A Deep Learning to Decision Support: A Survey of Imaging, Multi-Omics and Clinical AI for Lung Cancer

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Abstract:

Lung cancer remains the leading cause of cancer mortality, driving active research across imaging, multi- omics, and explainable AI (XAI). This survey reviews twenty recent studies across three themes: (i) imaging workflows for detection, segmentation, and classification, (ii) multi-omics and radiogenomics for subtype, stage, and mutation prediction, and (iii) clinical outcome modeling for immunotherapy response with interpretable decision support. In imaging, advances such as modified U-Net variants, multi-stage cascades, and 2D/3D CNN ensembles on LUNA16/LIDC-IDRI improve Dice/IoU scores and reduce false positives. Hybrid and transformer-based models further achieve 95–98% patch-level accuracy, though generalization is still hampered by dataset heterogeneity and limited multi-center validation. Multi-omics integration proves decisive: combining LUAD mRNA, miRNA, and methylation features with PCA–SMOTE–CNN yields Accuracy/F1 ≈0.97 and AUC≈1.00, outperforming single-omics and graph/autoencoder baselines. Similarly, Grad-CAM– guided CT models for EGFR/KRAS prediction achieve up to 0.98 accuracy with interpretable saliency linking peri-nodular morphology to genotype. Clinically, explainable ensembles (e.g., CatBoost) predict survival after immunotherapy with accuracies of 0.75–0.83, where SHAP highlights neutrophil-to-lymphocyte ratio and ECOG status over PD-L1. Collectively, evidence indicates imaging models excel at morphology, multi-omics drive robust classification, and clinical deployment demands XAI, calibration, and external validation. The review concludes with a roadmap for standardized preprocessing, multimodal late-fusion, and clinically aligned explainability to advance screening and treatment planning.

Keywords:

Lung cancer, medical imaging, convolutional neural networks, multi-omics integration, radiogenomics, immunotherapy prediction, explainable AI.