatGPT to use R studio packages like readxl, (ggplot2, and tidyverse to make the graphs. We will also be asking ChatGPT to suggest alternative packages with codes that can be used on R to generate the graphs. We will be using the datasets from the Albert *et al* 2024 paper to recreate the graph using ChatGPT and R. We will document the steps and generated codes from ChatGPT to see if the codes will give us the desired graphs.

5. 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. Atkinson, C.F. ChatGPT and computational-based research: benefits, drawbacks, and machine learning applications. Discov Artif Intell 3, 42 (2023). https://doi.org/10.1007/s44163-023-00091-3