

Radiogenomics For EGFR Mutation Status Prediction in CT Images:

Impact Of Model Design on Performance and Prospective Generalizability

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Disclosure

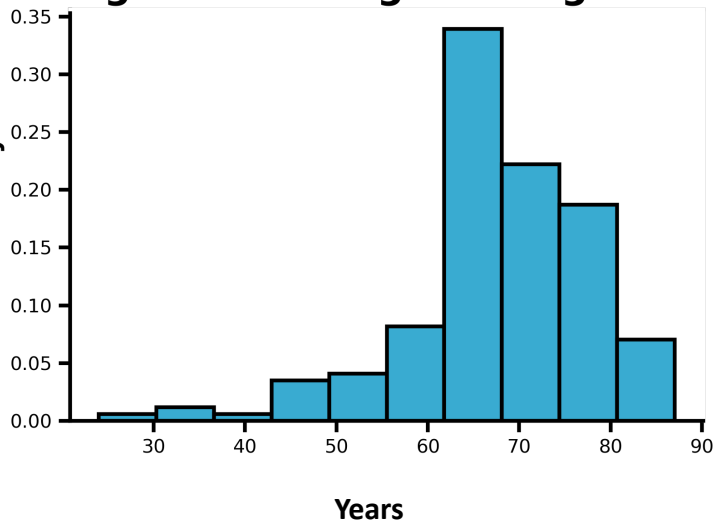
All authors were employees of Tempus Labs, a for-profit company, at the time of the research

Purpose

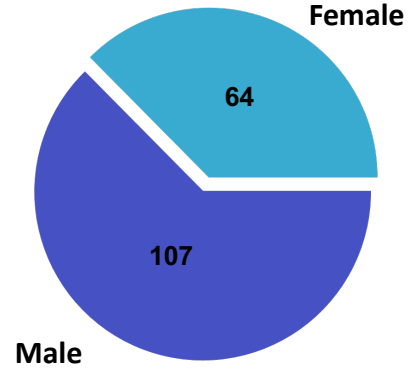
- Predict EGFR mutation status using CT scans
- Investigate how model design choices affect predictive power and robustness
 - CT Image exam: diagnostic CT vs CT from PET/CT
 - Feature extraction approach
 - Feature selection/dimensionality reduction approach
- Evaluate the prospective generalizability of models

Dataset

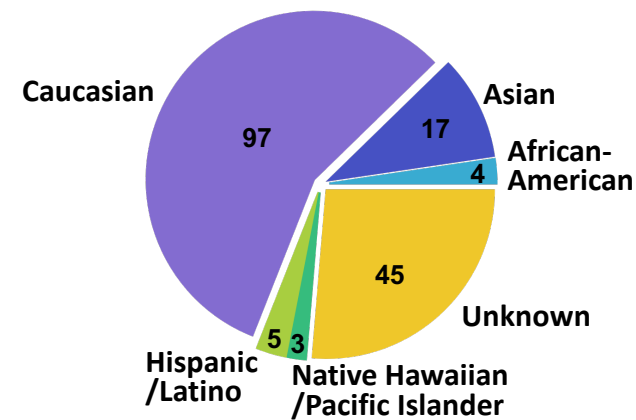
Age at Histological Diagnosis



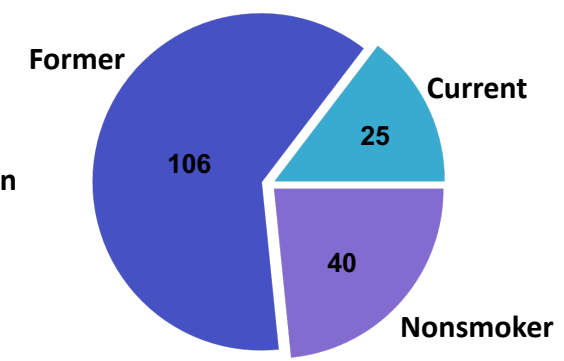
Gender



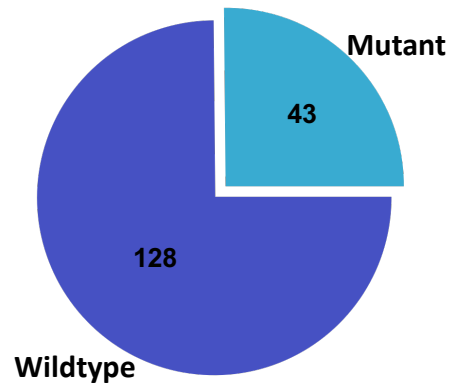
Ethnicity



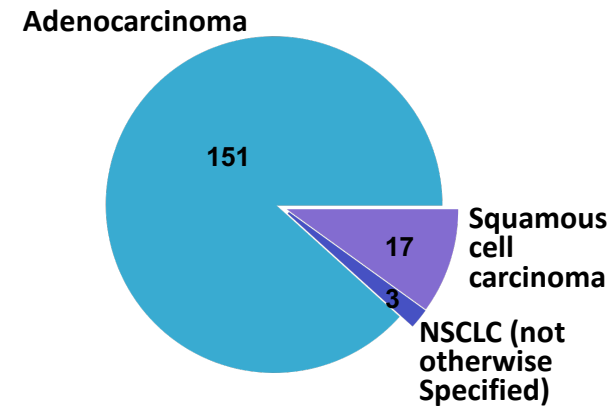
Smoking status



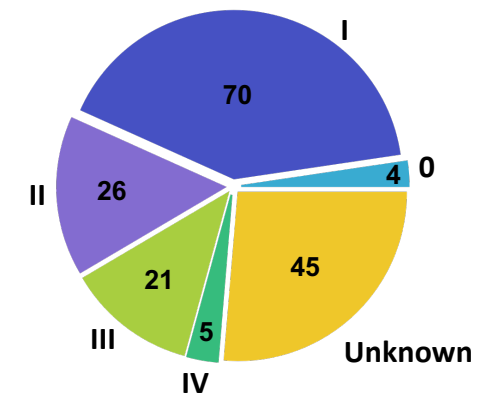
EGFR mutation status



Histology



Stage

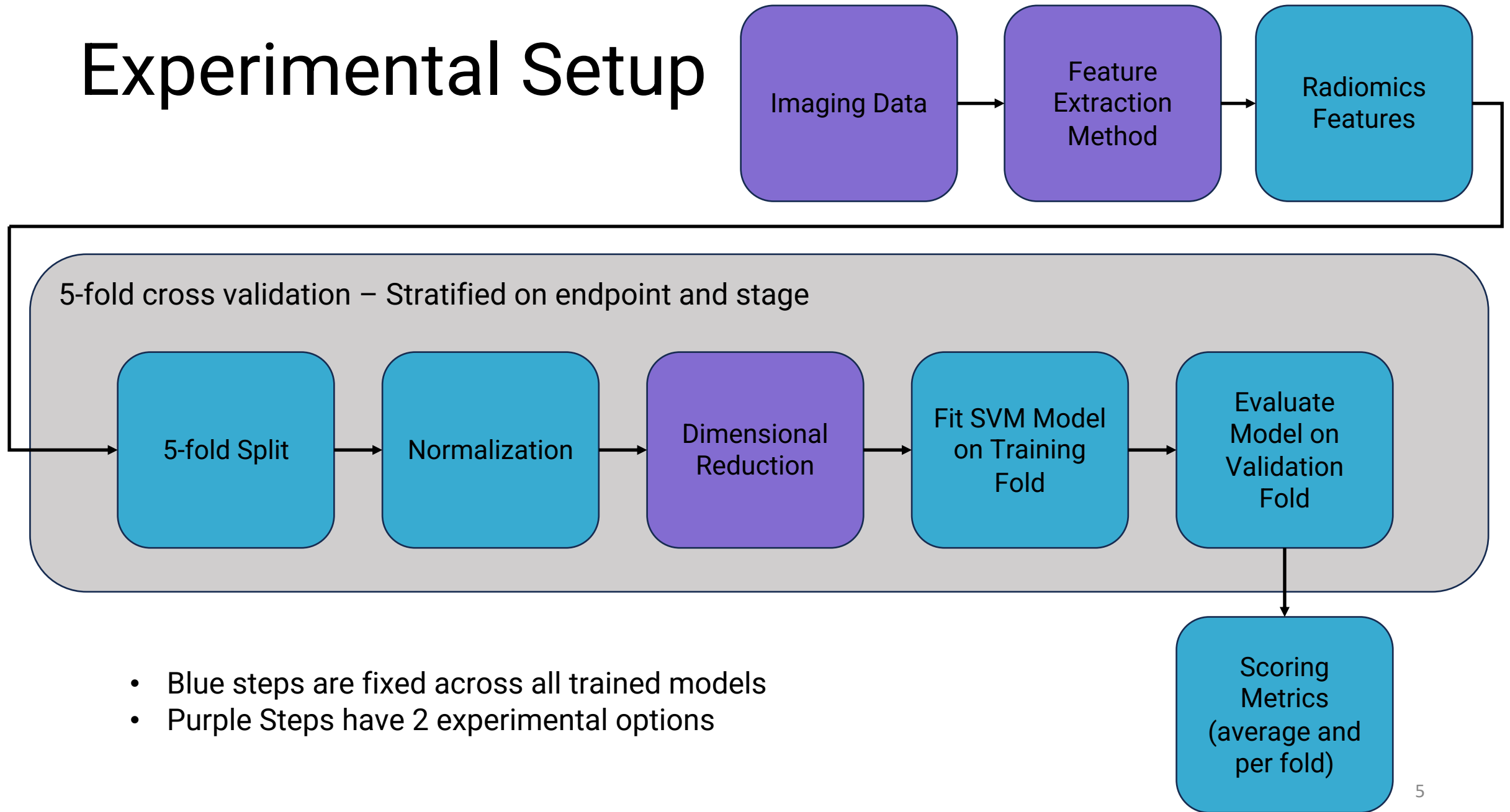


TCIA NSCLC-Radiogenomics public dataset*

171 NSCLC patients with radiology scans and EGFR mutation status

*Bakr, S., Gevaert, O., Echegaray, S. *et al.* A radiogenomic dataset of non-small cell lung cancer. *Sci Data* 5, 180202 (2018). <https://doi.org/10.1038/sdata.2018.202>

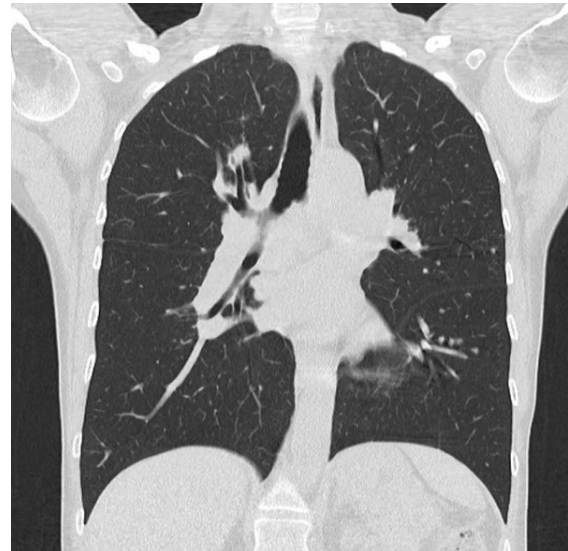
Experimental Setup



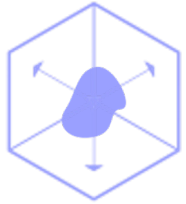
Experimental Variables

We compared model results from different:

- Image types:
 - Diagnostic CT scans
 - PET-CT CT scans
- Feature extractions method:
 - Standard radiomics features
 - Deep radiomics features
- Dimensionality reduction:
 - PCA
 - LASSO

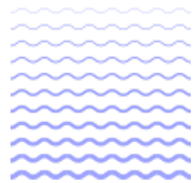


Standard Radiomics



SHAPE-BASED FEATURES

- Longest diameter
- Volume
- Surface Area
- Etc.



TEXTURAL FEATURES

- Contrast
- Non-uniformity
- Homogeneity
- Etc.



INTENSITY-BASED FEATURES

- Average
- Skewness
- Kurtosis
- Etc.

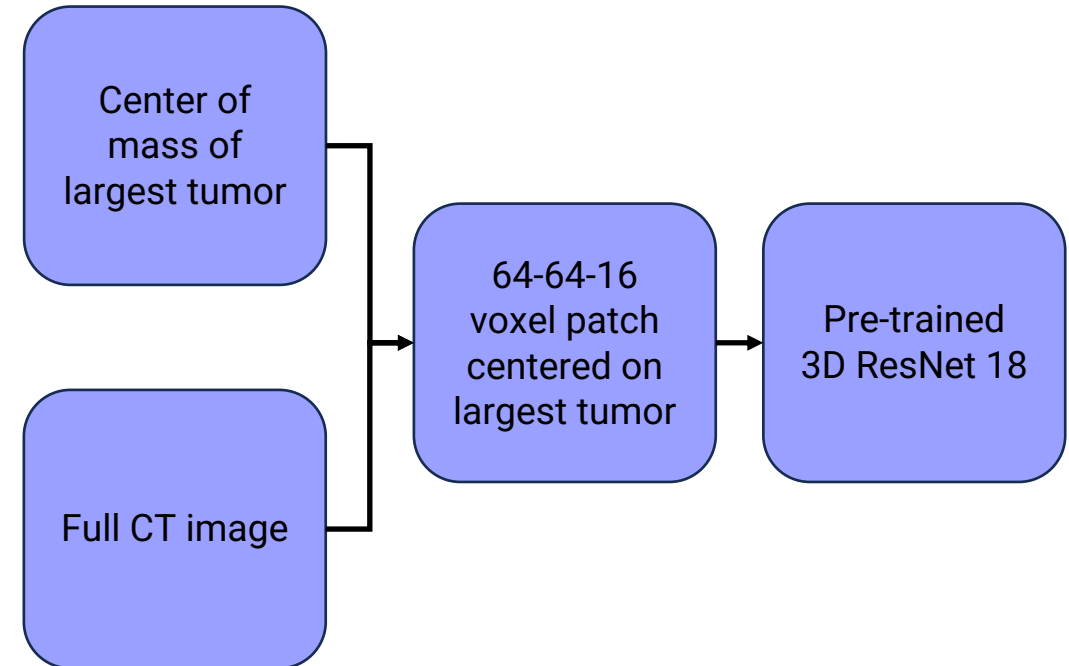


FILTER-BASED FEATURES

Wavelet and Laplacian of Gaussian filters are applied to the image prior to feature extraction

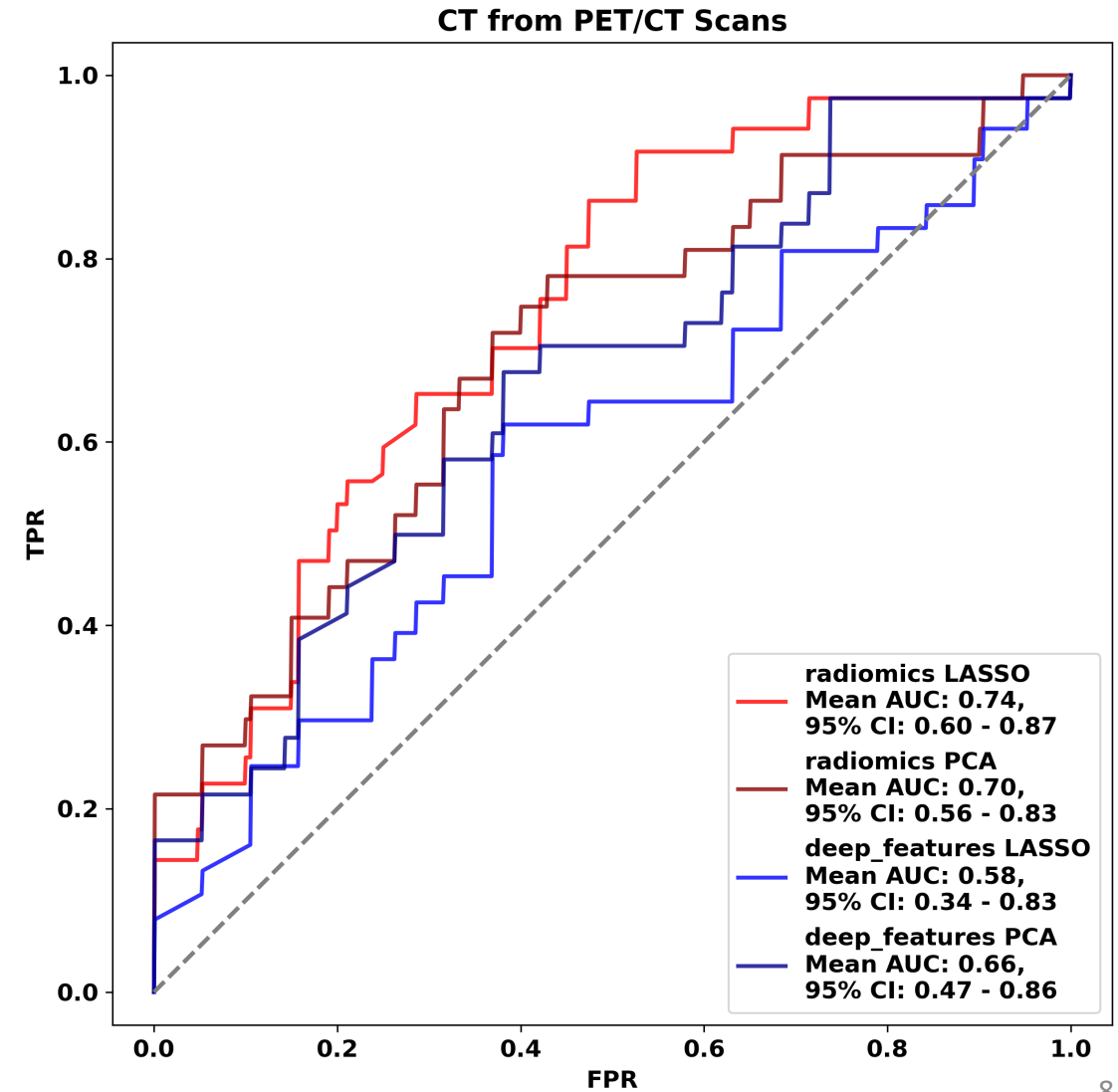
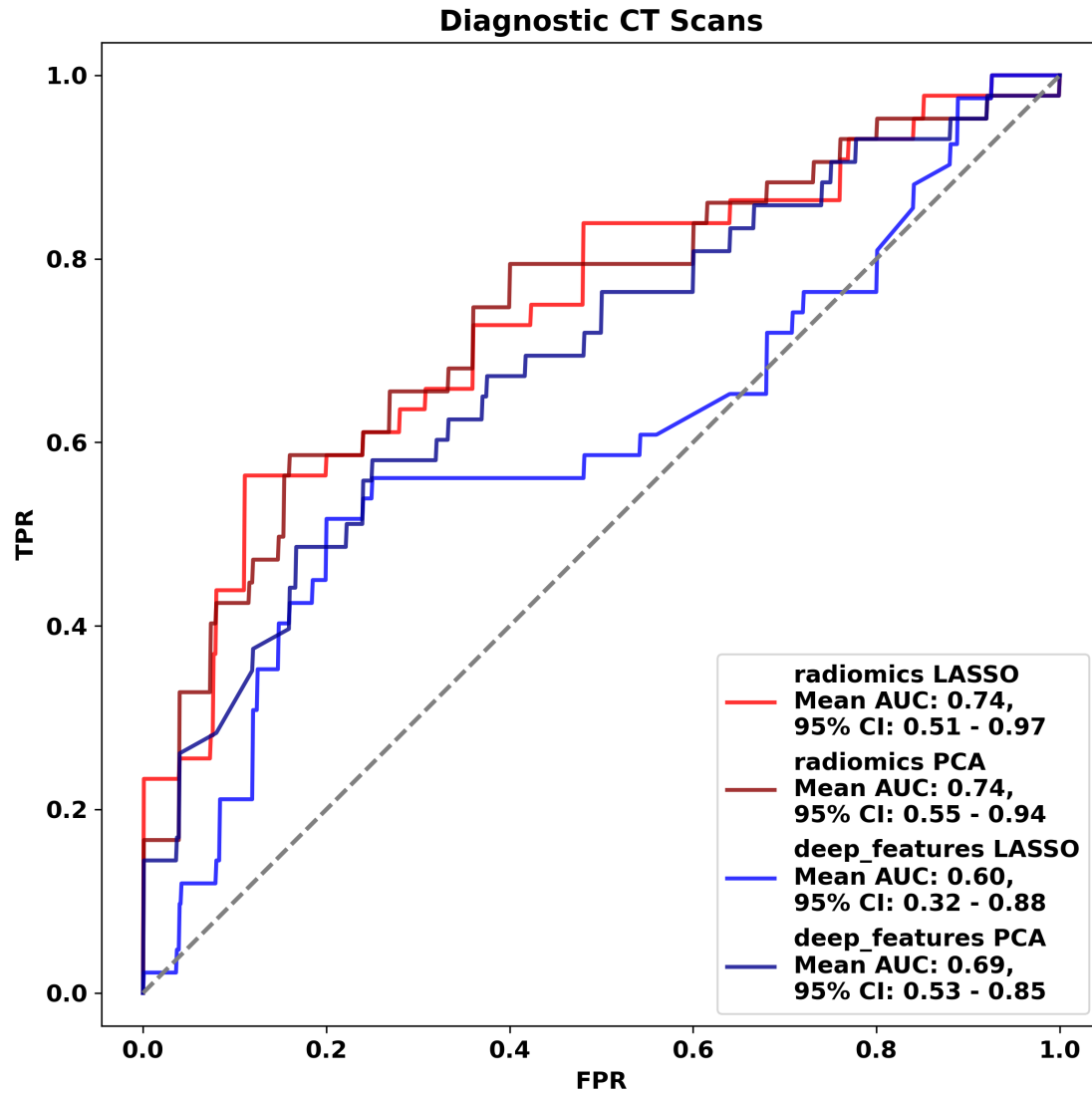
Output: 2072 features extracted using Tempus' dedicated radiomics feature extraction pipeline

Deep Radiomics

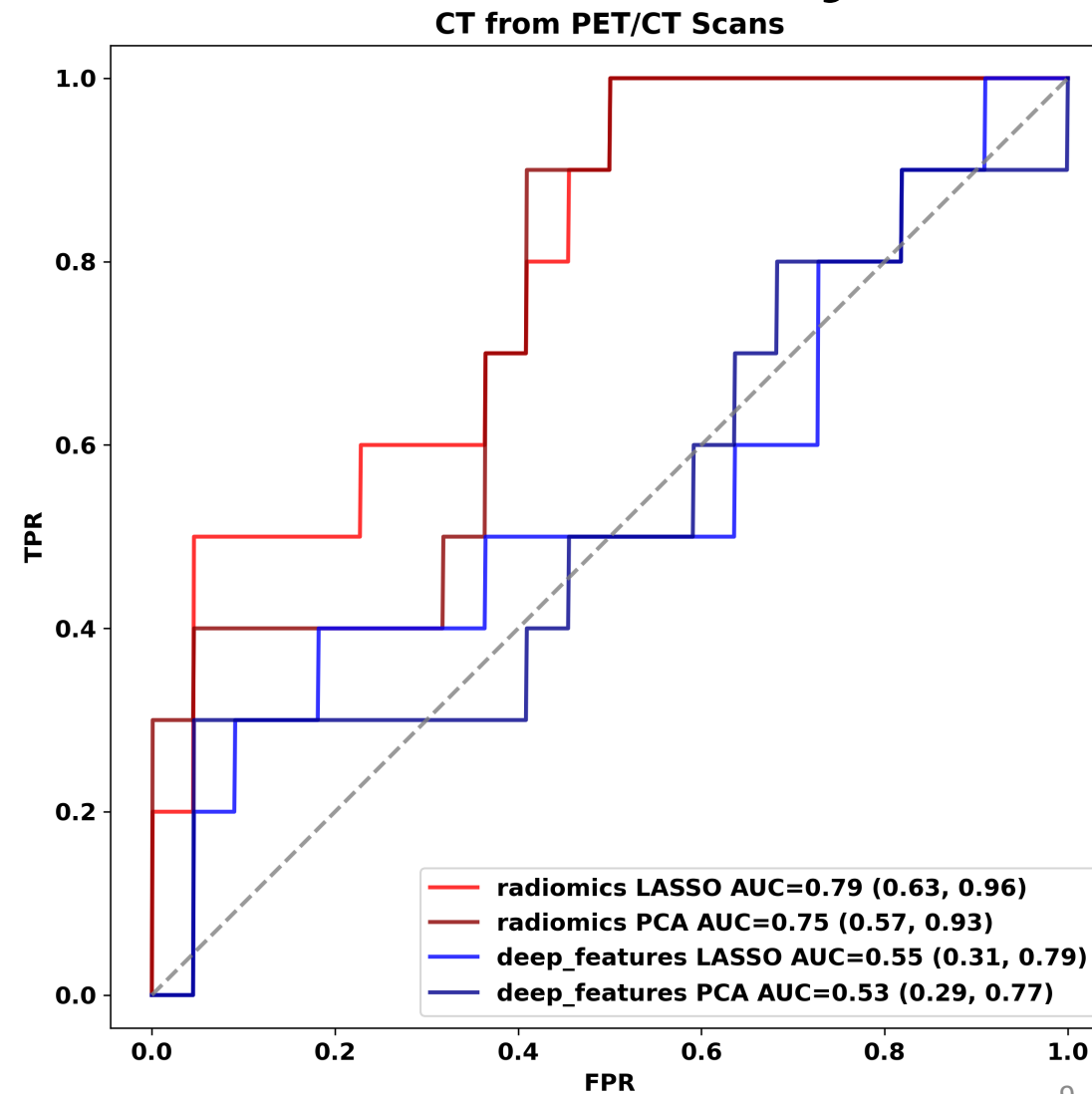
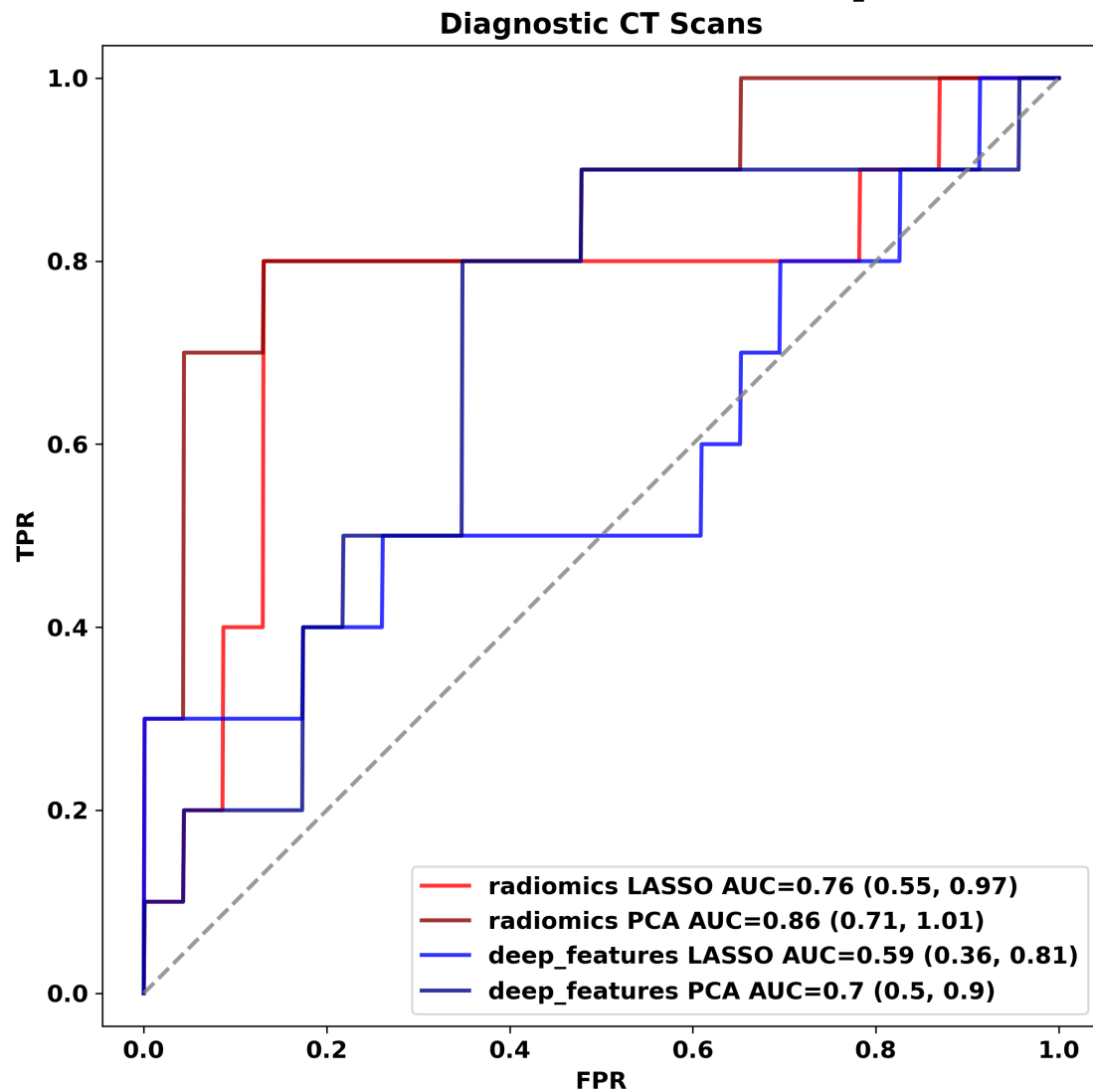


Output: 16,384 deep features/embeddings

Results – Validation Folds



Results – Prospective Generalizability



Common LASSO Selected Features

Percent of CV folds Feature Selected In

	PETCT CTs	Diagnostic CTs
GLSZM LargeAreaHighGrayLevelEmphasis	1	0.6
GLCM ClusterProminence	0.8	0.8
GLSZM ZoneVariance	0.6	0.8
Minimum Intensity	0	0.8
Local Binary Pattern feature 18	0.8	0

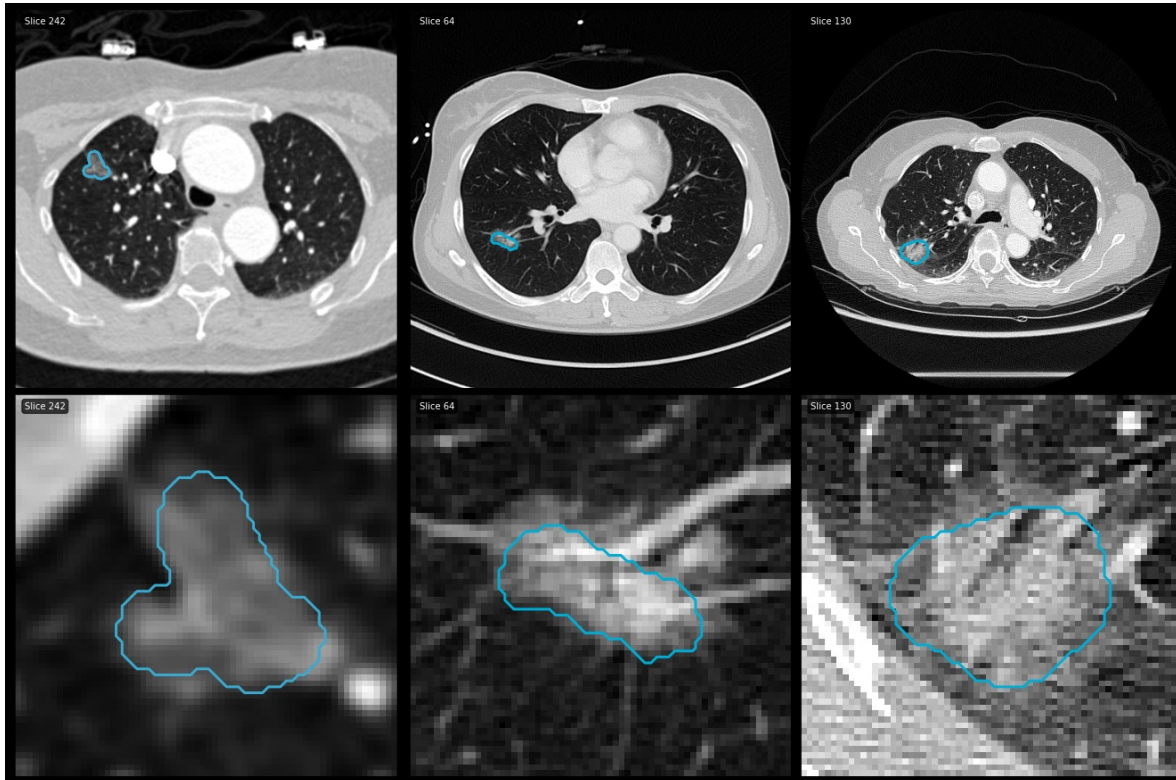
Example Scans

Mutation: EGFR+ Prediction: EGFR+

ID: AMC-027

ID: R01-136

ID: AMC-023

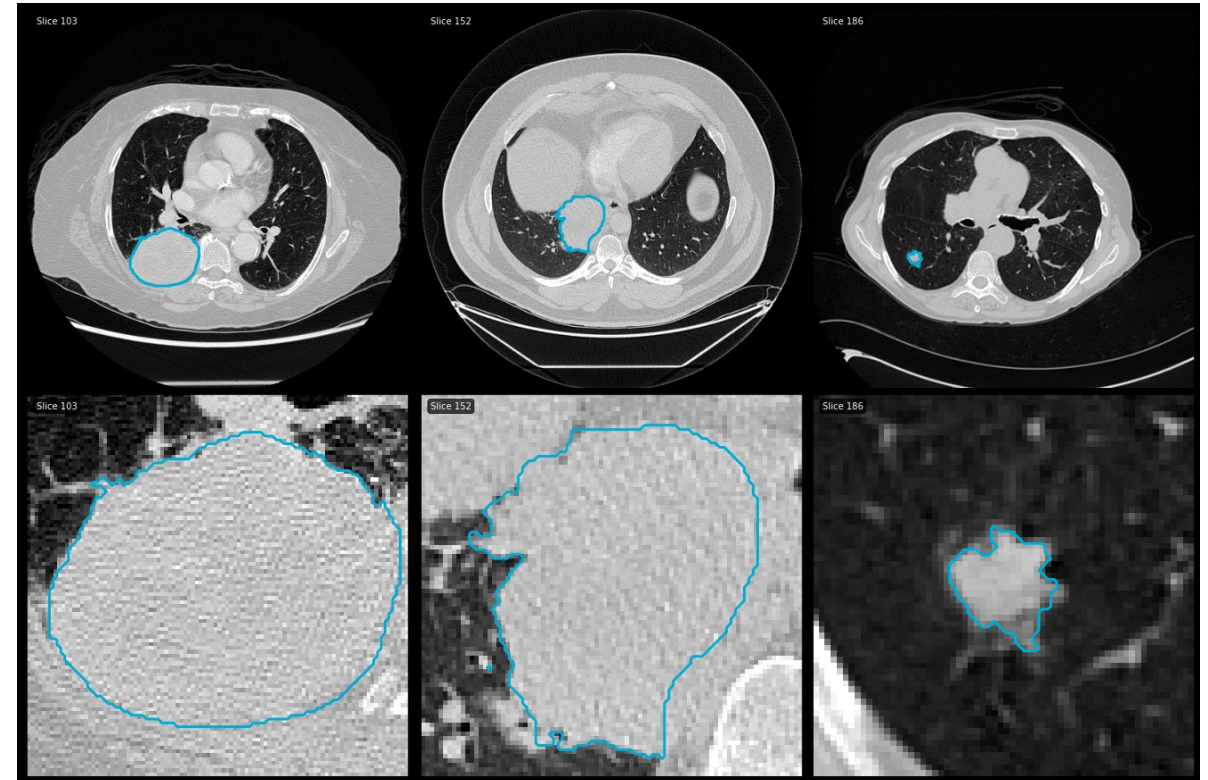


Mutation: EGFR- Prediction: EGFR-

ID: R01-090

ID: R01-036

ID: AMC-014



Discussion

- Tumor-based standard radiomics features performed better than deep feature-based approaches regardless of image type
- Model performance was similar using both diagnostic CT scans and CT scans from PET/CT exams, with PET/CT CT scans only slightly underperforming
- The effectiveness of standard radiomics feature models supports the ***potential of radiogenomics in early identification of patients likely to harbor EGFR mutations***