Identification of Pancreatic Cancer Driver Genes With a Novel Machine Learning Approach

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With the lowest 5-year survival rate (9%) among all types of cancer, pancreatic cancer is considered one of the most lethal diseases in the world. Current conventional treatments often fail because there are no reliable genes to target in pancreatic cancer therapies and drugs. Hence, there is a crucial need for the discovery of new pancreatic cancer driver genes for the development of better treatments. This study develops a state-of-the-art machine learning workflow for identifying key driver genes for pancreatic cancer. Our workflow identifies several genes, including KRT17, S100A4, and PTGS2, which have high potential as targets for pancreatic cancer therapies and have been validated with over hundreds of publications in literature. Our workflow also identifies novel genes, including SSFA2 and NDUFA6, that have never been studied before while showing great potential as therapy targets. These new genes provide directions for further experimental studies for advancing pancreatic cancer treatments.

Awards Won:

Second Award of $2,000

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