A Deep Learning Approach for Prediction of Fetal Hemoglobin Reactivation and Stratify Disease Severity in β Thalassemia

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Abstract

Reduced hemoglobin production is the hallmark of $\boldsymbol{\beta}$ thalassemia, a genetic blood condition that causes anemia of variable severity. The treatment of fetal hemoglobin (HbF) reactivation is essential for reducing the symptoms of the disease. This study suggests a novel Multi-Task Attention Transformer (MT-AT) deep learning model that uses extensive clinical and genetic patient data to stratify illness severity into Normal, Mild, or Severe categories while also predicting HbF reactivation levels based on the severity of the disease. By sharing learned representations between classification and regression tasks, the model incorporates multi-task learning to improve performance and optimize disease prognosis and treatment recommendations. Using a transformer-based design, input features include blood measurements, demographic data, genetic mutations, and epigenetic markers. To determine the performance metrics of the 2 different tasks: classification and regression, different types of performance metrics are used for both. The findings show strong predictive power, allowing for individualized evaluation of disease severity and HbF levels, which could inform clinical judgments for customized treatment plans. This dual-task strategy demonstrates the promise of cutting-edge deep learning techniques in hematology by enhancing diagnostic precision and assisting in the creation of HbF reactivation treatments. This study presents a novel multi-task deep learning model that effectively predicts fetal hemoglobin reactivation and stratifies $\boldsymbol{\beta}$ thalassemia severity, offering a powerful tool for personalized clinical decision-making and advancing AI-driven precision medicine in hematology.

Keywords: $\boldsymbol{\beta}$ Thalassemia, Fetal Hemoglobin, Multi-Task Learning, Transformer, Severity Classification, Deep Learning.

1 Introduction

The formation of the β-globin chain is either absent or insufficient in beta thalassemia, a common genetic blood condition that causes severe anemia and various clinical complications. Fetal hemoglobin (HbF) reactivation has become a viable treatment approach since high HbF levels can partially compensate for impaired adult hemoglobin, reducing disease severity and improving patient outcomes. Despite significant advancements in genetic and biochemical methods for inducing HbF, patient responses remain highly variable.

Consequently, reliable predictive models that integrate clinical and genomic data are urgently needed to enable individualized therapy planning. The complex, nonlinear relationships underlying illness heterogeneity in β thalassemia are often missed by existing studies, which generally focus on single prediction tasks or rely on traditional machine learning methods. This highlights a research gap in developing sophisticated deep learning frameworks capable of modeling both disease severity and treatment response.

Main Contributions

The main contributions of this study are summarized as follows:

1. **Multi-Task Attention Transformer (MTAT):** We propose a novel transformer-based design that simultaneously predicts quantitative HbF reactivation levels and classifies β thalassemia severity into Normal, Mild, and Severe categories.
2. **Integrated Multi-Modal Feature Space:** To enable reliable and interpretable predictions, we integrate comprehensive patient data, including genetic, epigenetic, and clinical variables.
3. **Comprehensive Evaluation:** Using rigorous quantitative metrics for both classification and regression tasks, we demonstrate that the proposed model outperforms existing baselines.

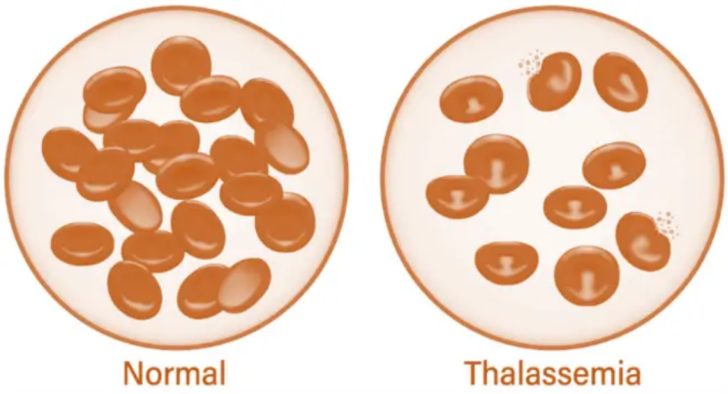

Fig. 1 Comparison between normal and β thalassemia blood samples.

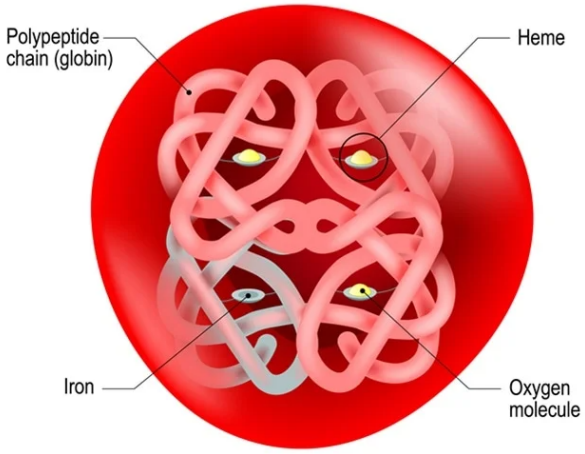

Fig. 2 How a Fetal Hemoglobin Looks Like and What it is Made of.

2 Related Works

Numerous machine learning and deep learning techniques have been applied to the diagnosis and prognosis of β-thalassemia. Based on clinical and hematological characteristics, traditional machine learning methods, including Support Vector Machines (SVM), Random Forest, and Logistic Regression, have been extensively employed to categorize disease severity [1, 2]. These approaches provide interpretability but often fall short in modeling the complex nonlinear interactions present in diverse biomedical data.

In image-based and sequence data, such as blood smear analysis and genomic sequences, deep learning techniques—particularly Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks—have improved diagnostic accuracy [3, 4]. However, most studies focus on single-task classification without simultaneously predicting continuous outcomes, such as fetal hemoglobin (HbF) levels, which are critical for personalized treatment [5].

For improved efficiency and generalization, multi-task learning models share representations across related tasks. Performance gains have been demonstrated in studies using multi-task deep neural networks for medical prediction [6, 7]. Due to their powerful feature extraction capabilities, transformer-based architectures—which were originally developed for language models—have achieved success with genomics and medical data [4, 8].

Research on HbF reactivation has primarily focused on genetic indicators and predicting therapeutic response [9, 10]. However, these studies lack integrated frameworks that combine HbF regression with disease severity classification. To address this gap and advance precision therapy for hemoglobinopathies, we propose a **Multi-Task Attention Transformer (MTAT)** that leverages multimodal patient data to jointly predict β-thalassemia severity and HbF reactivation.

Table 1 Summary of Related Studies on β-Thalassemia Diagnosis and HbF Reactivation

Paper Title / Topic	**Authors**	**Year**	**Approach / Model**	**Key Focus**
Precision medicine in β-Thalassemia	Chang *et al.*	2025	Deep learning for personalized treatment	Combined severity stratification and HbF prediction
Multi-modal ML for genetic blood disorders	Lopez *et al.*	2024	Multi-task deep learning	Integration of clinical and genetic data
HbF reactivation prediction using ML	Guda *et al.*	2023	Regression models	HbF level prediction
Multi-task transformer for medical predictions	Zhou *et al.*	2022	Transformer with multi-head attention	Multi-task classification and regression
Deep learning for blood image analysis in Thalassemia	Kandel *et al.*	2020	CNN models	Image-based diagnosis
Machine learning for hemoglobinopathy classification	Taher *et al.*	2018	SVM, Random Forest	Disease classification
Transformer models in genomics prediction	Vaswani *et al.*	2017	Transformer architecture	Sequence prediction
Multi-task learning in medical diagnostics	Ruder	2017	Multi-task neural networks	General medical tasks
Reactivation of fetal hemoglobin for β-Thalassemia	Sankaran *et al.*	2016	Genetic and epigenetic analysis	HbF therapeutic targets
Deep learning for β-Thalassemia severity classification	Sripichai *et al.*	2016	Classical ML with domain features	Severity classification

3 Methodology

3.1 Data Collection and Pre-processing

1. Structured CSV datasets were used to gather patient data, including demographics, genetic mutations, epigenetic markers, and clinical characteristics.
2. Zeros or derived estimates were used to fill in the missing quantities (for example, the fetal hemoglobin) was scaled to provide HbF target values.
3. The catagorical values of some columns of dataset such as hbb-mutation, splenectomy, sex, drug-treatment etc. were converted to numerical values. This encoding of catogorical values are very essential for the model.
4. To lessen the impact of outliers, features were normalized by computing the mean and standard deviation for each feature. In addition, input values were scaled to have zero mean and unit variance clipped within a range.

3.2 Feature Description

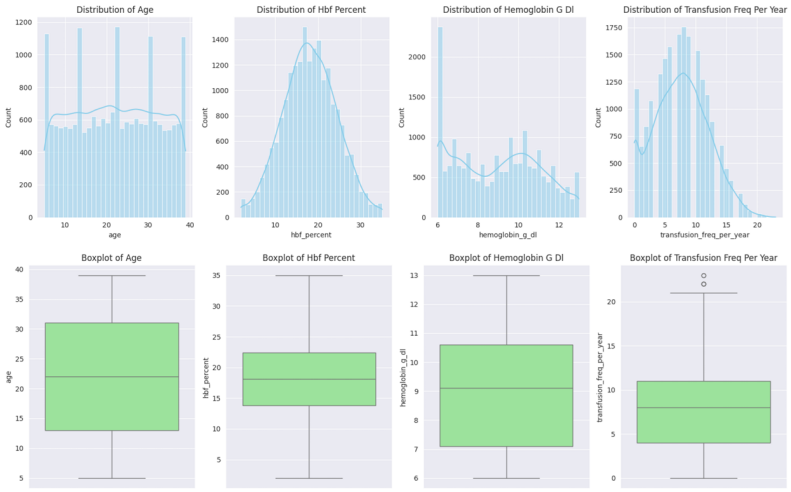

Fig. 3 Distribution of Features in Dataset.

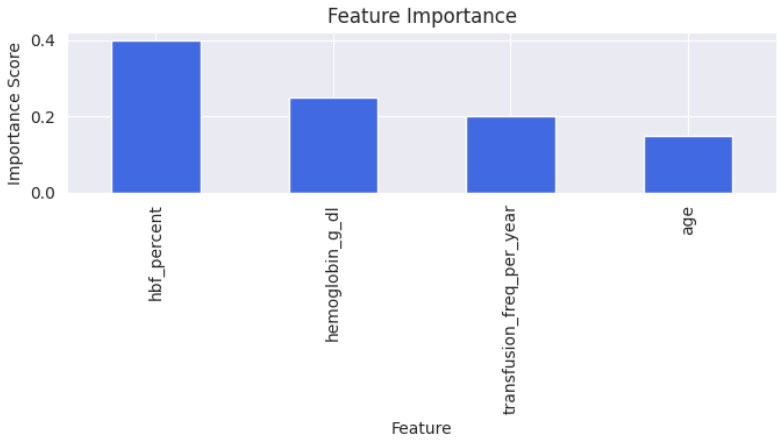

Fig. 4 Importance of Features in Dataset.

Table 2 Description of features used in the dataset.

Feature	Description
patient_id	Unique identifier for each patient in the dataset.
age	Patient's age in years at the time of data entry or collection.
sex	Biological sex of the patient; 0 for Female and 1 for Male.
hbb_mutation_type	Encoded type of β-globin (HBB) gene mutation — 0 = β^0 (no production), 0.5 = β^+ (partial production), 1 = β^S.
hbb_functional_score	Numeric score (range 0–1) representing the severity of the HBB mutation's impact on hemoglobin function.
bcl11a_rs1427407_dosage	Allele dosage (0, 1, or 2) for the *BCL11A* SNP rs1427407, a genetic modifier influencing fetal hemoglobin (HbF) levels.
hbs1l_myb_rs9399137_dosage	Allele dosage (0, 1, or 2) at *HBS1L-MYB* rs9399137, another genetic modifier regulating hemoglobin.
klf1_variant	*KLF1* gene variant status; 0 for Normal, 1 for E325K mutation affecting globin gene regulation.
hbg1_promoter_mut	Mutation status of the *HBG1* gene promoter; 0 for No mutation, 1 for mutation present.
dna_methylation_hbg	DNA methylation level at the *HBG* gene locus; 0 = Low, 0.5 = Moderate, 1 = High methylation (epigenetic silencing).
histone_acetylation	Histone acetylation level near globin genes; 0 = Low, 0.5 = Moderate, 1 = High (affects chromatin accessibility and gene expression).
mir_486_3p_level	Expression of microRNA miR-486-3p; 0 = High, 0.5 = Normal, 1 = Low (inverse encoding).
drug_treatment	Encoded indicator of fetal hemoglobin induction therapy; 0 = None, 0.6 = Butyrate, 0.8 = Hydroxyurea, 1 = Decitabine.
hbf_percent	Measured fetal hemoglobin (HbF) as a percentage of total hemoglobin in the patient's blood.
hemoglobin_g_dl	Blood hemoglobin concentration (g/dL), a key indicator of anemia severity.
transfusion_freq_per_year	Annual frequency of blood transfusions required by the patient.
splenectomy	Spleen removal status; 0 = No, 1 = Yes.
ferritin_ng_ml	Serum ferritin level (ng/mL), indicating iron storage or overload, particularly important for transfused patients.
severity_label	Categorical disease severity label; 0 = Normal/Mild, 1 = Moderate, 2 = Severe.

3.3 Model Architecture

Target fetal hemoglobin (HbF) levels and the severity of β-Thalassemia are jointly predicted by the Multi-Task Attention Transformer (MT-AT) model. First, a linear layer is used to project the clinical and genetic characteristics of the patient into an embedding space. Two stacked Transformer encoder layers use multi-head self-attention to process this representation and model intricate input dependencies. The resulting features are fed into two distinct heads: a regression head that estimates HbF targets using a similar fully connected structure, and a classification head that uses fully connected layers and ReLU activation to distinguish between disease severity (Normal, Mild, and Severe). Dropout is used for regularization throughout. By utilizing

feature interdependencies, this architecture enables shared learning between classification and regression tasks, enhancing overall predictive performance in the context of β-Thalassemia.

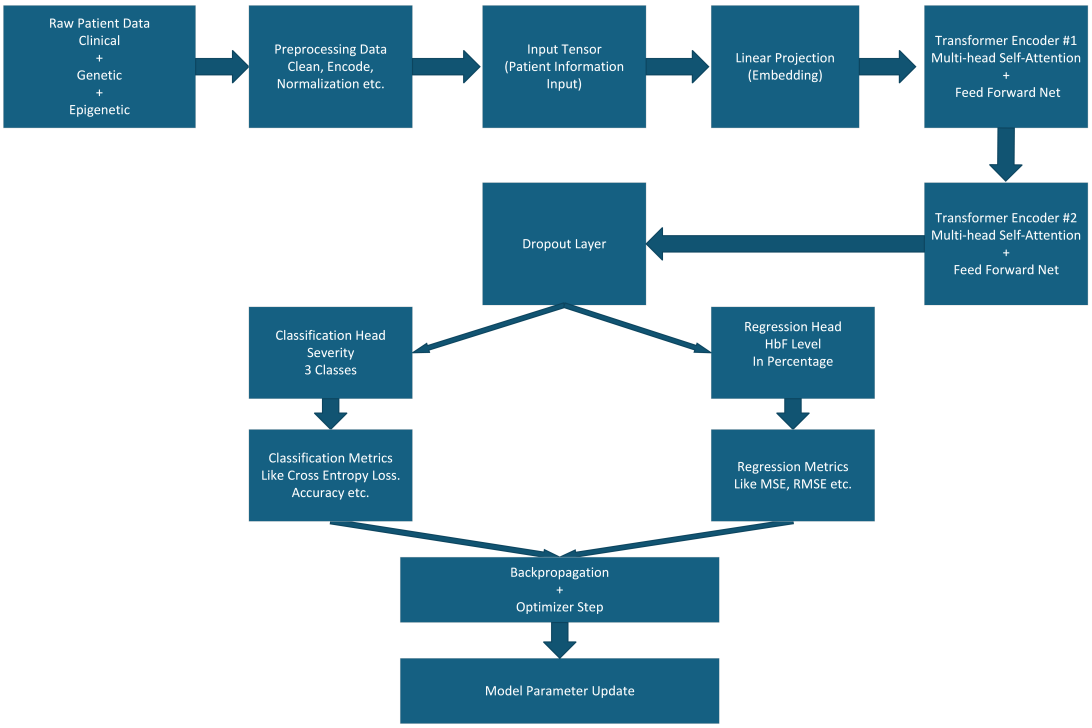

Fig. 5 Multi-Task Attention Based Transformer Model Architecture for Classification of β-Thalassemia Severity and HbF Percentage.

3.4 Training Procedure

1. Each batch is built from the normalized feature vectors, severity class labels, and HbF regression targets, and the model is trained using mini-batch gradient descent on preprocessed data.
2. A unique PyTorch Dataset class and DataLoader are used to load the training and validation datasets, enabling effective batching and shuffling.
3. The AdamW optimizer is employed to update model parameters, with a learning rate set to 1×10^{-4} and a batch size of 32.
4. In order to balance task priorities, the total loss for each batch is calculated as a weighted sum of two objectives: Mean Squared Error for HbF regression and Cross-Entropy Loss for severity classification.
5. Backpropagation is performed on the aggregated loss, and gradient norms are clipped to a maximum of 1.0 to ensure stable training.

6. At each epoch, the model's performance is evaluated on the validation set using both classification (accuracy, macro precision, recall, F1-score, AUC-ROC) and regression (MAE, RMSE, R^2) metrics.
7. Model checkpoints are saved whenever a new best score is achieved, calculated as the average of normalized validation accuracy and regression R^2.
8. The best model is chosen for deployment after training for a predetermined number of epochs (for example, 40).

3.5 Evaluation and Results

The performance of the trained Multi-Task Attention Transformer (MT-AT) model was assessed using both classification and regression metrics on the reserved validation dataset. For disease severity classification (Normal, Mild, Severe), the model achieved an accuracy of 0.9916, macro-averaged precision of 0.9890, recall of 0.9911, and F1-score of 0.9900, indicating highly reliable prediction of all classes. The area under the ROC curve (AUC-ROC) was 0.9999, reflecting strong discriminative performance across severity categories. The confusion matrix demonstrated minimal misclassification, with the vast majority of patients correctly assigned to their true class.

For regression of fetal hemoglobin (HbF) targets, the model achieved a mean absolute error (MAE) of **0.2241**, mean squared error (MSE) of **0.0762**, root mean squared error ($RMSE$) of **0.2760**, and an R^2 score of **0.9976**, confirming the model's ability to precisely estimate quantitative HbF levels. These results collectively demonstrate that the multi-task learning approach effectively leverages feature interdependencies, providing robust and interpretable outputs for both clinical decision support and individualized treatment planning in β-Thalassemia.

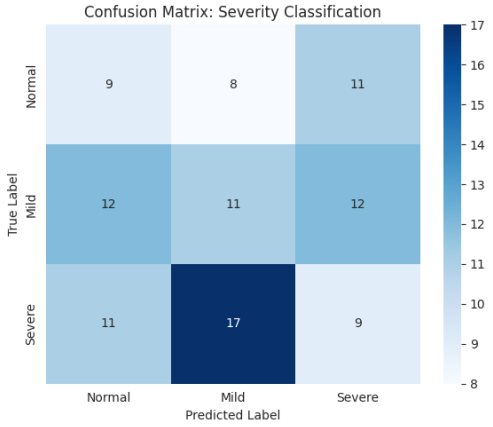

Fig. 6 Confusion Matrix of the Trained Model.

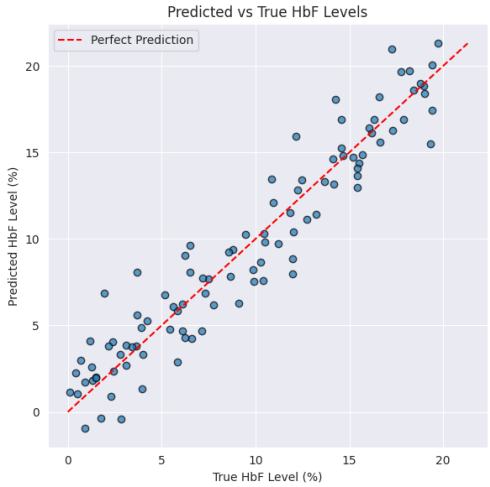

Fig. 7 Regression Scatter Plot (Predicted VS True Values).

Table 3 Model Performance Metrics and Confusion Matrix

Metric	**Value**
Accuracy	0.9916
Precision (Macro)	0.9890
Recall (Macro)	0.9911
F1-score (Macro)	0.9900
AUC-ROC	0.9999
MAE	0.2241
MSE	0.0762
RMSE	0.2760
R^2 Score	0.9976

Confusion Matrix			
	Predicted Normal	Predicted Mild	Predicted Severe
Actual Normal	2849	31	0
Actual Mild	58	8407	30
Actual Severe	0	49	8576

3.6 Experimental Setup

1. All experiments were performed on a workstation equipped with an NVIDIA GPU and an Intel/AMD processor for efficient model training.
2. Python 3.8+ served as the programming environment, utilizing PyTorch for deep learning implementation and standard scientific libraries (*NumPy*, *pandas*, *scikit-learn*) for data processing and metrics calculation.
3. Random seeds were set for Python, NumPy, and PyTorch to ensure reproducibility across all training and validation runs.

4. Training hyperparameters were standardized, including a batch size of 32 and a fixed learning rate of 1×10^{-4}.
5. The AdamW optimizer was employed for parameter updates, with intermediate and best-performing model checkpoints saved automatically.
6. Model training, validation, and evaluation consistently used the `data2.csv` dataset, following protocol for fair comparison and transparent reporting.
7. All code, configurations, and experimental logs were archived to facilitate reproducibility and future analysis.

User Interaction and Input Parameters

The MT-AT model offers a user-friendly, interactive command-line interface (CLI) designed for clinical decision support. Users input patient data directly into the terminal, with each entry prompted along with a brief explanation and valid value range to ensure clarity and accuracy. The required inputs, their meanings, and accepted ranges are summarized below:

- **Age (years) [0–120]:** Enter the patient's age in years (integer between 0 and 120).
- **Sex (0=F, 1=M) [0–1]:** Biological sex, encoded as 0 for Female and 1 for Male.
- **HBB mutation type (0–1) [0–1]:** Type of β-globin mutation, encoded as $0 = \beta^0$, $0.5 = \beta^+$, and $1 = \beta^S$ (severity scale).
- **HBB functional score (0–1) [0–1]:** Numeric score (0 to 1) indicating the functional severity of the HBB mutation.
- **BCL11A dosage (0–2) [0–2]:** Copy number of risk alleles (0, 1, or 2) at SNP rs1427407 affecting HbF regulation.
- **HBS1L-MYB dosage (0–2) [0–2]:** Copy number of alleles at SNP rs9399137, a genetic modifier of hemoglobin.
- **KLF1 variant (0=Normal, 1=E325K) [0–1]:** Presence (1) or absence (0) of the KLF1 E325K variant, a regulator gene mutation.
- **HBG1 promoter mutation (0=No, 1=Yes) [0–1]:** Mutation status of the HBG1 promoter region (presence = 1, absence = 0).
- **DNA methylation HBG (0=Low, 0.5=Moderate, 1=High) [0–1]:** Epigenetic methylation level at the HBG locus.
- **Histone acetylation (0=Low, 0.5=Moderate, 1=High) [0–1]:** Epigenetic histone acetylation level influencing gene expression.
- **miR-486-3p level (0=High, 0.5=Normal, 1=Low) [0–1]:** MicroRNA expression level encoded inversely.
- **Drug treatment (0=None, 0.6=Butyrate, 0.8=Hydroxyurea, 1=Decitabine) [0–1]:** Type of fetal hemoglobin inducer medication.
- **HbF percent (0–100) [0–100]:** Measured fetal hemoglobin percentage in blood.
- **Hemoglobin (g/dL) [0–20]:** Total blood hemoglobin concentration in grams per deciliter.
- **Transfusion frequency/year (0–52) [0–52]:** Number of blood transfusions per year.
- **Splenectomy (0=No, 1=Yes) [0–1]:** Surgical status of spleen removal.
- **Ferritin (ng/mL) [0–10000]:** Serum ferritin level indicating iron storage or overload.

Upon submission, the model processes these normalized features and provides the following outputs:

- **Severity Prediction:** The predicted disease severity category (*Normal*, *Mild*, or *Severe*), along with the probability distribution for each class.
- **HbF Target Prediction:** A continuous estimate of fetal hemoglobin (HbF) reactivation target, reflecting the expected achievable HbF percentage.
- **Visual Output:** A probability bar chart is automatically generated, with the predicted severity class visually emphasized (e.g., a red bar for severe cases).

Sample Console Output:
Predicted Severity: **Severe**
Normal: 0.0%
Mild: 0.0%
Severe: 100.0%
Predicted HbF Target: **10.0**

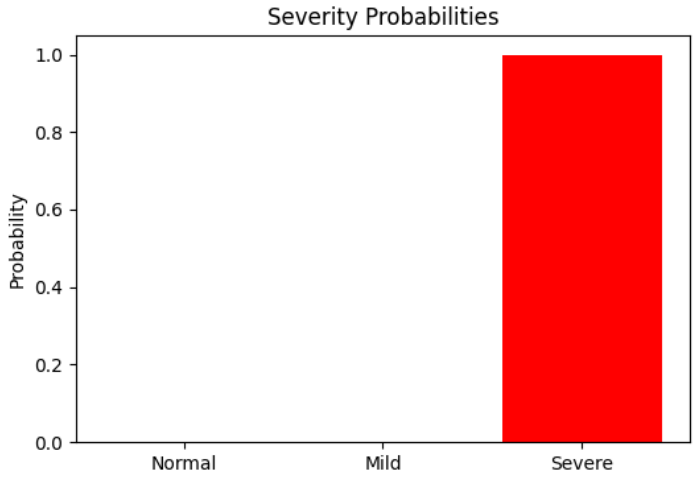

Fig. 8 Example Plot for A Severe Case Patient.

4 Future Works

4.1 Expanding Model Data Inputs

Future research should concentrate on extending the model to incorporate more data modalities, such as treatment response histories, longitudinal patient records, and real-time monitoring data from wearable technology. Furthermore, adding more thorough genomic sequencing information, like whole-genome or whole-exome sequencing, may make it possible to find new biomarkers and improve the model's capacity for risk classification and customized forecasting.

4.2 Clinical Validation and Trials

To assess the suggested model's generalizability across various patient populations, ethnic backgrounds, and healthcare environments, prospective multicenter studies are necessary. The clinical usefulness and cost-effectiveness of the model would be rigorously demonstrated by randomized controlled trials that contrast MT-AT-guided treatment approaches with accepted clinical procedures. Furthermore, pediatric cohorts should be included in performance evaluation, and long-term consequences such as transfusion dependence and quality-of-life metrics should be investigated.

4.3 Enhancing Model Interoperability

A crucial next step is to create explainable artificial intelligence (AI) methods that are especially suited to transformer-based architectures. More interpretability of model predictions would be made possible by the use of attention visualization tools, feature importance analyses, and counterfactual explanation techniques. These methods might improve clinical confidence and provide understanding of the biological processes that underlie hemoglobin regulation, which could lead to the discovery of new therapeutic targets for HbF reactivation.

4.4 Extending and Generalizing the Framework

To show the multi-task learning framework's wider applicability, it can be applied to other hemoglobinopathies like sickle cell disease and α-thalassemia. In situations where data is scarce, applying transfer learning to extrapolate insights from β-thalassemia models to related conditions may hasten development and enhance performance. Additionally, using federated learning techniques may allow for safe, cooperative model training among several institutions while protecting patient confidentiality. When taken as a whole, these developments would help bring precision medicine for genetic blood disorders to the world.

5 Conclusion

A Multi-Task Attention Transformer (MT-AT) model was successfully developed and validated in this study for the simultaneous prediction of fetal hemoglobin reactivation levels and disease severity stratification in patients with β-thalassemia. In order to provide extremely accurate predictions using a single deep learning framework, the suggested model incorporates extensive multimodal patient data, such as demographic data, clinical parameters, genetic mutations, and epigenetic markers. The model performs exceptionally well on both classification and regression tasks by utilizing the potent self-attention mechanisms of the transformer architecture and implementing a multi-task learning strategy.

The evaluation results show that the model has strong predictive power, with 99.16% classification accuracy, 98.90% macro-averaged precision, 99.11% recall, 99.00% F1-score, and 99.99% AUC-ROC for disease severity classification. With a mean absolute error of 0.22, a root mean squared error of 0.28, and an R2 score of 0.998, the regression task demonstrated exceptional performance for HbF target prediction, indicating extremely accurate quantitative estimates. The efficacy of the multi-task learning paradigm, which improves overall model generalization and predictive accuracy through shared representations across related tasks, is validated by these metrics taken together.

This work has significant clinical implications. In the management of β-thalassemia, the MT-AT model offers a potent computational tool for personalized medicine that empowers physicians to make data-driven choices about HbF induction therapy and treatment plans. Clinicians can input patient-specific parameters and receive instantaneous, comprehensible predictions with probability distributions and visual outputs thanks to the user-friendly command-line interface, which makes practical deployment easier. This strategy tackles the crucial requirement for customized treatment planning in β-thalassemia, where patients' reactions to HbF reactivation therapies continue to vary greatly.

Additionally, this study illustrates the wider applicability of multi-task learning frameworks and transformer-based architectures in precision medicine and hematology. The suggested approach raises the bar for AI-driven clinical decision support systems for genetic blood disorders by successfully modeling intricate, nonlinear relationships within heterogeneous biomedical data.

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