

Texas Society of Neuroradiology (TSNR)

Scientific Abstract

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MRI Radiomics for Survival Prediction in Brain Metastases: A Machine Learning Analysis

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Purpose

Background: Brain metastases (BM) carry poor prognosis, and accurate survival prediction is critical for treatment planning. Radiomics offers a means of extracting high-dimensional imaging biomarkers, but its prognostic utility in BM remains unclear.

Purpose: To evaluate whether MRI-derived radiomic features can improve survival prediction in patients with brain metastases.

Materials and Methods

This retrospective study used the public Pretreat-MetsToBrain-Masks MRI dataset (N=200 patients, 975 enhancing lesions) with multisequence MRI and tumor segmentations. 502 Radiomic features were extracted from T1 pre-contrast, T1 post-contrast, T2-weighted, FLAIR, and T1 subtraction images. Five machine learning survival models (XGBoost-Cox, Coxnet, Ridge-Cox, Random Survival Forest [RSF], Survival SVM) were trained on an 80% training set and evaluated on a 20% held-out test set. The primary outcome was overall survival; performance was assessed by Harrell's C-index and time-dependent AUC.

Results

The best-performing model (Survival SVM) achieved a test-set C-index of 0.65 (95% CI: 0.47-0.81) and a mean time-dependent AUC of 0.65. Ridge-Cox and RSF yielded similar performance (C-index 0.61



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and 0.60). XGB-Cox and Coxnet performed near chance (C-index 0.51 and 0.48). No model demonstrated statistically significant Kaplan-Meier separation between high- and low-risk groups.

Conclusion

MRI radiomic features yielded limited prognostic utility for overall survival in a heterogeneous brain metastasis cohort. These findings highlight the challenges of survival modeling based solely on intracranial imaging features and highlight the need for integrative prognostic approaches combining imaging, clinical, and systemic disease variables.

References

None

Figures

Table 1. Baseline cohort characteristics stratified by survival status

Characteristic	Overall (N = 200)	Alive (censored, n = 125)	Death (n = 75)	p-value
Demographics				
Age, years	65 [55-73]	65 [55-73]	65 [56-73]	0.838
Sex - male	74 (37.2)	48 (38.4)	26 (35.1)	0.757
female	125 (62.8)	77 (61.6)	48 (64.9)	
Race -White	172 (86.9)	107 (85.6)	65 (89.0)	0.415
Black/African American	9 (4.5)	5 (4.0)	4 (5.5)	
Asian/Pacific Islander	9 (4.5)	8 (6.4)	1 (1.4)	
Unknown	8 (4.0)	5 (4.0)	3 (4.1)	
Ethnicity - Hispanic/Latino	6 (3.0)	5 (4.0)	1 (1.4)	0.415
Unknown	193 (97.0)	120 (96.0)	73 (98.6)	
Smoking, pack-years	9.8 [0-24]	6.8 [0-20]	15 [0-30]	0.033
Imaging features				
Enhancing lesions, n	2 [1-5]	2 [1-5]	3 [1-6]	0.380
Necrotic lesions, n	1 [0-2]	1 [0-2]	1 [0.2-2]	0.372
Edema lesions, n	2 [1-4]	2 [1-4]	2 [1-5]	0.492
Enhancing volume, cm ³	3.2 [0.7-10.5]	4.2 [0.7-12.3]	1.8 [0.6-6.3]	0.070



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Necrosis volume, cm³	0.6 [0-3.3]	0.7 [0-3.3]	0.1 [0-4.1]	0.639
Edema volume, cm³	17.5 [0.8-89.8]	35.8 [0.8-98.0]	11.1 [0.9-52.2]	0.175
Necrosis/enhancing ratio	0.1 [0-0.3]	0.1 [0-0.3]	0.1 [0-0.3]	0.557
Edema/enhancing ratio	3.0 [1.2-7.8]	2.9 [1.3-7.6]	3.0 [1.0-8.8]	0.828
Primary tumor type				0.410
Breast	26 (13.1)	19 (15.2)	7 (9.5)	
Gastrointestinal	14 (7.0)	7 (5.6)	7 (9.5)	
Small cell lung	17 (8.5)	11 (8.8)	6 (8.1)	
Non-small cell lung	86 (43.2)	49 (39.2)	37 (50.0)	
Melanoma	40 (20.1)	29 (23.2)	11 (14.9)	
Renal cell carcinoma	16 (8.0)	10 (8.0)	6 (8.1)	
Other	0 (0.0)	0 (0.0)	0 (0.0)	
Disease distribution				
Extracranial metastasis - yes	95 (48.2)	57 (46.0)	38 (52.1)	0.498
Infratentorial disease - yes	91 (45.7)	56 (44.8)	35 (47.3)	0.846
Survival				
Overall survival, months	16 [7-32.5]	19 [8-46]	12.5 [6.2-24]	0.003

Table 2. Radiomic feature counts per sequence and preprocessing stage

Stage	T1 post-contrast (T1c)	T1 pre-contrast (T1n)	T2-weighted (T2w)	FLAIR	Subtraction (T1sub)	Other	Total
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Preprocessed	93	93	93	93	93	37	502
Post-near-zero variance	93	93	93	93	93	37	502
Scaled	93	93	93	93	93	37	502
Final (correlation-pruned, $R \geq 0.8$)	29	27	21	25	8	23	133

Table 3. Performance of survival models on the test set

Model	C-index (95% CI)	tdAUC (mean)
SurvSVM	0.65 (0.47-0.81)	0.65
Ridge-Cox	0.61 (0.44-0.77)	0.63
Random Survival Forest	0.60 (0.40-0.80)	0.57
XGB-Cox	0.51 (0.36-0.70)	0.51
Coxnet	0.48 (0.32-0.63)	0.48

Table 4. Top radiomic features selected by each survival model

Model	Top features (abbrev.)
SurvSVM	T1C GLCM InverseVariance; T2F GLCM DifferenceVariance; T1N GLDM DependenceVariance; T2F First-order IQR; T1N GLCM JointEntropy



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RSF	T1C GLCM Autocorrelation; T1C First-order Skewness; T1N GLCM JointEnergy; T2F GLSZM LargeAreaLowGrayLevelEmphasis; Necrosis volume
XGB-Cox	T1C GLCM JointEntropy; T2W First-order Median; T1N GLDM GrayLevelNonUniformity; T1sub GLCM JointEnergy; T2F First-order Entropy
Ridge-Cox	T2F First-order Range/Minimum/Maximum; Race indicators
Coxnet	T1N GLCM Id/Correlation/ClusterShade; T1sub GLRLM LongRun(High)GrayLevelEmphasis

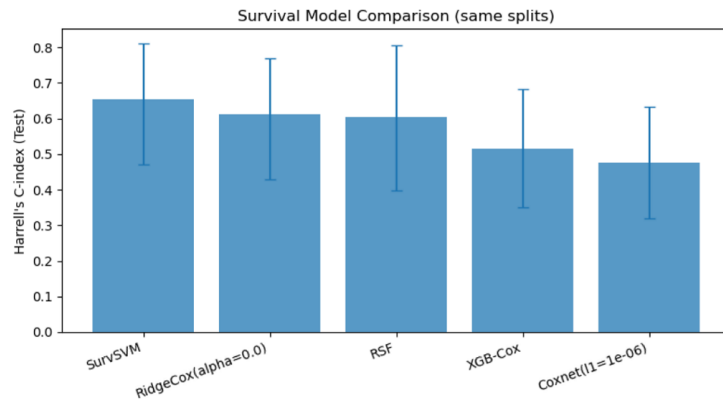


Figure 1. Comparison of survival model discrimination on the held-out test set. Bars represent Harrell's concordance index (C-index) with 95% confidence intervals.



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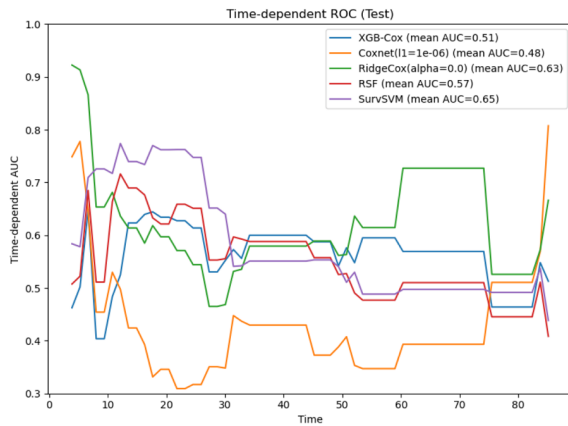


Figure 2. Time-dependent receiver operating characteristic (ROC) curves for the held-out test set. The plot displays time-dependent area under the curve (AUC) across follow-up for five survival learners: XGB-Cox, Coxnet, Ridge-Cox, Random Survival Forest (RSF), and Survival Support Vector Machine (SurvSVM).

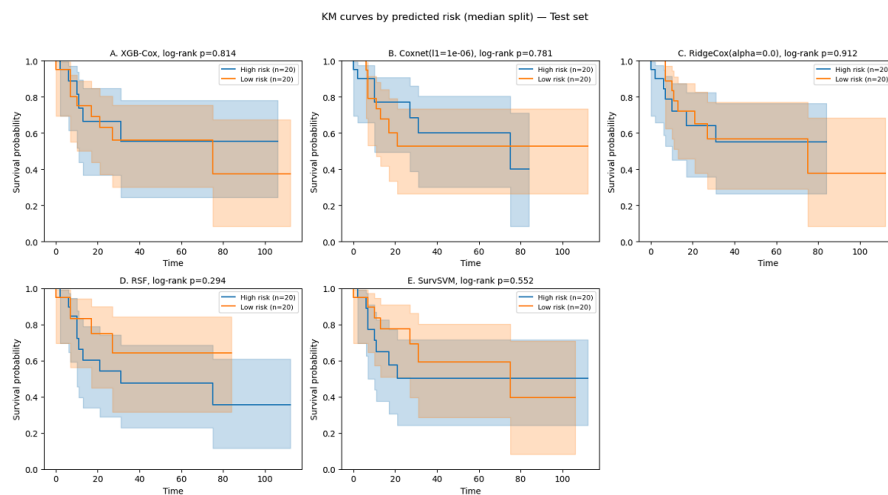


Figure 3. Kaplan-Meier curves stratified by predicted risk (median split) on the test set for (A) XGB-Cox, (B) Coxnet, (C) Ridge-Cox, (D) RSF, and (E) SurvSVM. Shaded areas indicate 95% confidence intervals; p-values from log-rank test.



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