



Multidomain Sequence Classification of Brain, Knee, and Prostate MRIs Through 3D-CNN and Gradient Boosted Trees

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Introduction

Numerous unique MR sequences are utilized in imaging each body part. Given human error and time constraints, DICOMs often contain incorrect image information, slowing radiologists' workflows but also limiting the accessibility of MR data for machine learning. Automated classification could lessen the manual burden of labeling sequences and improve accuracy. While specialized algorithms for classification of MR images for individual body parts have been reported, an algorithm for multiple body domains is demonstrated in this abstract.

Hypothesis

Classification of MRI sequences from multiple domains can be achieved above the 85% accuracy estimated of DICOM headers in practice (Guld et al, 2002).

Methods

A subset of brain, knee, and prostate MR images were obtained from the publicly available fastMRI dataset (Zbontar et al, 2018). Sequences included 1000 brain axial T1, T1 post-contrast, and T2 images; 1000 knee axial T2 fat suppressed (FS), coronal PD, coronal PD FS, sagittal PD, and sagittal T2 FS images; and 300 prostate axial T2 and ADC images. Images were partitioned 80/20 between training/validation and testing.

Metadata-agnostic sequence classification was performed using a 3D Convolutional Neural Network (CNN)-XgBoost approach (Figure-1). Briefly, images were first run through a 3D CNN based on a ResNet-18 architecture with default ImageNet weights, implemented from an open source library (Soloyev et al, 2021). Output before the final network layer was extracted as a feature vector and subsequently input into gradient boosted decision trees implemented with the XgBoost algorithm, allowing classification into each sequence/body part. Training/validation of the decision trees was optimized with 5-fold cross validation with a grid search to determine the hyperparameters producing the highest validation accuracy.

Results

An accuracy of 91.3% was achieved on the test dataset. The largest error rate occurred in misclassifying brain axial T1 noncontrast versus contrast images (Figure-2).

Conclusion

Accurate automated classification of multidomain MR sequences was demonstrated through a 3D CNN-XgBoost approach.

Figure(s)

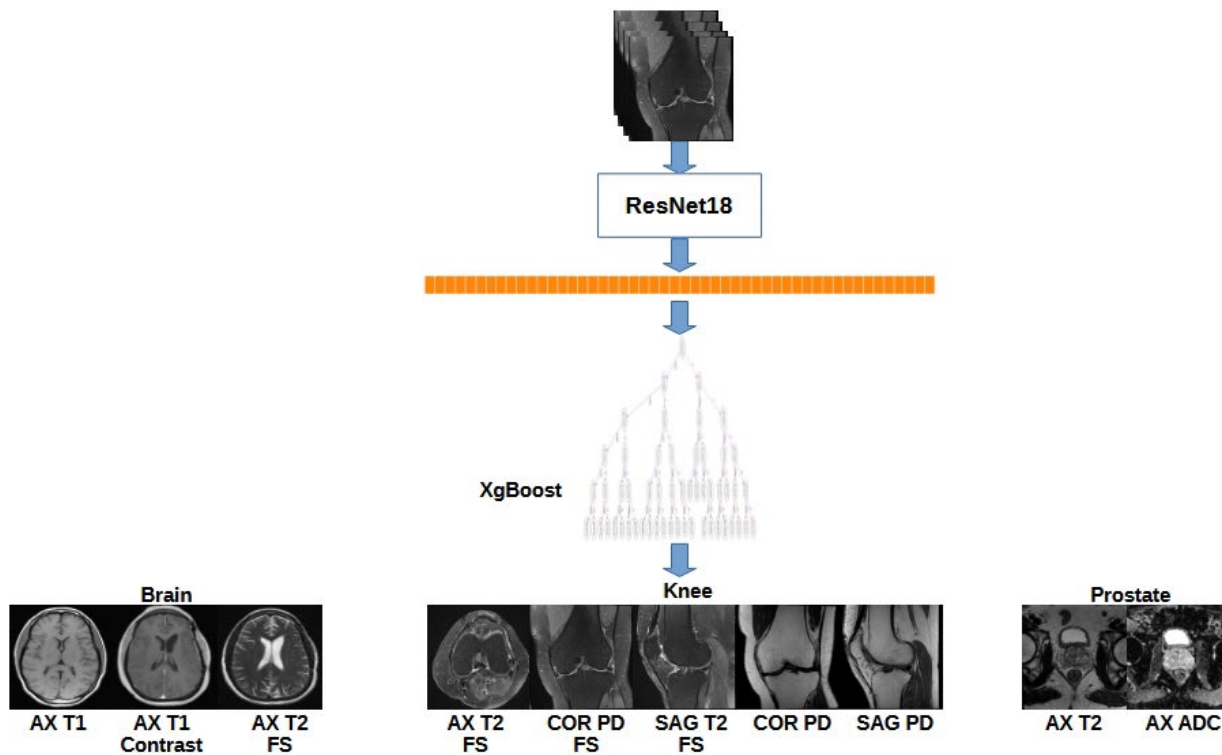


Figure 1. Pictorial of MR sequence classification by 3D CNN-XgBoost network

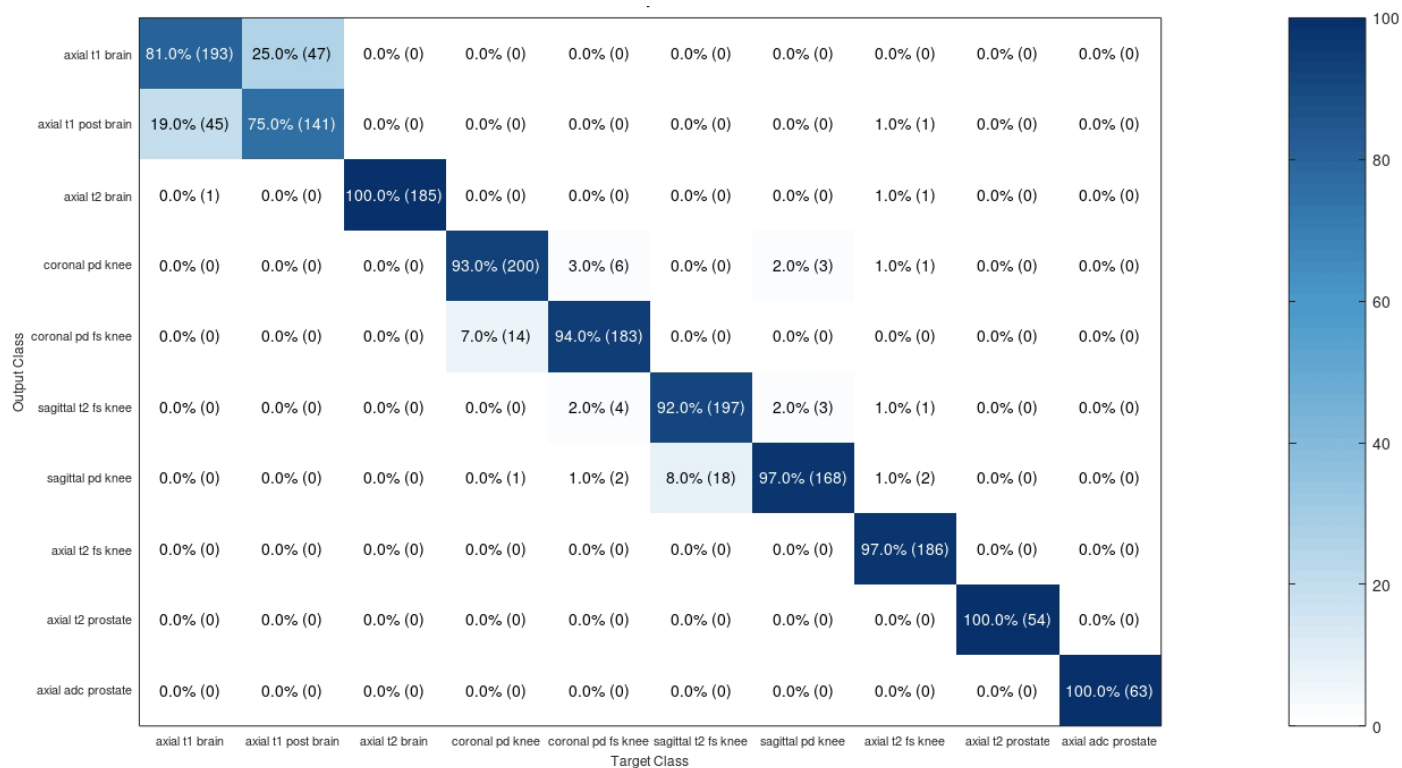


Figure 2. Confusion matrix with breakdown of error rates by sequence

Keywords

Artificial Intelligence/Machine Learning; Clinical Workflow & Productivity; Imaging Research