FDG-PET Radiomics Outperforms Conventional Biomarkers for Treatment Response Prediction in High-Risk Hodgkin Lymphoma: Evidence from the AHOD0831 Trial

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INTRODUCTION

- Metabolic tumor volume (MTV) and maximum standardized uptake value (SUVmax) are established PET imaging biomarkers
- These biomarkers lack spatial characterization of intratumor heterogeneity
- Radiomics is a field of quantitative image analysis that offers this spatial characterization
- If radiomics can better predict response to radiotherapy in high-risk Hodgkin lymphoma (HL), then patient outcomes can improve

AIM

The aim of this work was to build, validate, and compare radiomics-based models with other established PET imaging biomarkers

METHODS

- 115 PET/CT scans from high-risk HL patients in the AHOD0831 clinical trial were included
- 93 first- and second-order radiomics features were extracted from gross tumor volumes (GTV)
- 3 differing datasets were extracted based on the number of SUV per gray level bin for comparison (0.25, 0.50, and 0.75 SUV/bin)
- All features underwent univariate analysis via Mann Whitney U test
- Significant features underwent least absolute shrinkage and selection operator (LASSO) feature selection to identify which were most associated with response
- Cross-validated logistic regression (LR) models were constructed with top features and compared
- ROC curve analysis used to compare with baseline PET biomarkers MTV and SUVmax

RESULTS

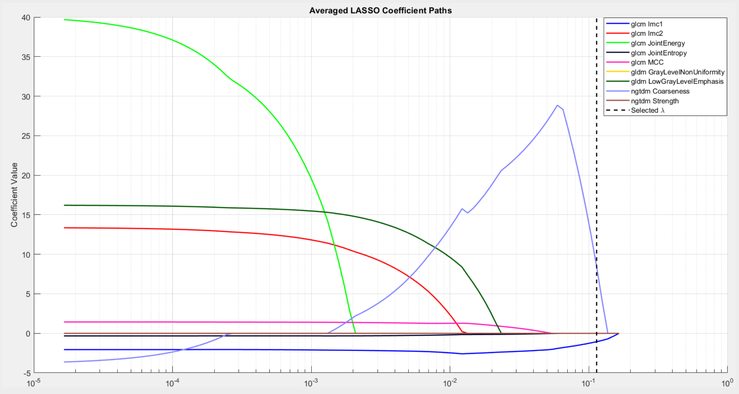

Figure 1: LASSO coefficient pathways for significant features. Coefficient values are averaged at each λ value across all 100 iterations. Chosen λ denoted as vertical dotted line.

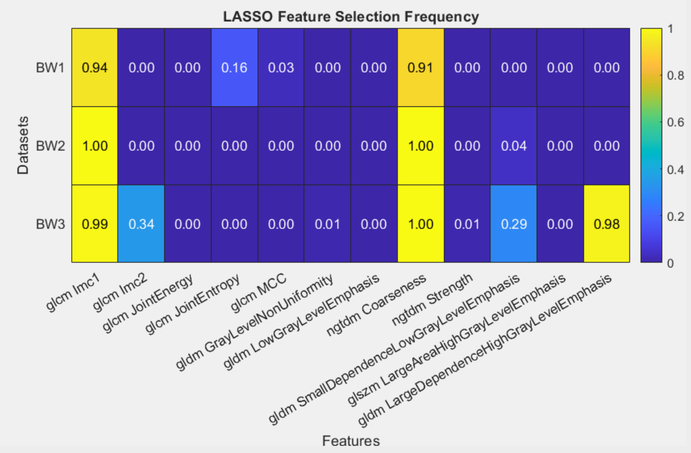

Figure 2: Frequency heatmap of features selected across 100 iterations of LASSO

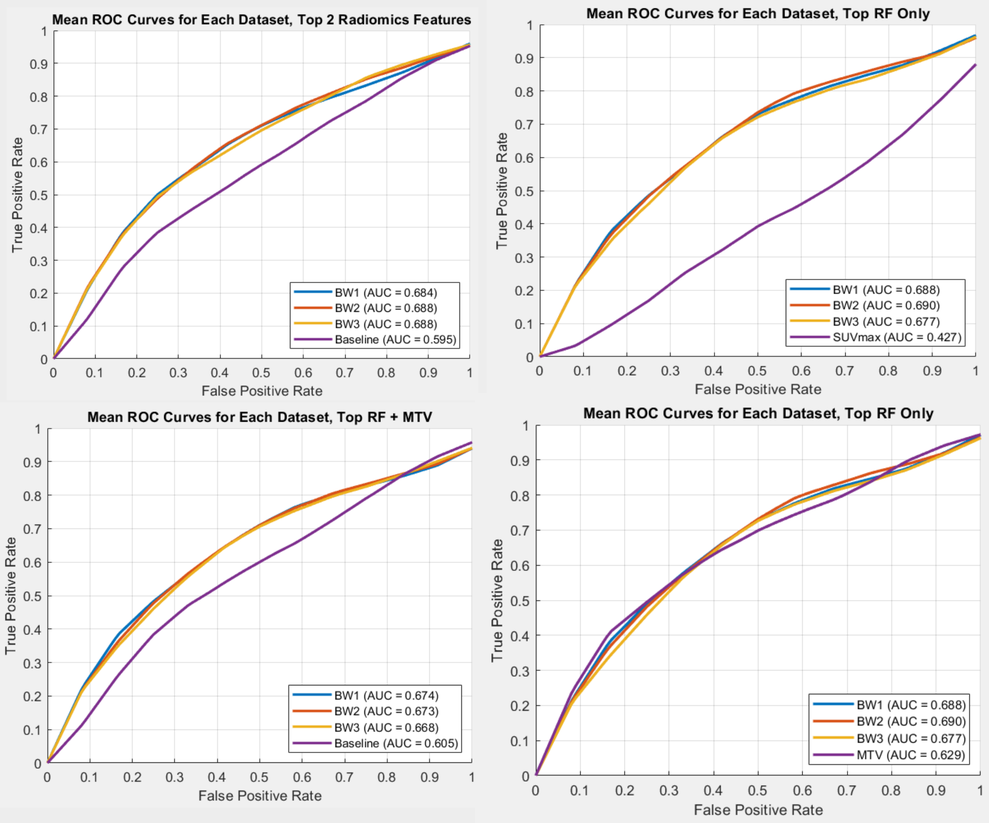

Figure 3: Averaged AUC curves for each model across all data sets

RESULTS

- 54 responders (47%) and 61 non-responders (53%) were identified
- 12 feature varied significantly between responder groups across all data sets
- Across 100 iterations of cross-validated LASSO selection, 2 radiomics features were consistently selected across all data sets:
  - GLCM IMC1
  - NGTDM Coarseness
- The baseline model constructed with MTV + SUVmax had poor performance overall, average AUC = 0.595
- MTV alone AUC = 0.629
- SUVmax alone AUC = 0.499
- Top 2 radiomics features AUC = 0.688
- There was a significant difference between the radiomics model and the baseline model (Delong p-value<0.001)
- AUCs did not differ significant between data sets
- Decision curve analysis revealed an average net benefit difference of 0.02 between the radiomics model and the MTV model

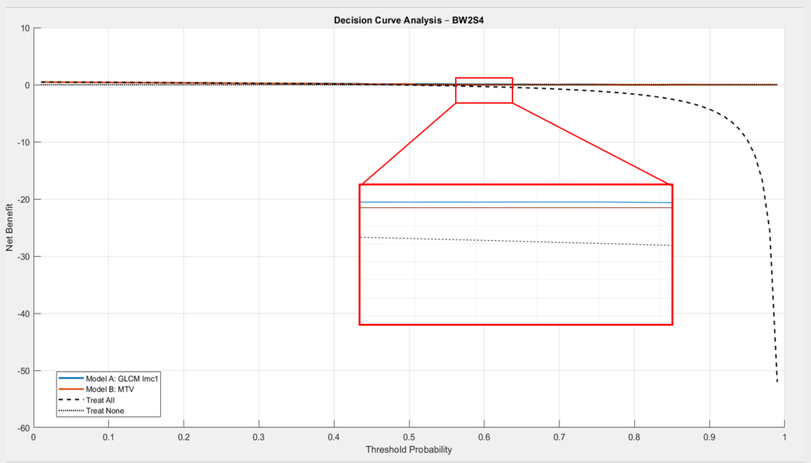

Figure 4: DCA curves comparing the best radiomics model to the best baseline model

DISCUSSION

- Radiomics-based models consistently outperformed baseline PET imaging biomarkers
- Bin width did not have a significant impact on feature selection or model performance
- SUVmax offered little discriminative performance
- While the difference was significant, the best performing radiomics model still had low performance (AUC = 0.689)
- Radiomics can likely be used as a supplementary biomarker for prognosis

CONCLUSIONS

- Radiomics features have value in prognosis for high-risk HL
- Future study is warranted on incorporating radiomics into clinical strategy

REFERENCES

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