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Letter to the Editor

Clinical Machine Learning Pitfalls: Reliability of Feature Importance in Prediction of Continuous Renal Replacement Therapy in Acute Type A Aortic Dissection Assessment

To the Editor:

Li et al. proposed a machine learning framework using Extreme Gradient Boosting (XGBoost) and SHapley Additive exPlanation (SHAP) to predict the need for continuous renal replacement therapy after acute type A aortic dissection repair.¹ They developed a predictive model for continuous renal replacement therapy using multiple clinical and laboratory variables derived from perioperative data from 588 patients from a single center. After comparative evaluation, XGBoost was selected over other machine learning algorithms due to its superior performance. Subsequently, SHAP values were used to evaluate feature importance, identifying key predictors including intraoperative peak lactate level, red blood cell transfusion volume, renal artery involvement status, and myoglobin, cystatin C, and creatine kinase-myocardial band concentrations. Despite the widespread adoption of such frameworks, it is essential to recognize that high predictive performance does not guarantee reliable feature rankings. We believe that inherent biases raise concerns about the reliability of feature importance. Several studies have highlighted the discordance between predictive performance and meaningful attribution, which reinforces the need for rigorous, model-independent frameworks to support clinically relevant interpretation. Feature importance rankings often reflect artifacts of the prediction process rather than genuine causal relationships. Indeed, overreliance on predictive accuracy to justify feature relevance is a well-documented issue, the details of which are discussed in the Supplementary Material in detail.^{2–5}

Tree-based machine learning models such as XGBoost are known to introduce biases in feature importance estimation, often favoring variables involved in early decision splits.^{6–10} These importance scores are further shaped by the model's internal logic, feature interactions, and multicollinearity. SHAP, a widely used explainable artificial intelligence technique, inherits these model-specific biases and may even amplify them due to its dependence on the model's output structure.^{11,12} Consequently, the combined use of XGBoost and SHAP can result in interpretability challenges. This issue may be particularly pronounced in high-dimensional datasets

with complex and correlated features, where overfitting becomes more likely and model reliability diminishes. We believe that claims of successful feature identification under such conditions, especially when accounting for nonlinearity and interactions, should be carefully examined in light of these limitations. Moreover, validating feature importance remains inherently difficult due to the lack of ground truth, which leads to inconsistent rankings across models. In Li et al.'s study, the presence of intricate feature relationships and data sensitivity further complicates interpretation, highlighting the need for cautious analysis and robust methodological design.

To ensure accurate interpretations in health risk assessment, a robust analytical framework is essential. This approach should incorporate methodologies better suited for capturing complex associations within health data, such as unsupervised learning techniques including feature agglomeration and highly variable gene selection.^{13,14} The use of nonparametric statistical methods like Spearman's rho or Kendall's tau would most likely also be highly beneficial.^{15,16} These methods can detect various types of relationships, offering enhanced interpretability crucial for translating findings into actionable clinical insights. Ultimately, this multifaceted approach is indispensable for generating accurate, reproducible, and clinically relevant information that can truly advance health risk assessment.

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No new data were generated or analyzed in support of this research.

Declaration of competing interest

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CRedit authorship contribution statement

Souichi Oka: Writing – original draft, Conceptualization.
Yoshiyasu Takefuji: Writing – review & editing, Supervision, Project administration.

Supplementary materials

Supplementary material associated with this article can be found in the online version at doi:10.1053/j.jvca.2025.08.035.

References

- Li K, Li Y, Gao Q, et al. Machine learning in risk prediction of continuous renal replacement therapy after surgical repair of acute type A aortic dissection. *J Cardiothorac Vasc Anesth* 2025;0:6–28. <https://doi.org/10.1053/j.jvca.2025.06.028>.
- Fisher A, Rudin C, Dominici F. All models are wrong, but many are useful: Learning a variable's importance by studying an entire class of prediction models simultaneously. *J Mach Learn Res* 2019;20:177. <https://doi.org/10.48550/arXiv.1801.01489>.
- Lipton ZC. The myths of model interpretability: In machine learning, the concept of interpretability is both important and slippery. *ACM Queue* 2018;16:31–57. <https://doi.org/10.1145/3236386.3241340>.
- Lones MA. Avoiding common machine learning pitfalls. *Patterns* 2024;5:101046. <https://doi.org/10.1016/j.patter.2024.101046>.
- Musolf AM, Holzinger ER, Malley JD, et al. What makes a good prediction? Feature importance and beginning to open the black box of machine learning in genetics. *Hum Genet* 2022;141:1515–28. <https://doi.org/10.1007/s00439-021-02402-z>.
- Alaimo Di Loro P, Scacciatelli D, Tagliaferri G. 2-Step gradient boosting approach to selectivity bias correction in tax audit: An application to the VAT gap in Italy. *Stat Methods Appl* 2023;32:237–70. <https://doi.org/10.1007/s10260-022-00643-4>.
- Adler AI, Painsky A. Feature importance in gradient boosting trees with cross-validation feature selection. *Entropy* 2022;24:687. <https://doi.org/10.3390/e24050687>.
- Huti M, Lee T, Sawyer E, et al. An investigation into race bias in random forest models based on breast DCE-MRI derived radiomics features. *Clin Image-Based Proced. Fairness AI Med Imaging* 2023;225:225–34. https://doi.org/10.1007/978-3-031-45249-9_22.
- Salles T, Rocha L, Gonçalves M. A bias-variance analysis of state-of-the-art random forest text classifiers. *Adv Data Anal Classif* 2021;15:379–405. <https://doi.org/10.1007/s11634-020-00409-4>.
- Touw WG, Bayjanov JR, Overmars L, et al. Data mining in the life sciences with random forest: A walk in the park or lost in the jungle. *Brief Bioinform* 2013;14:315–26. <https://doi.org/10.1093/bib/bbs034>.
- Huang X, Marques-Silva J. On the failings of Shapley values for explainability. *Int J Approx Reason* 2024;171:109112. <https://doi.org/10.1016/j.ijar.2023.109112>.
- Kumar I, Scheidegger C, Venkatasubramanian S, et al. Shapley residuals: Quantifying the limits of the Shapley value for explanations. *Adv Neural Inf Process Syst* 2021;34:26598–608. <https://doi.org/10.48550/arXiv.2106.10860>.
- Zhang J, Wu X, Hoi SCH, et al. Feature agglomeration networks for single stage face detection. *Neurocomputing* 2020;380:180–9. <https://doi.org/10.1016/j.neucom.2019.10.087>.
- Xie Y, Jing Z, Pan H, et al. Redefining the high variable genes by optimized LOESS regression with positive ratio. *BMC Bioinformatics* 2025;26:104. <https://doi.org/10.1186/s12859-025-06112-5>.
- Yu H, Hutson AD. A robust Spearman correlation coefficient permutation test. *Commun Stat Theory Methods* 2024;53:2141–53. <https://doi.org/10.1080/03610926.2022.2121144>.
- Okoye K, Hosseini S. Correlation tests in R: Pearson Cor, Kendall's Tau, and Spearman's Rho. *R Programming: Statistical data analysis in research*. Springer Nature 2024:247–77. https://doi.org/10.1007/978-981-97-3385-9_12.

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