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Comment on: AI-supported modified risk staging for multiple myeloma cancer useful in real-world scenario

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Artificial intelligence has made a revolution in cancer management, through categorizing patients needing concentrated therapy upfront and also in monitoring frequency throughout the follow-up stages. Machine learning approaches to progress a Modified Risk Staging works to enhance easy-to-acquire available laboratory parameters. Patients who recently have a diagnosis of multiple myeloma are confirmed on two-fold datasets. Evaluation of the suggested risk staging model with previously known RISS and ISS was assumed to investigate its efficacy proceeding the estimates through several terms for expectation as overall survival and progression-free survival [1].

Modified Risk Staging has shown very promising results, and it is being used for the first time to diagnose multiple myeloma and so far, may be used in the diagnosis of various malignancies including leukaemia and lymphoma. Many factors can lead to poor prognosis of tumours, due to the expensive genomic checks that cannot be implemented due to economic and/or ecologic limits [2]. A new online tool permits automatic determination of Modified Risk Staging according to the assessed parameters to subdue such obstacles. As a case in point, the parameters that in collective integration into risk staging, were given weighs to each through their respective hazard ratios for overall survival and progression-free survival gotten by the univariable Cox-proportional hazard check on the working out statistics for precise integration [3].

Another inspiration for Modified Risk Staging dependent this computerized database is that could be returned to a wider database related to not only Indian patients but also Asian ones that for which the laboratory and clinical information is available overtly, especially that the J48 tree for risk staging showed promising results in the real risk category for each case [4]. Farswan et al. [5] established Modified Risk Staging effectiveness in the identification of risk cases. This is the first study to evaluate the proposed thresholds of laboratory factors through KAP yielding distinctive overall survival and progression-free survival that are computed as minimum *p*-value with separation of Modified Risk Staging groups compared to individuals established with documented thresholds and later, accepted.

The study included total multiple myeloma patients (n=1,070) who were arbitrarily divided as training group (n=716) and test group (n=354). The test group did not include any missing parameters while in the training group, 41 cases (5.7% of 716) had some missing parameters assigned as the median value. Original thresholds were accepted for hemoglobin (12.3 g/dL), β2M (4.8 mg/L), albumin (3.6 g/dL), calcium (11.13 mg/dL) and eGFR (48.1 mL/min) on the multiple myeloma dataset by KAP. The authors examined the effectiveness by applying Modified Risk Staging for overall survival prediction in terms of C-index, hazard ratios, and its corresponding *p*-values, but had comparable C-index and p-values to ISS in the prediction of progression-free survival outdone ISS. On both datasets, Modified Risk Staging completed better RISS in expressions of *p*-values and C-index. A modest available tool was also considered to let computerized calculation of Modified Risk Staging dependent on the values of the parameters.

The main study limitations, were some differences in RISS groups were results of 57.48%, 70.49% and 35.27% for RISS-1, RISS-2 and RISS-3 respectively for the 5-year overall survival which suggested some anomaly because RISS-1 should have a higher overall survival as

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matched to RISS-2. This irregularity might be for assigning a larger number of cases to RISS-2 having larger overall survival as comparable to RISS-1. Secondly, the study commends working out on machine learning models applied on greater datasets to offer the effective upfront prediction that could be valuable to choose therapy mainly in high-risk multiple myeloma cases.

Based on these results, this study indicated that the thresholds of the investigated parameters through KAP yield distinctive overall survival and progression-free survival patterns. The accuracy of ten-fold cross-validation and receiver operating characteristic area approve that the ranked stratification model may properly categorize cases into diverse risk clusters. Indeed, the study offers a new significant method for machine learning techniques applied in Modified Risk Staging that resulted in good prediction of survivaland recognized varied risk groups with different features. While other studies looked at genetic markers to classify patients in different diseases either based on genetic markers or environmental parameters [6,7], this study is the first reliable and simple staging system which uses simple and easily available laboratory parameters. It is needed for situations wherever genomic testing is not available.

CRediT authorship contribution statement

Rania M. Khalil: Writing – original draft, Writing – review & editing. **Mohamed Gomaa Kamel:** Writing – original draft, Writing – review & editing.

Declaration of Competing Interest

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