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Introduction

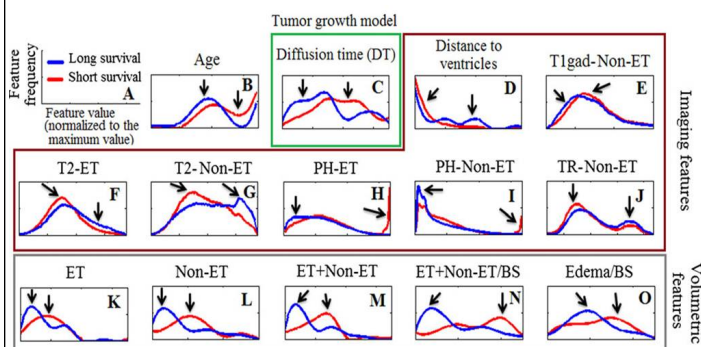
- Several studies have examined correlates between imaging features of neoplasm and patient survival or tumor genetic composition; however, few models have been robust enough to enter clinical practice.
- We used advanced pattern analysis and machine learning to identify a combination of imaging features on magnetic resonance (MR) images to predict overall survival and molecular subtype in patients with glioblastoma (GB).

Methods

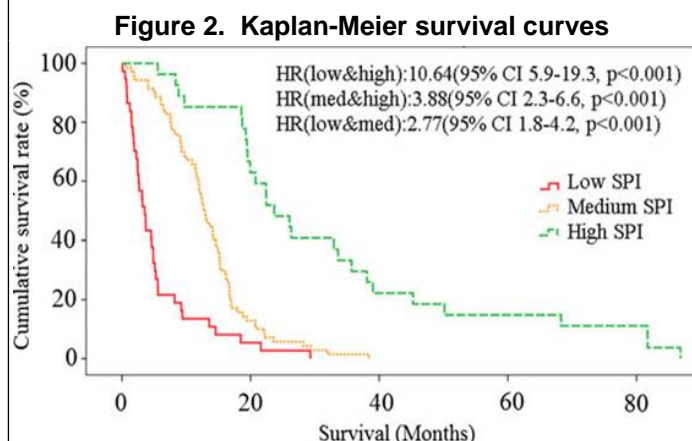
- Imaging features were extracted from structural, diffusion, and perfusion MR images at time of diagnosis in a cohort of GB patients.
- Machine learning was used to examine multiple imaging features simultaneously to determine which set of features was most predictive of survival, and, in a separate model, of molecular subtype.

Results

Figure 1. Histograms display the distribution of features most predictive of survival



The figures show the relationship between the value of each feature (x-axis) and frequency of each feature (y-axis) in short (red) and long (blue) survival. ET = enhancing tumor, Non-ET = non-enhancing core of tumor, BS = brain size, TR = trace, PH = peak height of perfusion signal, DT = diffusion time based on a biophysical tumor model.



Actual survival on x-axis is compared among each of the three survival groups based on predictions generated by the survival prediction index (SPI). Low survival = < 6 months, medium survival = 6-18 months, high survival = > 18 months.

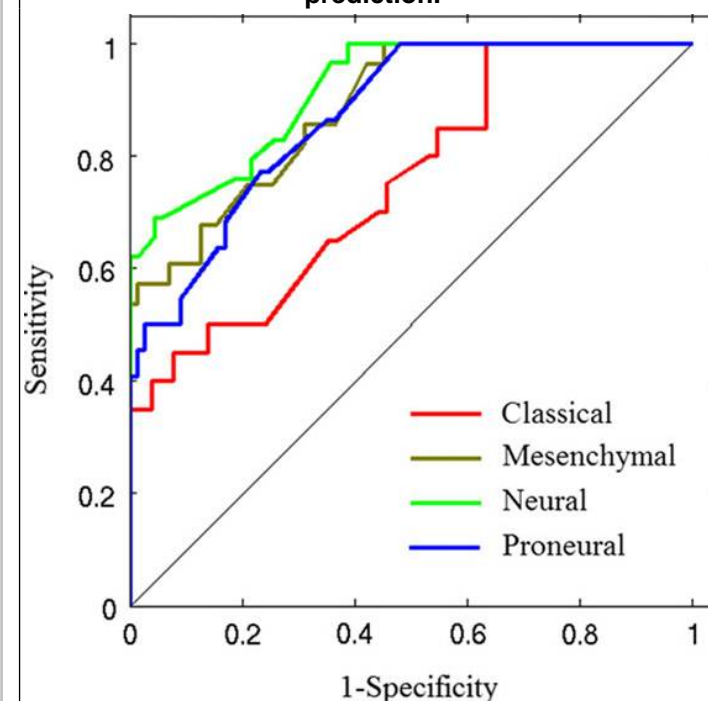
- Constellations of imaging markers related to infiltration and diffusion of tumor cells, microvasculature, and blood-brain barrier compromise were predictive of short survival.

Table 1.

	Study (n)	Accuracy (%)	AUC	
Survival	<6 mo	Retrospective (27)	87.62	0.87
	Prospective (11)	82.76	0.85	
>18 mo	Retrospective (29)	88.57	0.91	
	Prospective (7)	83.33	0.84	
6-18 mo	Retrospective (49)	79.05	N/A	
	Prospective (11)	87.5	N/A	
Overall	Retrospective (105)	77.14	N/A	
	Prospective (29)	79.17	N/A	
Tumor subtype	Proneural (22)	85.86	0.87	
	Neural (29)	87.88	0.92	
	Mesenchymal (28)	83.84	0.89	
	Classical (20)	84.85	0.75	
Overall (99)	75.76	N/A		

Accuracy of survival & molecular subtype predictions.

Figure 3. ROC curves for each GB molecular subtype prediction.



ROC curves are compared to chance (the diagonal line). AUC is shown in Table 1.

Conclusions

- Unlike prior studies, we analyzed the entirety of imaging data in an integrative fashion, leveraging the power of pattern analysis and machine learning to predict survival and molecular subtype with high accuracy and reproducibility in GB.
- Our non-invasive models utilize multi-parametric imaging obtained routinely for GB patients, making it readily translatable to the clinic.

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