The prescreening tool for gastric cancer in China

We read with interest the work by Cai *et al*[1] presenting a precise and cost-effective initial mass-prescreening tool for improving the detection of gastric cancer (GC), including early GC. However, we have several comments on the design and results of this study, hoping to improve the transferability and cost-effectiveness of this prescreening tool to other cohorts.

The first point is about the strategy of handling missing data. This study prevented all participants with any missing data from the analysis without reporting the percentage of those participants in the total cohort, which might lead to biassed results if the included records aren't a completely random subset of 'high-risk population of gastric cancer' in China. To minimise bias, imputation techniques, a more efficient group of methods to deal with non-random missingness, is recommended to obtain an integrated datasets for analysis.[2] Before and after using the interpolation method, sensitivity analysis should be conducted to assess the stability of the results. In such a situation, the results will be more reliable.

Another important point is in regard to division of the derivation cohort and validation cohort. In their study, the eligible participants were randomly split into two groups: two-thirds of them to develop the prediction rule and the remaining one-third to confirm its predictive performance. This design is usually not recommended in the Transparent Reporting of a multivariable prediction model for Individual Prognosis or Diagnosis statement,[3] because of weak power during model derivation and validation. Splitting the eligible participants non-randomly (eg, by location) into two groups is a better design for estimating model performance than Cai *et al* did in their study, because it allows non-random changes between two datasets. After non-random reclassification of the study population for model development and validation or further external validation, the transferability of the tool to other cohorts will be more credible.

Last but not least, although negative predictive value (98.8%) of the GC prescreening tool was high, its discrimination (area under curve 0.76) may not be good enough, with about 30% of GC and early GC wrongly classified as low risk category. This prediction rule was originally derived from a conventional logistic regression model, ignoring sophisticated non-linear interactions between variables which may play a crucial part in discriminating GC from non-GC. By capturing non-linear relationships in complex data, machine learning algorithms, such as support vector machines and random forest, have been successfully applied to develop useful classification tools recently, which predict clinical outcomes better than traditional regression models.[4–7] However, whether machine learning methods could operate as prescreening tools to improve cost-effectiveness of GC screening needs further investigation.

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