Genetic risk classifier to predict localised renal cell carcinoma recurrence

Jin-Huan Wei and colleagues[1] developed a reliable risk classifier, based on six single nucleotide polymorphisms, to refine prognosis of localised clear cell renal cell carcinoma. After internal and independent validation, this genetic classifier has apparent superiority over previous models when combined with clinicopathological characteristics.[2,3] The finding of this study is of clinical importance because it can complement the existing staging system in predicting localised renal cell carcinoma recurrence by integrating information about genetic alterations.

However, we have two concerns regarding the methods used for the study. First, to quantify effect-size estimation, Wei and colleagues[1] binarised patients in the training set using their median genetic risk score as the cutoff. Clearly, such a partition method did not take survival time into consideration. To overcome this drawback, the use of the survival tree-based technique, which has been applied to more survival scenarios by considering clinical outcome and survival time simultaneously on the basis of scientific judgement, is highly recommended.[4,5] Second, separating data into training and testing sets is an important part in the evaluation of data mining models, and by default (in the data mining field) the ratio of sample size in training versus testing sets is 70:30. In the Article,[1] there are small and equal sample sizes in the training and internal testing sets, but it seems unwise to ensure consistent reproducibility but sacrifice the statistical power of the training set. Whether our opinions can improve rigour and enhance prognostic accuracy is certainly of added interest and requires further exploration.

We declare no competing interests.

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