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Biomedical signal and image processing methods

Three-dimensional topological radiogenomics of epidermal growth factor receptor Del19 and L858R mutation subtypes on computed tomography images of lung cancer patients

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Highlights

- A 3DBN-based algorithm extracted topologically invariant lung cancer CT traits.
- 3DBN features could feasibly classify *EGFR* wild-type and Del19/L858R mutations.
- 3DBN features showed radiogenomic associations with *EGFR* subtype characteristics.

Abstract

Objectives

: To elucidate a novel radiogenomics approach using three-dimensional (3D) topologically invariant Betti numbers (BNs) for topological characterization of epidermal growth factor receptor (*EGFR*) Del19 and L858R mutation subtypes.

Methods

: In total, 154 patients (wild-type *EGFR*, 72 patients; Del19 mutation, 45 patients; and L858R mutation, 37 patients) were retrospectively enrolled and randomly divided into 92 training and 62 test cases. Two support vector machine (SVM) models to distinguish between wild-type and mutant *EGFR* (mutation [M] classification) as well as between the Del19 and L858R subtypes (subtype [S] classification) were trained

using 3DBN features. These features were computed from 3DBN maps by using histogram and texture analyses. The 3DBN maps were generated using computed tomography (CT) images based on the Čech complex constructed on sets of points in the images. These points were defined by coordinates of voxels with CT values higher than several threshold values. The M classification model was built using image features and demographic parameters of sex and smoking status. The SVM models were evaluated by determining their classification accuracies. The feasibility of the 3DBN model was compared with those of conventional radiomic models based on pseudo-3D BN (p3DBN), two-dimensional BN (2DBN), and CT and wavelet-decomposition (WD) images. The validation of the model was repeated with 100 times random sampling.

Results

: The mean test accuracies for M classification with 3DBN, p3DBN, 2DBN, CT, and WD images were 0.810, 0.733, 0.838, 0.782, and 0.799, respectively. The mean test accuracies for S classification with 3DBN, p3DBN, 2DBN, CT, and WD images were 0.773, 0.694, 0.657, 0.581, and 0.696, respectively.

Conclusion

: 3DBN features, which showed a radiogenomic association with the characteristics of the *EGFR* Del19/L858R mutation subtypes, yielded higher accuracy for subtype classifications in comparison with conventional features.

Keywords

Radiogenomics; Computational topology; Molecularly targeted drugs; Precision medicine