© Aluna Publishing

ORIGINAL ARTICLE

CONTENTS

Comparative analysis of machine learning models for survival prediction in patients with malignant melanoma

Maksym A. Chernykh[1], Olena O. Oshyvalova[1,2]

[1] NATIONAL TECHNICAL UNIVERSITY OF UKRAINE «IGOR SIKORSKY KYIV POLYTECHNIC INSTITUTE», KYIV, UKRAINE

[2] STATE INSTITUTION OF SCIENCE «CENTER OF INNOVATIVE HEALTHCARE TECHNOLOGIES» STATE ADMINISTRATIVE DEPARTMENT, KYIV, UKRAINE

ABSTRACT

Aim: To perform a comparative analysis of the effectiveness of contemporary machine learning models applied to survival prediction in patients with malignant melanoma and to assess their potential advantages over conventional staging systems as tools for personalised risk stratification.

Materials and Methods: A structured comparative analysis of published prognostic models developed using population-based databases was performed, comparing measures of discrimination (area under the ROC curve [AUC] and concordance index [C-index]), calibration (Brier score), and clinical utility (decision curve analysis). The clinical context was supplemented by data from a retrospective cohort study of patients with cutaneous melanoma.

Results: Ensemble and gradient-boosting algorithms (Random Forest, CatBoost, and XGBoost) consistently outperformed Cox proportional hazards regression models in terms of discrimination, achieving AUC values of approximately 0.76-0.84 for 1-, 3-, and 5-year survival. Ensemble models achieved a C-index of 0.732, compared with 0.685 for Cox regression and 0.537 for AJCC/NCCN criteria; the MIA nomogram demonstrated performance comparable to that of machine learning models (C-index, 0.739). Tumour stage, age, and surgical treatment were consistently identified as the leading prognostic factors. Retrospective cohort data confirmed the prognostic role of Breslow thickness, mitotic activity, and lymph node involvement in disease progression.

Conclusions: Machine learning models provide greater accuracy and more individualised prognostic assessment than conventional approaches and may serve as a supplement to standard staging systems. Their implementation requires prospective validation while preserving the physician's ultimate decision-making authority.

KEYWORDS: melanoma, machine learning, personalised medicine

Wiad Lek. 2026;79(9):2194-2200. doi: 10.36740/WLek/237519 DOI

INTRODUCTION

Melanoma, an aggressive skin cancer originating from melanocytes, represents a significant global health problem owing to its high metastatic potential, mortality, and variable prognosis [1]. Despite advances in treatment, outcomes in patients with melanoma remain dependent on factors such as tumour stage, tumour localisation, and individual patient characteristics [1].

Accurate survival prediction is important for clinical decision-making and for personalising treatment plans, ultimately improving outcomes for patients with melanoma. At present, the AJCC (American Joint Committee on Cancer) staging system, which is considered the global standard, is used to assess the risk of disease progression and prognosis in patients with cutaneous melanoma (Table 1) [2].

Since aggregate statistics do not reveal the full picture of the tumour process in melanoma, the additional use of specialised calculators employing several independent data points improves individual risk prediction. The most widely used is the melanoma calculator developed by Melanoma Institute Australia (MIA) [3, 4]. These calculators assess standard TNM features together with patient-specific variables [5]:

1) Age: older patients generally have lower survival rates;

2) Biological sex: statistically, women generally have a more favourable prognosis than men;

3) Anatomical location: melanomas on the extremities (arms and legs) have a better prognosis than those on the trunk, head or neck;

4) Mitotic rate: the rate at which cancer cells divide (although excluded from some principal T categories, it remains a powerful prognostic factor).

At the current stage of scientific research, modern oncology uses molecular tumour profiles to generate targeted risk estimates [6]:

1) Gene expression profiling (GEP): commercial GEP tests (such as DecisionDx-Melanoma) assess specific RNA signatures in the primary tumour to classify pa-

tients into low- or high-risk categories for metastasis, helping to reduce the number of unnecessary SLNB procedures;

2) Mutational status: detection of BRAF V600 mutations helps to determine prognosis, particularly in stage III disease, and guides the use of targeted adjuvant therapy [7];

3) Polygenic risk scores: academic models use signatures of between 5 and 14 different genes (for example, STAT1, CDK2, p21) combined with spatial single-cell RNA imaging in order to predict how the tumour will interact with the patient's immune system [8].

At present, machine learning and multimodal artificial intelligence (AI) models increasingly outperform conventional statistics by processing vast, heterogeneous datasets simultaneously [9]. The use of AI is therefore becoming a relevant direction for risk stratification in melanoma:

1) Algorithmic risk stratification – advanced gradient boosting algorithms such as CatBoost, XGBoost and Random Forest process large demographic and clinical datasets (such as the national SEER database) to accurately map survival curves [10];

2) Computer vision and digital pathology – deep learning models extract prognostic signals directly from routine digital tissue images;

3) Multimodal systems – by combining digital pathology images with electronic health records (EHR), AI models create personalised, practical clinical decision support tools for patients with early-stage melanoma [1].

It is also well established that, when developing an individualised prognosis for patients with melanoma, it is preferable to additionally consider established anatomical and pathological features of the tumour. These variables are therefore often combined using multivariable regression models, such as Cox proportional hazards models, to predict 1-, 5-, or 10-year survival [1].

Comparisons of different melanoma prognostic models are conducted continuously and form the basis of modern personalised oncology. The principal aim of such studies is to determine whether novel genetic and digital tools can outperform or provide a meaningful complement to the conventional international AJCC staging system [11].

Thus, the relevance of comparative studies evaluating artificial intelligence systems for melanoma prognostication is driven by the global trend towards personalised medicine (Table 2).

Contemporary research indicates that patients with the same melanoma stage may have radically different clinical outcomes, which requires the introduction of dynamic, multimodal and personalised tools. Further searches for new prognostic systems in melanoma are therefore directed at resolving a fundamental contradiction of modern oncology – the biological heterogeneity of melanoma has outgrown the capabilities of the standard AJCC staging system.

AIM

The aim of our study was to perform a comparative analysis of the effectiveness of contemporary machine learning models applied to survival prediction in patients with malignant melanoma, and to assess their potential advantage over the conventional AJCC staging system as a tool for personalised risk stratification. Our research hypothesis was that non-linear ensemble and gradient boosting models provide higher discriminative ability and clinical utility compared with classical regression methods.

MATERIALS AND METHODS

The study was designed as a structured comparative analysis of published machine learning prognostic models for survival assessment in patients with melanoma, supplemented by clinical context from a retrospective cohort study. The sources included peer-reviewed publications in which prognostic models were developed and validated using population-based databases and for which at least one quantitative performance measure was reported.

The eligibility criteria for models included in the comparison were as follows: development using structured clinical and demographic data from patients with melanoma; availability of internal or external validation; and reporting of measures of discrimination (area under the ROC curve [AUC] and concordance index [C-index]), calibration (Brier score), or clinical utility (decision curve analysis [DCA]). Models from the Cox proportional hazards regression (CoxPH), LASSO regression, Random Forest, XGBoost, gradient-boosting (GBM, CatBoost, and LightGBM), and neural network families were included. The methodological features of gradient-boosting algorithms are described in specialised technical publications [12, 13]. As reference non-machine-learning stratification tools, the AJCC/NCCN criteria and the MIA nomogram were additionally included in the comparison [3].

The clinical context was supplemented by data from the retrospective follow-up of 200 patients with cutaneous melanoma who were monitored by dermatovenereologists at a specialised institution over a 10-year period [5]. For the morphological characterisation of the primary tumour, Breslow thickness, the presence of ulceration, and mitotic activity were assessed; staging

Table 1. The AJCC melanoma staging system

Criterion	Characteristic
TNM criteria	the international standard for determining the extent of malignant tumours and cancer staging: T (Tumour) – describes the size of the primary tumour and its invasion into adjacent tissues or organs; N (Node) – indicates the presence or absence of metastases in regional lymph nodes; M (Metastasis) – determines the presence of distant metastases in other organs or tissues
Breslow thickness	Measures the exact depth of tumour invasion in millimetres. It remains the most important local prognostic factor
Ulceration	Absence or presence of ulceration of the epidermis overlying the tumour, indicating an aggressive phenotype
Mitotic rate	The rate of cellular proliferation, defined as the number of mitoses per square millimetre
Lymph node involvement	Confirmed by sentinel lymph node biopsy (SLNB), which determines whether the cancer has spread regionally

Source: compiled by the authors based on [2]

Table 2. Principal advantages of applying AI in melanoma prediction

Criterion	Advantage
Transition to personalised prognosis	Comparative AI studies help to create tools that account for dozens of microfactors simultaneously (age, genetics, the precise immune microenvironment of the tumour), calculating an individual survival trajectory for the patient with melanoma
Reduction in the number of unnecessary invasive procedures	Comparisons of AI models are aimed at training the accurate identification of low-risk patients in whom traumatic surgical interventions for sentinel lymph node removal may be avoided
Optimisation of healthcare system costs	Freely available AI models can deliver high-accuracy results, which will reduce the costs of high-cost diagnostic investigations
Selection of the optimal treatment strategy	Mathematical models will help to assess patient survival depending on the therapy applied

Source: compiled by the authors based on [1, 11]

was performed according to the 8th edition of the AJCC staging system [2].

Model performance was compared using the AUC, C-index, and Brier score values reported in the respective sources for 1-, 3-, and 5-year survival. Standard software packages (Microsoft Excel 2021 and IBM SPSS Statistics 29) were used for statistical processing and visualisation of the cohort data. In the primary studies included in the comparison, the models were implemented in R (mlr3, mlr3proba, randomForestSRC, and glmnet packages) and Python (XGBoost and CatBoost libraries). The gradient-boosting implementations differed in their handling of categorical predictors and regularisation; these differences were taken into account when interpreting the reported performance measures.

ETHICS

The study was conducted in accordance with the provisions of the Declaration of Helsinki of the World Medical Association and the ethical principles for medical research involving human subjects. The retrospective analysis of clinical data used to form the clinical context was carried out on de-identified data within the framework of an approved research project of the institution; additional informed consent for the retrospective analysis of de-identified data was not required in accordance with the applicable regulatory documents. The comparative analysis of prognostic models is based on openly published aggregate data that contain no individually identifiable information.

AI STATEMENT

The following artificial intelligence (AI) tools were used in this work: Claude Opus 4.8 (Anthropic) and ChatGPT GPT-5.5 (OpenAI). They were used for formation and formatting of the bibliography under the author's control and language checking and correction under the author's supervision. All AI-generated or AI-assisted content, including text and code, was reviewed, verified, and edited by the authors. All sections using AI were reviewed and edited personally by the authors. The scientific statements, conclusions, and results are the authors' own intellectual contribution.

RESULTS

The comparative analysis showed that non-linear ensemble and gradient boosting algorithms consistently outperform classical regression models in terms of

Table 3. Comparative characteristics of machine learning model families for survival prediction in melanoma

Model family	Reported discrimination measure	Features / limitations
Cox regression (CoxPH), LASSO	C-index ~0.67–0.69	Simplicity and interpretability; assumptions of linearity and proportional hazards
Random Forest	C-index ~0.70–0.73; AUC up to ~0.84	Highest stability; accounts for non-linear interactions; requires a sufficient sample size
Gradient boosting (CatBoost, XGBoost, GBM)	AUC ~0.76–0.87	Efficient handling of categorical and incomplete data; risk of overfitting
Neural networks	AUC ~0.55–0.66	Flexibility; sensitivity to sample size and class imbalance

Note: AUC – area under the ROC curve; C-index – concordance index. The ranges presented summarise values reported in population-based studies
Source: compiled by the authors based on [1, 10, 11]

discrimination. In population-based studies, Random Forest and gradient boosting models (CatBoost, XGBoost) reached AUC values of approximately 0.76-0.84 for 1-, 3- and 5-year survival, whereas Cox proportional hazards regression and LASSO demonstrated lower concordance index values [10, 11]. The generalised comparative characteristics of the principal model families are presented in Table 3, and the distribution of discrimination measures across prediction horizons is shown in Fig. 1.

As shown in Figure 1A, the advantage of ensemble algorithms was maintained across all prediction horizons. The Random Forest model demonstrated the highest AUC values –0.813, 0.808, and 0.840 for 1-, 3-, and 5-year survival, respectively – whereas the corresponding values for Cox regression did not exceed 0.749. The lowest discriminatory ability was observed for neural networks (AUC, 0.646-0.660), which is consistent with their sensitivity to limited sample sizes in rare tumour types. Gradient-boosting models (CatBoost, XGBoost, and GBM) occupied an intermediate position, with stable AUC values ranging from 0.713 to 0.766; CatBoost demonstrated the lowest variability across prediction horizons (0.756-0.760).

Ensemble models also demonstrated an advantage in terms of calibration: Brier score values for Random Forest were 0.175, 0.164, and 0.130 for 1-, 3-, and 5-year survival, respectively, representing the lowest (i.e., best) values among all compared algorithms. In external testing on independent samples, discrimination measures decreased as expected (C-index, 0.701; AUC, 0.715-0.776) but remained at an acceptable level, indicating satisfactory model generalisability.

A separate comparison of machine learning models with conventional risk-stratification tools used in routine clinical practice was performed (Fig. 1B). The AJCC/NCCN criteria, based predominantly on tumour thickness, yielded a C-index of only 0.537, with high sensitivity (95.0%) but extremely low specificity (12.4%). Cox regression increased the C-index to 0.685. The MIA nomogram, which additionally accounts for mitotic activity, histological subtype, and lymphovascular invasion, achieved a C-index of 0.739 and 0.750 on external validation, respectively, demonstrating performance comparable to that of ensemble machine learning models (C-index, 0.732) [3]. Thus, in terms of discrimination, the modern multiparametric nomogram and machine learning models demonstrated comparable performance and substantially outperformed the criteria-based AJCC/NCCN approach.

Analysis of feature importance in the best-performing models showed that tumour stage, patient age, and surgical treatment were the leading prognostic factors for survival; these variables made a substantially greater contribution than other predictors [1, 10]. The influence of stage and age was most pronounced in short-term predictions and gradually weakened as the prediction horizon increased. At the same time, in models built using an extended set of histological features, mitotic activity and pretreatment lactate dehydrogenase levels were among the most important predictors, indicating that the relative importance of predictors depends on the completeness of the source data [1]. Assessment of clinical utility using decision curve analysis confirmed that ensemble models provided greater net clinical benefit across a wide range of threshold probabilities (approximately 0.1-0.6) than classical methods [14].

The retrospective cohort follow-up data are consistent with the modelling results. The morphological characteristics of the primary tumour (Breslow thickness, mitotic activity, presence of ulceration) and the AJCC disease stage were associated with subsequent progression: the highest levels of mitotic activity and ulceration were observed at advanced (III–IV) stages. Tumour progression predominantly occurred in the first years of follow-up, and the leading routes of metastasis were regional and distant lymphatic collectors, the lungs, skin, liver and skeletal system [5]. This confirms the role of the same quantitative clinical parameters that are used as predictors in machine learning models.

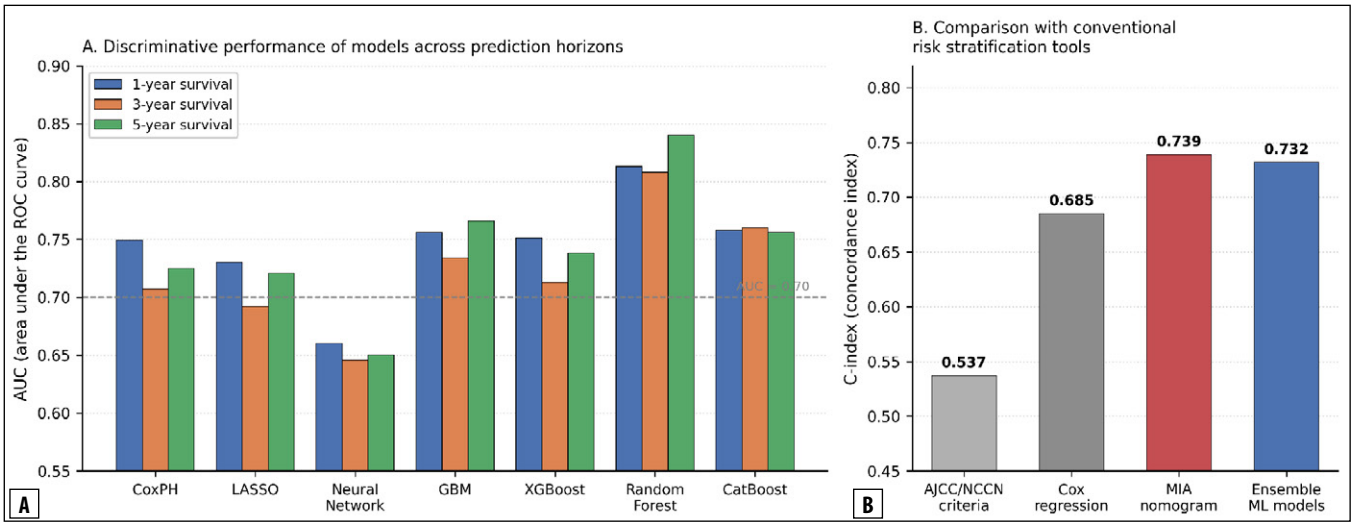


Fig. 1. Comparative performance of prognostic models in melanoma: A – discriminative ability (AUC) of machine learning models and regression approaches for 1-, 3- and 5-year survival; B – comparison of the concordance index (C-index) of ensemble machine learning models with conventional risk stratification tools (AJCC/NCCN criteria, Cox regression, MIA nomogram). Data summarised from published population-based studies
Source: compiled by the authors based on [1, 3, 4, 10]

DISCUSSION

Our results demonstrated that ensemble and gradient boosting models provide higher discriminative ability compared with Cox proportional hazards regression (C-index 0.732 versus 0.685; AUC up to 0.840 versus 0.749), which supports the research hypothesis put forward. These data are consistent with the results of F. Gao and X. Xu, who, when comparing six algorithms in a population-based sample, obtained a C-index of 0.732 and AUC values of 0.813–0.840 for the Random Forest model, whereas CoxPH and LASSO did not exceed 0.685 and 0.670, respectively [10]. A similar hierarchy of algorithms was described by E. Hu et al.: in their study of a sample of 4875 patients with cutaneous melanoma, the CatBoost model showed the best generalisability, with stable AUC values of 0.7557-0.7595, which is close to the ranges we obtained for gradient boosting algorithms [1].

The relatively low effectiveness of neural networks that we identified (AUC 0.646-0.660) also corresponds to the literature. K. Kourou et al. note that the advantage of deep architectures over ensemble methods manifests itself predominantly in large and multimodal data arrays, whereas in structured clinical samples of limited size ensemble decision trees retain their advantage [11]. This explains why, in melanoma studies where samples rarely exceed a few thousand observations, it is Random Forest and CatBoost rather than neural networks that occupy the leading positions.

Of key importance for the interpretation of our results is the comparison of machine learning models with the MIA nomogram. The C-index value we obtained for the MIA nomogram (0.739) corresponds to the data of S. N. Lo et al., who reported an accuracy of 73.9% on internal and 75.0% on external validation in an independent MD Anderson cohort [3]. Fundamentally, this measure is not inferior to the results of ensemble machine learning models. This calls for a critical appraisal of the widespread claim of an unconditional superiority of algorithmic approaches: according to our data, a carefully constructed multiparametric regression nomogram may be at least equivalent to more complex models. Instead, the genuine advantage of both approaches manifests itself precisely in comparison with the criteria-based AJCC/NCCN selection, which in our analysis provided a C-index of only 0.537. The same conclusion is drawn by S. N. Lo et al., who show that at an equal sensitivity of 95% the specificity increased from 12.4% for the NCCN/ASCO criteria to 22.1% for the MIA nomogram [3].

The structure of leading predictors identified in our analysis (stage, age, surgical treatment) corresponds to the results of population-based studies [10], but requires a caveat. In the work of E. Hu et al., where the feature set included extended histological parameters, the dominant predictors were mitotic activity and lactate dehydrogenase level, while demographic factors made a minimal contribution [1]. This discrepancy shows that the ranking of predictors largely reflects the completeness of the available data rather than the biological significance of the features alone. The meta-analysis by Q. Xia et al. confirms that Breslow thickness, ulceration and lymph node involvement remain the most stable prognostic factors regardless of the modelling method [15], and the systematic review by K. Lallas et al. additionally assigns mitotic activity and molecular markers to this group [7].

The results of the retrospective cohort follow-up that we used for clinical context confirm the pattern noted above: the highest levels of mitotic activity and ulceration were observed at advanced stages, and progression predominantly occurred in the first years of follow-up, with metastasis to regional lymphatic collectors, the lungs, liver and skeletal system [5]. This is consistent with meta-analytic data on predictors of distant metastasis [7, 15] and indicates that the predictors used by algorithms have a reproducible clinical and morphological basis rather than being purely statistical artefacts.

At the same time, our data showing a decline in performance on external validation (C-index, 0.701 vs. 0.732 on internal validation) reflect a systemic problem in the field. The systematic review by I. Kaiser et al., which examined prognostic models in melanoma, demonstrated substantial methodological heterogeneity in model development and validation, meaning that most published models are not directly comparable with one another [4]. K. G. M. Moons et al. emphasised that, in the absence of external validation, performance estimates are systematically overestimated owing to model optimism [16]. For this reason, the advantage of ensemble algorithms identified in our analysis should be interpreted with caution: it has been demonstrated using retrospective, population-based data but not in prospective cohorts.

The study has several limitations. The comparison was based predominantly on models developed using retrospective population-based databases, particularly SEER, which are subject to selection bias and data incompleteness. In addition, most models underwent only internal validation, limiting their generalisability [16]. Comparability between studies is further complicated by differences in cohorts, feature sets, and validation methodologies [4]. Molecular markers, including BRAF, KIT, and NRAS mutational status, as well as the effects of modern immunotherapy, are often not incorporated into available models, which may lead to underestimation of long-term survival. Studies based on single-cell and spatial tumour maps indicate considerable unrealised potential for incorporating such data into prognostic models [8]. Furthermore, beyond tumour-related characteristics, short-term survival in patients with cancer is influenced by general clinical factors, particularly nutritional status [17]. Further research should therefore focus on prospective multicentre validation, the integration of molecular data, and the standardisation of evaluation metrics.

CONCLUSIONS

Machine learning models, particularly ensemble algorithms (Random Forest) and gradient-boosting algorithms (CatBoost and XGBoost), provide more accurate and clinically useful individualised survival prognostication in patients with melanoma than classical regression methods, achieving AUC values of approximately 0.76-0.84 and a C-index of 0.732, compared with 0.685 for Cox regression. At the same time, the modern multiparametric MIA nomogram demonstrates comparable discriminatory performance (C-index, 0.739), whereas the criteria-based AJCC/NCCN approach is substantially inferior to both (C-index, 0.537). The leading prognostic factors are consistently tumour stage, age, and surgical treatment, consistent with both population-based data and the results of retrospective clinical follow-up. Machine learning models should be regarded as a supplement to, rather than a replacement for, the conventional AJCC staging system. The practical implementation of such tools requires prospective clinical validation, integration of molecular data, and the preservation of the physician's ultimate decision-making authority.

REFERENCES

1. Hu E, Tai M, Nie Z et al. Development of a machine learning-based model for prognostic prediction in melanoma. Sci Rep. 2025;15:45628. doi:10.1038/s41598-025-30377-8. DOI
2. Gershenwald JE, Scolyer RA, Hess KR et al. Melanoma staging: evidence-based changes in the American Joint Committee on Cancer eighth edition cancer staging manual. CA Cancer J Clin. 2017;67(6):472—492. doi:10.3322/caac.21409. DOI
3. Lo SN, Ma J, Scolyer RA et al. Improved risk prediction calculator for sentinel node positivity in patients with melanoma: the Melanoma Institute Australia nomogram. J Clin Oncol. 2020;38(24):2719—2727. doi:10.1200/JCO.19.02362. DOI
4. Kaiser I, Pfahlberg AB, Uter W et al. Risk prediction models for melanoma: a systematic review on the heterogeneity in model development and validation. Int J Environ Res Public Health. 2020;17(21):7919. doi:10.3390/ijerph17217919. DOI
5. Oshyvalova OO, Mazurenko SM, Voinov IG. Follow-up performance of patients with cutaneous melanoma: recommendations for an effective strategy. Wiad Lek. 2024;77(11):2215—2224. doi:10.36740/WLek/197099. DOI
6. Keung EZ, Gershenwald JE. The eighth edition American Joint Committee on Cancer (AJCC) melanoma staging system: implications for melanoma treatment and care. Expert Rev Anticancer Ther. 2018;18(8):775—784. doi:10.1080/14737140.2018.1489246. DOI
7. Lallas K, Kyrgidis A, Chrysostomidis A et al. Clinical, dermatoscopic, histological and molecular predictive factors of distant melanoma metastasis: a systematic review and meta-analysis. Crit Rev Oncol Hematol. 2024;202:104458. doi:10.1016/j.critrevonc.2024.104458. DOI

8. Love NR, Williams C, Killingbeck EE et al. Melanoma progression and prognostic models drawn from single-cell, spatial maps of benign and malignant tumors. Sci Adv. 2024;10(28):eadm8206. doi:10.1126/sciadv.adm8206. DOI
9. Tran KA, Kondrashova O, Bradley A et al. Deep learning in cancer diagnosis, prognosis and treatment selection. Genome Med. 2021;13:152. doi:10.1186/s13073-021-00968-x. DOI
10. Gao F, Xu X. Machine learning prediction of overall survival in patients with primary gastrointestinal melanoma. Transl Cancer Res. 2025;14(11):7494–7506. doi:10.21037/tcr-2025-1029. DOI
11. Kourou K, Exarchos TP, Exarchos KP et al. Machine learning applications in cancer prognosis and prediction. Comput Struct Biotechnol J. 2015;13:8–17. doi:10.1016/j.csbj.2014.11.005. DOI
12. Hancock JT, Khoshgoftaar TM. CatBoost for big data: an interdisciplinary review. J Big Data. 2020;7(1):94. doi:10.1186/s40537-020-00369-8. DOI
13. Jabeur SB, Gharib C, Mefteh-Wali S et al. CatBoost model and artificial intelligence techniques for corporate failure prediction. Technol Forecast Soc Change. 2021;166:120658. doi:10.1016/j.techfore.2021.120658. DOI
14. Nguyen TT, Nguyen QVH, Nguyen DT et al. Multidimensional machine learning for assessing parameters associated with COVID-19 in Vietnam: validation study. JMIR Form Res. 2023;7(1):e42895. doi:10.2196/42895. DOI
15. Xia Q, Ma Q, Zhu J et al. Prognostic factors in postoperative patients with cutaneous melanoma: a systematic review and meta-analysis. Am J Cancer Res. 2024;14(5):1947–1956. doi:10.62347/SQZT7285. DOI
16. Moons KGM, Kengne AP, Woodward M et al. Risk prediction models: I. Development, internal validation, and assessing the incremental value of a new (bio)marker. Heart. 2012;98(9):683–690. doi:10.1136/heartjnl-2011-301246. DOI
17. Datema FR, Ferrier MB, Baatenburg de Jong RJ. Impact of severe malnutrition on short-term mortality and overall survival in head and neck cancer. Oral Oncol. 2011;47(9):910–914. doi:10.1016/j.oraloncology.2011.06.510. DOI

CONFLICT OF INTEREST

The Authors declare no conflict of interest

CORRESPONDING AUTHOR

Maksym A. Chernykh
Igor Sikorsky Kyiv Polytechnic Institute
37 Beresteiskyi Ave., 03056 Kyiv, Ukraine
e-mail: maksym.chernykh@edu.kpi.ua

ORCID AND CONTRIBUTIONSHIP

Maksym A. Chernykh: 0009-0003-1301-7362 A B C D
Olena O. Oshyvalova: 0000-0002-0395-0269 A E F

A – Work concept and design, B – Data collection and analysis, C – Responsibility for statistical analysis, D – Writing the article, E – Critical review, F – Final approval of the article

RECEIVED: 22.03.2026
ACCEPTED: 28.08.2026

CREATIVE COMMONS 4.0