



## Texas Society of Neuroradiology (TSNR)

### Scientific Abstract

2026 Annual Meeting – Dallas, TX

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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.

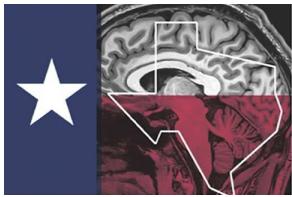
*Purpose:* To evaluate whether MRI-derived radiomic features can improve survival prediction in patients with brain metastases.

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



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<b>Necrosis volume, cm<sup>3</sup></b>	0.6 [0-3.3]	0.7 [0-3.3]	0.1 [0-4.1]	0.639
<b>Edema volume, cm<sup>3</sup></b>	17.5 [0.8-89.8]	35.8 [0.8-98.0]	11.1 [0.9-52.2]	0.175
<b>Necrosis/enhancing ratio</b>	0.1 [0-0.3]	0.1 [0-0.3]	0.1 [0-0.3]	0.557
<b>Edema/enhancing ratio</b>	3.0 [1.2-7.8]	2.9 [1.3-7.6]	3.0 [1.0-8.8]	0.828
<b>Primary tumor type</b>				0.410
<b>Breast</b>	26 (13.1)	19 (15.2)	7 (9.5)	
<b>Gastrointestinal</b>	14 (7.0)	7 (5.6)	7 (9.5)	
<b>Small cell lung</b>	17 (8.5)	11 (8.8)	6 (8.1)	
<b>Non-small cell lung</b>	86 (43.2)	49 (39.2)	37 (50.0)	
<b>Melanoma</b>	40 (20.1)	29 (23.2)	11 (14.9)	
<b>Renal cell carcinoma</b>	16 (8.0)	10 (8.0)	6 (8.1)	
<b>Other</b>	0 (0.0)	0 (0.0)	0 (0.0)	
<b>Disease distribution</b>				
<b>Extracranial metastasis - yes</b>	95 (48.2)	57 (46.0)	38 (52.1)	0.498
<b>Infratentorial disease - yes</b>	91 (45.7)	56 (44.8)	35 (47.3)	0.846
<b>Survival</b>				
<b>Overall survival, months</b>	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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<b>Preprocessed</b>	93	93	93	93	93	37	502
<b>Post-near-zero variance</b>	93	93	93	93	93	37	502
<b>Scaled</b>	93	93	93	93	93	37	502
<b>Final (correlation-pruned, R ≥ 0.8)</b>	29	27	21	25	8	23	133

**Table 3. Performance of survival models on the test set**

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

**Table 4. Top radiomic features selected by each survival model**

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



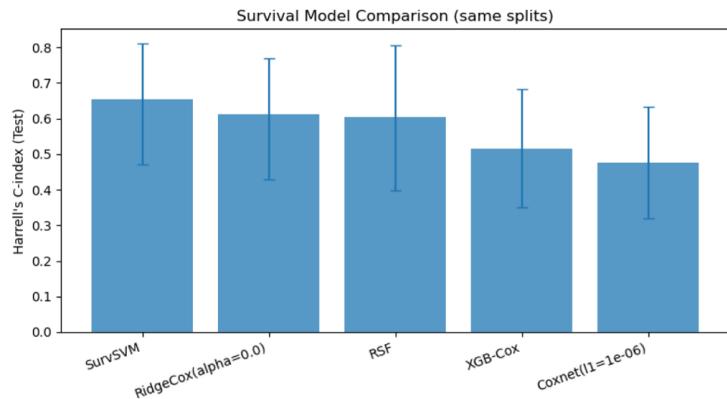
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<b>RSF</b>	T1C GLCM Autocorrelation; T1C First-order Skewness; T1N GLCM JointEnergy; T2F GLSZM LargeAreaLowGrayLevelEmphasis; Necrosis volume
<b>XGB-Cox</b>	T1C GLCM JointEntropy; T2W First-order Median; T1N GLDM GrayLevelNonUniformity; T1sub GLCM JointEnergy; T2F First-order Entropy
<b>Ridge-Cox</b>	T2F First-order Range/Minimum/Maximum; Race indicators
<b>Coxnet</b>	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.

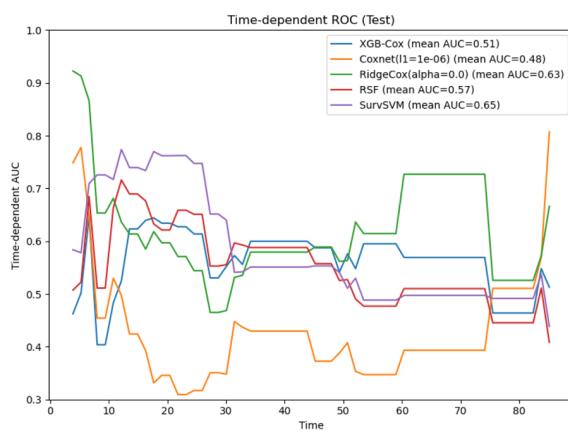


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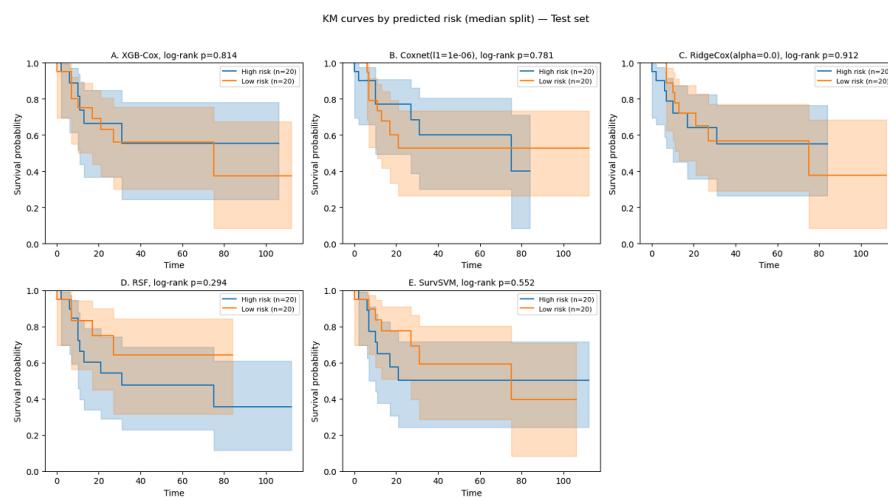
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**Figure 2.** Time-dependent receiver operating characteristic (ROC) curves for the held-out test set. The plot displays time-dependent area under the curve (AUC) across follow-up for five survival learners: XGB-Cox, Coxnet, Ridge-Cox, Random Survival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