

# Novel ML-based Prognostic Subgrouping of Glioblastoma: ReSPOND 2022 model

Case ID: upenn-gbm\_006

## **This report includes the following:**

1. ML results and flagged features
2. Snapshots of the preprocessed images with brain mask. Users should review these images to approve the quality of the preprocessing.
3. Snapshots of the preprocessed images with tumor segmentation. Users should review these images to approve the quality of the segmentation.
4. Overall Survival Map (OSM) atlas
5. Extracted feature values along with value ranges from the ReSPOND cohort. Users should proceed with caution if the values are flagged to be lower or higher

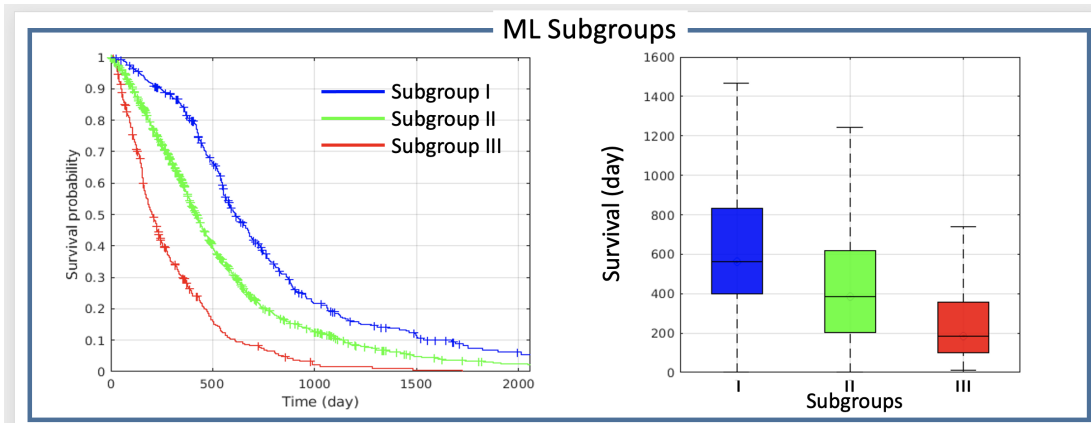
## **Disclaimers:**

1. This software has been designed for research purposes only and has neither been reviewed nor approved for clinical use by the Food and Drug Administration (FDA) or by any other federal/state agency.
2. This code (excluding dependent libraries) is governed by the license provided in <https://www.med.upenn.edu/sbia/software-agreement.html> unless otherwise specified.
3. This paper is currently under review by *Nature Medicine* (reference number: NMED-A124673)

# 1. ML results and flagged features

## Subgroup: II

The figures below show the survival distribution for the subgroups I,II,III from the ReSPOND 2022 cohort (n=2293). The left panel shows the Kaplan-Meier survival curves. The right panel shows boxplots of the subgroups versus patient survival. On each box, the central line indicates the median, and the bottom and top edges indicate the 25th and 75th percentiles, respectively. The whiskers extend to the most extreme data points not considered outliers. Please refer to the publication for more details [Nature Medicine reference number: NMED-A124673]



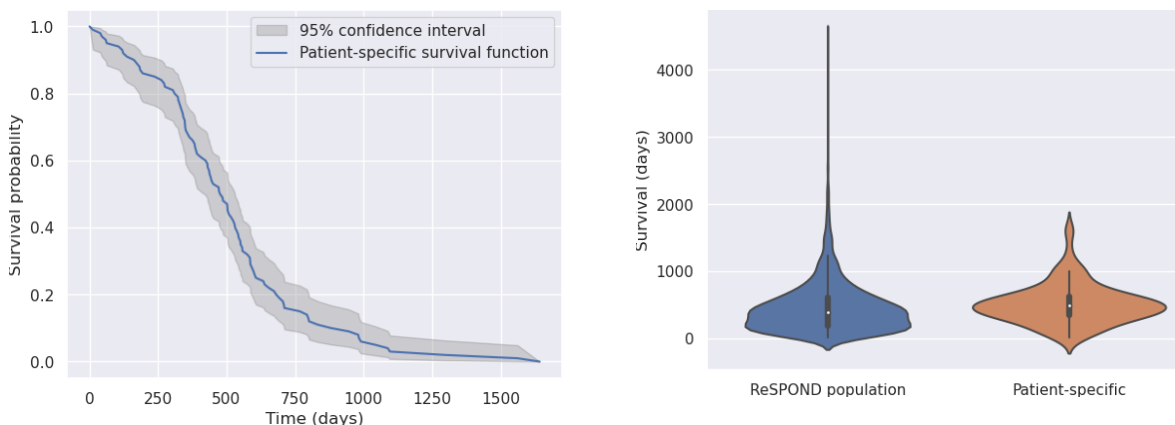
## Features outside of the ReSPOND range:

If any features are listed here, this indicates that these features were outside of the typical range we've seen in the ReSPOND cohort. Users should proceed with caution if this is the case.

None

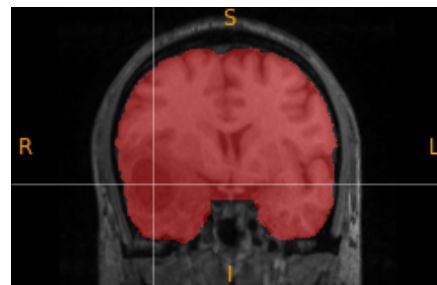
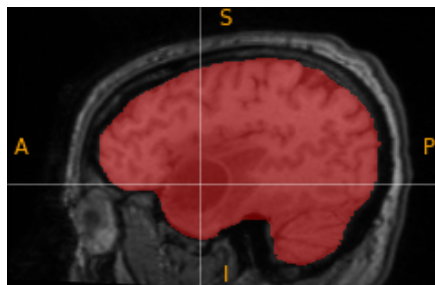
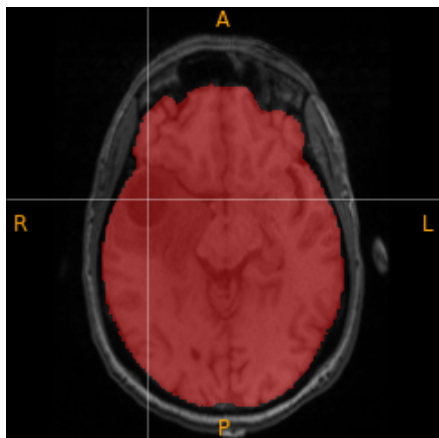
## Personalized survival estimate:

The figures below show the survival distribution for a patient-matched subset of the ReSPOND cohort. The subset is made up of 100 patients with the nearest SPI values to the user-provided patient. The left panel shows the Kaplan-Meier survival curve with 95% confidence interval. The right panel shows violin plots of patient survival for the overall ReSPOND cohort and patient-matched subset. On each box, the central point indicates the median, and the bottom and top edges indicate the 25th and 75th percentiles, respectively. The whiskers extend to the most extreme data points not considered outliers.

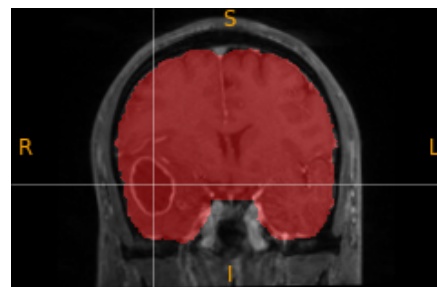
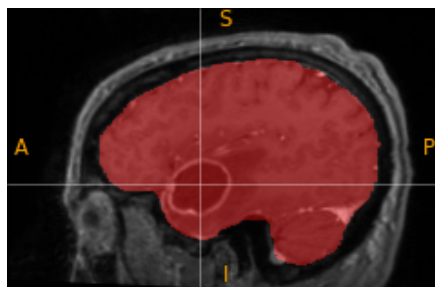
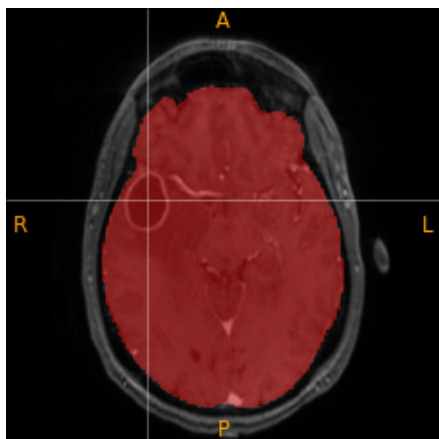


2. Preprocessed images and brain mask (shown in red). All 3D images can be found in the Results folder for further evaluation.

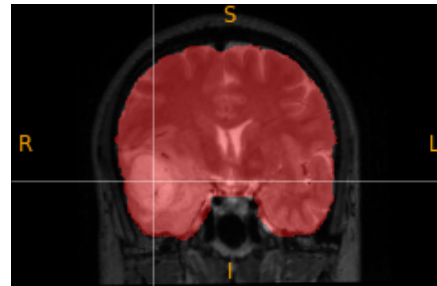
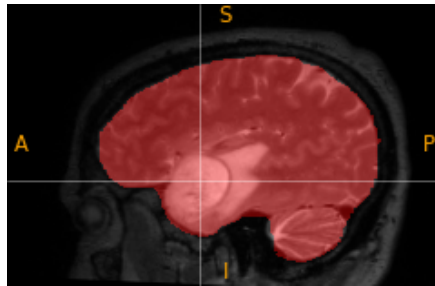
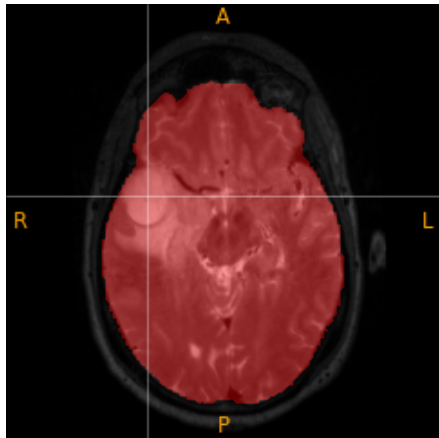
T1



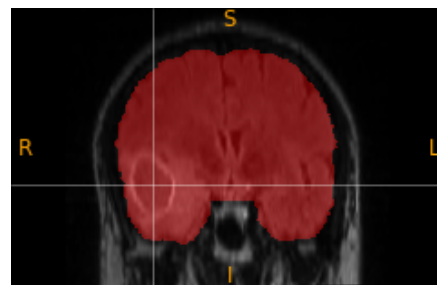
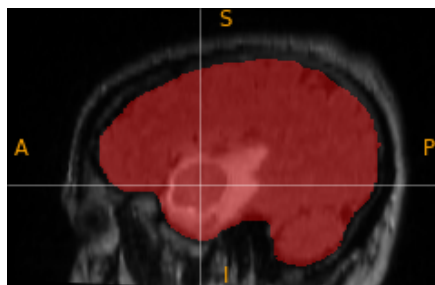
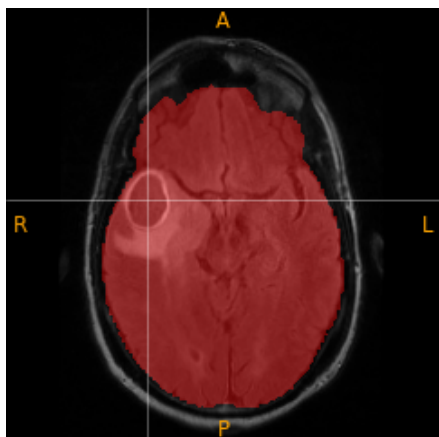
T1CE



T2

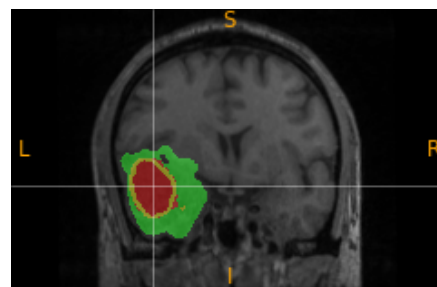
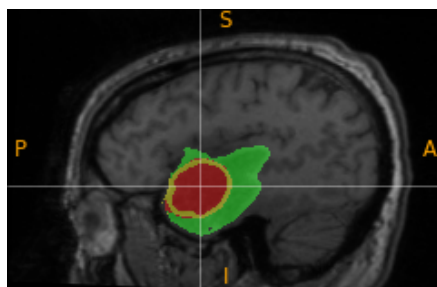
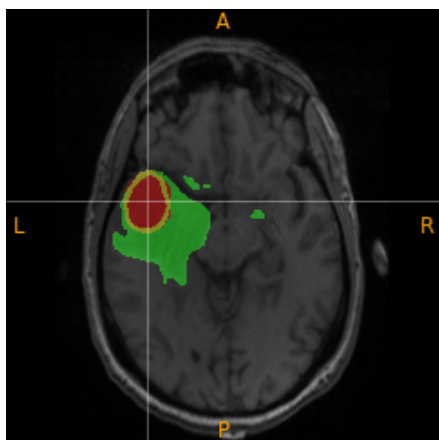


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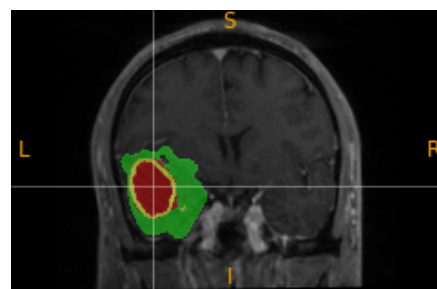
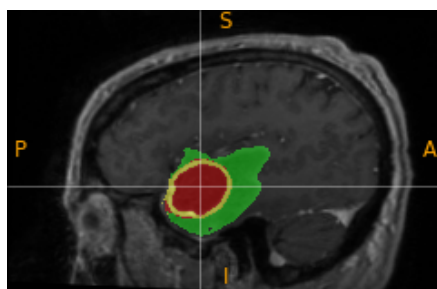
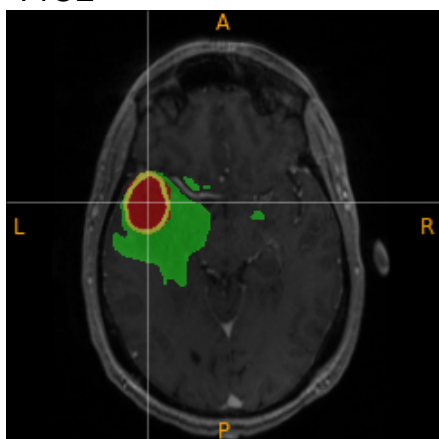


3. Tumor segmentation. Snapshot of the largest TC volume slice is shown. Labels follow the BraTS convention, enhancing tumor (ET; Yellow), peritumoral edematous/infiltrated tissue (ED; Green), and necrotic and non-enhancing tumor core (NC; Red). SegmOption=DeepMedic[3]

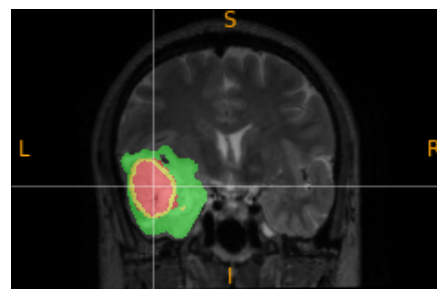
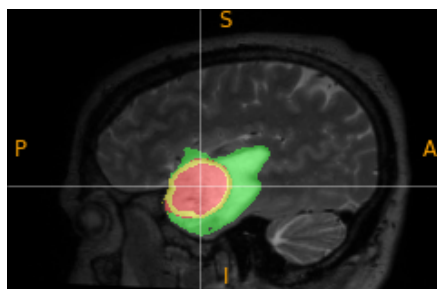
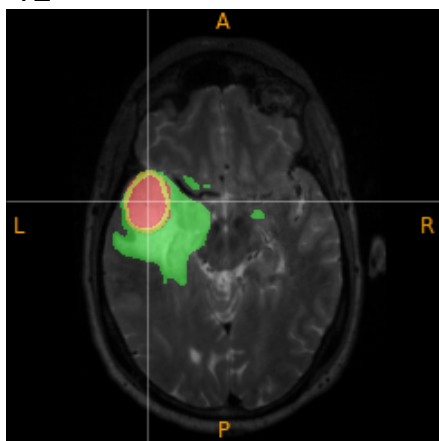
T1



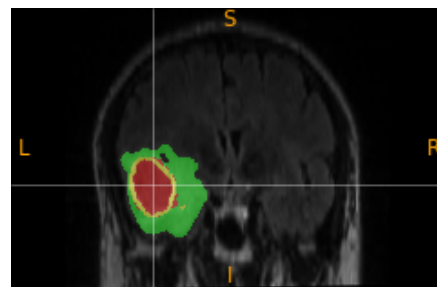
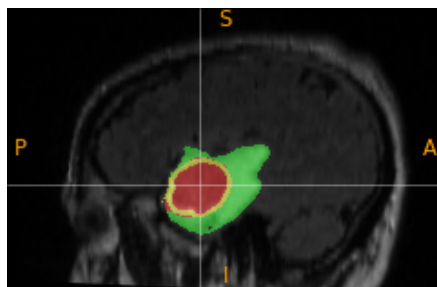
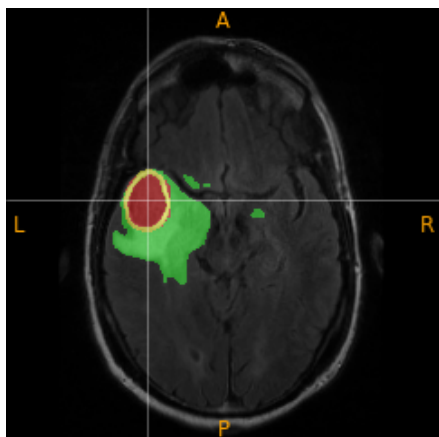
T1CE



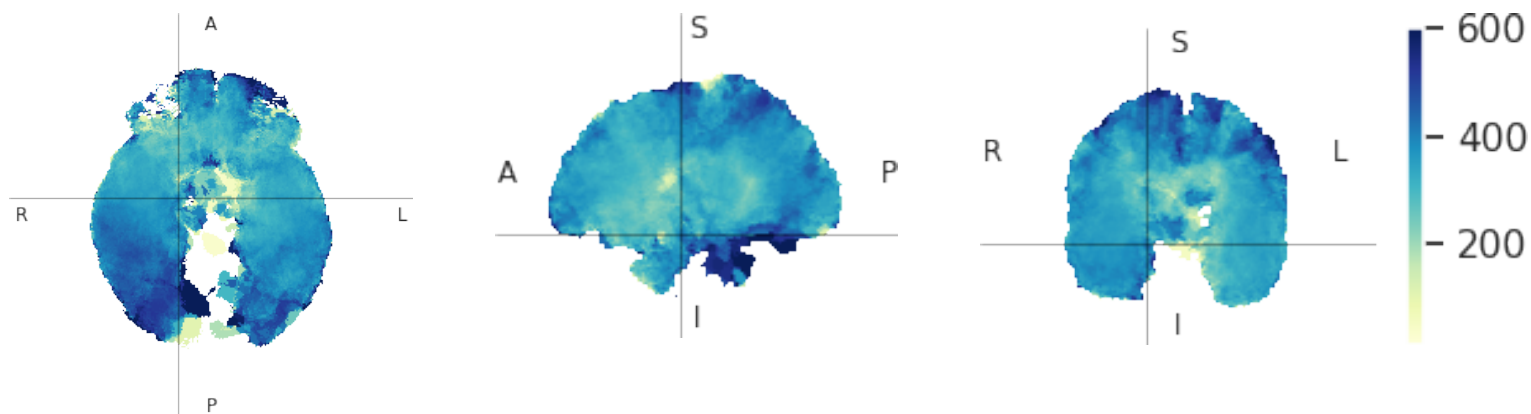
T2



FLAIR



**4.Overall Survival Map (OSM) atlas. The crosshair shows the slices at the largest TC volume.**



## 5. Radiomic Features

	Feature name	Feature value	ReSPOND.min	ReSPOND.mean	ReSPOND.med	ReSPOND.max	Flag
0	Size_NC	10088.000000	0.000000	12050.513300	6981.000000	140161.000000	
1	Size_ET	6889.000000	0.000000	23316.374620	18859.000000	143057.000000	
2	Dist2Vent	2.374377	0.000000	4.532068	1.191891	35.372128	
3	ED*100./(NC+ET)	343.411700	0.000000	423.749161	188.608411	118898.113200	
4	ED*100./(NC+ET+ED)	77.447590	0.000000	62.599502	65.350975	99.915965	
5	ET*100./BS	0.436756	0.000000	1.591563	1.289837	8.399922	
6	NC*100./BS	0.639570	0.000000	0.817516	0.474362	11.978201	
7	ED*100./BS	3.696232	0.000000	4.118192	3.614858	17.805036	
8	(NC+ET)*100./BS	1.076327	0.007233	2.409080	1.928902	16.337189	
9	(NC+ET+ED)*100./BS	4.772559	0.026242	6.527271	6.166784	21.395980	
10	(NC+ET)./(NC+ET+ED)	0.225524	0.000840	0.374005	0.346490	1.000000	
11	Number	1.000000	1.000000	1.345399	1.000000	9.000000	
12	Extent	0.475982	0.057138	0.379101	0.386651	0.594522	
13	AxisLength	87.464230	15.873803	105.279734	106.277307	202.318765	
14	AxisRatio	2.769327	2.085374	2.979922	2.830533	7.549256	
15	Left	0.000000	0.000000	7276.512865	1873.000000	95846.000000	
16	SSD_mean	331.825500	36.000000	384.943506	382.566558	688.250945	
17	SSD_min	244.416700	1.000000	176.129163	187.500000	468.333333	
18	SSD_median	333.411700	36.000000	384.172648	381.379310	740.000000	

## References

- [1] (Prognostic Subgrouping) Akbari et al. Novel AI-based Prognostic Subgrouping of Glioblastoma: A Multi-center Study, Nat Med, NMED-A124673
- [2] (Preprocessing Pipeline) Davatzikos et al. Cancer imaging phenomics toolkit: quantitative imaging analytics for precision diagnostics and predictive modeling of clinical outcome, J Med Imaging, 5(1):011018, 2018
- [3] (Brain mask) Thakur et al. Brain Extraction on MRI Scans in Presence of Diffuse Glioma: Multi-institutional Performance Evaluation of Deep Learning Methods and Robust Modality-Agnostic Training, Neuroimage. 2020 Oct 15;220:117081.
- [4] (DeepMedic) Kamnitsas et al. Efficient Multi-Scale 3D CNN with Fully Connected CRF for Accurate Brain Lesion Segmentation. Medical Image Analysis, 2016.
- [5] (FeTS) Pati et al. The federated tumor segmentation (FeTS) tool: an open-source solution to further solid tumor research. 2022 Phys. Med. Biol. in press.