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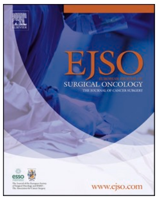

Enhancing feature importance analysis with Spearman’s correlation with p-values: Recommendations for improving PHLF prediction

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Famularo et al. employed several machine learning models to predict the risk of post-hepatectomy liver failure (PHLF) in hepatocellular carcinoma (HCC) patients [1]. They used Extreme Gradient Boosting (XGB), Random Forest (RF), and Support Vector Machine (SVM) models, trained with clinical and radiomic features. Hyperparameters were optimized through grid search, and model performance was evaluated using AUC, accuracy, sensitivity, and specificity. The feature importance of the models was assessed, and SHAP (Shapley Additive Explanations) was applied to the XGBoost and Random Forest models to explain the contribution of individual features to the model’s predictions.

Machine learning techniques like XGBoost are widely used, but different machine learning models employ distinct methodologies for calculating feature importance, and this can lead to varying degrees of bias. Feature importance from machine learning models is always inherently biased, which is a significant issue [2,3]. Therefore, although Famularo et al. possess considerable expertise, it is equally necessary to fully consider the complexities of algorithmic calculations and their associated biases. To avoid non-negligible biased feature importances, it is recommended to rely on robust statistical methods that assess genuine associations between variables, such as Spearman’s correlation with P-values, non-linear and nonparametric approaches [4].

XGBoost (Extreme Gradient Boosting) is a decision tree-based ensemble algorithm known for its effectiveness but may introduce biases in feature importance calculations. It uses metrics like gain (accuracy improvement contribution), coverage (relative observation association), and frequency (feature usage). These metrics are model-specific, meaning feature importance rankings vary with model configurations, making them non-absolute. Correlated features can distort importance evaluations, leading to underestimation or overestimation of contributions. Feature interactions further complicate assessments, and overfitting can inflate the importance of features that perform poorly on new data. The sequential tree-building approach may disproportionately emphasize features that correct previous errors [2].

Random Forest, another powerful machine learning algorithm, excels in feature selection and prediction. It constructs numerous decision trees and combines their predictions to improve stability and accuracy. However, Random Forest can introduce bias with categorical features having many unique values, which might give high importance to features with little predictive impact. Additionally, it may fail to capture non-linear relationships, underestimating feature importance in such cases. Class imbalance can also skew feature importance towards features prevalent in the majority class, neglecting crucial features in the minority class [2].

SHAP is a reliable explanation framework, but it is not without biases [3]. Its dependence on the model means SHAP values can inherit and amplify biases present in the model. Moreover, SHAP assumes that features are independent when assessing their contributions, which may not always hold true. When features are correlated, their combined impact may distort the overall interpretation. SHAP values can also be particularly sensitive to outliers or noise in the dataset, which can result in misleading evaluations of feature importance. Features that are typically of low importance can be disproportionately influenced by outliers, causing skewed importance metrics. Furthermore, SHAP may misrepresent contributions when features have non-linear relationships with the target, particularly in complex models like XGBoost.

In conclusion, while both XGBoost and Random Forest are widely used methods, caution is needed when interpreting feature importance due to the potential biases inherent in these models. Additionally, while SHAP values provide a structured approach to explaining model predictions, they are inherently influenced by the model’s biases and underlying assumptions, particularly regarding feature independence. Given these considerations, the authors may want to consider incorporating robust statistical methods, such as Spearman’s correlation with p-values [4], to supplement machine learning-derived feature importance. This would provide more reliable insights into the true associations between features and outcomes, thereby enhancing the validity of their findings. By doing so, they can uncover genuine relationships between features and outcomes, ultimately advancing knowledge in predicting PHLF occurrence preoperatively, while mitigating the risks associated with biased interpretations.

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