

Radiogenomic modeling predicts survival-associated prognostic groups in glioblastoma

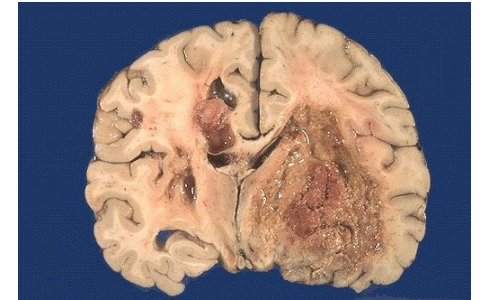
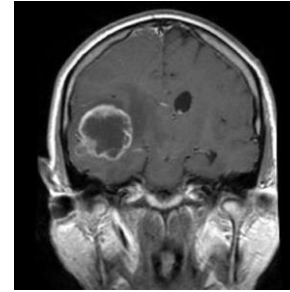
Nicholas Nuechterlein

10/25/2021

The University of Washington
Paul G. Allen School of Computer Science & Engineering

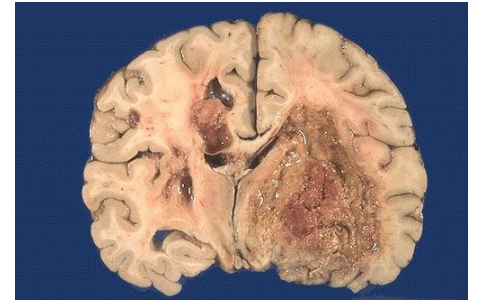
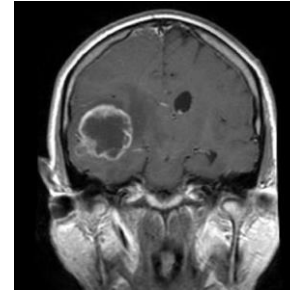
What is Glioblastoma?

- Most common and aggressive primary adult malignant brain tumor
- Median survival of 15 months
- Incurable because
 - Extremely heterogeneous
 - Blood brain barrier
- Last approved therapeutic agent was in 2005



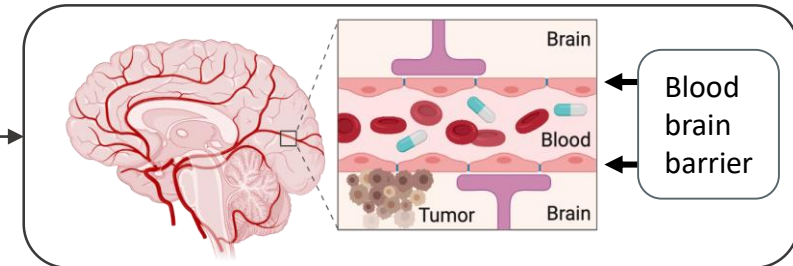
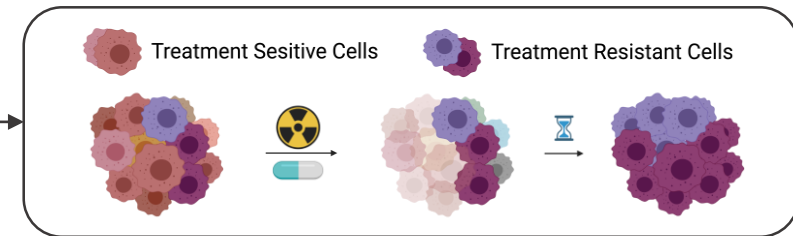
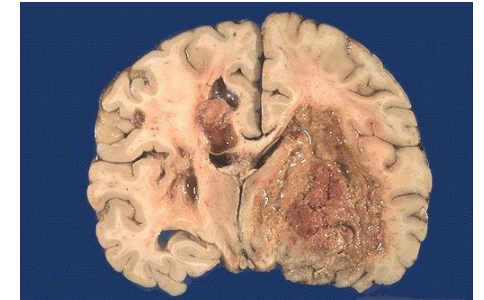
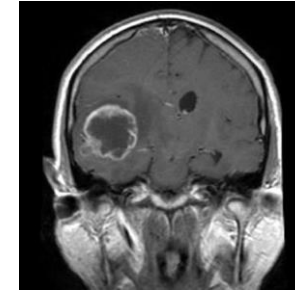
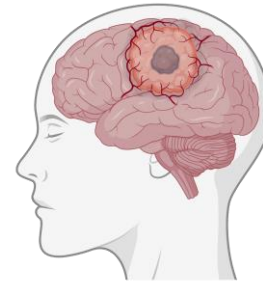
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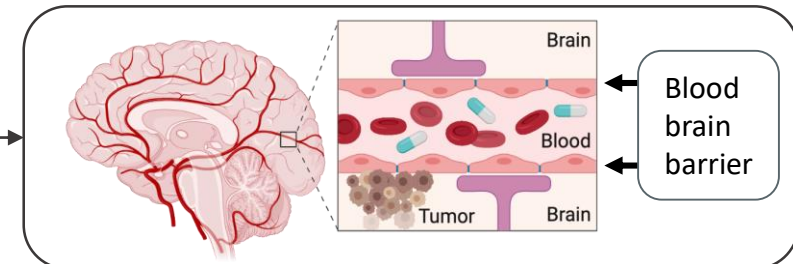
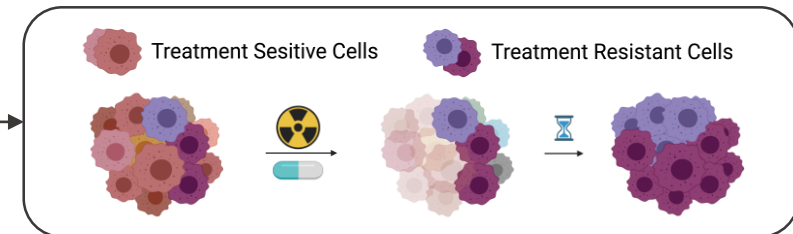
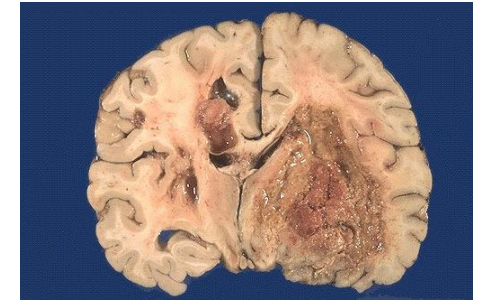
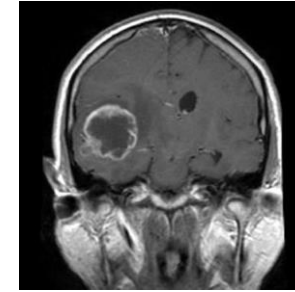
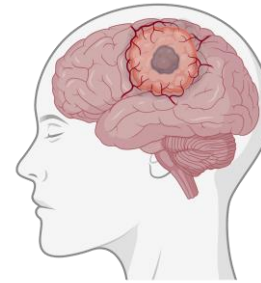
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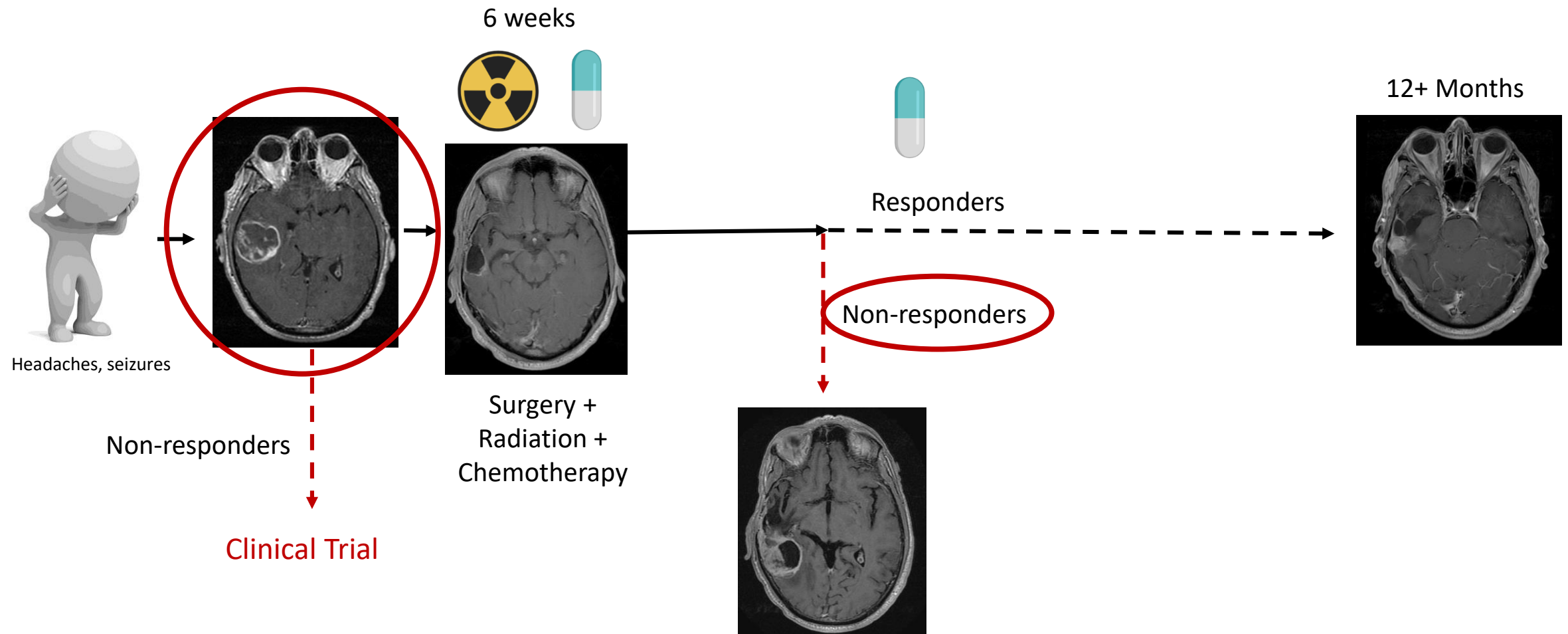


Report from the FDA

**Food and Drug Administration Drug Approval Summary:
Temozolomide Plus Radiation Therapy for the Treatment
of Newly Diagnosed Glioblastoma Multiforme**

Martin H. Cohen, John R. Johnson, and Richard Pazdur

Patient Clinical Course



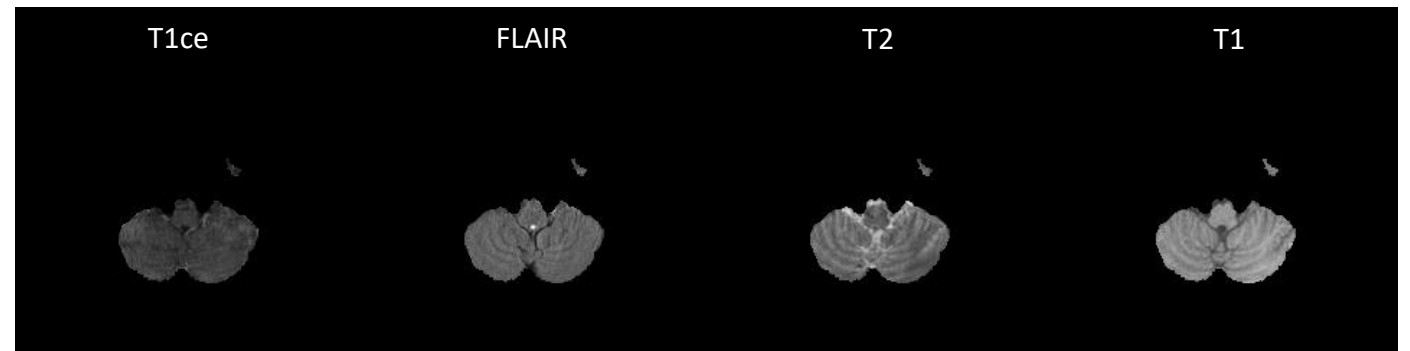
Motivation for predicting short-term survivors

- Better for patients
 - Poor survivors have the most to gain from upfront trials
- Better for trials
 - Identifying poor survivors upfront can help balance clinical trial arms
 - Trials will run faster with poor survivors
- **But we need to know **who** the poor survivors are **upfront****

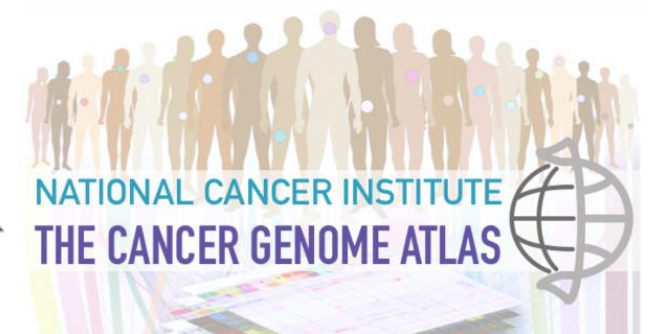
Data

- MRI
 - Rich, global representation of tumor
 - Cheap, fast, non-invasive, repeatable
 - Volumetric
 - $255 \times 255 \times 155 \times 4$
 - (> 50 M voxels)
- Our data
 - 46 TCIA preoperative glioblastomas MRI with T1ce, FLAIR, T2, T1

Magnetic Resonance Imaging (MRI)



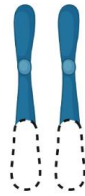
THE **CANCER**
IMAGING ARCHIVE



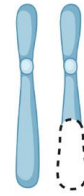
Copy Number

- Captures DNA structure
- Unlike MRI: invasive, expensive, not repeatable
- 23,000 x 1 (gene-level)
- Values in $\{-2, -1, 0, 1, 2\}$

Homozygous
Deletion



Single Copy
Loss



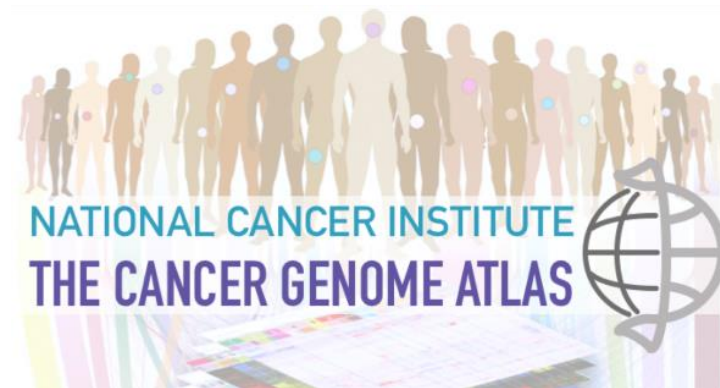
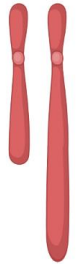
Diploid Normal
(Intact)



Gain

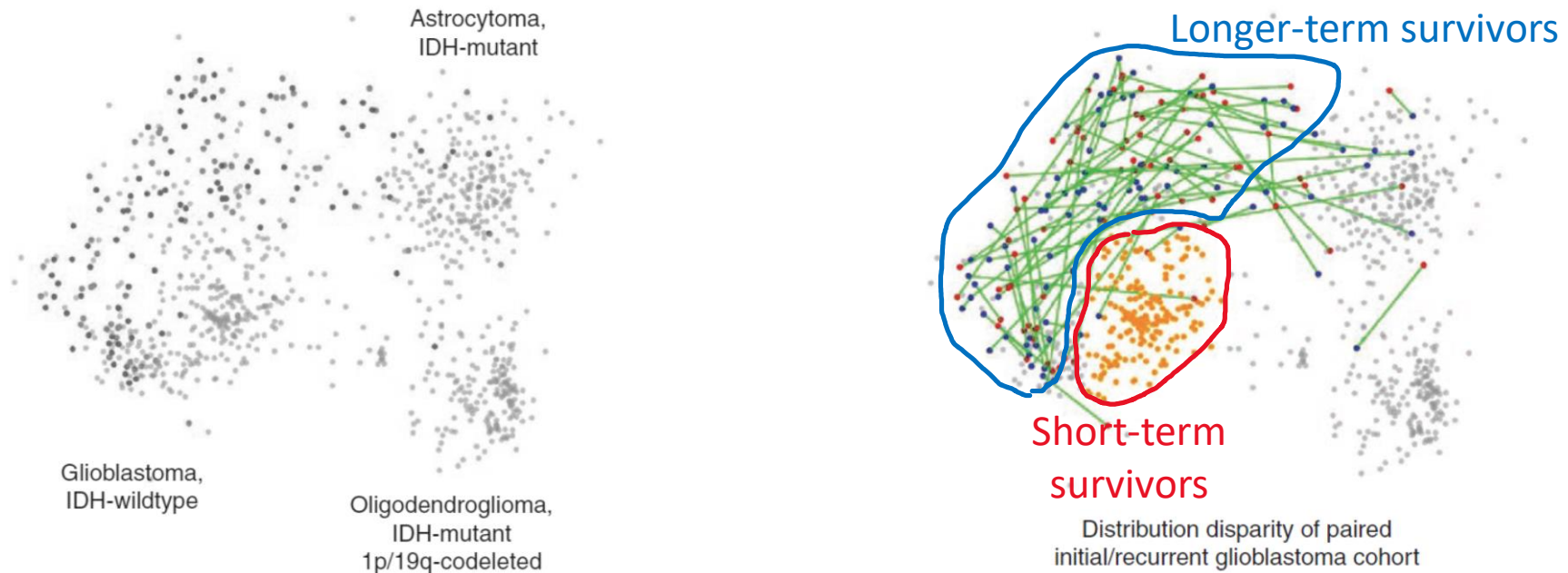


Amplification



Poor survivor definition

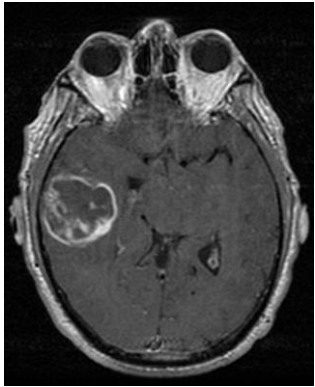
Glioblastoma patients who undergo second resections live longer



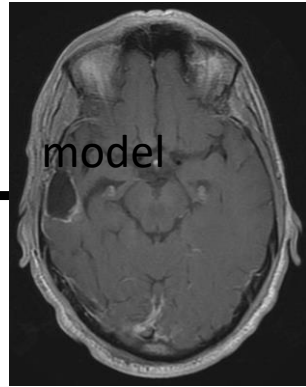
PJ Cimino



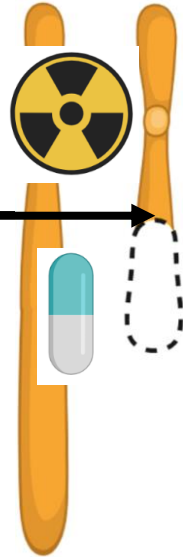
Baseline MRI



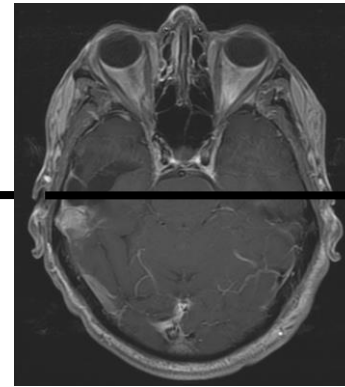
Post Resection MRI



Copy Number (SCNA)



MRI at recurrence

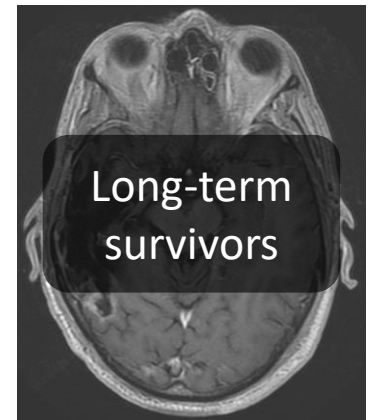


Patients eligible for second resections are generally healthier, better surviving patients

No 2nd Resection

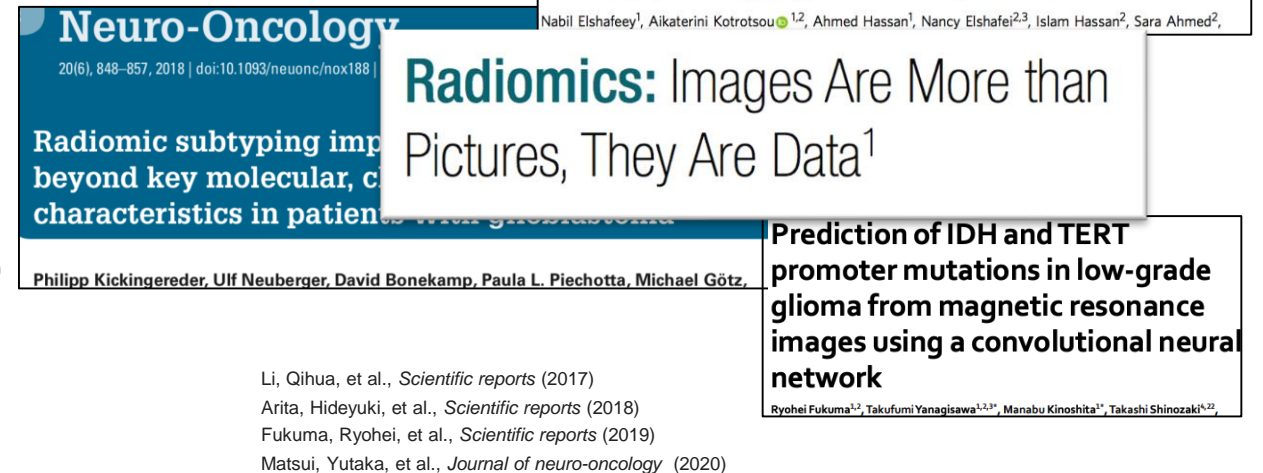


2nd Resection

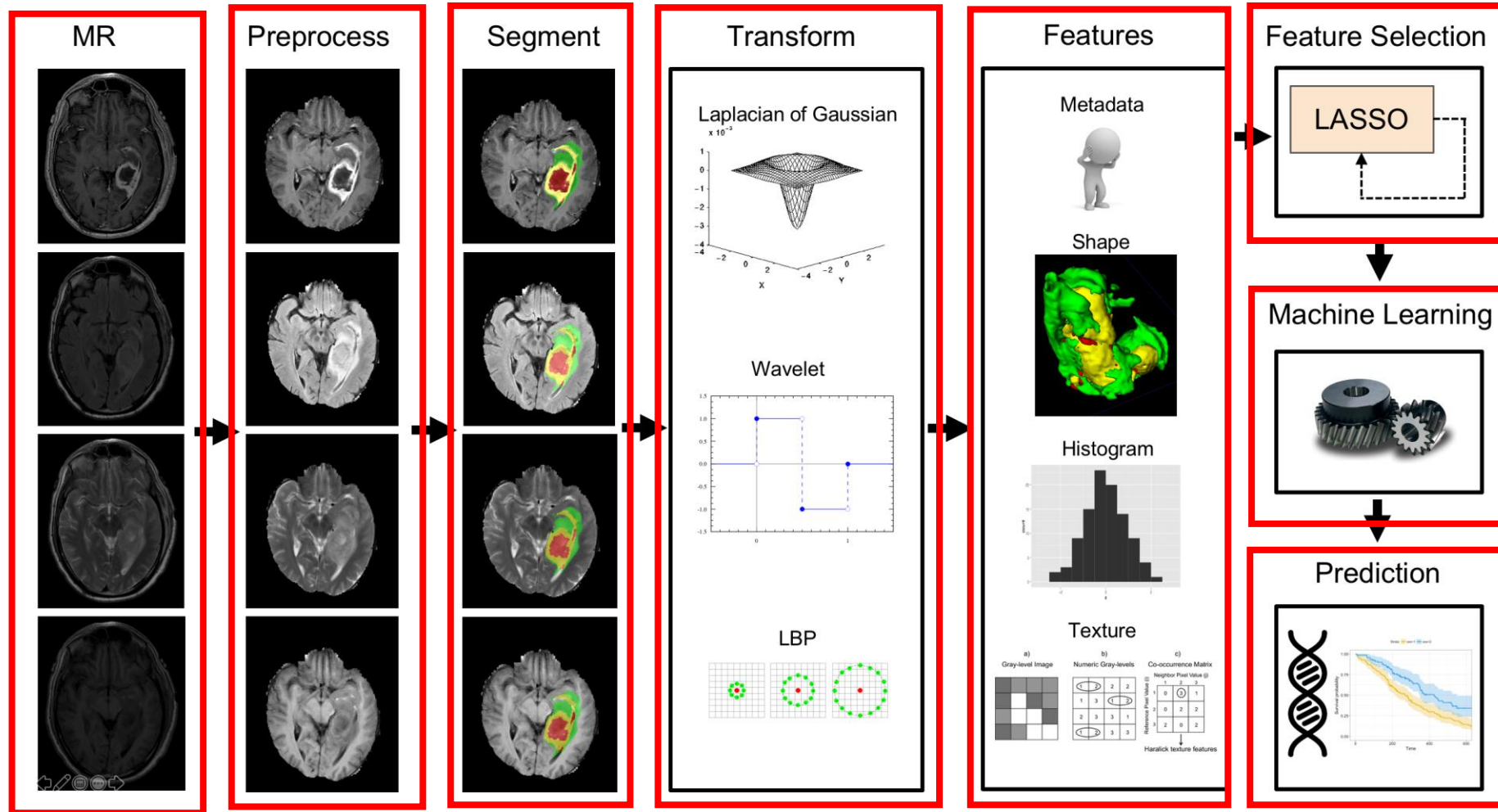


Methods

- Radiogenomics/radiomics
 - An evolving field in medical imaging that strives to equate quantitative image features with the genomic profile of pictured tissues
- Pipelines
 - Image acquisition
 - Image normalization
 - Feature extraction
 - Feature selection
 - Prediction using ML models
 - (Or end-to-end deep learning models)
- Novelty
 - Feature selection method
 - Unique clinical application

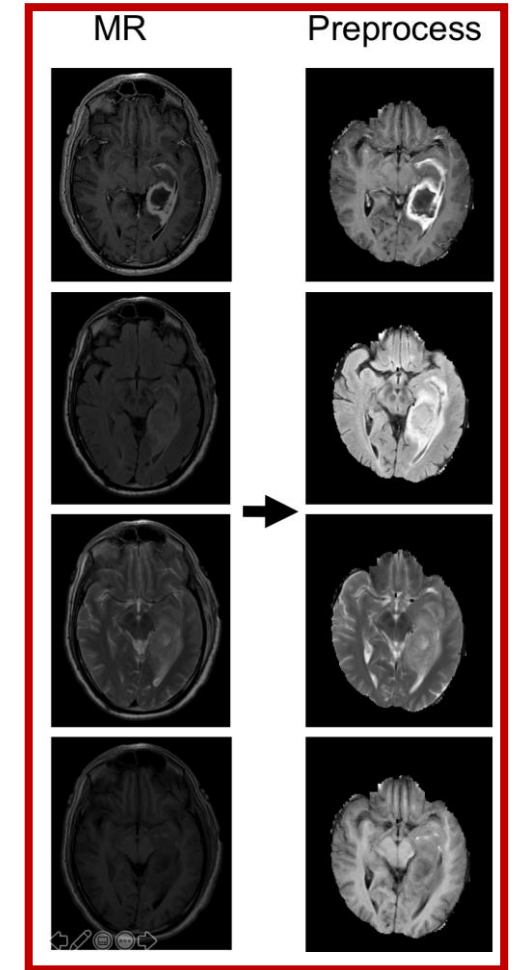


Method



Preprocessing

1. DICOM -> NiftI
 - dcm2niix
2. Skull-strip
 - The Brain Extraction Tool (BET)
3. Co-register same-subject MRI sequences
 - FMRIB's Linear Image Registration Tool (FLIRT) from the FMRIB Software Library (FSL)
4. Normalize/bias correct
 - N4 Bias Field Correction



Li, et al., J Neurosci Methods (2016)

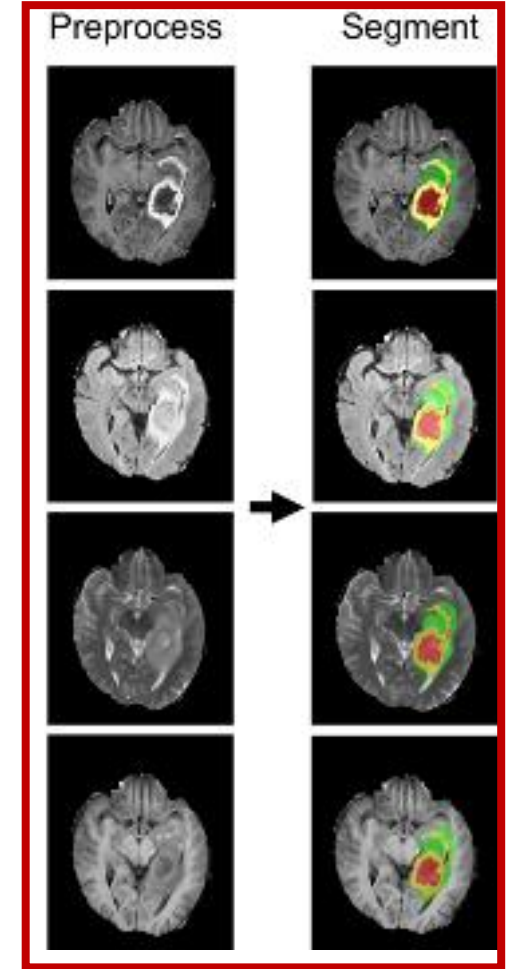
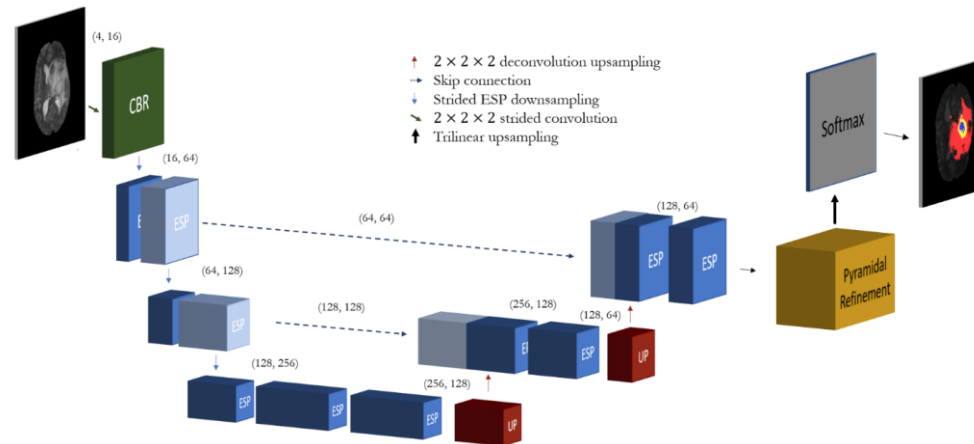
Jenkinson et al. Med Image Anal (2001)

Jenkinson et al. Neuroimage (2002)

Tustison NJ, Avants BB, et al. IEEE Trans Med Imaging (2010)

Segmentation

- U-net based architecture
- Used ESP blocks



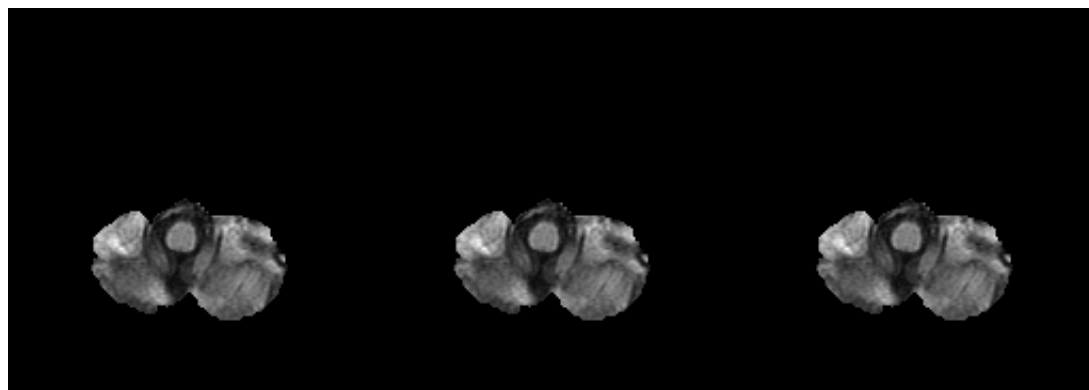
Nuechterlein, et al., *International MICCAI Brainlesion Workshop* (2018)
Mehta et al., *ECCV* (2018)
Ronneberger et al., *MICCAI* (2015)

Segmentation Results

Raw MR

Prediction

Ground Truth



Raw MR

Prediction

Ground Truth

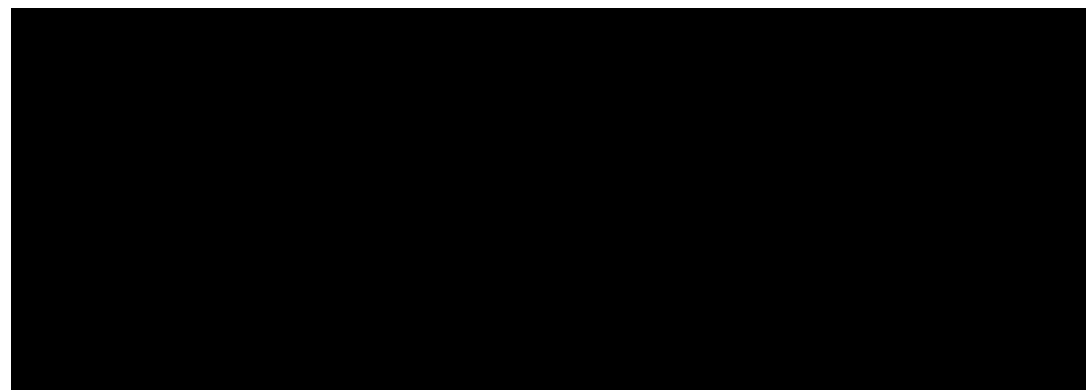


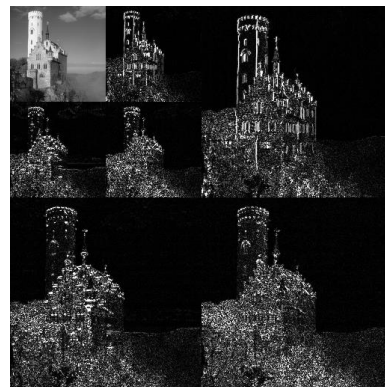
Image filters / transformations

- Identity
- Laplacian of Gaussian (LoG)
- Wavelet
- Local binary patterns (LBP)
- Exponential, logarithm, square , square root

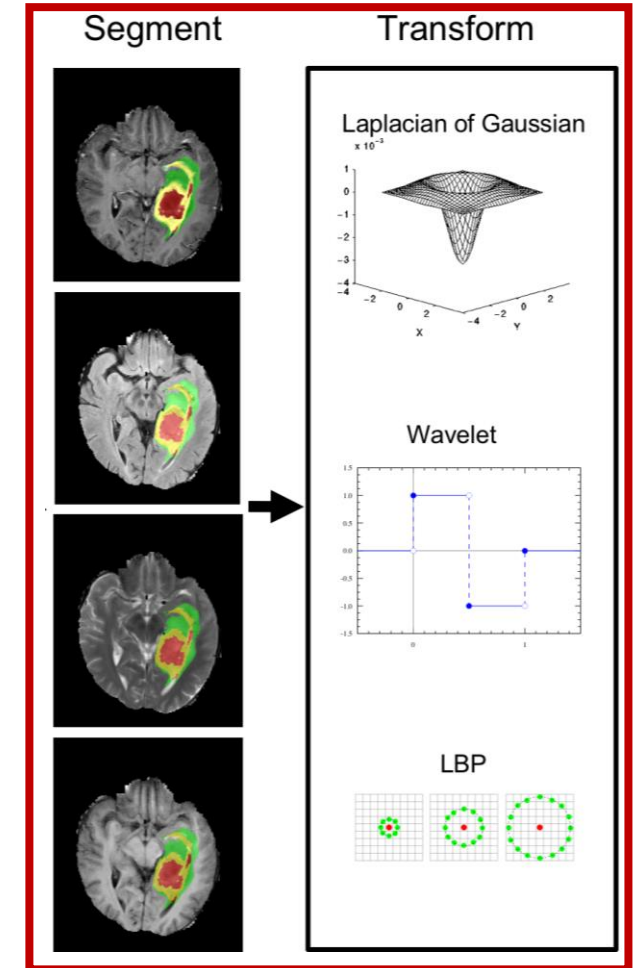
LoG



Wavelet



LBP



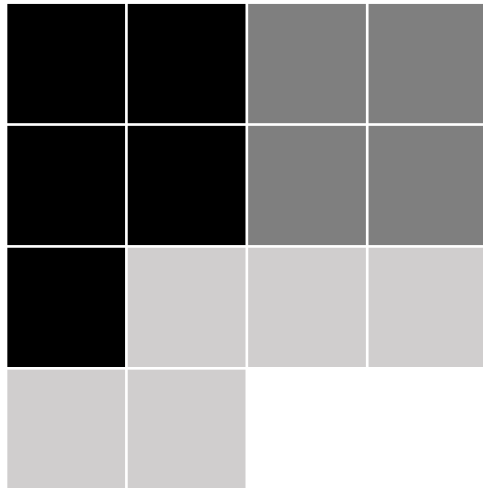
Texture analysis

- Image texture gives us information about the spatial arrangement of color or *intensities* in an image
- Example: Grey-level co-occurrence matrix (GLCM)



GLCM

Image



Values are image grey levels (GLs)

0	—	0	—	1	—	1
0	—	0	—	1	—	1
0	—	2	—	2	—	2
2	—	2	—	3	—	3

Prepare GLCM matrix: values are descriptions of GLCM values

i/j	0	1	2	3
0	(0,0)	(0,1)	(0,2)	(0,3)
1	(1,0)	(1,1)	(1,2)	(1,3)
2	(2,0)	(2,1)	(2,2)	(2,3)
3	(3,0)	(3,1)	(3,2)	(3,3)

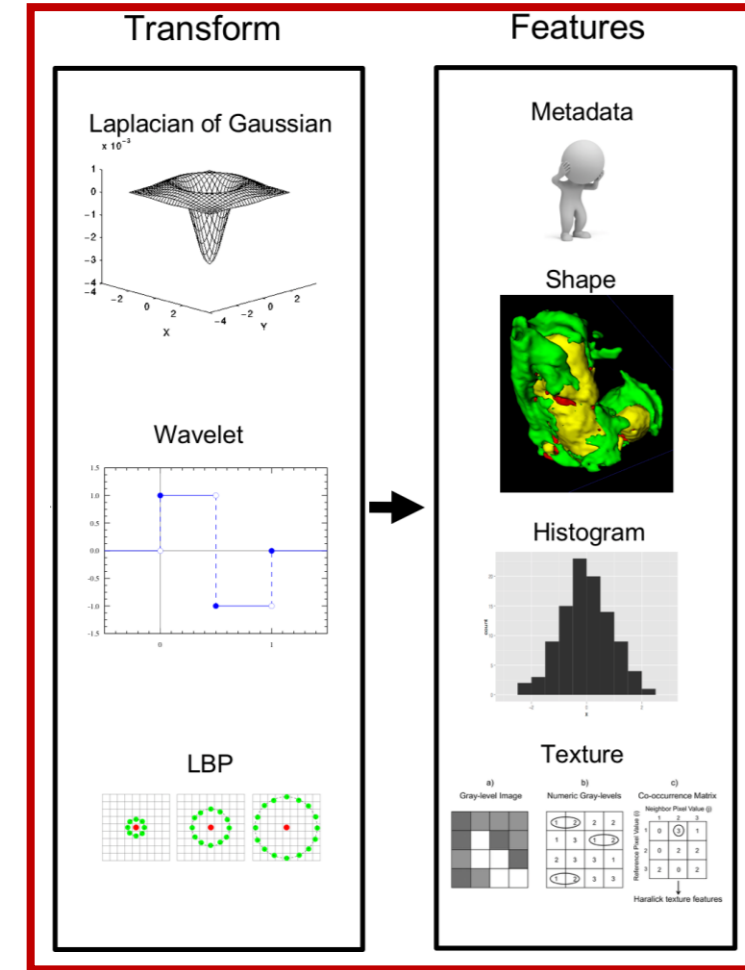
Values are counts of frequencies of the neighboring pairs of image pixel values

2	2	1	0
0	2	0	0
0	0	3	1
0	0	0	1

The diagonal elements all represent pixel pairs with no grey level difference

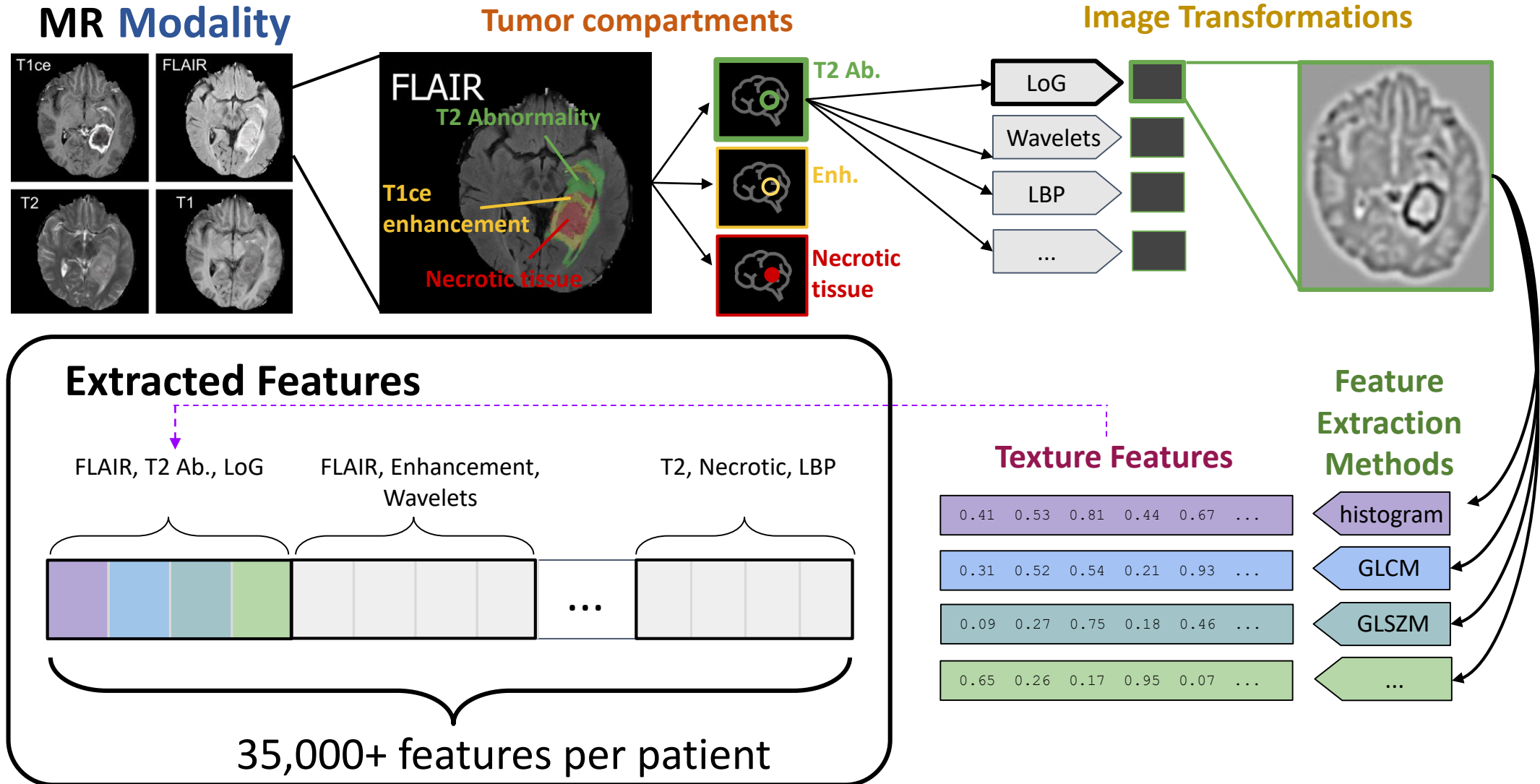
Feature Extraction

- Histogram
 - Percentile, energy, entropy, kurtosis, skewness, uniformity, etc.
- Texture
 - GLCM (Gray Level Co-occurrence Matrix)
 - Contrast, correlation, etc.
 - GLRLM (Grey-Level Run Length Matrix)
 - GLSZM (Gray Level Size Zone Matrix)
 - GLDM (Gray Level Dependence Matrix)
 - NGTDM (Neighboring Gray Tone Difference Matrix)
- Implementation
 - *pyradiomics*



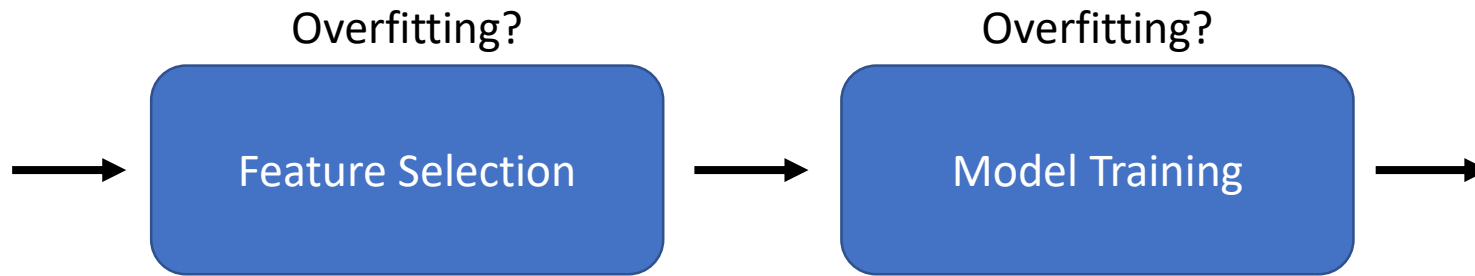
Putting it all together

Feature = $\{m, c, t, e, f\}$

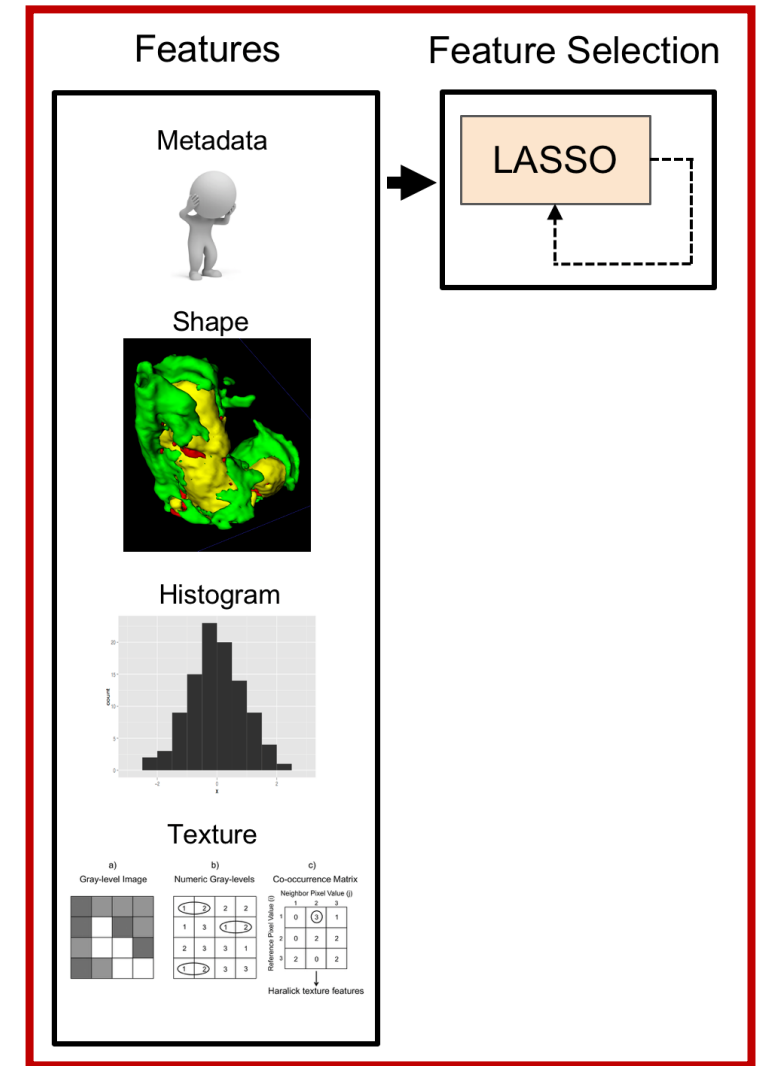


Feature selection

- Feature set is far too large for modeling a few number of samples
- Feature selection overfits
 - Recursive feature elimination
 - Variance thresholding
 - LASSO feature selection

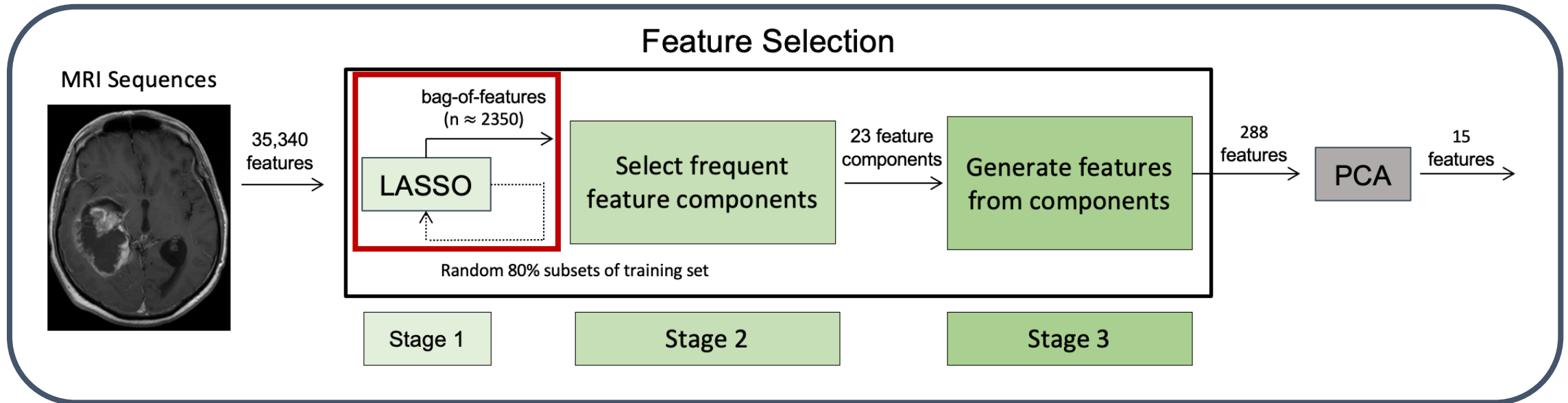


- We want to leverage the structure of our features

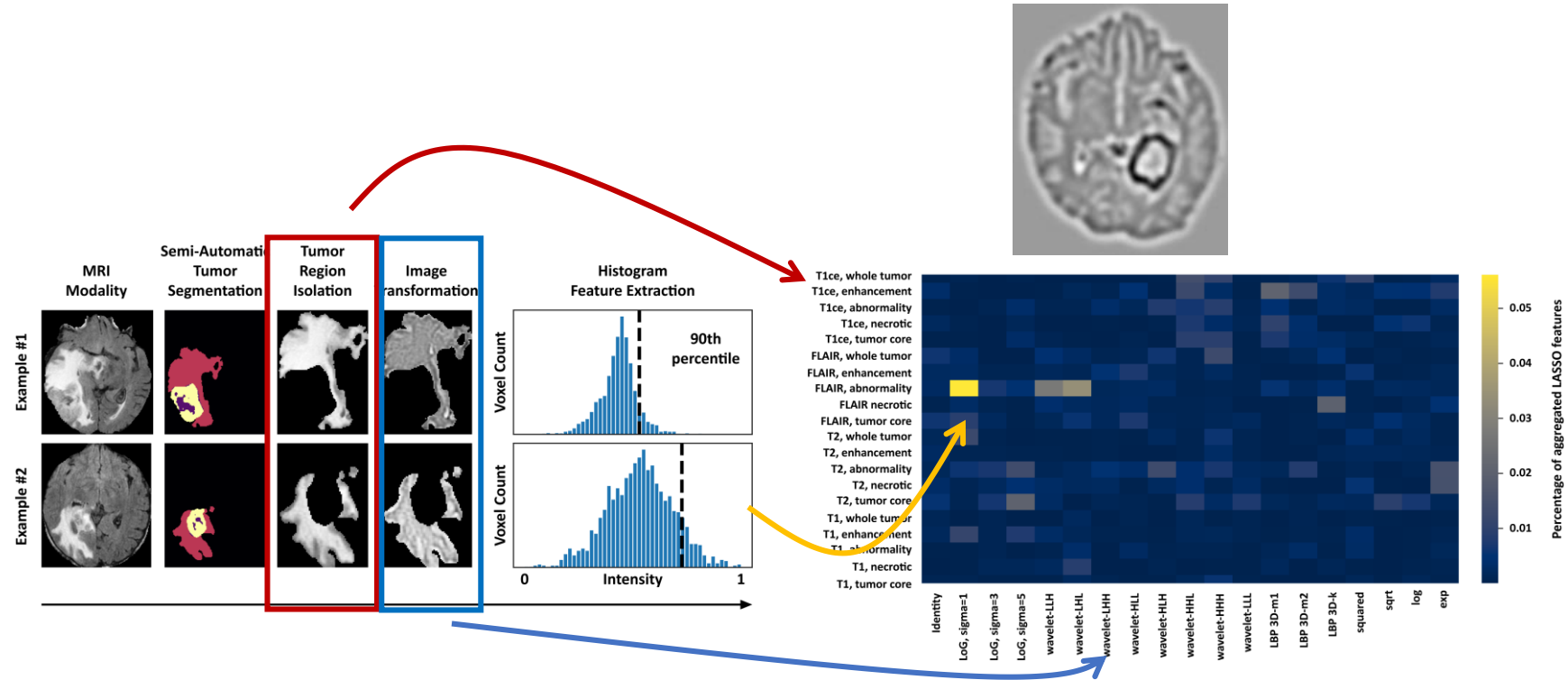


Feature Selection

- Stage 1
 - Aggregate a bag B of LASSO-selected features, including duplicates, by training LASSO models on random subsets of the training data

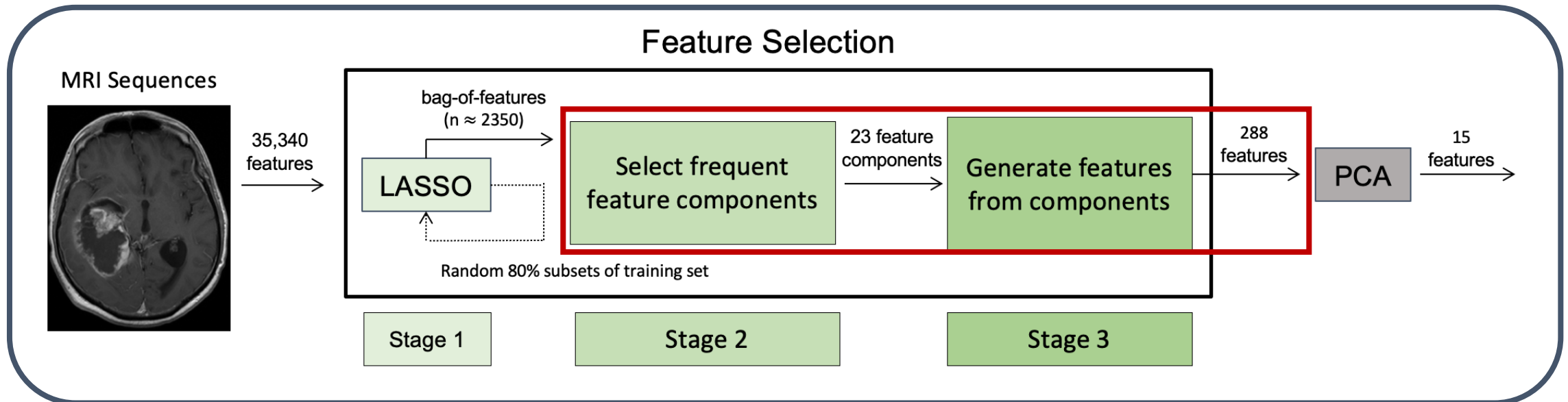


Feature Selection



Feature Selection

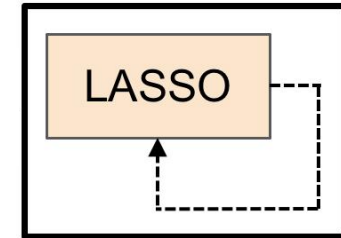
- Stage 2 & 3
 - Use B to determine which *feature components* (C) are most relevant to the classification task
 - Generate the set of 288 features whose components were determined from the set C
 - Use PCA to further reduce the dimensionality of our feature set to 15



Modeling

- 15 PCA Features
- Collection of small machine learning models
- Cross validation

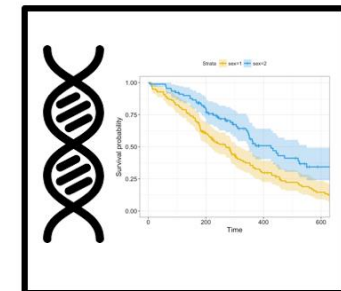
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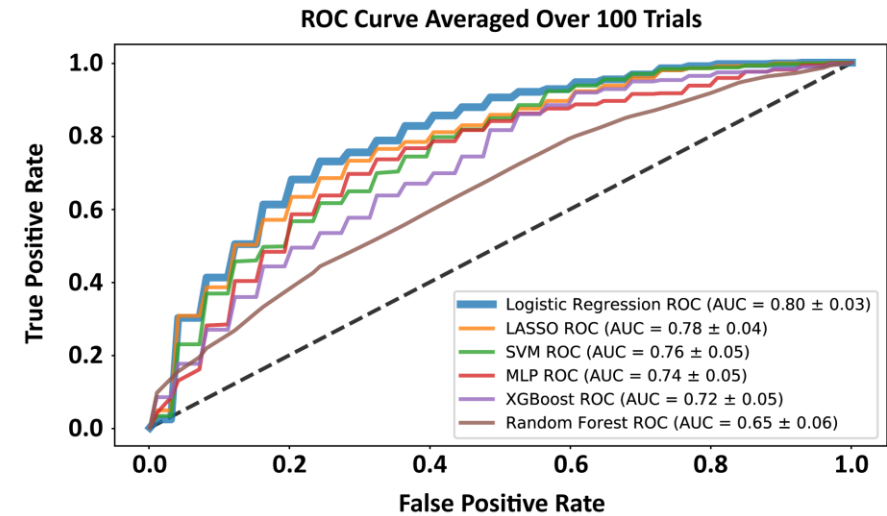
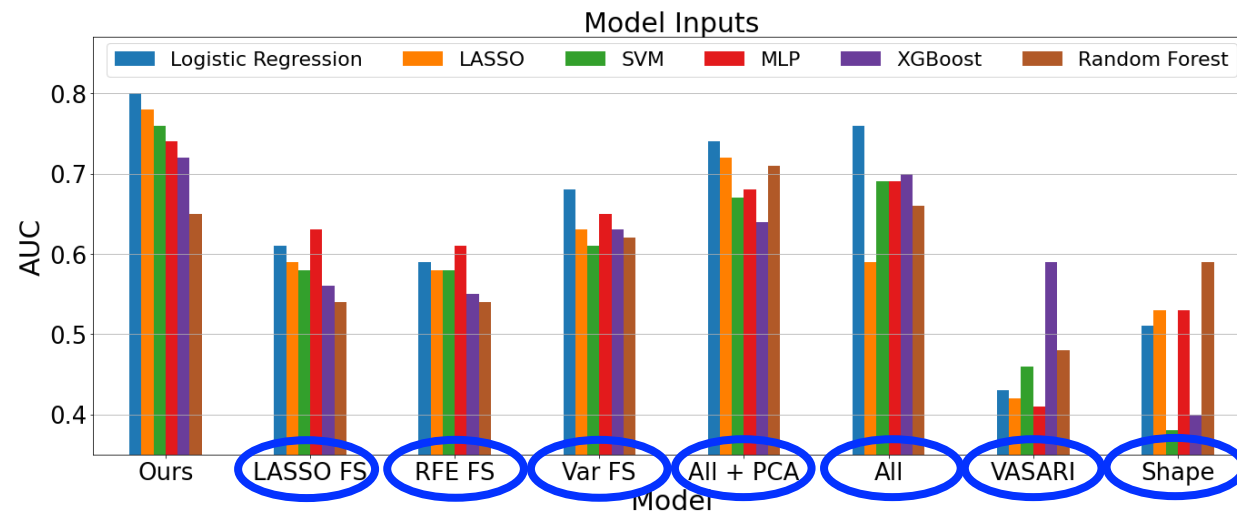
Machine Learning



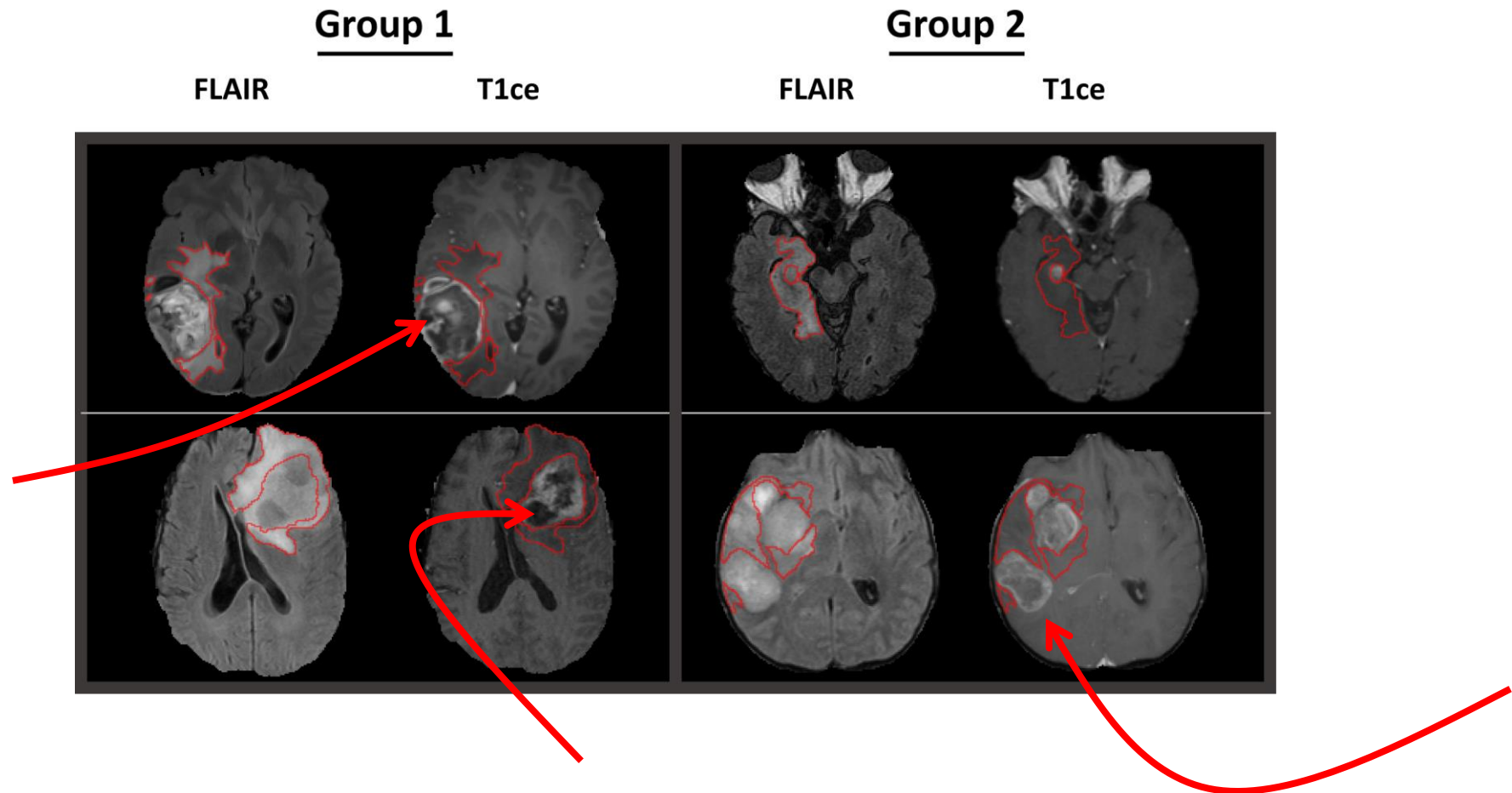
Prediction



Results



Results



Discussion

- $AUC > 0.80$
- Attributes Not Selected
 - Enhancing tumor!
 - Identity transformation
- Attributes Selected
 - Laplacian of Gaussian transform (edge detector)
 - T2 Abnormality on FLAIR

Imaging Summary

- Developed a custom feature selection method that allows for the prediction of poor surviving glioblastoma patients, but leaves room for improvement
- Imaging limitations
 - Until scanner protocol is standardized, noise will interfere with model reliability
 - Low sample counts
 - Patients almost always get first resections, thus the fact that MRI is cheap and non-invasive is not necessarily an advantage in the upfront setting

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