

CHAPTER V

CONCLUSIONS AND RECOMMENDATIONS

5.1. Conclusions

This study examined the application of Complete Blood Count (CBC) data for anemia classification using the CatBoost algorithm together with SHAP interpretability analysis. The conclusions in this section are formulated based on the research questions stated at the beginning of the study. They are derived from the results of model performance evaluation, SHAP-based interpretation, and system implementation.

1. The experimental results demonstrated that the CatBoost algorithm effectively classified anemia types based on Complete Blood Count (CBC) data. Across all experimental scenarios, the highest performance was achieved by the CatBoost model with class weights. This model obtained an Accuracy, Macro F1-score, and Weighted F1-score of 1.0000. The findings indicate that class weighting enabled the model to classify diagnosis classes more consistently, particularly when handling an imbalanced dataset. In contrast, applying hyperparameter tuning did not improve the classification performance. Instead, the tuned model achieved lower evaluation results while requiring substantially longer Training time.
2. The SHAP analysis showed that each anemia diagnosis class had distinct feature contribution patterns. For the Healthy class, the prediction was mainly influenced by Hemoglobin (HGB), Platelet Count (PLT), White Blood Cell Count (WBC), Red Blood Cell Count (RBC), and Mean Corpuscular Volume (MCV). Iron Deficiency Anemia and Other Microcytic Anemia were primarily associated with Mean Corpuscular Volume (MCV), Mean Corpuscular Hemoglobin Concentration (MCHC), Mean Corpuscular Hemoglobin (MCH), Hemoglobin (HGB), and Hematocrit (HCT). The Leukemia and Leukemia with Thrombocytopenia classes were mainly influenced by White Blood Cell Count (WBC), Platelet Count (PLT), Hemoglobin (HGB), Red Blood Cell Count (RBC), and Mean Corpuscular Hemoglobin Concentration (MCHC). Meanwhile, Macrocytic Anemia, Normocytic Hypochromic Anemia, and Normocytic Normochromic Anemia shared similar dominant features, namely

Hemoglobin (HGB), Mean Corpuscular Volume (MCV), Mean Corpuscular Hemoglobin (MCH), Mean Corpuscular Hemoglobin Concentration (MCHC), and Red Blood Cell Count (RBC). For the Thrombocytopenia class, the primary contributing features were Hemoglobin (HGB), Platelet Count (PLT), White Blood Cell Count (WBC), Mean Corpuscular Hemoglobin Concentration (MCHC), and Mean Corpuscular Volume (MCV)..

Overall, the features that most frequently contributed to the predictions were Hemoglobin (HGB), Mean Corpuscular Volume (MCV), Mean Corpuscular Hemoglobin (MCH), Mean Corpuscular Hemoglobin Concentration (MCHC), White Blood Cell Count (WBC), Platelet Count (PLT), and Red Blood Cell Count (RBC). These findings indicate that the proposed model achieved high classification performance while providing clear explanations of how CBC features contributed to the prediction results. Consequently, SHAP enhanced model interpretability by explaining both the direction and magnitude of each feature's contribution to anemia classification.

5.2. Recommendations

Based on the results of this study, several recommendations are proposed for future research.

1. Future studies are recommended to use datasets with a larger number of samples and more varied characteristics. The use of data from healthcare institutions or real clinical records may help evaluate the model's generalization ability in conditions that are closer to actual medical practice.
2. Future research can also compare class weighting with other methods for handling imbalanced data, such as Random Oversampling, SMOTE, ADASYN, or a combination of oversampling and undersampling techniques. Such a comparison may assist in determining the most appropriate approach for handling class imbalance in anemia classification based on Complete Blood Count (CBC) data.
3. The interpretability analysis may be further enhanced by incorporating additional visualization techniques beyond **the** SHAP beeswarm plot, there by providing more comprehensive and easier-to-understand model explanations, particularly in medical applications.