

used to evaluate the performance in the testing set. **Results:** In the training set, the 3 different ML pipelines selected slightly different sets of features (25, 27 and 37 variables for RF, SVM and LR) and reached similar although slightly different accuracy (90%, 95% and 74% for RF, SVM and LR respectively). In the testing set the accuracy was 68%, 67% and 65% for RF, SVM and LR respectively. The majority voting of their outputs reached a higher performance (accuracy of 100% in the training set and 75% in the testing set). **Conclusion:** Different ML pipelines reached similar accuracy in predicting the notoriously difficult endpoint of survival in NSCLC. Implementing simple majority voting of these outputs allowed to increase the accuracy. Even though the level of accuracy reached can seem relatively low (~75%), the resulting prognostic stratification is higher than when relying on clinical stage (58%), and of interest for clinical practice as it could help identifying patients with higher risk amongst stage II and III patients, that could benefit from intensified treatment and/or more frequent follow-up after treatment. **References:** None.

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Radiogenomics analysis of PET/CT images in lung cancer patients: Conventional radiomics versus deep learning

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Aim/Introduction: Analysis of the mutation status of epidermal growth factor receptor (EGFR) and Kirsten rat sarcoma viral oncogene (KRAS) mutations are frequently used as treatment management tools in non-small cell lung cancer (NSCLC). The objective of this study was to investigate and compare EGFR and KRAS mutation status in PET images using conventional radiomics (explicit-feature-extraction) versus deep learning (implicit-feature-extraction). **Materials and Methods:** 147 NSCLC patients were included in the study, where 32 had effective EGFR mutations, 37 had KRAS mutations, and 110 and 115 had no EGFR or KRAS mutations, respectively. Tumors were segmented by semiautomatic method from the PET images (expert radiologist). For conventional radiomics analysis, images were first discretized into 64 bin levels. 105 features were subsequently extracted from the lesions, including statistical

(SUV), shape, GLCM, GLSZM, GLRLM, NGTDM and GLDM. Following feature extraction, we apply a union on embedded feature selection with different methods to get a set of useful features. After getting the union, we investigated correlations between features to eliminate high correlate features. The selected features were fed into different classifiers including decision tree (DT), bagging, gradient boosting (GB), random forest (RF), ada-boost (AB), logistic regression (LR), support vector machine (SVM), naïve Bayesian (NB), LASSO, multi-layer perceptron (MLP), and an ensemble of the above methods. By comparison, our deep learning framework included a 3D deep convolution neural network (CNN) composed of 3×3×3 convolutions, batch norm, LeakyReLU, and 2×2×2 max pooling blocks followed by fully connected layers. The final layer is a soft-max for binary classification. We evaluated the performance of classifiers using receiver operating characteristic (ROC) area under the curve (AUC) analysis with 10-fold cross validation.

Results: NB and RF with AUCs of 75.04 and 72.02 had the highest performance in predicting EGFR and KRAS mutations, respectively. Ensemble methods had AUCs of 86.98 and 77.05 for predicting EGFR and KRAS, respectively. Finally, CNN had AUCs of 89.95 and 79.02 in predicting EGFR and KRAS mutations, respectively. **Conclusion:** Radiogenomics analysis of PET images in NSCLC patients was undertaken to link PET uptake and heterogeneity quantitation with genomics. Ensemble learning in the context of radiomics analysis can result in significantly higher performance compared to individual learning models, while deep learning (CNN; implicit feature extraction) showed the highest performance in prediction of EGFR and KRAS status. The results of the current study indicate the potential of advanced machine learning methods within radiogenomics analysis towards non-invasive prediction of mutation status in patients with NSCLC. **References:** None.

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Towards fully automated image processing in the clinic

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Aim/Introduction: Machine learning has huge potential in Nuclear Medicine for increasing efficiency and improving accuracy. In particular, numerous authors have demonstrated high performance in segmentation, classification and regression tasks. However, many studies are based on assumptions which may not be reflective of the clinic, for instance using research rather than clinical data. Implementation for routine patient care has so far been limited. This study aims to demonstrate the performance of established machine learning methods for two routine nuclear medicine processing tasks, currently performed manually in clinic: 1) segmentation of the myocardium in MPS stress-rest scans (the segmentation mask being used to guide a rigid registration, to quantify differences in patient position) and 2) segmentation of the left ventricle blood pool for ejection fraction estimation on MUGA scans. Automating either of these tasks would achieve significant reductions in workload.