Deep Learning Pipeline for Automated Identification of Osteoarthritic Degenerative Changes in the Hip

Eugene Ozhinsky*, Radhika Tibrewala*, Valentina Pedoia, Sharmila Majumdar (*contributed equally)

HIGHLIGHTS: Manual identification of bone and cartilage abnormalities in MR images can be laborious and time consuming. The goal of this study was to develop a fully automated deep learning pipeline to identify morphological and degenerative changes in patients with hip osteoarthritis (OA).

INTRODUCTION: Osteoarthritis (OA) is a debilitating joint disease that involves the degeneration of the articular cartilage and affects more than 25% of the adult population. Previously, SHOMRI (Scoring Hip Osteoarthritis with MRI) has been proposed as an MR-based hip OA evaluation system, based on the presence of morphological abnormalities, such as bone marrow edema, cartilage lesions, labral abnormalities and cysts. However, manual identification of bone and cartilage abnormalities in MR images can be laborious and time consuming. Thus, the goal of this study was to develop a fully automated deep learning pipeline to identify morphological and degenerative changes in patients with OA of the hip joint that would act as a radiology assist in image interpretation.

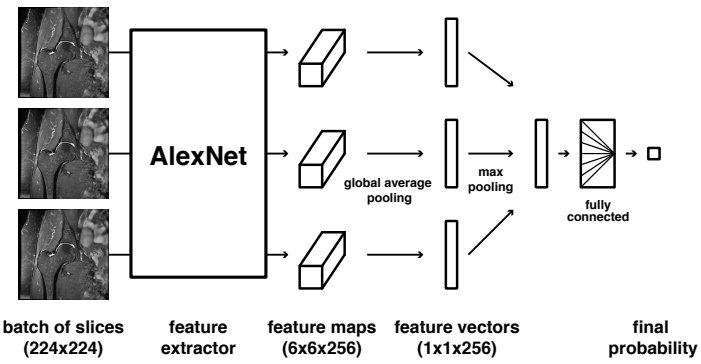
METHODS: 594 T2-weighted fat saturated coronal hip volumes from subjects with radiographic or symptomatic hip OA were used in this study. The data were split into training, validation, and testing set with the ratio of 65-25-15%. Per volume labels (Lesion/No Lesion in cartilage) were derived from SHOMRI grades.

A weekly-supervised multislice classification model, based on MRNet architecture (Bien, et al. PLoS Medicine. 2018) was implemented in Python using PyTorch framework. The image slices were center cropped to 150x150 mm. Feature maps from each slice were generated using AlexNet feature extractor, pre-trained on ImageNet dataset. The features were pooled within each slice and across slices into a combined feature vector. Finally, a fully connected classification layer was trained using the ground truth image labels.

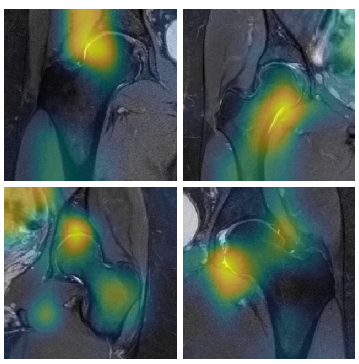
The network was trained for 50 epochs with weighted cross-enthropy loss (P=0.4), Adam optimizer with scheduler (LR = 10^{-5}) and data augmentations: random rotation (±5°), shift (±10 px), affine transformations, Gaussian noise. Saliency maps were generated to visualize the regions of the images that were most important for classification.

RESULTS: It took 11 training epochs for the network to reach the optimal classification performance. The network achieved an AUC of 0.74 (validation) and 0.71 (test) on binary lesion detection. Saliency maps tended to highlight areas of cartilage and bone marrow, indicating that the network has learned that features of those areas are important for OA detection.

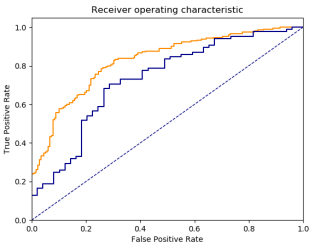
CONCLUSIONS: Our results have demonstrated the feasibility of automated identification of OA degenerative changes using deep learning models. Multislice network architecture allowed training with weak supervision (global labels only).



Multislice classification model architecture



Examples of class activation maps for cartilage lesion classification



ROC curves for train (orange) and validation (blue) datasets.