µCT Images from Clinical CT of the Human Proximal Femur using Deep Learning Super-Resolution

Simon Gremaud

,
Supervisor(s): MSc Osman Berk Satir, MSc Gabriela Gerber, Prof. Dr. Philippe Büchler
Institution(s): ARTORG Center for Biomedical Engineering Research
Examiners: MSc Osman Berk Satir, Prof. Dr. Philippe Büchler

Introduction

The image resolution provided by Quantitative Computed Tomography (QCT) scans is insufficient for the detailed characterization of bone structure and its morphometric properties. These parameters can be acquired with high resolution scans and they improve the outcomes of the biomechanical simulations. Micro-Computed tomography (µCT) scans can deliver the high resolution required for such analyses, however, they are limited by their capability to only image small volumes and are not available in clinical settings. To overcome these limitations, this study investigated the application of Super-Resolution Generative Adversarial Networks (SRGANs) to reconstruct µCT images from QCT scans.

Materials and Methods

The dataset includes scans of 58 proximal femurs from 33 human donors (age:82), each scanned with both QCT and µCT. Initially, the SRGAN used in this study followed the same architecture of Ledig et al. [1] for 2D images. This architecture was later modified to generate volumetric scans with a high resolution (HR) patch size of 64x64x64 voxels and an upsampling factor of 4. In the volumetric analysis bone morphometric parameters such as bone volume fraction (BV/TV), the degree of anisotropy (DA), and the main direction of trabecular orientation were compared. The DA and the main directions were calculated using the bone fabric tensor [2]. The main orientation was identified by the largest eigenvalue of the fabric tensor, and the DA was determined by the ratio between the largest and the smallest eigenvalues.

Results

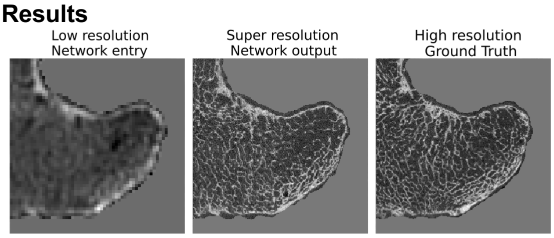

Figure. 1 Results of the 2D SRGAN for HR patches of (256x256 pixels) with an upsampling factor of 4. The HR resolution is 0.137 mm/px.

From a visual assessment, the 2D SRGAN network showed impressive fidelity in replicating bone structure, accurately reflecting its density, thickness, and spacing (Fig 1). The bone morphometric analysis of 100 patches from the 3D SRGAN test dataset showed a very high correlation (r=0.98) on the BV/TV. The DA analysis showed a weaker correlation (r=0.43). The median angle between the main trabeculae direction was 12.06°. These findings were confirmed by the evaluation of a complete reconstruction of the proximal femur (Fig 2).

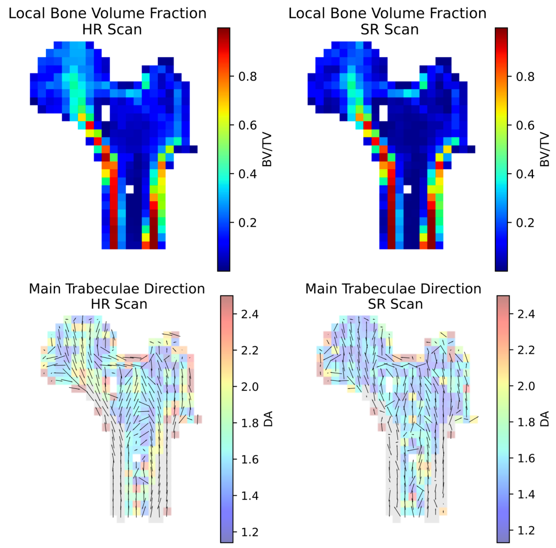

Figure. 2 Comparison of the bone morphometric quantities between the generated super resolution (SR) scan and the HR scan from the 3D SRGAN.

Discussion

This study examines the application of SRGAN in bone imaging and confirms the results of Ledig et al. for 2D images. The 3D SRGAN effectively duplicated BV/TV and the primary trabecular orientation. However, it was less successful in accurately generating finer structures, and the DA assessment showed a weak correlation. The study also pointed out the limitations of 3D patch size, as the resulting larger network led to training instability. In this study, only morphometric parameters of the bone were evaluated, and it would be important to evaluate the impact of upsampling accuracy on the biomechanical simulation derived from these reconstructed images.

References

[1] Ledig et al., Proceedings of the IEEE conference on computer vision and pattern recognition, 4681-4690, 2017.
[2] Hosseini et al., Bone, 97:114-120, 2017