

Letter to the Editor

Clinical Readiness of Vital Sign–Based Sepsis Prediction

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JMIR Med Inform 2026;14:e111475; doi: [10.2196/111475](https://doi.org/10.2196/111475)

Keywords: sepsis prediction; deep learning; vital signs monitoring; temporal modeling; clinical readiness

I read with interest the study by Yang et al [1], which proposed a lightweight transformer-based model for real-time sepsis prediction using six vital signs. The clinical motivation is laudable, but several methodological and interpretational issues warrant clarification.

First, from the original 40,336 PhysioNet records, only 3766 qualified sequences were retained after filtering for vital-sign completeness [1]. For septic records, the authors required <50% missingness within a 16-hour window around sepsis onset, whereas nonseptic sequences were sampled with missingness ≤50%. This selection favors records with greater temporal completeness, yet the model is promoted for low-resource settings where data sparsity may be substantial. The manuscript also does not clearly specify how residual missing values within retained sequences were handled. Because missingness patterns may themselves carry clinical information and influence model estimates [2], reporting the preprocessing strategy, comparing included and excluded patients, and evaluating performance across varying levels of missingness would better demonstrate robustness.

Second, the validation strategy requires greater transparency. The Methods describe a 4:1 train/test split, whereas Table 2 reports averages from 5-fold cross-validation [1]. Although these approaches are compatible, their relationship is not explained. More importantly, the contrastive-learning margins were selected from three candidate configurations according to the lowest mean absolute error (MAE), while

Figure 3 tracks area under the receiver operating characteristic curve, area under the precision-recall curve, and MAE on the “test dataset” across training epochs. To avoid potentially optimistic performance estimates, it would be important to clarify whether hyperparameter and epoch-related model-selection decisions were made independently of the data used for final performance estimation. Nested validation or a strictly held-out test set would provide a clearer estimate of generalizability and would address concerns emphasized by contemporary reporting and risk-of-bias frameworks such as TRIPOD+AI (Transparent Reporting of a Multivariable Prediction Model for Individual Prognosis or Diagnosis + AI) and PROBAST+AI (Prediction Model Risk of Bias Assessment Tool + AI) [3,4].

Third, the interpretation of prediction timing requires clarification. The abstract reports a normalized MAE of 0.11%, whereas Table 2 of the original study reports 0.11 and the Methods define MAE as prediction error normalized by input-sequence length [1]. If 0.11 represents a proportion, it corresponds to 11% rather than 0.11% of sequence length. Because input sequences are variable in length, this normalized metric does not directly indicate how many hours before or after sepsis onset predictions occurred. Reporting absolute timing error and clinically interpretable warning time in hours would therefore substantially improve interpretation. The probability threshold used to derive the reported sensitivity (89.29%) and specificity (73%) should also be specified.

These clarifications would not diminish the technical contribution of the Multi-Scale Temporal-aware Contrastive Learning (MSTCL) model but would strengthen its reproducibility, transportability, and clinical readiness.

Generative AI Use

ChatGPT (GPT-5.6; OpenAI) was used to assist with manuscript organization and language refinement. All scientific arguments, factual statements, and references were independently reviewed and verified by the authors, who take full responsibility for the final content.

Funding

This work was supported by the Health Commission of Sichuan Province Medical Science and Technology Program (grant 25LCYJ34).

Authors' Contributions

LL and SL contributed equally to the conceptualization of the commentary, methodological appraisal, verification and interpretation of the published results and methods, literature review, and critical revision of the manuscript. LL additionally contributed to funding acquisition. CN contributed to the conceptualization of the commentary, conducted the literature review and critical appraisal, drafted the manuscript, and supervised the overall intellectual content. All authors contributed to the final interpretation, critically reviewed the manuscript, read and approved the final version, and accept accountability for the work.

Conflicts of Interest

None declared.

Editorial Notice

The corresponding author of “Online Sepsis Prediction Using Vital Signs and Multiscale Temporal-Aware Contrastive Learning: Model Development and Validation Study,” did not respond to our invitation to reply to this letter.

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Abbreviations

MAE: mean absolute error

MSTCL: Multi-Scale Temporal-aware Contrastive Learning

PROBAST+AI: Prediction Model Risk of Bias Assessment Tool + AI

TRIPOD+AI: Transparent Reporting of a Multivariable Prediction Model for Individual Prognosis or Diagnosis + AI

Edited by Andrew Coristine; This is a non-peer-reviewed article; submitted 07.Sep.2026; accepted 16.Oct.2026; published 27.Oct.2026

Please cite as:

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JMIR Med Inform 2026;14:e111475

URL: <https://medinform.jmir.org/2026/1/e111475>

doi: [10.2196/111475](https://doi.org/10.2196/111475)

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