Radiomic Features From Multi-Institutional Glioblastoma MRI Offers Additive Prognostic Value to Clinical and Genomic Markers

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Objective

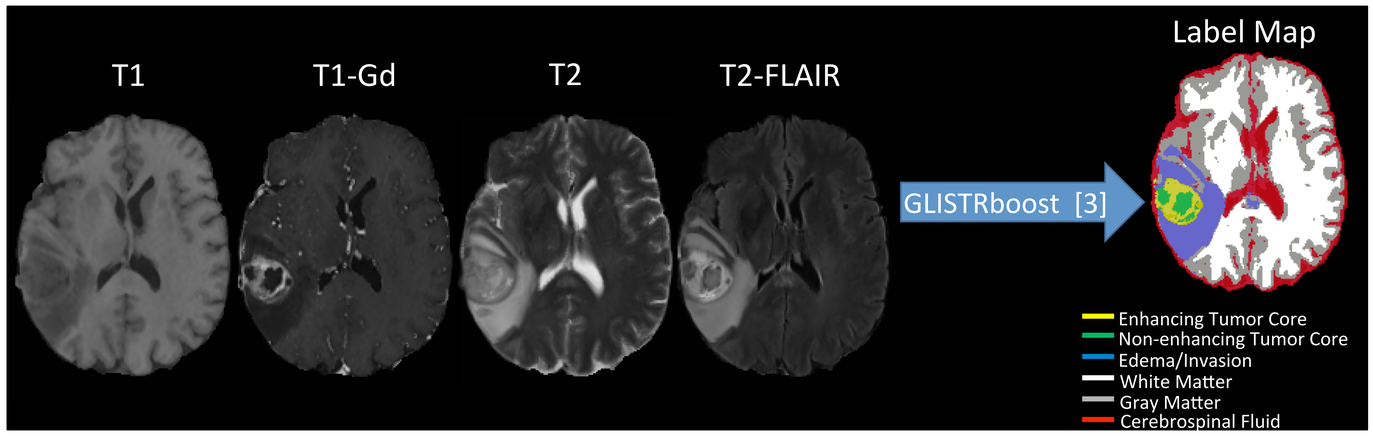
Synergies between clinical, genomic, and radiomic features should improve the predictive value of each group of features and their combinations through a prognostic classifier based on machine learning in patients with glioblastoma.

Materials

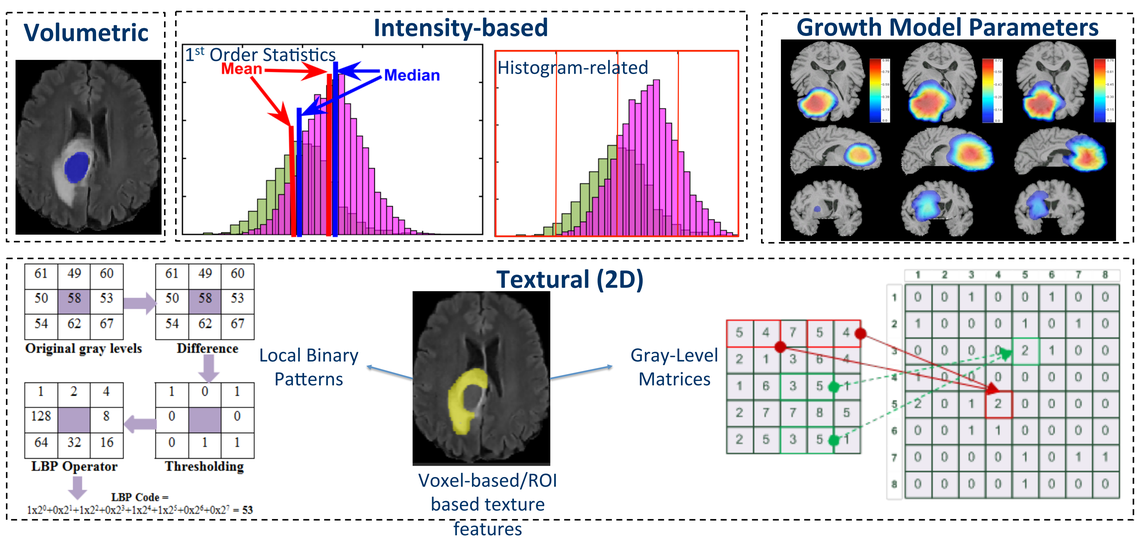
- N=168 Jefferson patients
- Combined with Penn (n>300) and TCGA (n=105)
- Selection based on availability of:
  - Pre-operative structural modalities, i.e. T1, T1-Gd, T2, FLAIR
  - Gene expression (AgilentG4502A),
  - miRNA (Agilent Human microRNA8x15K), and
  - DNA methylation (Illumina Infinium Human Methylation BeadChip 27)
- Median age = 60 years (range 17-84)
- Median post-resection survival = 420 days (range 7-1731)
- Low survival group: 35 patients with survival below the 33rd percentile (<210 days)
- High survival group: 35 patients with survival above the 67th percentile (>470 days).

Methods

Multimodal Tumor Segmentation using GLISTRboost

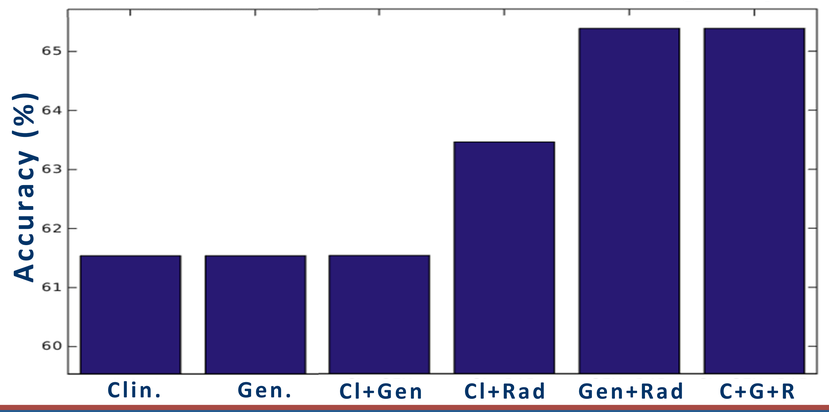


Quantitative Imaging Features Extraction



Results

SVM 10-fold CV between survival groups



- 10-fold CV to test the predictive models on new patient data.
- Accuracy
  - Highest when using combination of all data
  - Lowest with clinical data alone
  - Highest SVM weights associated with radiomic data

Conclusions

- Combination of data allows for better prediction of survival as compared to using any one type of dataset individually.
- Combining data increases the complexity of the analysis.
- However, the boost in the signal outweighs the increase in noise, while predicting survival.
- More accurate prediction models will better guide treatment options

Future Directions

- Using automated tools such as CaPTk to extrapolate tertiary tumor measurements for better prognosis
- Apply model to different institutions' cohorts to further validate prediction accuracy
- Explore other radiomic features that more accurately predict GBM outcomes

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