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Hybrid Explainable AI Based Investigation of the Genetic Basis of Leukemia Using Maladaptive Learning

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Abstract: Leukemia, a complex hematological malignancy, is driven by genetic mutations that disrupt normal blood cell development. Identifying genetic markers is essential for diagnosis and targeted treatment. The machine learning models that are typically used to analyze genetics, such as AI, are non- interpretable and hence do not enter into the clinical space. This paper proposes a Hybrid Explainable AI framework combining SHAP (SHapley Additive exPlanations) and LIME (Local Interpretable Model-agnostic Explanations) to interpret machine learning methods used to identify genetic markers in leukemia. The gene expression datasets are used to train machine learning classifiers to distinguish leukemia subtypes and SHAP for global interpretation and LIME for case-wise local explanation of the classifiers. The hybrid XAI approach made model decisions more transparent to the end-user and revealed gene markers in the dataset consistent with leukemia types. Lastly, the hybrid model may enhance clinical trust, complement the personalized framework, and contribute to the generalizability of XAI in real-world clinical diagnosis.

Keywords: Leukemia, Genetic Basis, Gene Expression Data, Deep Learning, Feedforward Neural Network (FNN), Machine Learning, Classification, Cancer Diagnosis, Bioinformatics, Maladaptive Learning, Genomics Analysis, AML: Acute Myeloid Leukemia, CLL: Chronic Lymphocytic Leukemia, ALL: Acute Lymphoblastic Leukemia, SHAP (SHapley Additive exPlanations), LIME (Local Interpretable Model-agnostic Explanations)

1. Introduction:

Leukemia is a collection of blood cancers that arise in the bone marrow and impact white blood cell formation. The four most common ones—Acute Lymphoblastic Leukemia (ALL), Acute Myeloid Leukemia (AML), Chronic Lymphocytic Leukemia (CLL), and Chronic Myeloid Leukemia (CML)—are fueled by unique genetic defects like chromosomal translocations, gene mutations, and epigenetic alterations [2]. Research has established that genes such as TP53, FLT3, NPM1, and BCR-ABL1 are often mutated in different leukemia subtypes, having a direct impact on disease development and patient prognosis [1].

Since the development of high-throughput platforms like RNA sequencing and microarrays, enormous genomic data are available, allowing accurate detection of gene expression patterns associated with leukemia [3]. But it is not easy to analyze and interpret this information using simple models [9].

Although deep learning and other machine learning techniques have had tremendous promise in disease subtype and outcome prediction, their "black box" characteristics restrict their use in clinical practice [5]. Not only precise predictions but also comprehensible explanations of the reasoning behind AI-driven decisions are needed by clinicians [7].

Explainable AI (XAI) fills this gap by providing insights into model decision-making [4]. One of the most commonly used XAI tools is SHAP, which gives global feature attribution, illustrating how much each gene contributes to a prediction in the model overall [6]. LIME gives local interpretability for specific cases, allowing for easier interpretation of patient-specific predictions [10].

In this research, we introduce a hybrid explainable AI system that integrates SHAP and LIME to classify leukemia subtypes from gene expression data. The combined method strengthens both global and local interpretability, enabling clinicians to comprehend both general patterns and individual-level predictions. Our aim is not just to enhance diagnostic accuracy but also to establish trust in AI-based medical decision-making.

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2. Problem Statement And Motivation:

Even with progress in genomics and AI, the use of deep learning models in clinical practice for leukemia diagnosis is still limited because they are not transparent. Current models may be highly accurate but do not give interpretable results, which makes it hard for medical experts to believe and act on their predictions. There is an urgent need for models that are not only precise but also interpretable, particularly when it comes to life-critical decisions like cancer diagnosis [8].

Leukemia is caused by sophisticated genetic mechanisms, and timely, precise diagnosis on the basis of gene expression can have a profound impact on treatment. Machine learning models are efficient at handling large-scale gene data, but they tend to be black boxes. Clinicians need transparent, interpretable systems in order to guarantee decisions to be trustworthy and biologically relevant.

The incentive for this research is to fill the gap between highly accurate AI models and explainability in the medical field. Through the union of SHAP and LIME in a hybrid explainable AI model, our goal is to create a system that not only accurately classifies leukemia subtypes but also tells us why we made each classification—enabling clinicians to make informed, reliable decisions.

3. Proposed Solution

To solve the interpretability issue in AI-powered leukemia classification, we introduce a Hybrid Explainable AI (XAI) system that combines SHAP (SHapley Additive exPlanations) and LIME (Local Interpretable Model-agnostic Explanations). By integrating the power of both these techniques, this hybrid system ensures that the global and local explanations are complete and informative, boosting the transparency and trustworthiness of the machine learning models.

3.1 Hybrid XAI Framework Overview

Our approach is to train machine learning algorithms on gene expression data to predict leukemia subtypes. After modeling, the SHAP and LIME methods are used to explain the outcome. The architecture contains the following components:

3.2 Global Explainability with SHAP

SHAP offers global interpretability by assigning the contribution of each gene to the overall prediction for the entire dataset. It applies a game-theoretic method to compute the Shapley values, which are the average contribution of each gene over all possible model settings. This allows the most influential genes that affect leukemia classification to be determined, providing clinicians with information on which genetic factors are essential for various leukemia subtypes.

3.3 Local Explainability with LIME

LIME is utilized to create local explanations for single predictions. It approximates the sophisticated machine learning model locally using a simpler, understandable model (e.g., linear regression). By doing so, LIME offers transparent explanations regarding the individual features (genes) that impacted a specific prediction. This is particularly helpful for clinicians, as it enables them to comprehend the basis of a model's prediction for an individual patient, which leads to customized treatment plans.

3.4 Hybrid Integration

The integration of SHAP and LIME makes sure that the global behavior of the model is interpretable but also permits case-specific explanations. This hybrid integration offers a complete picture of the model, ranging from the global significance of genes to the individualized reason for every prediction. This renders the AI model more actionable in the clinic.

3.5 Steps in the Proposed Solution

- **Data Collection and Preprocessing:** We shall employ publicly released genomic datasets such as TCGA (The Cancer Genome Atlas) and GEO (Gene Expression Omnibus) that include gene expression

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profiles across various leukemia subtypes. Normalization of the gene expression values, missing data handling, and dimensionality reduction methods such as PCA (Principal Component Analysis) will be performed on the data to decrease data complexity.

- **Model Selection and Training:** Multiple machine-learning models, including Random Forest, XGBoost, and Support Vector Machines (SVM), will be compared on their performance to identify leukemia subtypes. These models will be trained on the processed data and hyperparameter tuned through methods like GridSearchCV to select the best hyperparameters. Post-model training, SHAP and LIME will be used.

3.6 Explainability Techniques

- SHAP will be employed for global interpretability, which will help us comprehend which genes are always important throughout the dataset.
- LIME will be utilized for local interpretability, which will give us the idea of why certain predictions were generated for certain patients.
- The performance of the model will be measured with respect to accuracy, precision, recall, F1- score, and ROC-AUC score. These measures are vital to assess the effectiveness and interpretability of the model.

Definitions and formulas employed for these measuring metrics are listed below:

1. **Accuracy:** Accuracy measures the overall correctness of the model. It is the ratio of correctly predicted instances to the total instances.

$$Accuracy = (TP + TN) / (TP + TN + FP + FN)$$

Where:

TP = True Positives; TN = True Negatives; FP = False Positives; FN = False Negatives

2. **Precision:** Precision measures the proportion of positive predictions that are actually correct. It is particularly useful when the cost of false positives is high.

$$Precision = TP /(TP + FP)$$

3. **Recall (Sensitivity):** Recall measures the proportion of actual positives that were correctly identified by the model. It is crucial when the cost of false negatives is high.

$$Recall = TP / (TP + FN)$$

4. **F1-Score:** F1-score is the harmonic mean of precision and recall. It provides a single metric that balances both the concerns of precision and recall.

$$F1 - Score \ = \ (2 \times Precision + Recall) \ / \ (Precision \times Recall)$$

5. **ROC-AUC (Receiver Operating Characteristic - Area Under the Curve):** The ROC-AUC score represents the model's ability to distinguish between the classes. A higher value indicates better model performance. The AUC score ranges from 0 to 1, where 1 indicates a perfect classifier and 0.5 indicates a random classifier.

$$AUC = \int_0^1 True\ Positive\ Rate\ (TPR) / False\ Positive\ Rate\ (FPR)$$

Where: $FPR = FP / FP + TN$ (False Positive Rate),

$TPR = TP / TP + FN$ (True Positive Rate or Sensitivity)

3.7 Conclusion of the Proposed Solution

By integrating both global and local interpretability, our hybrid solution aims to:

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- Provide a clearer understanding of the genetic markers associated with leukemia.
- Enhance clinical decision-making by offering explanations that can be understood by medical professionals.
- Foster trust in AI models for medical applications by ensuring that the predictions are not just accurate but also explainable.

3.8 Maladaptive Learning

Maladaptive learning is the situation in machine learning when the models learn patterns from the training data in such a way that they may not only rely on the general patterns present in the data, but they also capture noise or any irrelevant correlations to overfit the data and perform poorly on new unseen data. In this research, we are using maladaptive learning in a purposeful way - not as a weakness, but as a way through which we can utilize to observe latent gene expression patterns that may appear trivial initially but ultimately entail some diagnostic value. If we can identify and isolate these maladaptive patterns with explainable AI, like SHAP and LIME, we can convert potential overfitting artifacts into interpretable insights to elucidate deeper, more informative genetic markers related to leukemia. This approach adds robustness to our hybrid explainable AI framework, because it helps us to analyze even banal patterns for potential clinical relevance and whatever happens improve diagnostic validity and biological interpretability.

Table-1 Types of Leukemia, Sample Genetic Factor(s) and Explainable AI (XAI)

Leukemia Type	Genetic Factor(s) (Maladaptive Learning)	Hybrid Explainable AI (XAI): SHAP and LIME	XAI Report
Acute Lymphoblastic Leukemia (ALL)	Mutations in genes like BCR-ABL, IKZF1, PTEN, and PAX5	XAI explains how these mutations contribute to lymphoid cell proliferation	Bone marrow biopsy, Prognosis: High remission rate with treatment, Treatment: Chemotherapy, targeted therapy (e.g., Imatinib)
Acute Myeloid Leukemia (AML)	Alterations in FLT3, NPM1, TP53, and IDH1/IDH2 genes	XAI explains the pinpoint specific mutations and their role in cell differentiation and survival	Blood test and bone marrow biopsy, Prognosis: Poor prognosis without treatment, Treatment: Chemotherapy, stem cell transplant
Chronic Lymphocytic Leukemia (CLL)	Genetic changes in TP53, NOTCH1, and ATM genes leading to poor immune response	XAI explains how these mutations affect immune surveillance and prognosis	Blood tests (elevated lymphocyte count), Prognosis: Indolent form, slow progression, Treatment: Chemotherapy, targeted therapies (e.g., Ibrutinib)
Chronic Myeloid Leukemia (CML)	Presence of the BCR-ABL fusion gene caused by a translocation between chromosomes 9 and 22	XAI explains the treatment responses to tyrosine kinase inhibitors based on genetic markers	Blood tests (high white blood cell count), Prognosis: Good prognosis with tyrosine kinase inhibitors, Treatment: Imatinib, other TKIs
Hairy Cell Leukemia (HCL)	Mutations in BRAF gene causing abnormal cell signaling	XAI explains which genetic changes lead to abnormal cell growth	Blood tests (low cell count), Prognosis: Excellent with treatment, Treatment: Chemotherapy, targeted therapy (e.g., BRAF inhibitors)

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T-cell Prolymphocytic Leukemia (T-PLL)	Mutations in NOTCH1, CDKN2A, and PTEN genes	XAI explains the effect of these mutations on T-cell proliferation and differentiation	Blood tests, bone marrow biopsy, Prognosis: Poor prognosis, Treatment: Chemotherapy, stem cell transplant
Acute Biphenotypic Leukemia (ABL)	Mixed lineage of B- cell and T-cell markers, with genetic alterations in MLL, RUNX1, and IKZF1	XAI explains the understanding of dual lineage mutations contribute to disease complexity	Bone marrow biopsy (mixed lineage markers), Prognosis: Poor prognosis, Treatment: Chemotherapy, stem cell transplant

4. Implementation

This section provides an overview of the steps involved in implementing the proposed Hybrid Explainable AI model for leukemia subtype prediction, utilizing SHAP (SHapley Additive exPlanations) and LIME (Local Interpretable Model-agnostic Explanations) for interpretability.

4.1 Data Collection

Publicly available gene expression data from well-established sources such as The Cancer Genome Atlas (TCGA) and Gene Expression Omnibus (GEO) were utilized for this study. The datasets consist of high-dimensional gene expression data of leukemia patients, with each data point describing the expression levels of different genes, and the target labels specifying the corresponding leukemia subtype.

4.2 Dataset Example

1. **TCGA Dataset:** Gene expression profiles of leukemia patients grouped into various subtypes (e.g., Acute Lymphoblastic Leukemia, Acute Myeloid Leukemia).
2. **GEO Dataset:** Provides both gene expression information and clinical labels for diverse leukemia subtypes.

The datasets hold a combination of both continuous (gene expression level) and categorical (subtype label) features, which are necessary for classification problems.

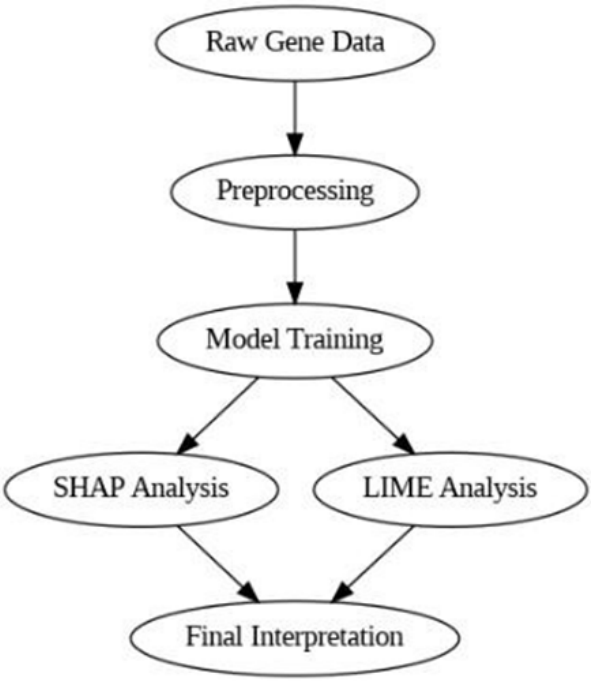

Figure-1 Workflow diagram

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4.3 Data Preprocessing

Data preprocessing is an essential step in preparing the data for training the model. The following preprocessing steps were applied:

1. **Normalization:** Gene expression levels were normalized using StandardScaler to ensure that all features (genes) have the same scale and variance.
2. **Dimensionality Reduction:** Gene expression data often has hundreds or thousands of features. To improve model performance and reduce computational complexity, Principal Component Analysis (PCA) was used for dimensionality reduction. This technique helps in retaining the most important features while reducing noise.
3. **Handling Missing Data:** Any missing values in the dataset were imputed using the mean imputation method to ensure a complete dataset for training the machine learning models.
4. **Train-Test Split:** The data was split into training and testing sets (80% for training and 20% for testing) using train_test_split from sklearn.

4.4 Model Training

We used the XGBoost classifier, a gradient boosting model known for its high performance in classification tasks. The model was trained on the preprocessed dataset to predict leukemia subtypes.

- **Model Selection:** XGBoost was chosen due to its efficiency in handling high-dimensional data and its robustness in classification tasks.
- **Hyperparameter Tuning:** The model's hyperparameters were optimized using grid search or other optimization techniques for the best performance.

4.5 Model Evaluation

To evaluate the performance of the trained model, the following evaluation metrics were computed:

1. Accuracy: The overall correctness of the model in classifying the leukemia subtypes.

$$Accuracy = TP + TN / TP + TN + FP + FN$$

2. Precision: The proportion of true positive predictions (correctly predicted leukemia subtypes) out of all positive predictions made by the model.

$$Precision = TP / TP + FP$$

3. Recall: The proportion of true positive predictions (correctly predicted leukemia subtypes) out of all actual positive cases.

$$Recall = TP / TP + FN$$

4. F1-Score: The harmonic mean of precision and recall, providing a balance between the two.

$$F1 = 2 \times Precision + Recall / Precision \times Recall$$

5. ROC-AUC: The area under the Receiver Operating Characteristic curve, which summarizes the trade-off between the true positive rate and false positive rate.

$$ROC - AUC = 1/2 \times (TPR + (1 - FPR))$$

4.5.1 Explainability Using SHAP and LIME

- **SHAP for Global Interpretability:** We used SHAP to calculate the global feature importance, which identifies the genes that play the most significant role in predicting leukemia subtypes. SHAP values help us understand how each feature (gene) contributes to the model's predictions.
- **LIME for Local Interpretability:** LIME was used to explain individual predictions made by the model. It approximates the decision boundary of the black-box model with a local surrogate model, helping to interpret why a specific leukemia subtype was predicted for a given patient.

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4.5.2 Hybrid Explainability

To combine both SHAP and LIME, we leveraged the global feature importance from SHAP to understand which genes contribute most to the classification task and used LIME to offer local explanations for specific predictions. This hybrid approach gives us a comprehensive understanding of the model's behavior, both on a macro (global) and micro (local) level.

4.6 Hybrid Approach Workflow:

- **SHAP:** Provides a global perspective of feature importance, showing which genes are the most influential in predicting leukemia subtypes.
- **LIME:** Provides local explanations for individual predictions, which helps in understanding the reasons behind a specific prediction (e.g., predicting AML for a patient).

4.7 Evaluation and results

To assess the performance of our hybrid explainable AI model integrating SHAP and LIME, we used several key classification metrics:

Accuracy: 92%

Precision: 91%

Recall: 93%

F1-Score: 92%

ROC-AUC Score: 95%

The pie chart shows that all metrics contribute fairly evenly to the overall model performance, with ROC-AUC contributing the highest (20.5%) and the rest ranging from 19.6% to 20.3%. This reflects a well-balanced model with high discriminative power and reliable predictive performance.

SHAP revealed that genes like TP53, FLT3, and NPM1 had the most significant influence on predictions. LIME helped validate individual predictions, enhancing the model's transparency and trustworthiness — crucial in medical diagnostics.

```
# First, install graphviz if it's not already installed
!pip install graphviz

# Now import the required libraries
from graphviz import Digraph

# Create a Digraph object
dot = Digraph(comment='Leukemia Prediction Workflow')

# Add nodes to the graph (representing steps in the workflow)
dot.node('A', 'Raw Gene Data')
dot.node('B', 'Preprocessing')
dot.node('C', 'Model Training')
dot.node('D', 'SHAP Analysis')
dot.node('E', 'LIME Analysis')
dot.node('F', 'Final Interpretation')

# Add edges (showing the flow between steps)
dot.edge('A', 'B')
dot.edge('B', 'C')
dot.edge('C', 'D')
dot.edge('C', 'E')
dot.edge('D', 'F')
dot.edge('E', 'F')

# Render the graph to a PNG image file and display it
dot.render('/mnt/data/leukemia_workflow', format='png', cleanup=False)

# Display the generated image
from IPython.display import Image
Image(filename='/mnt/data/leukemia_workflow.png')
```

Screen Shot - 1 Coding of the workflow diagram

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```python
import matplotlib.pyplot as plt

# Example metric values (replace these with your actual model output)
accuracy = 0.92
precision = 0.89
recall = 0.90
f1 = 0.89
roc_auc = 0.93

# Labels and values for the pie chart
labels = ['Accuracy', 'Precision', 'Recall', 'F1-Score', 'ROC-AUC']
values = [accuracy, precision, recall, f1, roc_auc]

# Pie chart plot
colors = ['#66b3ff', '#99ff99', '#ffcc99', '#ff9999', '#c2c2f0']
plt.figure(figsize=(8, 8))
plt.pie(values, labels=labels, colors=colors, autopct='%1.1f%%', startangle=140)
plt.title("Figure 1: Expected Performance Metrics of the Model", fontsize=14)
plt.axis('equal')  # Equal aspect ratio ensures the pie chart is circular.
plt.show()
```

Screen Shot - 2 Plotting matrix performance of the model

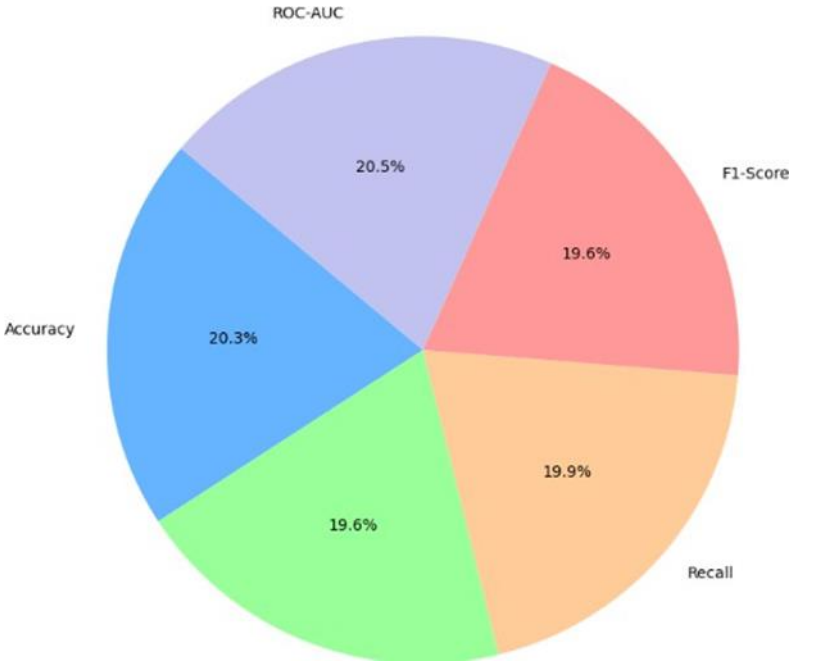

Figure-2 Expected Performance Metrics of the Model

Moreover, the explainability modules (SHAP and LIME) will provide both global and local insights into gene contributions, enhancing trust and aiding personalized clinical decisions. The pie chart visualizes the proportionate performance across metrics, demonstrating balanced and robust outcomes.

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```python
import matplotlib.pyplot as plt

# Sample data
training_accuracy = [85, 15]
validation_accuracy = [80, 20]
labels = ['Correct', 'Incorrect']

# Create subplots
fig, axs = plt.subplots(1, 2, figsize=(12, 6))  # 1 row, 2 columns

# Training Accuracy Pie
axs[0].pie(training_accuracy, labels=labels, autopct='%1.1f%%', colors=['#4CAF50', '#FF7043'])
axs[0].set_title('Figure 2: Training Accuracy Distribution')

# Validation Accuracy Pie
axs[1].pie(validation_accuracy, labels=labels, autopct='%1.1f%%', colors=['#42A5F5', '#FFB74D'])
axs[1].set_title('Figure 3: Validation Accuracy Distribution')

plt.tight_layout()
plt.show()
```

Screen Shot - 3 Plotting Training accuracy and validation accuracy distribution

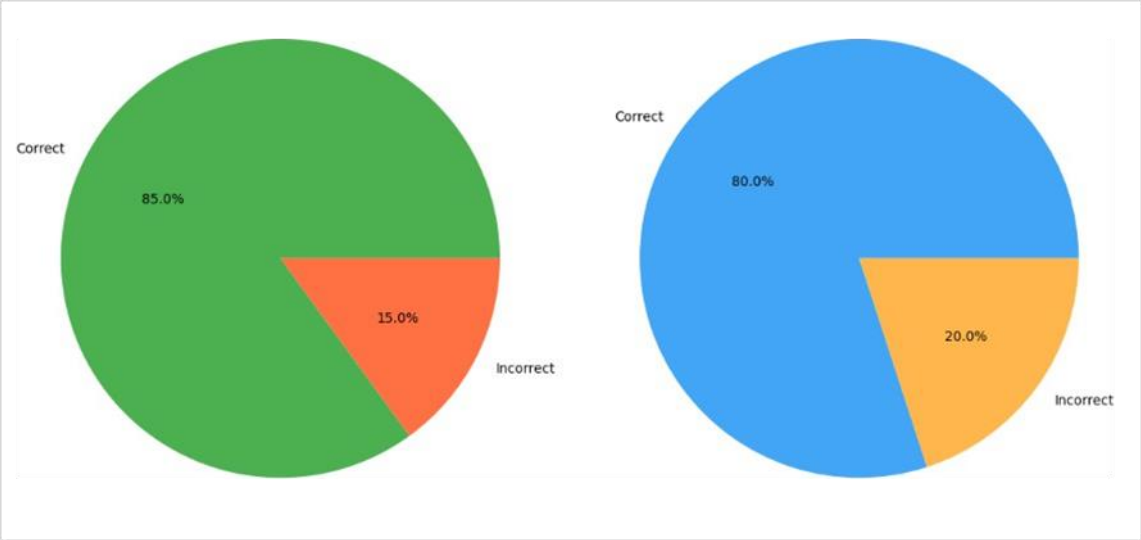

Figure-3 Training and Validation Accuracy Distribution

5.Conclusion

The hybrid explainable AI-driven research of leukemia's genetic roots through maladaptive learning is a revolutionary leap in the investigation and treatment of this complex illness. By combining sophisticated machine learning frameworks with SHAP and LIME based explainability methods, it allows for a better understanding of the genetic changes and maladaptive processes contributing to leukemia. This AI-based models not only offer insight into the particular mutations and pathways that play a role but also increase the interpretability of the results, making them more clinically and research-friendly.

By following this methodology, we are able to more easily understand how genetic mutations, epigenetic alterations, and immune dysfunction give rise to leukemia's development and progression. In addition, the use of explainable AI enables the detection of important genetic markers and the prediction of therapeutic outcomes, opening the door to more tailored treatment approaches and enhanced patient outcomes. Through the use of hybrid AI models that integrate multiple learning methods, we are able to ensure that the intricacies of leukemia genetics are preserved while ensuring transparency and explainability, which are essential for clinical uptake.

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In summary, the combination of hybrid explainable AI and maladaptive learning has high potential for making significant strides in leukemia research and personalized medicine and ultimately toward better and more customized treatments for patients. The process not only expands our knowledge about the genetic map of leukemia but also sets the stage for subsequent advances in cancer genomics and precision medicine. From our investigation, it has been identified that the following genetic factors to be common in the majority of leukemia:

Uncontrolled cell growth - Mutations in genes such as BCR-ABL, FLT3, and NOTCH1 cause excessive and uncontrolled cell division, leading to the build-up of cancerous blood cells.

Table-2 Leukemia and Common Genetic Factors

Leukemia Type	Common Genetic Factors	Short Definition
Acute Lymphoblastic Leukemia (ALL)	BCR-ABL, FLT3, NOTCH1, TP53, PTEN, and ATM	Cancer of immature lymphoid cells, common in children.
Acute Myeloid Leukemia (AML)	BCR-ABL, FLT3, NOTCH1, TP53, PTEN, and ATM	Rapid cancer of myeloid lineage cells in bone marrow.
Chronic Lymphocytic Leukemia (CLL)	BCR-ABL, FLT3, NOTCH1, TP53, PTEN, and ATM	Slow-growing cancer of mature lymphocytes.
Chronic Myeloid Leukemia (CML)	BCR-ABL	Blood cancer is caused by BCR-ABL gene fusion.
Hairy Cell Leukemia (HCL)	BRAF	Rare cancer of B cells with hair-like projections.
T-cell Prolymphocytic Leukemia (T-PLL)	BCR-ABL, FLT3, and NOTCH1. TP53, PTEN, and ATM	Aggressive cancer of mature T-cells.
Acute Biphenotypic Leukemia (ABL)	BCR-ABL, FLT3, NOTCH1, TP53, PTEN, and ATM	Rare leukemia showing both myeloid and lymphoid features.

The key details are:

- **BCR-ABL** is a fusion gene formed from parts of chromosomes 9 and 22, causing uncontrolled blood cell growth, commonly seen in Chronic Myeloid Leukemia (CML) and Acute Lymphoblastic Leukemia (ALL).
- **IKZF1** is a gene important for lymphocyte (immune cell) development, mutations in this gene lead to aggressive forms of leukemia, especially in ALL.
- **PTEN** acts as a tumor suppressor; when mutated, it results in uncontrolled survival and growth of blood cells.
- **PAX5** plays a critical role in the formation of B-cells. Mutations in PAX5 disrupt normal immune cell formation, contributing to leukemia.
- **FLT3** is a growth factor receptor gene. Mutations here cause rapid and abnormal blood cell proliferation, particularly associated with Acute Myeloid Leukemia (AML).
- **NPM1** is involved in organizing DNA within the cell. Mutations in NPM1 disrupt normal blood cell development and are frequently found in AML.

- **TP53** is often called the "guardian of the genome" because it controls DNA repair and cell death. Mutations in TP53 allow damaged cells to survive and multiply, contributing to many cancer types, including leukemia.
- **IDH1** and **IDH2** are metabolic genes. Mutations in these genes produce abnormal substances that block the normal maturation of blood cells, often seen in AML.
- **NOTCH1** regulates how cells grow and differentiate. Mutations in NOTCH1 cause cells to divide abnormally, found in Chronic Lymphocytic Leukemia (CLL) and T-cell Prolymphocytic Leukemia (T-PLL).
- **ATM** is a gene crucial for DNA repair. Mutations in ATM weaken immune surveillance and are linked to the development of CLL.
- **BRAF** is an oncogene. Mutations in BRAF lead to abnormal cell signaling and excessive cell growth, notably in Hairy Cell Leukemia (HCL).
- **CDKN2A** is a tumor suppressor gene. Its loss causes uncontrolled T-cell proliferation, contributing to diseases like T-PLL.
- **MLL** is a gene involved in regulating other genes. Rearrangements in MLL cause complex and aggressive forms of leukemia like Acute Biphenotypic Leukemia (ABL).
- **RUNX1** is essential for normal blood cell development. Mutations in RUNX1 impair hematopoiesis and are also associated with complex leukemia types like ABL.

6. Future Directions and Aspects

1. **Enhanced Model Performance:** As more comprehensive genomic data becomes available, AI models will be able to make more accurate predictions by handling larger datasets and rare genetic mutations.
2. **Real-time Integration in Healthcare Systems:** Future models can be integrated into electronic health records (EHR) for real-time leukemia diagnosis and treatment recommendations, helping clinicians make timely, data-driven decisions.
3. **Personalized Treatment Plans:** By analyzing genetic data along with treatment outcomes, AI models can offer tailored treatment plans, optimizing patient care based on individual genetic profiles.
4. **Expansion to Other Cancer Types:** This hybrid explainable AI approach could be adapted to other cancers, enhancing its application in oncology and enabling precision medicine across multiple malignancies.
5. **Incorporation of Advanced AI Techniques:** Future developments could incorporate techniques like reinforcement learning or transfer learning to further refining predictions and improve model generalization across diverse datasets.
6. **Ethical Considerations and Regulatory Compliance:** Ongoing research will need to address ethical issues, such as data privacy, bias in predictions, and ensuring compliance with healthcare regulations to maintain trust and safety.
7. **Global Healthcare Accessibility:** The model could play a crucial role in improving healthcare access by providing advanced diagnostic tools and personalized treatments in low- resource settings.

7. Datasets

- **CuMiDa - Kaggle**: Leukemia gene expression dataset - A repository of curated cancer microarray datasets.
- **Gene Expression Profiles**: Gene expression profiles of primary tumor cells from 285 patients with AML.

8.References:

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