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Training of deep convolutional neural nets to extract radiomic signatures of tumors

Author Block: Jiwon Kim¹, Sophia Seo¹, Saeed Ashrafinia², Arman Rahmim, PhD¹, Vesna Sossi¹, Ivan S. Klyuzhin, PhD¹.

¹University of British Columbia, Vancouver, BC, Canada, ²Johns Hopkins University School of Medicine, Baltimore, MD, USA.

Abstract:

Objectives: Radiomics-based analysis of FDG PET images has been shown to improve the assessment and prediction of tumor growth rate, response to treatment and other patient outcomes [1]. An alternative new approach to image analysis involves the use of convolutional neural networks (CNNs), wherein relevant image features are learned implicitly and automatically in the process of network training [2]; this is in contrast to radiomics analyses, where the features are "hand-crafted" and are explicitly computed (EC). Although CNNs represent a more general approach, it is not clear whether the implicitly learned features may, or have the ability to include radiomics features (RFs) as a subset. If this is the case, CNN-based approaches may eventually obviate the use of EC RFs. Further, the use of CNNs instead of RFs may completely eliminate the need for feature selection and tumor delineation, enabling high-throughput data analyses. Thus, our objective was to test whether CNNs can learn to act similarly to several commonly used RFs. Using a set of simulated and real FDG PET images of tumors, we train the CNNs to estimate the values of RFs from the images without the explicit computation. We then compare the values of the CNN-estimated and FC features.

Methods: Using a stochastic volumetric model for tumor growth, 2000 FDG images of tumors confined to a bounding box (BB) were simulated (40x40x40 voxels, voxel size 2.0 mm), and 10 RFs (3 x morphology, 4 x intensity histogram, 3 x texture features) were computed for each image using the SERA library [3] (compliant with the Image Biomarker Standardization Initiative, IBSI [4]). A 3D CNN with 4 convolutional layers, and a total of 164 filters, was implemented in Python using the Keras library with TensorFlow backend (https://www.keras.io). The mean absolute error was the optimized loss function. The CNN was trained to automatically estimate the values each of the 10 RFs for each image; 1900 of images were used for training, and 100 were used for testing, to compare the CNN-estimated values to the EC feature values. We also used a secondary test set comprised of 133 real tumor images, obtained from the head and neck PET/CT imaging study [5] publicly available at the Cancer Imaging Archive. The tumors were cropped to a BB, and the images were resampled to yield similar image size to the simulated image set.

Results: After the training procedure, on the simulated test set the CNN was able to estimate the values of most EC RFs with 10–20% error (relative to the range). In the morphology group, the errors were 3.8% for volume, 12.0% for compactness, 15.7% for flatness. In the intensity group, the errors were 13.7% for the mean, 15.4% for variance, 12.3% for skewness, and 13.1% for kurtosis. In the texture group, the error was 10.6% for GLCM contrast, 13.4% for cluster tendency, and 21.7% for angular momentum. With all features, the difference between the CNN-estimated and EC feature values were statistically insignificant (two-sample t-test), and the correlation between the feature values was highly significant (p<0.01). On the real image test set, we observed higher error rates, on the order of 20–30%; however, with all but one feature (angular momentum), there was a significant correlation between the CNN-estimated and EC features (p<0.01).

Conclusions: Our results suggest that CNNs can be trained to act similarly to several widely used RFs. While the accuracy of CNN-based estimates varied between the features, in general, the CNN showed a good propensity for learning. Thus, it is likely that with more complex network architectures and training data, features can be estimated more accurately. While a greater number of RFs need to be similarly tested in the future, these initial experiments provide first evidence that, given the sufficient quality and quantity of the training data, the CNNs indeed represent a more general approach to feature extraction, and may potentially replace radiomics-based analyses without compromising the descriptive thoroughness.

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