

Supplementary Materials:

Table S1. Detailed description of each article included

Reference (APA 7th format)	First autor	Year	Number of radiomics features	Features selection method	Model	Study	Metrics/ Performance	Data base size	Ground thruth	Histology
Agazzi, G et al. (2021). CT texture analysis for prediction of EGFR mutational status and ALK rearrangement in patients with non-small cell lung cancer. Radiologia Medica	Agazzi, G	2021	Not available (only texture)	SMOTE	GBM with a nested cross-validation approach	R	Median accuracy: 81.76% [95% CI 81.45–82.06]	84	Segmentation: radiologists EGFR: direct sequencing	Adenocarcinoma Metastatisis
Dang, Y., et al. (2021). Clinical and radiological predictors of epidermal growth factor receptor mutation in nonsmall cell lung cancer. Journal of Applied Clinical Medical Physics	Dang, Y	2021	1287	Mann-Whitney U test Spearman CC RF based Boruta algorithm	Rad-Score calculated with respective weighted coefficients by using a LR	R	ROC AUC of 0.798 (95% CI: 0.664 to 0.931)	132	Segmentation: radiologists EGFR: not mentioned (EGFR mutations identified on 4 tyrosine kinase domains (exons 18–21))	SCC
Digumarthy, S. et al. (2019). Can CT radiomic analysis in NSCLC predict histology and EGFR mutation status? Medicine	Digumarthy, S	2019	11	Not mentionned	Not used (multivariable logistic regression for assessment)	R	Radiomic features (kurtosis, K2) [ROC AUC 0.656–0.713, P = .03 to .003]; radiomics, clinical & imaging features : (ROC AUC 0.890, P < .0001)	93	Segmentation: radiologists EGFR: not mentioned (EGFR mutations identified on 4 tyrosine kinase domains (exons 18–21))	SCC
Dong, Y., et al. (2022). Development and validation of novel radiomics-based nomograms for the prediction of EGFR mutations and Ki-67 proliferation index in non-small cell lung cancer. Quantitative Imaging in Medicine and Surgery	Dong, Y	2022	638	Wilkinson's ICC (intraclass correlation coefficient)	LASSO logistic regression analysis	R	ROC AUC : 0.786 (95% CI: 0.621-0.95)	118	Segmentation: radiologists EGFR: PCR	SCC
He, R., et al. (2022). A Machine Learning-Based Predictive Model of Epidermal Growth Factor Mutations in Lung Adenocarcinomas. Cancers	He, R	2022	622	PCA LASSO	K-nearest neighbor, RF, LGBM, SVM	R	ROC AUCs : RF 0.66±0.06; KNN 0.62±0.05; SVC = 0.67±0.04; LGBM model = 0.66±0.07	758	Segmentation: radiologists EGFR: direct sequencing	Adenocarcinoma
Hong, D., et al. (2020). Radiomics Signature as a Predictive Factor for EGFR Mutations in Advanced Lung Adenocarcinoma. Frontiers in Oncology	Hong, D.	2020	396	LASSO	LR	R	ROC AUC : 0.851 (95% CI, 0.750 to 0.951)	201	Segmentation: radiologists EGFR: PCR	Adenocarcinoma
Jia, T. Y., et al. (2019). Identifying EGFR mutations in lung adenocarcinoma by noninvasive imaging using radiomics features and random forest modeling. European Radiology	Jia, T	2019	440	pvalue of each feature in the training cohort (performance driven)	EF classifiers	R	ROC AUC: 0.802. ROC AUC further improved to 0.828 by adding sex & smoking history. Se & sp: 60.6% & 85.1% at the best diagnostic decision point	503	Segmentation: radiologists EGFR: PCR	Adenocarcinoma

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Jiang, M., et al. (2019). Assessing EGFR gene mutation status in non-small cell lung cancer with imaging features from PET/CT. Nuclear Medicine Communications	Jiang, M	2019	512	LASSO	SVM 10-fold cross validation	R	ROC AUC of predicting results for 31 (18 for CT & 13 for PET) quantitative results 0.833 (95% CI: 0.74–0.93), counterpart to ROC AUC of outcomes for 4 qualitative features 0.731 (95% CI: 0.62–0.85). When quantitative features combining qualitative features: ROC AUC of predicting results for the whole 35 features: 0.953 (95% CI: 0.88–1)	80	Segmentation: radiologists EGFR: PCR	SCC
Koyasu, S., et al. (2020). Usefulness of gradient tree boosting for predicting histological subtype and EGFR mutation status of non-small cell lung cancer on 18F FDG-PET/CT. Annals of Nuclear Medicine	Koyasu, S	2020	7 type (not mentioned)	Not mentioned	RF classifiers Gradient tree boosting	R	ROC AUC values: RF, single type: 0.625; XGB, single type: 0.617; RF, multiple types: 0.577; XGB, multiple types: 0.659.	138	Public database	SCC
Le, N. Q. et al. (2021). Machine learning-based radiomics signatures for egfr and kras mutations prediction in non-small-cell lung cancer. International Journal of Molecular Sciences	Le, N	2021	851	Univariate selection, RFE, Feature importance, Filter methods, F-score, GA, minimum redundancy feature selection KBest algorithm	kNN, LR, RF, XGBoos	R	ROC AUC : 0.89	161	Public database	SCC
Li, S., et al. (2019). Radiomics for the prediction of EGFR mutation subtypes in non-small cell lung cancer. Medical Physics	Li, S	2019	580	Not mentioned	LR 5-fold cross validation	R	ROC AUC: 0.7925	312	Segmentation: radiologists EGFR: PCR mutations in EGFR exons 18 or 20, or simultaneous mutations in EGFR exons 19 & 21	SCC
Li, X. et al. (2018). Detection of epithelial growth factor receptor (EGFR) mutations on CT images of patients with lung adenocarcinoma using radiomics and/or multi-level residual convolutionary neural networks. Journal of Thoracic Disease	Li, X	2018	Not mentioned	RF classifiers	Multi-level residual CNNs based model	R	ROC AUC : 0.74 CI 0.670 0.811	1010	Segmentation: radiologists EGFR: PCR	Adenocarcinoma
Liu, Y. et al. (2016). Radiomic Features Are Associated With EGFR Mutation Status in Lung Adenocarcinomas. Clinical Lung Cancer	Liu, Y.	2016	Not mentioned	Not mentioned	multiple LR	R	ROC AUC : 0.667(95% CI, 0.604-0.721)	298	Segmentation: radiologists EGFR: PCR	Adenocarcinoma
Liu, Y et al. (2022). Development and Validation of Machine Learning Models to Predict Epidermal Growth Factor Receptor Mutation in Non-Small Cell Lung Cancer: A Multi-Center Retrospective Radiomics Study. Cancer Control	Liu, Y.	2022	1085	Intraclass correlation coefficient, hypothesis tests and LASSO.	LR, DT, RF, SVM	R	ROC AUC: .88, 95% CI: .75-.946	346	Segmentation: cardiothoracic disease imaging physicians EGFR: not mentioned	SCC; Large cell carcinoma pulmonary sarcomatoid carcinoma

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Lu, L et al. (2020). Radiomics prediction of egfr status in lung cancer—our experience in using multiple feature extractors and the cancer imaging archive data. Tomography	Lu, L	2020	IBEX (1563 features) & Pyradiomics (1319 f.), & in-house software, CIFE (1160 f.)	Included in the model	KNN, SVM, LASSO, RF bagging	R	IBEX, Pyradiomics, and CIFE yielded similar areas under the ROC of 0.68, 0.67, & 0.69. However, in validation, areas under the ROC of multivariate prediction models from IBEX, Pyradiomics, & CIFE decreased to 0.54, 0.56 & 0.64	228	Public database	SCC
Nair, J. et al. (2021). Radiogenomic Models Using Machine Learning Techniques to Predict EGFR Mutations in Non-Small Cell Lung Cancer. Canadian Association of Radiologists Journal	Nair, J	2021	326	LR	LR	R	0.8307+/-0.07	50	Segmentation: radiologists EGFR: PCR	Adenocarcinoma
Ninomiya, K et al. (2021). Robust radiogenomics approach to the identification of EGFR mutations among patients with NSCLC from three different countries using topologically invariant Betti numbers. PLoS ONE	Ninomiya, K	2021	52	Not mentioned	SVM 5-fold cross validation	R	0.86(0.78–0.93	194	Segmentation: radiologists EGFR: PCR	SCC
Rossi, G et al. (2021). Radiomic Detection of EGFR Mutations in NSCLC. Cancer Research	Rossi, G	2021	104	Variation test-retest PCA	SVM	R	ROC AUC : 0.85	109	Segmentation: radiologists EGFR: PCR	SCC
Shiri, I., et al. (2022). Impact of feature harmonization on radiogenomics analysis: Prediction of EGFR and KRAS mutations from non-small cell lung cancer PET/CT images. Computers in Biology and Medicine	Shiri, I	2022	218	ML-based feature selection (not specified)	RF	R	ROC AUCs 0.92–0.94 for EGFR	136	Public database	SCC
Tu, W et al. (2019). Radiomics signature: A potential and incremental predictor for EGFR mutation status in NSCLC patients, comparison with CT morphology. Lung Cancer	Tu, W.	2019	234	ICCs, Mann-Whitney U, Unsupervised consensus clustering	Multivariable logistic regression	R	ROC AUC 0.775 (0.703-0.847)	404	Segmentation: radiologists EGFR: not mentioned	NSCLC (no precision)
Li, X., et al. (2019). Predictive Power of a Radiomic Signature Based on. Front Oncol	Li,X	2019	38	LASSO	LASSO	R	ROC AUC (95%CI) = 0.83 (0.68, 0.92)	115	Segmentation: radiologists EGFR: PCR	
Li, Y., et al. (2018). CT Slice Thickness and Convolution Kernel Affect Performance of a Radiomic Model for Predicting EGFR Status in Non-Small Cell Lung Cancer: A Preliminary Study. Scientific reports	LI,Y	2018	1695	SVM	CCC	R	0.83 (0.68, 0.92)	51	Segmentation: radiologists EGFR: PCR	Adenocarcinoma
Wang, C., et al. (2022). Predicting EGFR and PD-L1 Status in NSCLC Patients Using Multitask AI System Based on CT Images. Frontiers in Immunology	Wang, C	2022	1247	LASSO	NLP	R	ROC AUCs: DL 0.906(0.885-0.930) Radiomics 0.860(0.816-0.902) Joint 0.928(0.909-0.946)	3629	Segmentation: Not mentioned EGFR: not mentioned	SCC

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Yang, C et al. (2020). Application of CT radiomics features to predict the EGFR mutation status and therapeutic sensitivity to TKIs of advanced lung adenocarcinoma. Translational Cancer Research	Yang, C	2020	715	LASSO	LR 10-fold cross validation	R	ROC AUC values of the unenhanced, arterial & venous phases in the EGFR mutation status training group: 0.6713, 0.8194 & 0.8464	253	Segmentation: radiologists EGFR: PCR ARMS	Adenocarcinoma
Yang, L., et al. (2022). PET/CT Radiomic Features: A Potential Biomarker for EGFR Mutation Status and Survival Outcome Prediction in NSCLC Patients Treated With TKIs. Frontiers in Oncology	Yang, L	2022	1037	Univariate LR analysis to select features with P<0.05 for the subsequent analysis. Secondly, multivariate LR analysis applied to choose features closely related to different EGFR status. Informative features retained using the LASSO	SVM, DT, RF	R	ROC AUC of EGFR-WT, EGFR-19-WT, and EGFR-21-WT, with 0.881, 0.851, and 0.849, respectively, and validation ROC AUCs of 0.926, 0.805 & 0.859, respectively	313	Segmentation: radiologists EGFR: PCR	Adenocarcinoma
Yang, X., et al. (2022). Using contrast-enhanced CT and non-contrast-enhanced CT to predict EGFR mutation status in NSCLC patients—a radiomics nomogram analysis. European Radiology	Yang, X	2022	1092	Mann-Whitney U test, Spearman CC, RF based Boruta algorithm	ML methods included SVM, LR, RF, GBDT, & NBC	R	0.850 (0.608–1.000)	412	Segmentation: radiologists EGFR: PCR	NSCLC (no precision)
Zhang, J., et al. (2020). Value of pre-therapy 18F-FDG PET/CT radiomics in predicting EGFR mutation status in patients with non-small cell lung cancer. European Journal of Nuclear Medicine and Molecular Imaging	Zhang, J	2020	45	LASSO	RF	R	0.87 (95%CI [0.79–0.95])	248	Segmentation: radiologists EGFR: PCR	Adenocarcinoma
Zhang, L., et al. (2018). Quantitative Biomarkers for Prediction of Epidermal Growth Factor Receptor Mutation in Non-Small Cell Lung Cancer. Translational Oncology	Zhang, L.	2028	485	LASSO	A multivariable logistic regression	R	AUXC wkith and without clinical feartures0.62 to 0.85	180	Segmentation: radiologists EGFR: PCR	Adenocarcinoma: 48.6% (68/140) of cases; SCC: 38.6% (54/140); others: 12.8% (18/140)

CCC=Concordance correlation coefficient; CIFE=Columbia Image Feature Extractor; DT=decision tree; Feature Extractor; GBDT=gradient boosting decision tree; GBM=Generalized boosted regression model; ML=Machine learning; NBC=naïve Bayesian classification; LASSO=Least absolute shrinkage and selection operator; LR= logistic regression; R=retrospective; RF=Random forest; SCC=Squamous cell carcinoma; Se=Sensitivity; SMOTE=Synthetic minority oversampling technique; Sp=specificity; ; SVM=support vector machine; RFE=Recursive feature elimination; ROC=receiver operating characteristic curve; PCA=Principal component analysis