Personalized Patient Blood Management for oncological patients with Machine Learning

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ABSTRACT

Background

Machine Learning (ML) techniques are increasingly recognized for their potential to enhance the safety and efficacy of blood transfusions [1], supporting PBM (Patient Blood Management) strategies.

Aim

This study focused on developing and validating a predictive model for intraoperative transfusion risk in oncological patients undergoing complex surgeries.
The goal is to improve transfusion appropriateness and facilitate access to personalized and effective preoperative pathways within PBM programs.

Methods

We analyzed clinical and laboratory data from 338 surgical oncology patients treated at the AUSL-IRCCS of Reggio Emilia between September 2021 and December 2023. The dataset included demographic information, medical history, laboratory tests, and surgical procedures specifics.
A Catboost model [2] was trained to predict transfusion risk, with hyperparameter tuning via Hyperopt functions. Feature importance and explainability analyses to identify the most critical predictors of transfusion risk were managed through the SHapley Additive exPlanations (SHAP) library.
Model performance was evaluated in terms of Area Under the Receiver Operating Characteristic Curve (AUC), Positive Predictive Value (PPV), and Negative Predictive Value (NPV).

Conclusion

Our findings demonstrated the model's distinct predictive capability for intraoperative transfusion risk, providing valuable insights into the clinical and laboratory predictors that influence transfusion needs.

Considerations

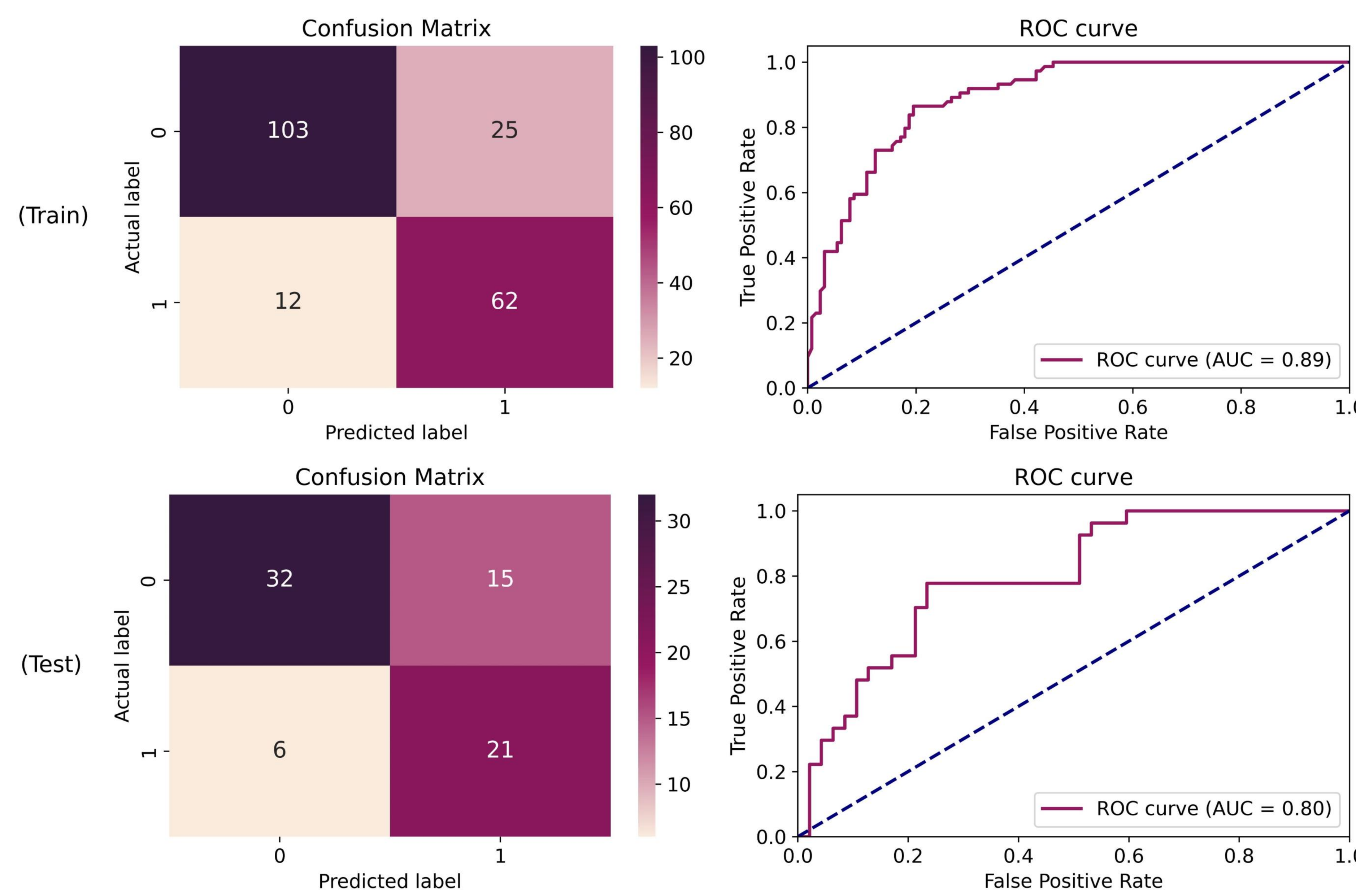
When fully optimized, this model could significantly support transfusion medicine specialists during preoperative assessments. Efforts to enhance the model's performance and generalizability are ongoing, with validations across larger and multicentric patient cohorts. Further analysis is required to evaluate the feasibility of integrating our model into clinical practice.

Relevance

Early prediction of intraoperative transfusion risk can enable transfusion medicine specialists to implement patient-specific preoperative strategies, reducing the risk of transfusion.
Our approach not only has the potential to minimize transfusion-related complications and enhance surgical outcomes for oncological patients but also offers significant benefits for patient health and cost reduction for the healthcare system.

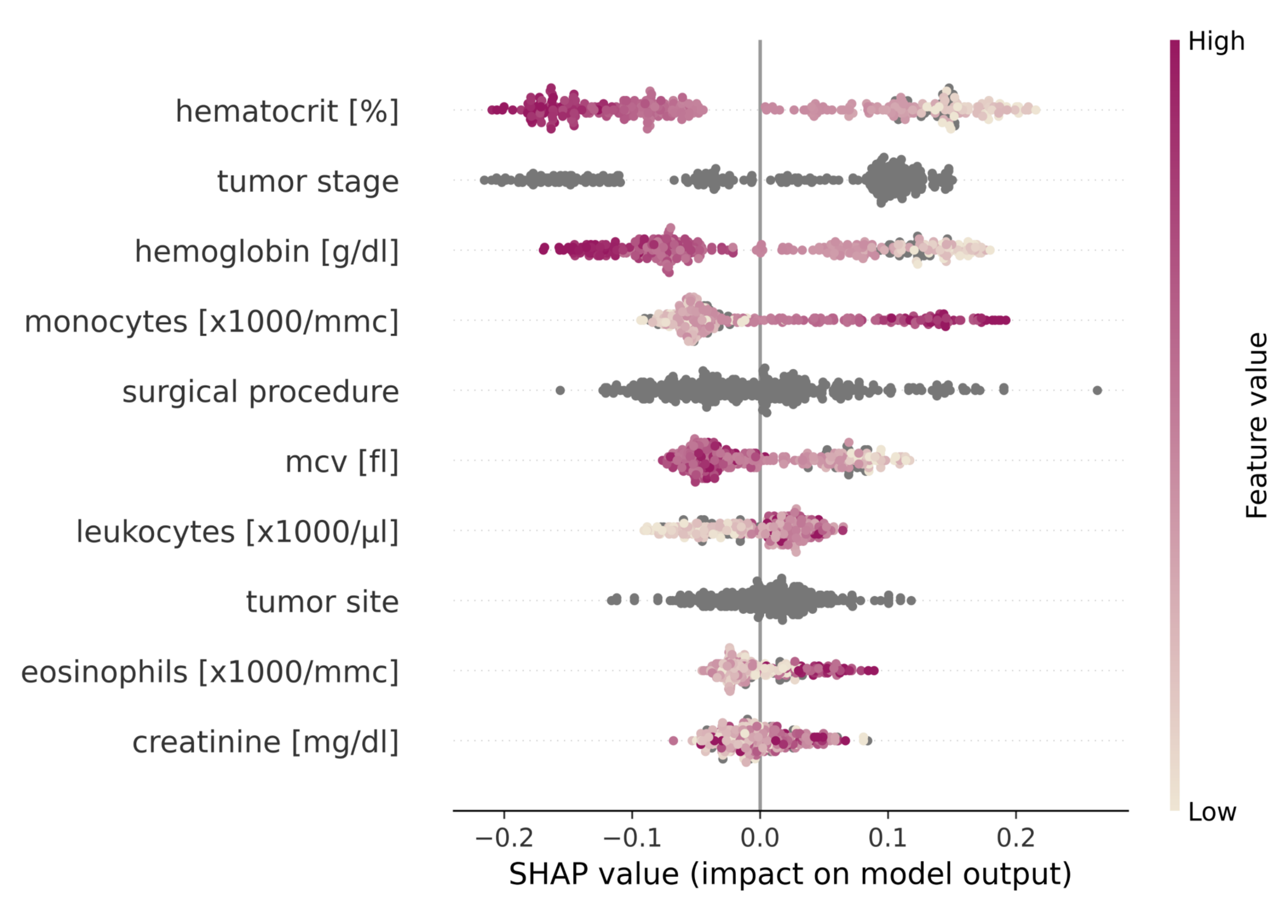
RESULTS

1 Confusion matrices and ROC curves for training (above) and testing (below) datasets



Label '0' in the confusion matrices indicates 'not transfused' and '1' indicates 'transfused'. PPV and NPV can be computed from the matrices, and result in: PPV = 0.7 and 0.6, NPV = 0.9 and 0.8 for training and testing sets, respectively. We aimed to minimize the misclassification of actual transfused cases, at the expense of increasing the false positives. This trade-off is generally acceptable in the medical context, as overlooking a real positive case (false negative) is often considered worse than the additional scrutiny of false positives. AUC values for training and testing highlighted distinct predictive performance for intraoperative transfusion risk.

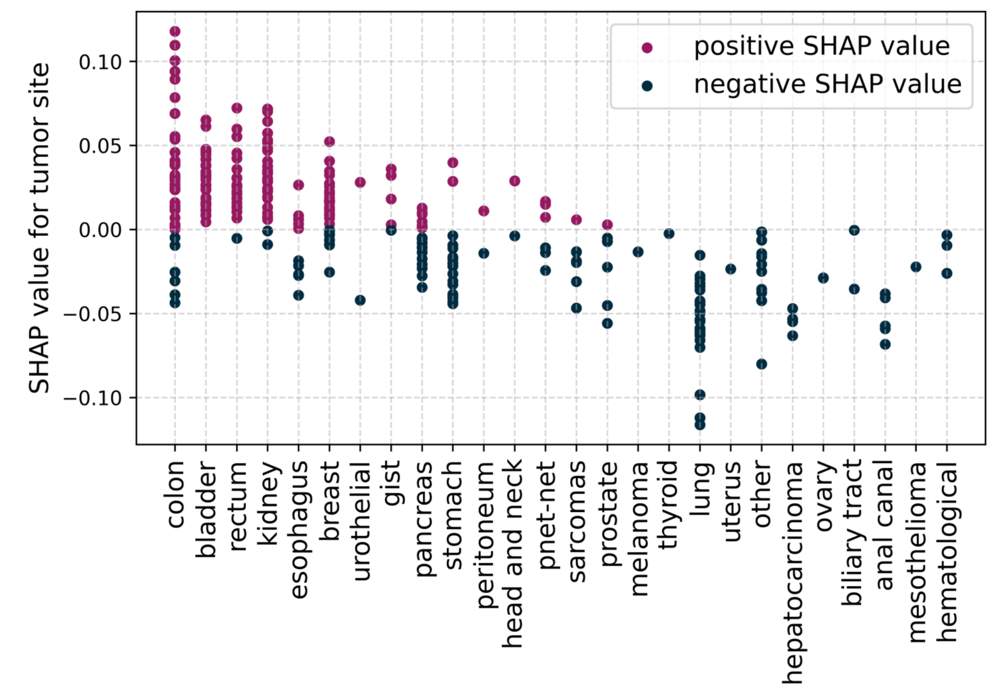
2 SHAP summary plot compiles the effects of all input features across all instances (each point), illustrating the importance of each feature whether the feature increases (positive values) or decreases (negative values) the prediction



Overall, the SHAP analysis clarifies which features most significantly affect the model's predictions by showing how different values of these features impact the outcomes. Features are arranged from the most impactful at the top to the least impactful at the bottom of the plot. The colour coding indicates the feature value for each observation, with dark purple denoting high feature values, and light pink indicating low values. For example, high hematocrit, hemoglobin and mean corpuscular volume (mcv) levels generally contribute positively towards the transfusion risk. Conversely, high monocyte and leukocyte levels tend to decrease the likelihood of needing a transfusion. The tumour stage, surgical procedure and tumour site are grey-coloured because they are categorical features.

3 Shap scatter dependence plot showing the impact of tumour site on the model's predictions

Tumor sites like colon, bladder, rectum, and kidney mostly show positive SHAP values, indicating they typically increase the transfusion risk.
Tumor sites such as lung, hepatocarcinoma, and biliary tract generally have negative SHAP values, suggesting they reduce the transfusion risk.
Tumor sites like pancreas and esophagus, show a wide spread of SHAP values, indicating variable impacts on the model's output.



References

1. Maynard S, et al. Machine learning in transfusion medicine: A scoping review. Transfusion. 2024 Jan;64(1):162-184.
2. https://catboost.ai/

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OECI COMPREHENSIVE Cancer Centre

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