DEEP LEARNING ANALYSIS OF BONE STRUCTURE IN OSTEOGENESIS IMPERFECTA USING HR-PQCT IMAGES

Pouyan Asgharzadeh (1,2), Annette Birkhold (1), Elizabeth Zimmermann (2), Frank Rauch (2), Oliver Röhrle (1), Bettina Willie (2)

1. *Institute for Modelling and Simulation of Biomechanical Systems, University of Stuttgart, Germany*
2. *Research Centre, Shriners Hospital for Children-Canada, Department of Pediatric Surgery, McGill University, Canada*

Introduction

Osteogenesis imperfecta (OI), also known as "brittle" bone disease, is a rare heritable bone disorder. In most cases, OI is caused by mutations in genes encoding type I collagen (COL1A1 and COL1A2), leading to increased bone fragility attributed to reduced bone mass and quality. OI can be categorized according to disease severity into type I (mild), type II (perinatally lethal), type III (severe) and type IV (moderate) [1]. OI types differ quite markedly in disease severity and thus in fracture rates [2]. High resolution peripheral quantitative tomography (HR-pQCT) has emerged as an imaging modality that may allow improved clinical fracture prediction in individuals with OI [3]. Surprisingly, despite differences in disease severity, HR-pQCT parameters overlap considerably between OI types (I, III, or IV), which complicates the relationship between disease phenotype and bone fragility [4-5]. The aim of the study was to use a classification deep neural network (DNN) and random forest (RF) model capable of predicting OI types, to identify, in a non-biased manner, structural factors learned by the models from HR-pQCT images of human radii that explain differences in bone fragility between OI types.

Method

Ninety-six HR-pQCT images were acquired (XtremeCT II, 60.8µm voxel size, 168 slices, 95mA, 60 kVp) of distal radii (4% of limb length) from adult OI patients (age: 24-75, male and female, OI type I, III and IV). A deep neural network (Bone structure assessment model [BSAM]: 15 layers with eight convolutional, three pooling and two fully connected layers and two dropout layers) was developed as a refined version of our published BAAM network [6] to perform the OI type classification task. An 80/20 training/test split was used, and standard augmentation was performed. Training was carried out for 2000 iterations (TensorFlow 1.7). Saliency maps (SM) were calculated resulting in a heat map demonstrating the localization of pixel importance for the OI classification task. Masks for trabecular, cortical and soft tissue were extracted. Attention, as normalized summation of pixel intensities of the saliency maps for each mask were determined. A RF model was trained on HR-pQCT morphological parameters (BV/TV, Tb.vBMD, Tt.vBMD, Met/Inn, TbTh, Tb.Sp, Tb.N., Tb.1/N.SD, Tt.Ar., Tb.Ar., Ct.vBMD, Ct.Th, Ct.Ar,). The importance of each structural feature on the model predictions was analyzed to identify OI type-related alterations. The trained models are then applied on the test set.

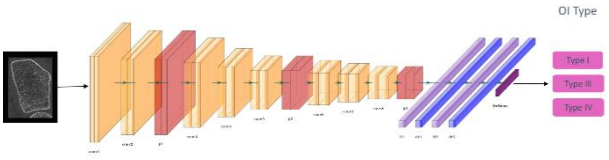

Figure 1: BSAM architecture

Results

The BSAM reached 94% accuracy in OI type classification (loss: 0.03). Trabecular compartment received higher attention than cortical ($p<0.01$, ANOVA). The RF model reached 15 out of 16 correct predictions. Analyzing the importance of each morphological parameter on OI classification revealed Tb.N. (14%), Ct.Th. (12%), Tb.1/SD (10%) and Tb.Sp. (10%) as the most decisive features for the model.

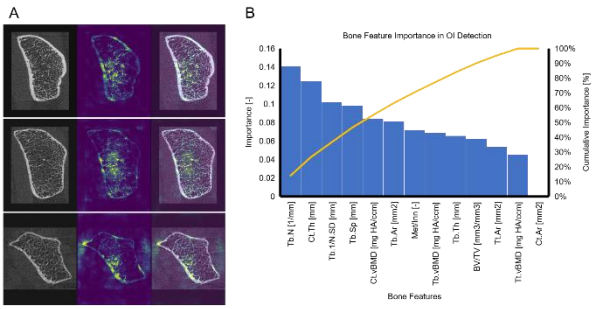

Figure 2: A) BSAM sample saliency maps and corresponding structural features to OI type I (top), III (middle) and IV (bottom). B) Morphological feature importance for OI classification of the RF model.

Discussion

Our DNN model points toward OI type being primarily manifested in the trabecular bone compartment. This is further supported by the RF model, as 3 of the 4 most important features are trabecular. The developed BSAM can further automatically extract structural features and precise locations correlated to each OI type through relating SMs to bone morphological parameters and their importance. This allows a more detailed assessment of OI manifestation in bone. In future, BSAM could be trained on HR-pQCT-based FE simulations to further include mechanical parameters.

References

1) Mortier et al. Am J Med Genet A. 2019. 2) Lindahl K et al. Eur J Hum Genet. 2015. 3) Mikolajewicz et al JBMR 2019. 4)Hald et al. Osteoporos Int 2016, 5) Kocijan Osteoporos Int 2015, 6) Asgharzadeh et al. arXiv preprint arXiv:1905.08099