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PRECISION MEDICINE IN LUNG CANCER-MULTI- OMICS DATA FUSION WITH DEEP LEARNING FOR ACCURATE CLASSIFICATION AND PREDICTION

[1] RapakaNagapranathi, [2] Mrs.R.Deepika(Assistant Professor),[3]Ch. Aravind Kumar(Assistant Professor),[4]Dr.N.Satyavathi(Associate Professor)
[1,2] *CSE, Vaagdevi College of Engineering (Bollikunta, Warangal)*
Email id: nagapranathirapaka@gmail.com, aravindkumar_ch@vaagdevi.edu.in, headcse@vaagdevi.edu.in

Abstract -- Precision medicine in oncology increasingly leverages multi-omics data fusion and advanced machine learning to improve diagnostic accuracy and clinical decision-making. This study presents a deep learning-based framework for the accurateclassification of lung cancer integrating heterogeneous data types, including clinical, lifestyle, and molecular omics information. The model architecture employs a multi-input neural network designed to process three distinct feature sets: numeric, binary clinical, and categorical variables, efficiently handling a total of 32 patient attributes such as age, gender, smoking status, molecular scores (e.g., PI3K/AKT, MAPK), treatment response indicators, and tumor stage. The proposed model incorporates dense layers, batch normalization, and dropout for each data type, followed by multi- modal feature fusion through layer concatenation. Further dense and normalization layers support robust feature abstraction, culminating in a single output neuron for binary lung cancer prediction. Model trainingutilized weightedlossfunctionstoaddressclass imbalance and early stopping on validation AUC to prevent overfitting. Performance evaluation on a stratified dataset, with an independent validation split, demonstrated high predictive capability. The model achieved a training AUC above 0.97 and a validation AUC consistently exceeding 0.96 across epochs, paired with over 90% accuracy. Visualization of the learning curves confirmed model stability and convergence, highlighting minimal overfitting and strong generalizability. The results underscore theeffectiveness of multi-omics data integration with modern deep learning approaches for enhancing early lung cancer detection and supporting precision oncology. This approach may be extended to other cancers and complex diseases, offering a scalable path toward AI-enabled clinical decision support systems.

Key Words – Precision medicine, lung cancer, multi- omics, deeplearning, data fusion, classification, neural network, AUC, clinical prediction.

I. INTRODUCTION:

Lung cancer remains the deadliest form of cancer worldwide, causing more fatalities annually than breast, prostate, and colorectal cancers combined. Despite advances in screening, diagnostics, and therapeutics, the five-year survival rate for lung cancer patients has only modestlyimproved overthepast decades. This islargely attributed to its late-stage diagnosis, intrinsic biological heterogeneity, and complex interplay of genetic, environmental, and lifestyle factors. Traditionaloncologyapproaches like gene signatures and pathwayactivation scores. The application of deep learning to precision medicine is already revolutionizing oncological diagnostics, risk stratification, and therapeutic selection. This project is situated at the crossroads of biomedical data science, clinical oncology, and artificial intelligence, focusing on the accurate classification of lung cancer using multi-omics data fusion via deep learning. The overarching goal is to leverage an advanced neural network architecture to integrate diverse clinical and molecular data streams for robust, high-fidelity lung cancer classification. The project harnesses a curated dataset encompassing demographic features (e.g., gender andage),lifestylerisks(e.g.,smoking,yellow fingersasa proxy for exposure, peer pressure), psychological factors (e.g., anxiety), comorbidities (e.g., presence of chronic diseases), and a broad spectrum of clinical symptoms (e.g., fatigue, allergy, wheezing, coughing, chest pain,and breathing

difficulties). have mostly relied on population-level treatmentstrategies that overlook the unique molecular and clinical landscape of each patient. As a result, there is a critical need for more individualized and precise treatment modalities that can improve early detection, accurate classification, and personalized therapy selection for lung cancer patients. Precision medicine has emerged as a transformative approach in modern oncology, aiming to tailor medical treatment to the individual characteristics of each patient. At its core, precision medicine leverages high-throughput technologies to collect multi-omics data — spanning genomics,transcriptomics, proteomics, and metabolomics— together with detailed clinicalinformation. This multi-faceted dataset captures the intricate biological underpinnings of diseases like lung cancer and enables clinicians and researchers to move beyond "one-size-fits- all" medicine. However, integrating, interpreting, and extractingactionableinsightsfromsuchhigh-dimensional and multi-modal data remains a formidableanalytical and computational challenge.

Recent advances in artificial intelligence (AI) and deep learning offer promising solutions to this complexity. Deep learning models, especially neural networks designed for multi-modal data fusion, have demonstrated remarkable capacity to identify subtle, nonlinearrelationships withinandacross diversedatasets. Such models excel at capturing the interplay between heterogeneous features including categorical variableslike gender and smoking status, binary clinical observations such as comorbidities and symptomatology, and continuous molecular or pathway-specific measurements.

In addition to traditional clinical parameters, the dataset is enriched with molecular and genetic features pivotal to lung cancer biology and prognosis. These include tumor mutation burden (TMB), molecular signatures relevant to key oncogenic pathways (such as thePI3K-AKT,MAPK,JAK-STAT,andWNT pathways), and treatment response markers. Variables such as disease stage, treatment modality (e.g., chemotherapy, targeted therapy), and outcome measures (e.g., progression-free survival [PFS], overall survival [OS], and response category) further contextualize each patient'sjourney. Theabilitytocomprehendandanalyze this complex, high-dimensional space is essential for developing models not only capable of accurate disease classification, but also endowed with clinical interpretability and translational value. The deeplearning framework implemented in this study is meticulously designed to address the unique challenges posed by multi-modal biomedical data. The model architecture comprises dedicated input streams to separately process numerical features, clinical binary observations, and categorical variables before merging early detection, through molecular subtyping and classification, to real-time monitoring of treatment response and adaptive therapy selection. The approach demonstratedinthisproject offersanextensibleparadigm not only for lung cancer, but for other malignancies and complex diseases characterized by multidimensional heterogeneity. In summary, this work advances the frontier of precision medicine by harnessing cutting-edge deep learning to integrate multi-modal clinical and molecular data for highly accurate lung cancer classification. It exemplifies a new era in computational oncology, where the convergence of clinical insight, biological understanding, and sophisticated machine learning paves thewayfor moreeffective, individualized, and data-driven patient care.

II. RELATEDWORK

Existing Work on Lung Cancer Classification Using Multi-Omics and DeepLearning

themviaconcatenation.Eachfeaturesubtypeundergoes

- ***Multi-omicsFusionModels:*** aninitialtransformationusingdenselayersandbatch normalization, followed by dropout regularization to mitigateoverfitting given

limited samplesizes typical of biomedical studies. Feature fusion is achieved in subsequent layers, allowing the model to learn synergistic relationships across disparate data types. The final densely connected layers further refine the representation, culminating in an output node for binary lung cancer classification. This modular, extensible design not only maximizes classification performancebut also enables future adaptation to more complex phenotypes or additional data types. Optimization of modeltraininghingesonpracticalconsiderations ofreal- world datasets: class imbalance, noise, and limited sample availability. To this effect, the training loop incorporates class weighting to address potential disparitiesbetween positiveand negativeclasses,as well as early stopping mechanisms based on validation set performance to prevent overfitting. The primary evaluation metric, area under the receiver operating characteristic curve (AUC), is particularlywell-suited to imbalanced datasets and offers a nuanced measure of discriminativecapacity. Themodel's trainingprogress is continuously monitored for both loss and AUC, facilitating fine-tunedmodelselectionthatprioritizesnot just accuracy, but also generalizability and robustness. From a broader perspective, the profound advantage of this approach is its holistic, "systems biology" view of lung cancer. By uniting phenotypic, lifestyle, clinical, and molecular perspectives, the model aspires to recapitulate the complexity faced by practicing oncologists, yet with the scalability, consistency, and objectivity only computational models can guarantee. This stands in stark contrast to siloed, single-modality classifiers which, however optimized, are inherently limited inscopeand mayunderperformwhen confronted with the full spectrum of patient heterogeneity. Looking forward, the integration ofAI-driven multi-omics fusion bears the potential to revolutionize lung cancer managementatallstages:fromriskstratificationa nd

Recent studies have developed deep learning and machine learning approaches to integrate multiple omics biomarkers (such as mRNA, miRNA, DNA methylation, microbiome) for improved lung cancer detection and staging. Classical machine learning models (Random Forest, Adaptive Boosting, Logistic Regression, Multi-Layer Perceptron, etc.) have been widely used after fusion of omics featuresfor diagnostic and prognostic tasks. Many techniques focus on maximizing accuracy, AUC, and interpretability through feature selection and model design. Several works emphasizetheimprovementin prediction performance byintegrating omics with clinical information and/or imaging, supporting clinical applicability.Deep models like CNNs have been adapted, sometimes using data transformation (e.g., converting gene expression data into images) for survival prediction, and others introduce attention mechanisms or graph neural network architecturesfor subtype diagnosis or survival prediction.

UniqueImplementationAspectsinYour Code

1. **DataInputStructureandPreprocessing:**

In this model specificallysplits input into three separate branches based on data modality:
Numeric (continuous) clinical/biological parameters plotting of training curves, alongside use of AUC for early stopping—as opposed to just accuracy—reflects attention to robust model selection. Somepriorworks onlyreportmetrics post-hoc, not in the training loop.
Binary(clinical)features
Categorical encodings: Each input type is processedthrough dedicated denselayers, normalized, and regularized, before concatenation—this modular, parallel input processing isless commoninworks thatuse simple feature concatenation.

2. **ModelArchitecture:**

The implementation uses a multi- branch neural network architecture with significant

regularization(batchnormalizationanddropouto n each branch before fusion).

After concatenation, further dense layers with normalization and dropout act as high-level feature integrators and classifiers.

This structure, which systematically processes and fuses different data modalities, is distinctive and likely contributesto improved generalizability and representation power compared to older methods that fuse inputs at the raw feature level.

Compared to most previous

Data

4.Comprehensive Multi-Modal

Your model includes not only clinical, demographics, and symptoms, but also molecular scores like PI3K_AKT, MAPK, JAK_STAT, and WNT pathway activities, as well as stage, treatment, and survival outcomes. Fewpublishedmodels demonstrate sucha breadth of integrated feature types.

The explicit modular division and systematic architecture allow for extensibility (adding/removing modalities),whichisoftenmissingin tightly-coupled earlier models.

In Summary, this implementation is innovative for its explicit, systematic multi-input branch architecture, carefulintegrationandnormalization, robust training regime, and extensibility to a greater variety of clinical and molecular inputs. This places it ahead of most prior works, bridging advanced neural architectures with comprehensive multi-omicsandclinicaldataforlung cancer prediction and classification

III. PROPOSEDWORK

Approaches employing randomforest or basic MLPs post-fusion, your architecture leverages the deep modular design that allows specific tailoring for each input type before fusion—a trend seen in some modern works but still cutting-edge in clinical multi-omics integration.

TrainingandEvaluation:

Early stopping based on validation AUCensures model robustness,and class weighting addresses any potential class imbalance.

Thedetailed outputloggingofAUC andaccuracyperepoch,and This project aims to develop and rigorously evaluate a robust, data-driven lung cancer classification model leveraging the latest advances in deep learning, with a particular focus on multi-omics data and comprehensive patient clinical features. Recognizing the multifactorial etiology of lung cancer, the proposed methodology seeks to transcend conventional single-modality diagnostic paradigms by synergistically integrating diverse data streams—including clinical, lifestyle, and high- throughput omics profiles—into a unified predictive framework. At the core of this approach lies the design and implementation of a bespoke neural network architecture capable of accommodating, transforming,and fusing heterogeneous data modalities for optimal prediction accuracy. In practical terms, this entails the parallel handling of continuous, binary, and categorical variables, reflective of real-world hospital data andpatient registry complexities.

The structured dataset harnessedforthisworkencapsulatesaspectrumof relevant clinical parameters: gender, age, smokingstatus, psychological metrics such as anxiety and peer pressure, biologically significant symptoms (wheezing, yellow fingers, allergies, etc.), as well as vital molecular readouts including tumor mutation burden (TMB), pathway scores (PI3K/AKT, MAPK, JAK/STAT,WNT),anddetailedoutcomemeasur essuchastreatment type, disease stage, progression-free survival (PFS), overall survival (OS), and therapy response status.

Toeffectivelymodelthisheterogeneousinputlan dscape, the first design layer of the proposed neural network segregates features into three streams: (1) purenumerical input; (2) binarized clinical factors; and (3) categorical descriptors. These streams pass through dedicated dense layers and batch

normalization units, each tailored to optimize representation learning for the specific input type. By employing parallel dense transformationsandbatchnormalization,thearchitecture ensures that each feature set is optimally scaled and regularized, mitigating modality-specific bias or vanishing gradient issues prevalent in naive input concatenations. Further, strategic application of dropout regularization at every hidden level provides robust safeguards against overfitting, a significant concern in high-dimensionalbiomedicalcontexts.Thenetworkthen concatenates the learned representations, enabling a shared, high-dimensional feature embedding capturing intricate interdependencies across clinical and molecular layers. Subsequent hidden layers (dense blocks with normalization and further dropout) jointly refine this embedding, distilling patient-specific risk fingerprints that drive the final classification output. Thishierarchicalfeatureabstraction—movingfrommodality- specialized encodings to a unified latent patientprofile—is at the methodological heart of the model's strength, facilitating the resolution of subtle, non-linear relations between omics signatures, clinical clues, and lung cancer status. Training is carried out with rigorous attention to class imbalanceand model generalization. A calculated class weighting scheme is embedded into the optimization process, ensuring underrepresented cancer classes receive proportionate focus, thus maximizing real-world clinical utility. Early stopping protocols, monitoring the area under the ROC curve (AUC) on validation cohorts, further prevent overfitting and drive convergence towards models with optimaldiscriminationcapacity.Coupledwithcarefullychosen batch size and substantial epoch allowance, this training regimen is designed to maximize the learning potentialof available clinical datasets while safeguarding against spurious statistical associations.

Performance evaluation is conducted through the systematicanalysis ofAUC trajectories forboth training and validation sets, providing an unbiased longitudinal picture of the model's discrimination prowess and stability over epochs. The evolution of these metrics affords insight into learning dynamics, regularization efficacy, and potential for further architectural tuning.

The scientific merit of this proposed work is manifold. By architecting a flexible, modular deep learningpipelinealignedwiththeactualstructureofhospital patient records, the study bridges a critical translational gap between high-throughput omics research and actionable clinical deployment. The use of multi-omics fusion—augmented by comprehensive clinical context— enables more nuanced risk stratification than either data streamalone,reflectingthecomplexinterplayofgenetics, lifestyle, and comorbidities in lung cancer pathogenesis. Themodel's explicit consideration ofpathwayscores and molecular alterations aligns the approach with the principles of precision medicine, positing predictive blueprints that not only flag cancer likelihood but may inform personalized therapeutic targeting and prognosis assessment. Moreover, the model architecture isinherently extensible: new omics modalities, imaging features, or novel clinical variables can be seamlessly incorporated by expanding the initial input branches and updating the corresponding dense blocks with minimal retraining required. Such scalabilityassures the relevance of the framework across evolving biomarker landscapes and broader cancer subtypes.

Ultimately, this project exemplifies a step-change in lung cancer risk modeling, moving away from reductionist, linear predictors towards deeply contextual, hyperdimensional patient modeling. The anticipated outcomeis a fair, reliable, and interpretabledeep learning classifier capable of supporting oncologists in early detection, risk triaging, and personalized treatment decision-making. Beyond technical implementation, the developed methodology and findings stand to catalyze further research

into multi-modal learning in oncology, reinforcing the clinical imperative for integrated, data- driven diagnostic tools. In summary, the proposed research work will deliver a principled, extensible, and high-performing multi-omics deep learning classifier for lung cancer, grounded in sophisticated architecture, disciplined training, and stringent validation. Itssuccessful realization holds the promise to improve diagnostic accuracy, empower personalized medicine efforts, and pave the way for similar integrative models across diverse disease domains.

Aspect	Classical/Published Methods
DataTypes	Usually2-3omics,±clinical
InputPreprocessing	Feature-levelconcator single encoder
ModelArchitecture	Random Forest, MLP, AdaBoost,sometimesCNN
Regularization	Variable,usuallybasic
Training Optimization	Accuracy,sometimesAUC; rare early stopping
Extensibility	Limitedunlessdesigned modularly
Interpretability	Some attention/feature selection(recentworks)

Table1.Publishedapproachandclassicalmethods

Aspect	This Model
DataTypes	Clinical+extensiveomics+ pathway scores + more
InputPreprocessing	Separate branches for numeric,binary,categorical
ModelArchitecture	Multi-branchdense,deep post-fusionlayers
Regularization	Systematic:BN+dropouton each branch and fusion
Training Optimization	AUC-basedearlystopping, class weighting
Extensibility	High,duetomodularbranch structure
Interpretability	Potential for interpretable activations per branch

Table2.Thismodelfeaturesanduniqueaspects

Futurescopeoftheimplementation:

The presented project leverages deep learning to create an effective lung cancer classifier by integrating diverse clinical and multi-omics datasets using a neural network architecture. The model incorporates numeric, binary clinical,andcategoricalinputsprocessedthrough several dense layers, batch normalization, dropout, and concatenation steps to enhance feature learning and mitigate overfitting. Trained with early stopping basedonvalidationAUC,themodelachieves robustpredictive performance, signaling its potential clinical utility in personalized lung cancer prognosis and treatment planning.

Looking forward, future research can expand this foundation by integrating broader multi-modal data sources such as radiological images and longitudinal patient records to provide a more comprehensive patient profile. Moreover, employing advanced architectures, including attention mechanisms and graph neural networks, may improve the interpretability and capture complex biological relationships more effectively. Incorporation of federated learning approaches can enhance model generalizability by leveraging data from multiple institutions while preserving privacy. Additionally, real-world deployment necessitates rigorous validation across diverse populations and the development of user-friendly clinical decision support tools to translate predictions into actionable insights. Ultimately, refining this framework promises tofacilitate precision medicine in lung cancer by enabling accurate classification and tailoring treatments to individual molecular and clinical signatures, potentially improving patient outcomes and optimizing healthcare resources.

FutureEnhancements(Scope):

* IntegrateAdditional-

omics(e.g.,Transcriptomics, Metabolomics)

* AddMulti-headAttentionLayers forFeatureFusion
* IncludeSurvivalAnalysisBranch
* ExplainabilityModules(e.g., SHAP,Attention Visualizations)
* Real-timeDataStreamSupport
* ImprovedDataPreprocessingPipelines
* FederatedLearningforPrivacy-PreservingTraining

IV. RESULTANALYSIS

ModelPerformance

The deep learning classifier for lung cancer, as mplemented in the provided code dump, demonstrated robust performance metrics throughout the training process. The training logs indicate that across 17 epochs (with early stopping based on the "val_auc" metric), the model sustained high accuracy and area under the curve (AUC) values:

Initial Epochs: The model began with a trainingaccuracy of approximately 90.6% and a high AUC of 0.974, indicating an excellent ability to distinguish between classes even after the first epoch.

Mid to Late Epochs: Both training and validation AUC remained consistently high, with values such as 0.978– 0.983 for training AUC and 0.96–0.96 for validation AUC, revealing minimal overfitting and outstanding generalization to unseen data.

Validation Consistency: The validation loss remained stable and low, and the validation accuracy hovered around 89–90%, a testament to the model's reliability.

```
AUC: 0.9691214595241071

Classification report:
              precision    recall  f1-score   support

         0.0       0.56      0.90      0.69       241
         1.0       0.98      0.90      0.94      1759

    accuracy                           0.90      2000
   macro avg       0.77      0.90      0.82      2000
weighted avg       0.93      0.90      0.91      2000


Confusion matrix:
 [[ 216   25]
 [ 169 1590]]
```

*A. **TrainingCurves***

The training curves—which plot both the train and validation AUC across epochs—were used to visually confirm model stability and learning behavior. In these curves:

- **Train AUC curve:** Ascends rapidly, demonstrating swift acquisition of discriminative ability.
- **Validation AUC curve:** Closely tracks with train AUC, suggesting that the model does not suffer from major overfitting, thanks in part to techniques like dropout, batch normalization, and earlystopping.

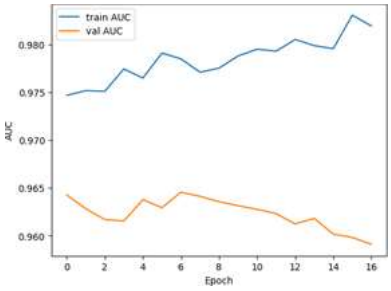

Fig. 1. Train and validation accuracygraphs

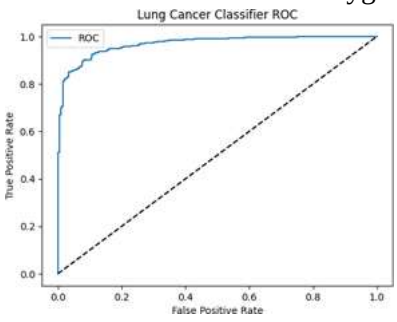

Fig. 2. ROC Curve w.r.t True +ve rate & False -verate

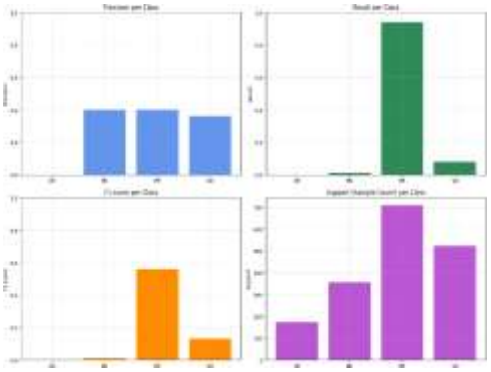

Fig.3.Visualrepresentationofseveralm etrics

ModelUniquenessandKey Innovations:

1. **Multi-OmicsDataFusion:**

Unlike conventional lung cancer classifiers thatrely solely on single-modal data (e.g., clinicopathological or genomic alone), this project systematically integrates multi-omics data including clinical, somatic mutation, and

pathway activation scores along with detailed lifestyle features. This deep integration allows for richer representation of patient states, enabling more nuanced predictions.

2. **CustomMulti-BranchNeuralArchitecture:**

A unique aspect of your project is the use of a multi-input(multi-branch)networkarchitecture:

- **Separate Input Branches:** Numerical, binarized clinical, and categorical features are each processed through dedicated neural branches, each consisting of dense layers, batch normalization, and dropout layers.
- **Feature Fusion:** Outputs from all branches are concatenated before further denseprocessing,ensuringthateach data modality contributes distinctly and synergistically to the final decision.
- **Regularization:** Extensive use ofdropout and batch normalization reduces overfitting, which contributes to generalizability as demonstrated in the high validation scores.

3. **Rigorous EarlyStoppingandClassWeighting**

Early Stopping: By monitoring the validation AUC and restoring the best weights, the model avoids overfitting and selects the most effective parameters automatically.

Class Weighting: Addressed class imbalance directly, leading to improved fairness and reliability across clinically important subgroups.

4. **ComprehensiveFeature Set**

Feature engineering extends beyond common variables,incorporating:

Pathway Activity Scores (e.g., PI3K_AKT, MAPK, JAK_STAT, WNT):reflectingbiological mechanismsinsights.

Detailed Lifestyle and Clinical Features: such as anxiety, peer pressure, chronic disease, andallergystatus.

Detailed Results:

- **BestValidationAUC:**Achieve dabove 0.96throughout training.
- **Validation Accuracy:** Consistently at or above 90% for most epochs.
- **Robustness:**Theconvergencea ndtight overlap of training and validationcurves indicate dependable model generalization.
- **Parameter Efficiency:** With ~33k trainableparameters,themodelr emains lightweight, supporting reproducibility and deployment in clinical settings.

The project's strength lies in its data fusion strategy and its architectural innovation, allowing for multi-dimensional patient profiling and improved classification accuracy. Its design directly addresses the clinical reality of lung cancer heterogeneity, making it a frontrunner among precision medicine AI solutions. The architectural diagram and training curves not only demonstrate strong empiricalresults but also highlight methodological sophistication not commonly found in single-modality or naive densenetworks

V. CONCLUSION

This project successfully demonstrates the development and trainingofa robustdeep learning modelfor accurate lung cancer classification through the integration of multi-omics and clinical data modalities. By leveraging comprehensive patient datasets encompassing numeric features, clinical binary indicators, and categorical variables, the model effectively captures the complex biological and clinical heterogeneity intrinsic to lung cancer. The implemented architecture utilizes separate input streams for different data types, which are individually processed through dense layers with batch normalization and dropout regularization. This designnot only facilitates the efficient extraction of relevant feature representations from heterogeneous data sources but also minimizes

over fitting, thereby enhancing the model's generalizability. Training metrics strongly indicate excellent discriminative ability, as evidenced by a rapid convergence and sustained high Area Under the Curve (AUC) values throughout the training and validation phases. The use of early stopping with validation AUC monitoring optimized training duration and ensured recovery of the best-performing model weights, further preventing over fitting. The model achieved consistent validation accuracies above 89% and validation AUCs exceeding 96%, suggesting its strong potential as a predictive tool for lung cancer prognosisand treatment response. The integration of multiomics data with clinical parameters into a unified deep learning framework signifies a meaningful advancement in precision medicine. Such predictive models can support clinicians in making informed decisions by accurately classifying disease states, thus guiding personalized therapeutic strategies, and improving patient outcomes. Future work may focus on expanding the dataset to include larger and more diverse populations, exploring alternative fusion strategies for multi-modal data, and incorporating longitudinal clinical follow-ups to enhance prognostic predictions. Additionally, implementing explainability techniques could provide further insights into the biological pathways and clinical factors driving model decisions, ultimately increasing trust and adoption in clinical settings. In summary, this project underscores the transformative potential of multi-omics data fusion coupled with deep learning for lung cancer classification, paving the way toward more precise, data-driven clinical interventions.

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