

Machine Learning Model Interpretation Tools Reveal Sub-Populations with Differing Predictors in a Clinical Prediction Model

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Background

Machine learning (ML) models are increasingly proposed for clinical prediction. The “black box” nature of ML models may limit model interpretability and credibility. Model interpretation tools can provide insight into the factors driving prediction and shed light on the key predictors in different groups. We demonstrate this through an ML model for outcome prediction in pediatric central line-associated bloodstream infections (CLABSIs) – an important class of infections in medically-complex children.

Methods

A cohort of 969 pediatric CLABSIs at a tertiary-care children’s hospital was extracted from the electronic health record. A set of 516 CLABSIs with sufficient data to be assessed for infection recurrence within 91 days was selected for analysis. A random forest (RF) model was derived from a training set (80%) to predict CLABSI recurrence within 91 days of infection onset and evaluated on a test set (remaining 20%)¹. SHapley Additive exPlanations (SHAP) was applied to generate global and sub-population predictor importance.

Results

The RF model had an area under the receiver operating characteristic curve (AUC) of 0.77 on the test set, suggesting good overall predictive performance. Based on SHAP values, the most influential overall predictors reflected a child’s history of prior CLABSI (Fig 1). In some cases, such as for the highest- and lowest-risk quartiles for CLABSI recurrence, predictor influence varied significantly (Fig 2A). In other cases, such as microbe type, predictor influence did not vary significantly across groups (Fig 2B).

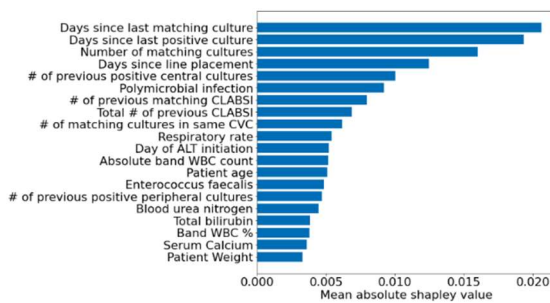


Figure 1: Twenty globally most-influential predictors for CLABSI recurrence. CLABSI: Central line-associated bloodstream infection, ALT: Antibiotic lock therapy, CVC: Central venous catheter, WBC: White blood count

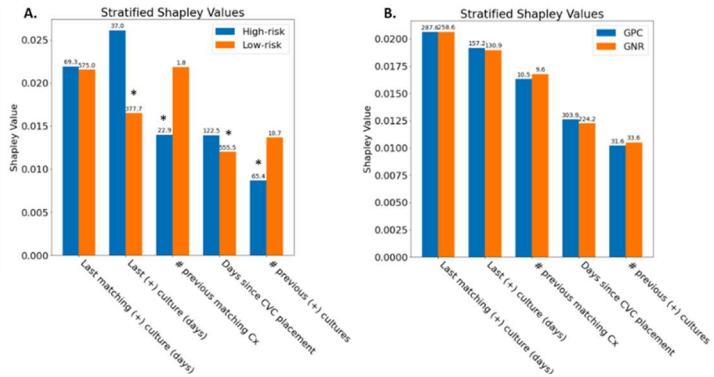


Figure 2: Influential predictors varied significantly when stratified by high- and low-risk patients (A), but not for different pathogen types (B). Cx: Culture, CVC: Central venous catheter, GPC: Gram-positive cocci, GNR: Gram-negative rods. * = $p < 0.05$.

Discussion

ML models can provide predictions that may be useful to clinicians. Model interpretation improves model credibility and may provide new insights. For instance, for high-risk children, recent past infections were particularly influential, whereas for low-risk children a low number of total prior infections was protective.

Conclusion

SHAP provided patient-level predictor importances, augmenting the potential of ML models in the clinical realm. Interpretations can help users interpret the output of an otherwise “black box” model and reveal patterns in predictor importance. SHAP may help generate new insights to improve our understanding of the clinical process of interest.

1. Walker LW, Nowalk AJ, Visweswaran S. Predicting outcomes in central venous catheter salvage in pediatric central line-associated bloodstream infection. *J Am Med Inform Assoc.* 2021 Mar;28(4):862-867.