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Meta-Analysis

Use of artificial intelligence models for prognosis and survival prediction in brain tumor patients: a systematic review and meta-analysis

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ABSTRACT

Brain tumors are associated with significant morbidity and mortality. Early prognostication of preoperative cases via AI models may improve treatment planning and clinical outcome. This systematic review and meta-analysis followed PRISMA 2020 guidelines. Literature review was conducted across various databases including PubMed, Web of Science, Cochrane etc. Out of the 433 papers obtained, 17 retrospective observational studies met the inclusion criteria. Risk of bias assessment was carried out using PROBAST+AI tool. Meta-analysis was carried out for the reporting area under the curve (AUC) or C-index for survival prediction models. With a total of 98,464 observations across 17 studies, machine learning (ML) and deep learning (DL) models were used to predict survival and prognosis in brain tumor patients. The risk of bias was low in 6% studies, moderate in 59% studies and high in 35% of the studies. The pooled AUC was 0.87 (SE: 0.04) with a 95% prediction interval between studies ranging between 0.61 and 1.13. Cochran's Q statistic for heterogeneity was 48.81 ($p<0.001$). Subgroup analyses showed pooled AUCs of 0.92 for ML models and 0.81 for DL models. Significant publication bias was demonstrated by Funnel plot and Egger's test. This systematic review and meta-analysis are the first to include multiple brain tumor types for predicting prognosis via AI models, with ML models showing slightly higher pooled performance than DL models. However, variability in datasets, limited external validation, and high heterogeneity among studies highlight the need for standardization and further research.

Keywords: Brain tumor, Artificial intelligence, Prognosis, Machine learning, Deep learning

INTRODUCTION

Brain tumors are abnormal growths of cells within the central nervous system which can be benign/ malignant.[1-3] They have considerable clinical impact due to high morbidity and mortality.[4,5] In United States the average annual incidence of primary malignant brain and CNS tumors is estimated at 7.08 per 100,000 population.[6,7] While in India, incidence of CNS tumors ranges from 5 to 10 per 100,000 population and accounts for 2% of malignancies.[8,9]

Common presenting features such as persistent headache, cognitive decline, seizures, and focal neurological deficits often bring patients first to general physicians. Early recognition of these symptoms is critical in initiating timely neuroimaging and specialist referral.[10-13]

Important prognostic predictors for brain tumors include, symptoms like visual changes, sensory complaints, altered mental status, with possibilities of metastasis and imaging findings including location of the tumor which predicts its histological grading of the tumor and its response to chemotherapy and radiotherapy.[14-17]

This highlights the need for early prognosis determination to ensure timely intervention with personalized treatment approach. Accurate detection through MRI is required as traditional image processing techniques often struggle due to noise and variability.[18,19]

Keeping these factors in mind, it becomes imperative that we have a better method for estimation of survival years in such patients.

Therefore, training AI models for the same, and improving them over time can help in quick and effective estimation of prognosis from just a CT or MRI image and reduce the healthcare burden on patients by specific treatment planning.[20]

METHODS

We conducted a systematic review under the PRISMA 2020 guidelines for systematic reviews and meta-analyses.[21]

Data sources and search strategy

A comprehensive systematic review of major electronic databases, including PubMed, Wiley Online Library, Web of Science, COCHRANE, and Embase, was conducted, encompassing studies from 2015 to April 2025. The literature search aimed to identify published studies on the use of artificial intelligence/machine learning models in predicting the overall survival of brain tumor patients.

To create a search string, keywords such as "Artificial Intelligence," "Machine Learning," "Deep Learning," "Brain Tumor," "Glioma," "Meningioma," "Astrocytoma," "Preoperative Planning," “Prognosis,” and “Survival Prediction” were used in combination with “AND” and “OR” Boolean operators. Additionally, reference lists of included studies were manually reviewed to identify further studies.

Eligibility criteria

Inclusion criteria

This systematic review evaluated individual studies using the PICOS framework (population, intervention, comparison, outcomes, and study designs). Studies were included if they were case-control/ cohort studies, included patients with any kind of brain tumor, involved the development of a ML model or used artificial intelligence (AI), and reported one of the outcomes of interest.

Study selection

The outcome of interest included survival prediction in brain tumor patients, prognosis prediction before surgical intervention, and prediction of the life expectancy of patients. Studies were excluded if they were systematic/ narrative reviews, did not involve the use of AI/ ML models, focused on diagnosis/ classification of brain tumors, focused on pediatric patients.

Study selection

All retrieved records from the systematic literature search were imported into Zotero.[22–38] The entire selection of records underwent the duplicate removal process. All authors were involved in preliminary screening using titles and abstracts to include relevant studies. Potentially relevant studies were considered eligible for a full-text review for inclusion. Any disagreements were resolved through consensus.

Data extraction

All authors independently performed data extraction using a predefined spreadsheet. The extracted data included the first author’s name, publication year, title of the study, journal, study type, AI model used, clinical task, tumor type, dataset used, sample size, outcome metrics, validation methods used, and limitations of the study.

After data extraction from the included studies as shown in the Table 1, two separate meta-analyses were conducted using meta-essentials (version 1.5): one for AUC values and another for Harrell’s C-index. These indices show the prognostic accuracy of AI-based models in predicting survival outcomes in brain tumor patients.

The pooled effect sizes were calculated using random-effects models. Heterogeneity was assessed using I^2, τ^2, and the Cochran’s Q test. Publication bias was evaluated using the funnel plot asymmetry and the Egger’s regression test.

We used meta-essentials 1.5, an excel-based tool developed by Erasmus University Rotterdam and random-effects model to account for inter-study variability and calculated pooled AUC, pooled C-index, heterogeneity (I^2), forest plots, publication bias (funnel plots, Egger's test).[40]

Subgroup analyses were conducted based on AI model type (ML vs DL) and dataset source (SEER, BraTS and institutional). Risk of bias was evaluated using PROBAST+AI. Meta-regression was not performed due to an insufficient number of covariate-rich studies.

Some studies reported AUC without SE or CI; therefore, AUC was computed via the equation A1 (shown in the Appendix A).

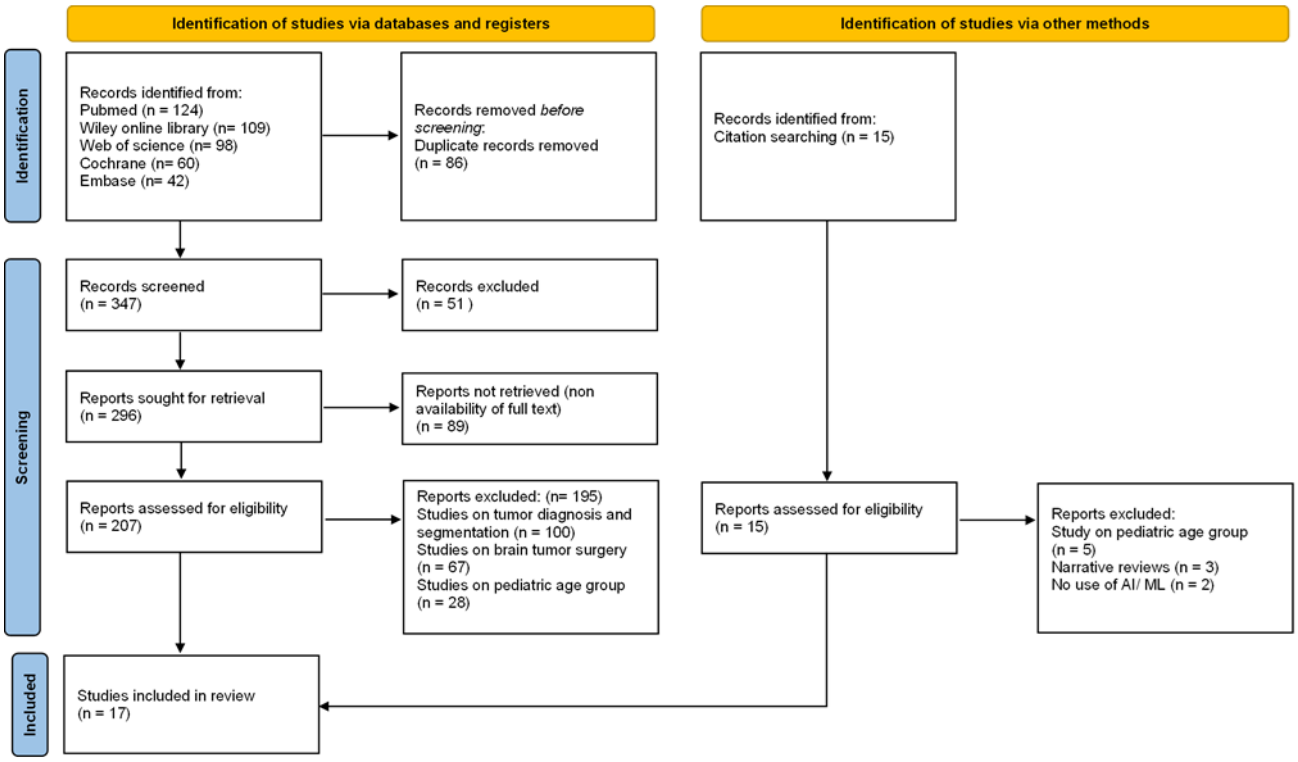

Figure 1: PRISMA flowchart of the study screening and selection process.

Table 1: Data extraction for meta-analysis.

Authors	Clinical outcome	AUC (95% CI) of validation dataset	SE	C-index (95% CI) of validation dataset	SE	N (validation set)	Best model
Chen et al[22]	OS	0.924 [0.8363-0.9999]	0.0417 via Eqn A3 [Appendix A]	0.847	0.05839	38	Random survival forest (RSF)-ML
Wei et al[23]	MGMT methylation prediction	0.902	Not calculated	Not reported		31	Radiomic Signature- ML
Li et al[24]	PFS	Not reported		0.861 (0.760-0.963)	0.026 Equation A4 [Appendix A]	43	Multiparameter radiomic model-ML
Liu et al[25]	PFS	Not reported		0.823	0.0255 Equation A3 [Appendix A]	84	Radiomic Signature- ML
Nath et al[26]	OS	0.972	0.0116 via equation A2 [Appendix A]	Not reported		83,599	Random forest (RF) with Cook's distance elimination (CDE) and SMOTE-ML
Musigmann et al[27]	Postoperative resection status (GTR vs STR)	0.886 [0.717:0.980]	0.0671	Not reported		31	2-feature logistic regression- ML
She et al[28]	OS	0.81	0.03	Not reported		11	3D ResNet using T1Gd MRI with transfer learning (TL)- DL
Marcus et al[29]	Surgical resectability	0.871 (95% CI: 0.849-0.895)	0.0117	Not reported		135	ANN- DL

Continued.

Authors	Clinical outcome	AUC (95% CI) of validation dataset	SE	C-index (95% CI) of validation dataset	SE	N (validation set)	Best model
Link et al[30]	OS	Not reported		Not reported			Univariable and multivariable Cox models-ML
Pan et al[31]	OS	0.937 (0.813-0.989)	0.0449 via Equation A4 [Appendix A]	0.757 (0.663-0.851)	0.0480	30	RF-ML
McGarry et al[32]	OS	Not reported		Not reported		81	Cox regression model-ML
Shaheen et al[34]	OS	0.73	0.0817 via Equation A2 [Appendix A]	Not reported		31	RF classifier-ML
Baid et al[35]	OS	0.799	0.0357 via Equation A2 [Appendix A]	Not reported		130	Neural network-based model-DL
Nie et al[33]	OS	Not reported		Not reported		25	3D multi-channel CNN-based model- DL
Beig et al[37]	OS	Not reported		0.74	0.0801 Equation A3 [Appendix A]	30	Radiomic-based model-ML
Wahed et al[36]	Post-surgical complications	0.930	0.0226 via Equation A2 [Appendix A]	Not reported		128	Neural network-DL
Leon et al[38]	survival prediction	Not reported		Not reported			Radiomic-based ML models-ML

RESULTS

Study selection

The initial database search retrieved 433 potential records. After removing duplicates (n=86), 347 records were subjected to preliminary screening, and 51 records were excluded. The rest of the 296 records were sought for retrieval, out of which 89 were excluded due to the non-availability of full text. The remaining 207 records underwent a full-text review against the predetermined inclusion criteria. During the full text review, 195 records were excluded due to studies on tumor diagnosis and segmentation (n=100), records focusing on brain tumor surgery (n=67), and records focusing on the pediatric age group (n=28). A total of 15 records were identified from searching the references of similar studies. Out of them, 5 were excluded due to focus on the pediatric population, 3 were narrative reviews, and 2 did not involve the use of AI/ML models. Finally, 17 studies were included in this systematic review. The entire study selection process is depicted in Figure 1 using the PRISMA guidelines.

Characteristics of the included studies

The 17 included studies were published between 2015 and April 2025. All the studies are retrospective observational studies, one is a case-control study, and the others are retrospective cohort studies. AI models included ML and DL models. ML models assessed were SVM-Support vector machine, RF, RSF, LASSO logistic regression etc. While DL models included ResNet- Residual network, 3D ResNet-ResNet adapted for 3D image volumes, DenseNet-densely connected convolutional networks etc. The total sample size across all studies was 98,464 observations, individual study sample sizes ranging from 56 to 90,390 observations.

Risk of bias assessment

Risk of bias was assessed via the PROBAST+ AI tool to classify studies as low, moderate/uncertain, or high risk of bias.[39] Authors evaluated all the studies based on the PROBAST + AI checklist using the official targeted signalling questions. Any discrepancies were resolved by the lead author. It was assessed across four domains-participants, predictors, outcomes, and analysis within both model development and evaluation phases. Notably, 6% of studies exhibited a consistently low risk of bias across all domains, due to their large sample size, proper data handling methods, and use of external validation techniques such as K-fold cross-validation. On other hand, 35% of studies showed high concern due to single-center design, selection bias and lack of external validation. Remaining 59% of studies had moderate concerns.

Applicability concerns were generally low across studies. 100% of studies have been assigned to have low concerns by the authors. These findings have been visualized as a traffic light plot via RoBvis web application (Figure 2).[45]

The various categories which lead to introduction of bias have been listed below (Figure 3).

Meta-analysis results

We used the meta-essentials effect size data 1.5 file. Each model's performance was entered as a separate effect size for meta-analysis. The meta-essentials tool (v1.5) was used to pool these results and generate forest plots. Among all the 17 studies, 11 studies reported outcomes related to overall survival (OS), 2 studies reported on progression-free survival (PFS), 3 studies assessed surgical outcome classification (e.g., gross total vs. subtotal resection), 1 study focused on post-surgical complication prediction and 1 study focused on MGMT methylation prediction.

Study inclusion and grouping

Studies were grouped by primary outcome type**.** A total of 6 studies were included in the AUC meta-analysis, which have both complete data available and report OS as an outcome (Table 2). Each study's contribution to the pooled estimate is represented by its weight. It is calculated based on inverse variance under a random-effects model.

Pooled AUC

The pooled AUC is 0.87 (SE=0.04), with a 95% confidence interval (CI) ranging from 0.77 to 0.97. This indicates a statistically significant effect in favor of the outcome measured. The Z-value is 23.21, and both one-tailed and two-tailed p<0.001. This demonstrates strong statistical significance. To account for potential between-study variability and to estimate the possible effect in a future comparable study, we calculated a 95% prediction interval (PI). The value ranges from 0.61 to 1.13. This suggests that while the overall effect is robust, future studies may observe slightly weaker or even non-significant effects, despite the significant pooled estimate (Figure 4).

Table 2: Studies included for AUC meta-analysis.

Study name	Effect size	CI lower limit	CI upper limit	Weight
Chen et al[22]	0.92	0.84	1.01	16.75%
Nath et al[26]	0.97	0.95	0.99	19.85%
She et al[28]	0.81	0.74	0.88	18.24%
Pan et al[31]	0.94	0.85	1.03	16.31%
Shaheen et al[34]	0.73	0.56	0.9	11.32%
Baid et al[35]	0.8	0.73	0.87	17.54%

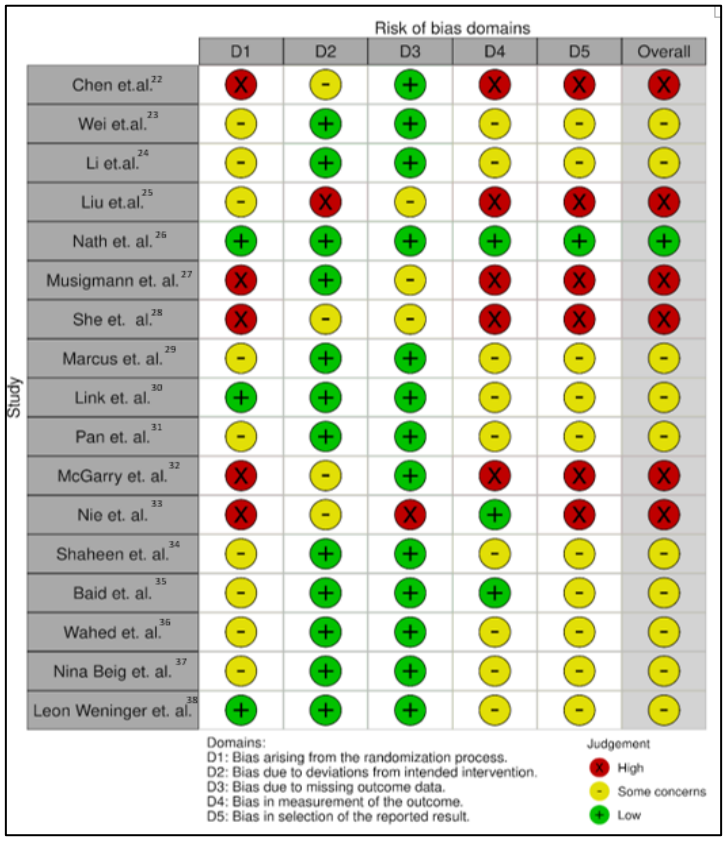

Figure 2: Traffic light plot showing the risk of bias assessment in selected studies.

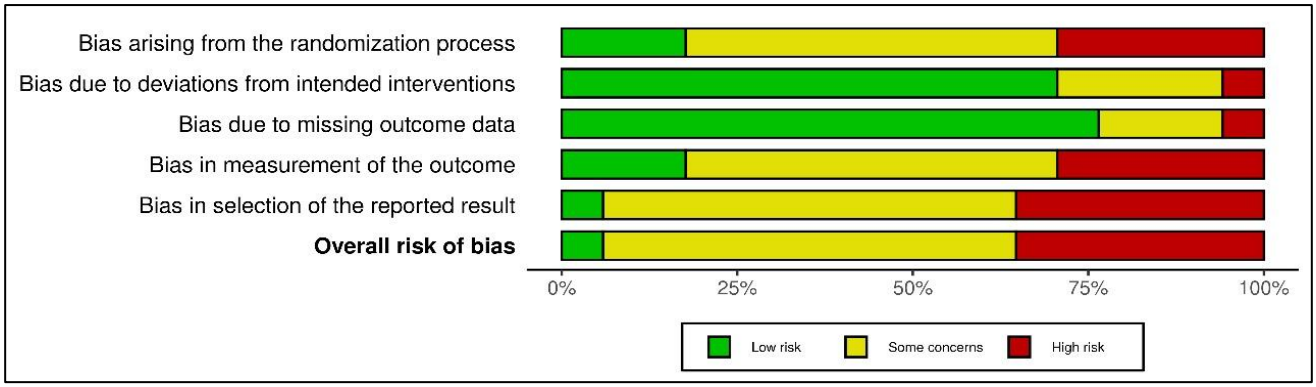

Figure 3: Risk of bias distribution across five domains (randomization, interventions, outcome data, outcome measurement, selection of reported result.

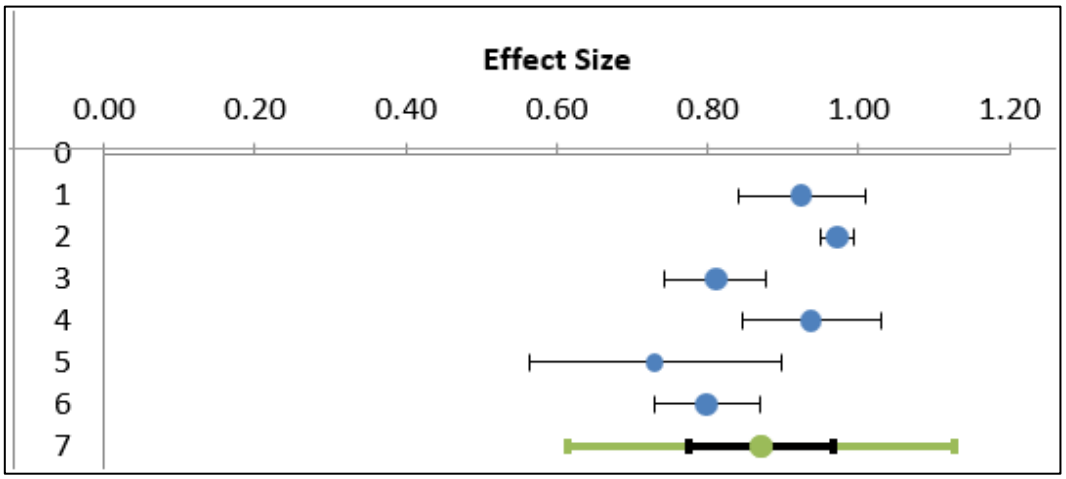

Figure 4: Forest plot illustrating AUC and 95% CI for included studies.

Heterogeneity

There is substantial heterogeneity across the included studies. Cochran's Q-statistic is 48.41 ($p<0.001$). This suggests true heterogeneity beyond random variation. The I^2 statistic is 89.67%. This suggests that approximately 89.67% of the total variation across studies was due to true heterogeneity rather than sampling error. This degree of heterogeneity is considered substantial, warranting the use of a random-effects model for pooling. The tau-squared (τ^2) value, representing the between-study variance, is 0.01, and the tau (τ) value is 0.09. This suggests low but non-negligible dispersion of effect sizes around the pooled estimate.

Assessment of publication bias

To evaluate the presence of publication bias among the included studies, a combination of visual and statistical approaches was employed.

Funnel plot (with trim-and-fill)

Figure 5 shows a funnel plot with trim-and-fill adjustment which showed moderately asymmetric, with more studies falling on one side. The funnel is slightly skewed to the right, which could mean possible small study effects.

Egger regression

To statistically examine funnel plot asymmetry and the presence of small-study effects, Egger's regression test was conducted.[42] The intercept estimate was-5.86 (standard error=3.96), with a 95% confidence interval of -16.04 to 4.33. While the negative intercept suggests a potential small-study effect, the confidence interval includes zero, and the test was not statistically significant ($t=-1.48$, $p=0.213$). This indicates no strong evidence of publication bias. Additionally, the slope estimate of the regression line was 1.46 (SE = 0.40, 95% CI: 0.43 to 2.50). This shows a consistent linear relationship between effect size and its standard error. This slope was also not significantly different from zero. This further supports the absence of asymmetry in the distribution of study results. Taken together, both the intercept and slope estimates from Egger's test provide no statistically significant evidence of publication bias in this meta-analysis.

While our results suggest low publication bias, these findings must be interpreted with caution because we had

a limited number of studies (n=6), which reduces the reliability of such assessments.

Subgroup analysis

To find out probable sources of heterogeneity, we conducted a subgroup analysis stratifying studies based on the type of model used for survival prediction. A random-effects model was applied with separate estimation of τ^2 within each subgroup.

The pooled effect size for DL-based studies was 0.81 (95% CI: 0.74-0.87), with no observed heterogeneity (I^2=0.0%). ML-based studies yielded a slightly higher pooled effect size of 0.92 (95% CI: 0.78-1.06), though with considerable heterogeneity (I^2=69.83%). The test for subgroup differences was statistically significant (Q=7.50, df=1, p=0.006) (Table 3). This indicates that model type significantly moderated the effect size. This subgroup variable accounted for approximately 61.93% of the between-study variability (pseudo-R^2) (Table 4). This indicates estimated average effect size and its dispersion across populations (Figure 6).

Table 3: Subgroup analysis based on type of model used i.e. DL and ML showing pooled effect size of 0.85 (95% CI: 0.74-0.87) and 0.92 (95% CI: 0.78-1.06) respectively.

Study name	Effect size	CI LL	CI UL	Weight	Q	P_Q	I^2	T^2	T	PI LL	PI UL
Chen et al[22]	0.81	0.74	0.9	58.61%							
Nath et al[26]	0.8	0.73	0.9	41.39%							
DL	0.81	0.74	0.9	57.00%	0.06	0.814	0%	0	0	0.74	0.87
Chen et al[22]	0.92	0.84	1	25.43%							
Nath et al[26]	0.97	0.95	1	37.83%							
Pan et al[31]	0.94	0.85	1	24.07%							
Shaheen et al[34]	0.73	0.56	0.9	12.66%							
ML	0.92	0.78	1.1	43%	9.94	0.019	69.83%	0	0.06	0.69	1.15
Combined effect size	0.86	0.71	1		48.4	0	89.67%	0.01	0.09	0.61	1.1

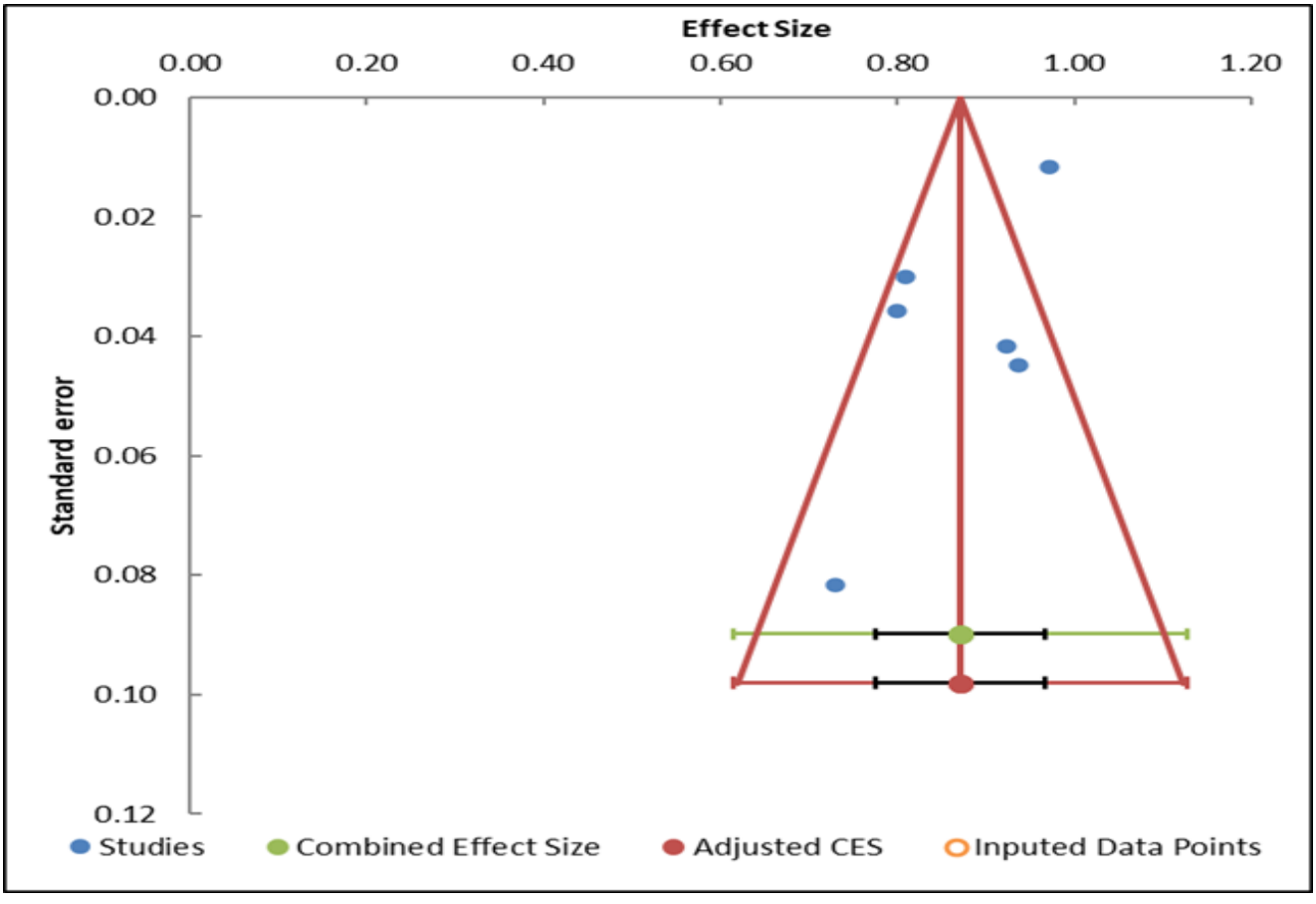

Figure 5: Funnel plot for assessment of publication bias.

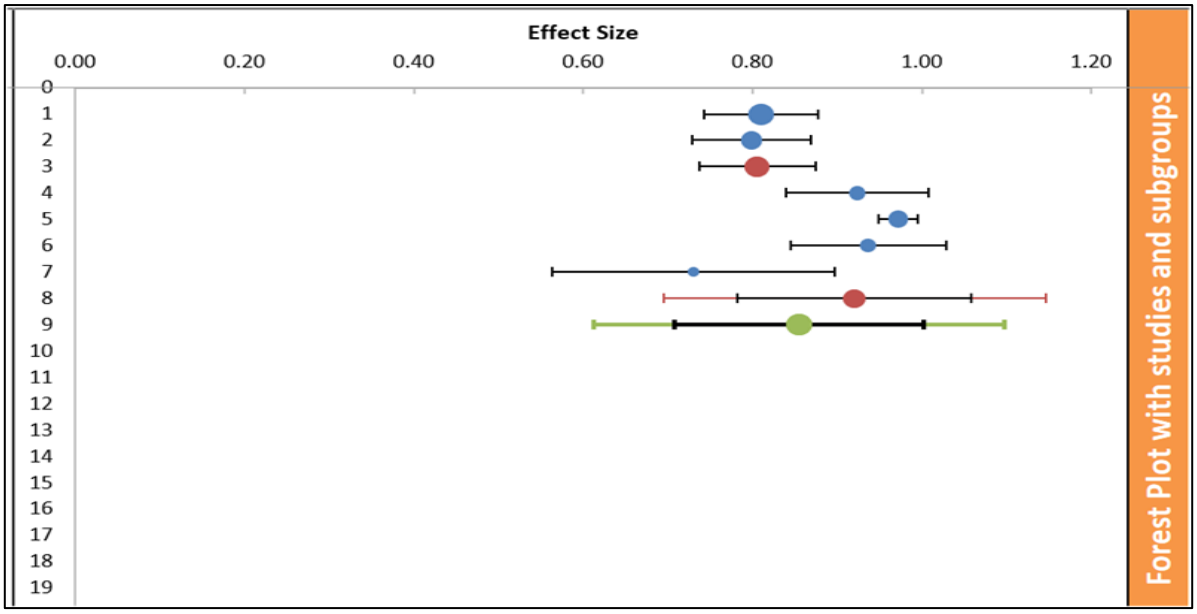

Figure 6: Forest plot showing effect sizes with studies and subgroups.

Table 4: Combined effect size, analysis of variance, pseudo R^2.

Variables	N		
Meta analysis model			
Between subgroup weighting	Random effects		
Within subgroup weighting	Random effects (Tau separate for subgroups)		
Confidence level	95%		
Combined effect size			
Effect size	0.86		
SE	0.06		
CI LL	0.71		
CI UL	1		
PI LL	0.61		
PI UL	1.1		
No. of included observations	83839		
No. of included studies	6		
No. of subgroups	2		
Analysis of variance	**Sum of squares (Q*)**	**Df**	**P**
Between/ model	7.5	1	0
Within/ residual	4.61	4	0
Total	12.11	5	0
Pseudo R^2	61.93%		

Pooled C-index

While 5 of the included studies report C-index for overall survival (OS) and PFS, the number of studies providing sufficient and comparable quantitative data for these outcomes is limited (n=3 for OS and n=2 for PFS). On qualitative analysis, Chen et al reported Harrell's C-index 0.847 with estimated SE 0.05839 for RSF; it used multiple models, best among them was RSF.[22] Li et al reported C-indices and CI for validation set: C-index=0.861, 95% CI=[0.760-0.963].[24] It used a multiparameter radiomic model. Liu et al reported C-index (Validation): 0.823.[25] It used the radiomic signature for PFS. Pan et al provided Harrell's C-index values with 95% confidence intervals for evaluating a radiomics-based ML model in predicting response to radiotherapy and overall survival in GBM patients.[31] Beig et al attempted to identify MRI surrogate markers of the tumor hypoxia pathway and assign an HES score using radiomics and predict the survivability of Glioblastoma patients.[37] They reported C index 0.74 (radiomic features only) and 0.83 (radiomic+clinical), hazard ratio STS vs. LTS: HR=0.9722-1.6271; MTS vs. LTS: HR=0.8443-1.5108, p value STS vs. LTS: p=0.0056, MTS vs. LTS: $p=9.21\times10^{6}$.

DISCUSSION

Clinical relevance

AI devices must meet regulatory standards (e.g., FDA, CE marking), including validation studies, safety assessments, and post-market surveillance in order to deliver effective predictive outcomes. Overall, the available data suggests promising performance of AI models, though validation remains limited.

Future directions

Future studies must focus on enhancing the methodological rigor by conducting prospective studies with multicenter collaborations to improve generalizability and reduce selection bias by increasing the dataset. Evaluation of AI models should be done in clinical workflows to assess their impact on decision-making, patient outcomes, and cost-effectiveness. Expansion of research to paediatric populations and understudied tumor types currently excluded from most studies should be performed. Validation of models should be done in low-resource settings using portable imaging modalities (for example- low-field MRI) and address algorithmic biases in underrepresented ethnic groups for better acceptance.

Strengths and limitations

A key strength and novel aspect of our systematic review and meta-analysis is its inclusive approach where we have evaluated multiple adult tumor types (glioma, meningioma, astrocytoma etc). To our knowledge, this is among the first meta-analyses to quantitatively synthesize AI model performance for prognosis across multiple brain tumor histologies, rather than restricting analysis to a single subtype.

The overall performance by AI models in predicting survival outcomes for brain tumor patients was positively encouraging. Our meta-analysis found a pooled AUC of 0.88 which suggests that these models have good performance in distinguishing in patients with better and worse prognosis. Additionally, many studies have reported high C-index values (often above 0.80) suggesting that models were generally good at predicting patient survival.

Nevertheless, we acknowledge a few limitations that should be considered when interpreting our results. A key limitation of this review was the limited number of studies reporting comparable AUC and C-index for survival related outcomes such as OS and PFS which makes it prone to high uncertainty, substantial influence from individual studies and inability to assess heterogeneity or publication bias meaningfully. Overfitting Bias due to small sample sizes could be present in the evaluation of the different model's performance, with an estimated impact of around 15-25%.

Finally, we would like to acknowledge that our study does not provide definitive evidence to warrant an immediate change in current standard of care or directly challenge existing guidelines. However, our results do offer valuable insights to inform patients about their predicted prognosis and contributes to development of patient specific treatment plan.

CONCLUSION

This systematic review and meta-analysis highlight the impact of AI in predicting overall survival and prognosis in patients with brain tumor. Our study reports with significant accuracy that AI models can be used effectively for prediction of prognosis in case of brain tumors. The potential clinical benefits these AI models could offer would include: earlier and more accurate prognosis due to the ability to identify subtle imaging features leading to faster initiation of treatment response. Personalised treatment planning by predicting survival and tumour aggressiveness would help tailor surgery, chemotherapy, and radiotherapy strategies. It will reduce diagnostic burden by triaging urgent cases, flagging high-risk tumours, and reducing inter-observer variability. This will lead to efficient resource utilization as it would automate survival outcomes allowing specialists to allocate more time to complex cases.

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REFERENCES

1. Louis DN, Ohgaki H, Wiestler OD, Cavenee WK. Overview of primary brain tumors: pathologic classification, epidemiology, molecular biology, and prognostic markers. Hematol Oncol Clin North Am. 2012;26(4):715-32.
2. Nejo T, Mende A, Okada H. The current state of immunotherapy for primary and secondary brain tumors: similarities and differences. Jpn J Clin Oncol. 2020; 50(11):1231-45.
3. Louis DN, Perry A, Wesseling P, Brat DJ, Cree IA, Figarella-Branger D, et al. The 2021 WHO classification of tumors of the central nervous system: a summary. Acta Neuropathol. 2021;142(1):11-28.
4. Global Burden of Disease Cancer Collaboration. Global, regional, and national burden of brain and other CNS cancers, 1990-2019: A systematic analysis for the Global Burden of Disease Study 2019. Front Neurol. 2022;13:950725.
5. Ostrom QT, Cioffi G, Gittleman H. CBTRUS statistical report: Primary brain and other central nervous system tumors diagnosed in the United States in 2015-2019. Neuro Oncol. 2022;24(5):v1-95.
6. Sung H, Ferlay J, Siegel RL, Laversanne M, Soerjomataram I, Jemal A et al. Global cancer statistics 2020: GLOBOCAN estimates of incidence

and mortality worldwide for 36 cancers in 185 countries. CA Cancer J Clin. 2021;71(3):209-49.
7. Ostrom QT, Patil N, Cioffi G, Waite K, Kruchko C, Barnholtz-Sloan JS. CBTRUS statistical report: Primary brain and other central nervous system tumors diagnosed in the United States in 2013-2017. Neuro Oncol. 2020;22(2):iv1-96.
8. Nair M, Varghese C, Swaminathan R. Cancer: Current Scenario, Intervention Strategies and Projections for 2015. NCMH Background Papers. 2015.
9. Yeole BB. Trends in the brain cancer incidence in India. Asian Pac J Cancer Prev. 2008;9:267-70.
10. Mayo Clinic. Pituitary tumors-Symptoms and causes. Mayo Clinic; 2023. Available at: https://www.mayoclinic.org/diseases-conditions/pituitary-tumors/symptoms-causes/syc-20350548. Accessed on 15 November 2025.
11. Darnell RB, Posner JB. Paraneoplastic syndromes involving the nervous system. N Engl J Med. 2003;349(16):1543-1554.
12. American Academy of Family Physicians. Primary brain tumors in adults. Am Fam Physician. 2008;77(10):1423-30.
13. Rahman AMJZ, Gupta M, Aarathi S, Mahesh TR, Vinoth Kumar V, Yogesh Kumaran S, et al. Advanced AI-driven approach for enhanced brain tumor detection from MRI images utilizing EfficientNetB2 with equalization and homomorphic filtering. BMC Med Inform Decis Mak. 2024;24:113.
14. Rauschenbach L, Kolbe P, Engel A, Ahmadipour Y, Oppong MD, Santos AN, et al. Predictors and surgical outcome of hemorrhagic metastatic brain malignancies. J Neurooncol. 2024;169(1):165-73.
15. Cacho-Díaz B, Lorenzana-Mendoza NA, Chávez-Hernandez JD, González-Aguilar A, Reyes-Soto G, Herrera-Gómez Á. Clinical manifestations and location of brain metastases as prognostic markers. Curr Probl Cancer. 2019;43(4):312-23.
16. Cagney DN, Martin AM, Catalano PJ, Redig AJ, Lin NU, Lee EQ, et al. Incidence and prognosis of patients with brain metastases at diagnosis of systemic malignancy: a population-based study. Neurooncol. 2017;19(11):1511-21.
17. Arvanitis CD, Ferraro GB, Jain RK. The blood–brain barrier and blood–tumour barrier in brain tumours and metastases. Nat Rev Cancer. 2020;20(1):26-41.
18. Mustaf M, Sali AF, Illzam EM, Sharifa AM, Nang MK. Brain cancer: Current concepts, diagnosis and prognosis. IOSR J Dent Med Sci. 2018;17(3):41-6.
19. Michel A, Dinger TF, Santos AN, Pierscianek D, Darkwah Oppong M, Ahmadipour Y, et al. Time interval between the diagnosis of breast cancer and brain metastases impacts prognosis after metastasis surgery. J Neurooncol. 2022;159(1):53-63.
20. GBD 2016 Brain and Other CNS Cancer Collaborators. Global, regional, and national burden of brain and other CNS cancer, 1990-2016: a systematic analysis for the Global Burden of Disease Study 2016. Lancet Neurol. 2019;18(4):376-93.
21. Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, et al. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. BMJ. 2021;372:n71.
22. Chen H, Li C, Zheng L, Lu W, Li Y, Wei Q. A machine learning-based survival prediction model of high grade glioma by integration of clinical and dose-volume histogram parameters. Cancer Med. 2021;10(8):2774-86.
23. Wei J, Yang G, Hao X, Gu D, Tan Y, Wang X, et al. A multi-sequence and habitat-based MRI radiomics signature for preoperative prediction of MGMT promoter methylation in astrocytomas with prognostic implication. Eur Radiol. 2019;29(2):877-88.
24. Li Y, Bao L, Yang C, Deng Z, Zhang X, Xu P, et al. A multiparameter radiomic model for accurate prognostic prediction of glioma. MedComm-Future Med. 2023;2(2):e41.
25. Liu X, Li Y, Qian Z, Sun Z, Xu K, Wang K, et al. A radiomic signature as a non-invasive predictor of progression-free survival in patients with lower-grade gliomas. NeuroImage Clin. 2018;20:1070-7.
26. Nath G, Coursey A, Li Y, Prabhu S, Garg H, Halder SC, et al. An interactive web-based tool for predicting and exploring brain cancer survivability. Healthc Anal. 2023;3:100132.
27. Musigmann M, Akkurt BH, Krähling H, Brokinkel B, Spille DC, Stummer W, et al. Analysis of the Predictability of Postoperative Meningioma Resection Status Based on Clinical Features. Cancers. 2024;16:22.
28. She Z, Marzullo A, Destito M, Spadea MF, Leone R, Anzalone N, et al. Deep learning-based overall survival prediction model in patients with rare cancer: a case study for primary central nervous system lymphoma. Int J Comput Assist Radiol Surg. 2023;18(10):1849-56.
29. Marcus AP, Marcus HJ, Camp SJ, Nandi D, Kitchen N, Thorne L. Improved Prediction of Surgical Resectability in Patients with Glioblastoma using an Artificial Neural Network. Sci Rep. 2020;10(1):5143.
30. Link KE, Schnurman Z, Liu C, Kwon YJF, Jiang LY, Nasir-Moin M, et al. Longitudinal deep neural networks for assessing metastatic brain cancer on a large open benchmark. Nat Commun. 2024;15(1):8170.
31. Pan ZQ, Zhang SJ, Wang XL, Jiao YX, Qiu JJ. Machine Learning Based on a Multiparametric and Multiregional Radiomics Signature Predicts Radiotherapeutic Response in Patients with Glioblastoma. Behav Neurol. 2020;2020(1):1712604.
32. McGarry SD, Hurrell SL, Kaczmarowski AL, Cochran EJ, Connelly J, Rand SD, et al. Magnetic Resonance Imaging-Based Radiomic Profiles Predict Patient Prognosis in Newly Diagnosed Glioblastoma Before Therapy. Tomography. 2016;2(3):223-8.
33. Nie D, Lu J, Zhang H, Adeli E, Wang J, Yu Z, et al. Multi-Channel 3D Deep Feature Learning for Survival Time Prediction of Brain Tumor Patients

Using Multi-Modal Neuroimages. Sci Rep. 2019;9:1103.
34. Baid U, Rane SU, Talbar S, Gupta S, Thakur MH, Moiyadi A, et al. Overall Survival Prediction in Glioblastoma With Radiomic Features Using Machine Learning. Front Comput Neurosci. 2020;14:61.
35. Shaheen A, Bukhari ST, Nadeem M, Burigat S, Bagci U, Mohy-ud-Din H. Overall Survival Prediction of Glioma Patients With Multiregional Radiomics. Front Neurosci. 2022;16:911065.
36. Wahed SA, Wahed MA. Predicting Post-Surgical Complications using Machine Learning Models for Patients with Brain Tumors. Int J Open Inf Technol. 2025;13(4):43-8.
37. Beig N, Patel J, Prasanna P, Hill V, Gupta A, Correa R, et al. Radiogenomic analysis of hypoxia pathway is predictive of overall survival in Glioblastoma. Sci Rep. 2018;8(1):7.
38. Weninger L, Haarburger C, Merhof D. Robustness of Radiomics for Survival Prediction of Brain Tumor Patients Depending on Resection Status. Front Comput Neurosci. 2019;13:73.
39. Moons KGM, Damen JAA, Kaul T, Hooft L, Navarro CA, Dhiman P, et al. PROBAST+AI: an updated quality, risk of bias, and applicability assessment tool for prediction models using regression or artificial intelligence methods. BMJ. 2025;388:e082505.
40. Suurmond R, van Rhee H, Hak T. Introduction, comparison, and validation of Meta-Essentials: A free and simple tool for meta-analysis. Res Synth Methods. 2017;8(4):537-53.
41. Duval S, Tweedie R. Trim and fill: A simple funnel-plot-based method of testing and adjusting for publication bias in meta-analysis. Biometrics. 2000;56(2):455-63.
42. Egger M, Smith GD, Schneider M, Minder C. Bias in meta-analysis detected by a simple, graphical test. BMJ. 1997;315(7109):629-34.
43. Begg CB, Mazumdar M. Operating characteristics of a rank correlation test for publication bias. Biometrics. 1994;50(4):1088-101.
44. Rosenthal R. The file drawer problem and tolerance for null results. Psychol Bull. 1979;86(3):638-41.
45. McGuinnes LA. "robvis: An R package and web application for visualizing risk of bias assessments. 2019.

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APPENDIX A

A1: Hanley-McNeil formula

$SE=\sqrt{[AUC(1-AUC) + (n_1-1)(Q_1-AUC^2)+(n_0-1)(Q_2-AUC^2)]/n0n1}$

n_1=number of positive cases

n_0=number of negative cases

AUC = area under ROC curve

Q_1=AUC/2-AUC

$Q_2=2\times AUC^2/1+AUC$

A2: Hanley and McNeil approximation for standard error of AUC

$SE=\sqrt{[AUC (1-AUC)/ n]}$

A3: Hanley and McNeil's simplified formula for c-index

$SE (C)=\sqrt{[c (1-c)/ N]}$

C=Concordance index,

N=number of independent comparable pairs

Assumption

Independent survival pairs and uniform censoring, as exact comparable pairs were unavailable in most included studies.

A4: Estimation of standard error from confidence interval

SE=[Upper CI-lower CI]/2×Z

Z=z-score for the 95% confidence interval i.e. 1.96

SE=[Upper CI-lower CI]/2×1.96