Spatial Transcriptomics and Adaptive Multi-Modal Encoding: A Novel Approach to Early Metastasis Profiling and Therapeutic Targeting Treatment

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Lung cancer remains the leading cause of cancer-related mortality, primarily due to its high metastatic potential and the difficulty of early detection. Current clinical approaches rely on assessments which have low sensitivity for early-stage metastases. To address these challenges, this project introduces a computational framework to predict metastatic potential directly from the primary tumor site, eliminating the need for secondary site biopsies and enabling earlier intervention. Leveraging spatial transcriptomics, this system captures cellular interactions and sequences missed by traditional methods, identifying high-risk tumor regions and metastatic drivers. The machine learning (ML) pipeline integrates neural networks, autoencoders, and clustering to reveal metastatic signatures with high accuracy. In silico testing aligned the received outputs with known signatures from open datasets. Building on these findings, an ML-guided lipid nanoparticle optimization pipeline was developed to design RNA-loaded formulations for inhibition of the given genetic pathways. A deep learning model was employed to enhance drug delivery candidates for the siRNA gene silencers. In vitro, cellular validation demonstrated high encapsulation efficiency, stability, and biocompatibility, showing potential to deliver therapeutics, offering a scalable, personalized therapeutic solution for metastatic suppression. This study bridges AI-driven profiling and treatment with precision nanomedicine for metastatic cancer at its earliest stages. Shifting cancer metastasis treatment from late-stage intervention to proactive, gene-targeted suppression, this work offers a revolutionary, data-driven solution to one of the deadliest challenges in oncology.

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