Computational Study of Targets in Lung Adenocarcinoma

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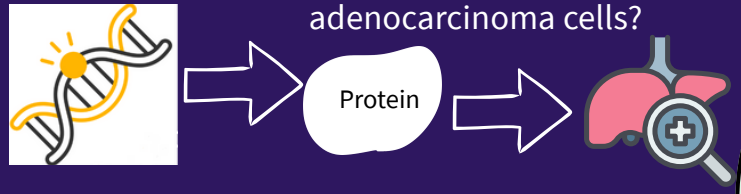
Research Question

Can a specific drug or peptide sequence be found that can mitigate the common somatic mutations in lung adenocarcinoma cells?

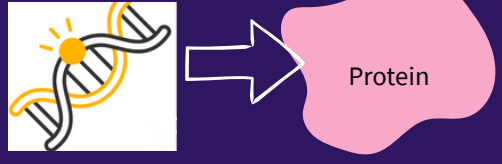
Hypothesis

Can a specific drug or peptide sequence be found that can mitigate the common somatic mutations in lung adenocarcinoma cells?



Bioinformatics opens research and gives more accurate tools for targeted therapies.

Phase 1 - Mutated Genome and Protein Selection



Phase 2 - Analyzing Mutated Proteins and Interactions

Phase 3 - Cancer Model Construction

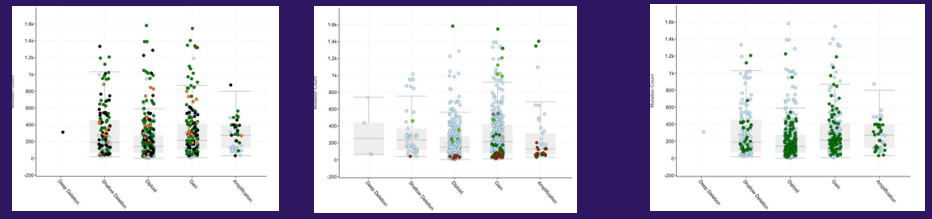


Fig 2-4: Graphs on how mutations occur according to type of mutation (EGFR, KRAS, and TP53).

Differential gene analysis gave understanding of where genes in LUAD sample are under expressed or overexpressed compared to adjacent normal lung tissue cells.
Identify occurrence of common mutations such as KRAS, EFGR, and TP53.
Use data to find target protein

Results: Analysis of common mutations gives something to specific allows to understand mutations in LUAD cells.

Conclusion: Helped me in analyzing specific genome mutations such as KRAS, EFGR, TP53 and look closely at tumor development.