



LETTER TO THE EDITOR

Machine-learning models for prediction of sepsis patients mortality: A needed consideration



Predicción de mortalidad en pacientes sépticos mediante modelos de machine-learning: una reflexión necesaria

Dear Editor:

The article “Machine-learning models for prediction of sepsis patients mortality”¹ is very interesting for many reasons: the methodology used, the adoption of advanced statistical techniques, the huge sample size, and the aim of universalize the results comparing different populations. However, for us, it is remarkable that they do not emphasize the struggle between the clinical prediction and the model prediction.

QuickSOFA (QS) scale intend to predict mortality as a brief version of a more complex scale, thresh from the Sepsis-3 recommendations. It is based on 3 variables: respiratory rate (RR), neurological impairment (following the Glasgow coma scale: GCS), and systolic blood pressure (SBP) < 100 mmHg.

As it is said in the paper, the SOFA scale had not had the good clinical prediction that it has in the model. In the search of why this could happen, if we focused on the variables included, they were some of the least important in the predictive model: RR (13th out of 15), GCS (9th out of 15) and SBP (15th out of 15). The most exciting point is that there are other accessible and more valuable variables for the model at our reach, as age, median blood pressure, and temperature.

The interesting thing is that there are easily accessible variables that are more relevant to the model, such as age, mean blood pressure, and temperature, than those used by QS.

The importance of variables is not entirely equivalent to the punctuation in the logistic regression results; it is more related to the need for that variable for decision-making by the algorithm. Therefore, a frequently used variable is relevant when predicting and a less frequently used variable does not contribute as much.

Here lies the crucial issue. Traditionally, we have made use of predictors based on linear statistical models (multivariate logistic regression) that have offered us predictive variables which allow us to detect and grade the risk of patients in an objective manner. Currently, machine learning techniques - based on non-linear statistical models - grant us a greater predictive capacity with a different priority of variables than we knew.²

This represents a key change, as it not only implies the generation of “new and different prediction for the same patient, but also forces us to think of new predictors for diseases that we already thought we understood enough.³ The predictive success of these models should encourage us to create datasets (collaborative databases) that allow us to exploit their predictive and hierarchical potential of the variables employed, which would lead us to prioritize areas of knowledge in diseases that we may have been neglecting.

We don't just have traditional statistics, but we have a multi-purpose tool machine learning. Our responsibility is to know how to use all the tools we have properly, to identify the problem we want to solve and therefore choose the appropriate statistical tool.⁴ This is not an invitation to give up on tradition, but rather a need to include new statistical tools to improve our knowledge in a complex clinical scenario.⁵

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Conflicts of interest

The authors declare that none have conflicts of interest.

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