Correspondence on Letter regarding “Toward Hepatitis C Virus Elimination Using Artificial Intelligence”

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Dear Editor,

We are grateful for the comments from Professor Hur and Professor Lee on our recent publication. We developed artificial intelligence (AI) models for predicting direct-acting antiviral agents (DAA) failure among a large chronic hepatitis C (HCV) cohort. In patients with decompensated liver cirrhosis, the AI model is beneficial in determining the optimal timing for the initiation of DAA therapy. We agreed that more intensive antiviral therapy beyond the current guidelines may be considered in HCV patients who are susceptible to DAA failure.

Since the presence of overfitting in the training dataset, the current AI model needs further optimization to improve its generalizability. We have ever tried hyperparameter tuning and simplifying the input features through dimensional reduction to avoid overfitting. In such an imbalanced dataset, it is a challenge to maintain the accuracy of the AI model and avoid overfitting. Unsolved overfitting may imply there are unidentified risk factors regarding treatment response. Our study only incorporated 55 clinical host and virologic features before and after treatment in the current model. The diversity of host genetics, cytokine dynamic, immunity, metabolism, baseline or treatment-emergent resistance-associated substitutions of HCV,...etc. may simultaneously affect the DAA efficacy. A combination of multi-omics in the AI model may enhance the predictive accuracy of the validation datasets in the future. Furthermore, all the subjects were enrolled from a single ethnic population. It is necessary to validate this AI model in independent cohorts of various ethnicities. Seeking opportunities for international research collaboration to verify and optimize this AI model is mandatory.
Reference