

Automatic Segmentation of Bone Marrow in T1-weighted Lumbar Spine Magnetic Resonance Images Using U-Net

Background: Robust localization and segmentation of bone marrow (BM) is crucial for accurate diagnosis of hematologic diseases. Although a number of studies have attempted to solve the segmentation problem, many methods are semi-automatic, which are prone to error and time-consuming [1-7].

Purpose: We propose a fully automatic segmentation of lumbar BM in T1-weighted magnetic resonance images (MRI) using U-Net: Convolutional Networks for Biomedical Image Segmentation [8].

Materials and Methods: This retrospective study included sagittal T1-weighted lumbar spine MRI acquired from 75 healthy subjects and 25 patients with hematologic diseases including multiple myeloma. The lumbar BM of each subject was segmented using a 3-dimensional GrowCut algorithm [9], which is a semi-automatic way of segmenting the area of interest from multiple slices of an image, to be used as a “ground-truth” for training. The 2D implementation of U-Net was designed to receive the images in size of 528 x 528 x 19 pixels per subject and was trained on Radeon Pro Vega 64X GPU with 16GBs RAM, using ADAM as an optimizer and a learning rate of 1×10^{-2} during 200 epochs. The 50 healthy subjects were used for training, and 25 healthy and 25 diseased subjects were used for validation.

Results: Figure 1 displays the representative slices of the (a) original T1-weighted lumbar spine MRI, (b) ground-truth for segmented lumbar BM with the GrowCut algorithm, (c) segmentation result with U-Net and (d) overlay of the original image with the U-Net segmented BM (red) of a healthy subject (top) and a patient with multiple myeloma (down). The Dice coefficient for all subjects was 0.768.

Conclusion: The use of U-Net demonstrated good performance on lumbar BM segmentation on T1-weighted lumbar spine MRI.

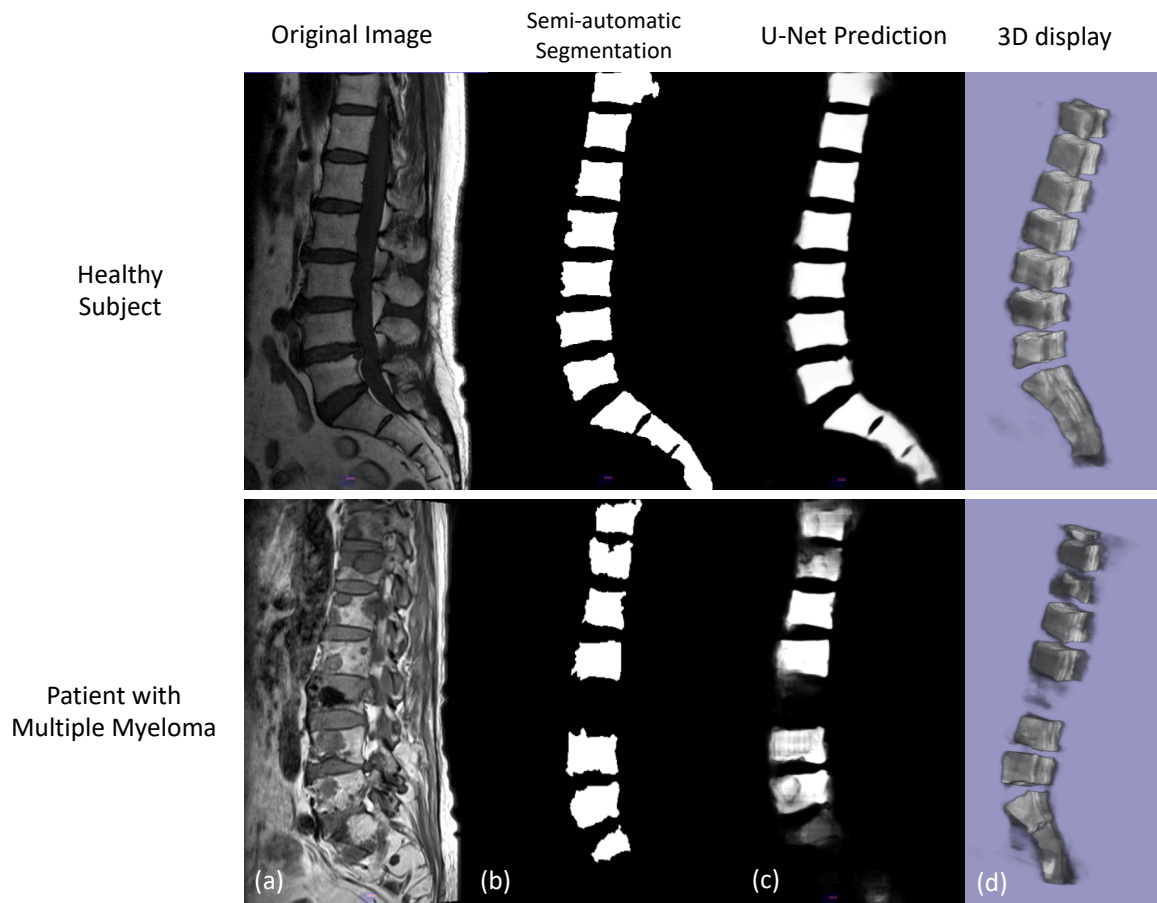


Figure 1. Representative slices of the (a) original images, (b) semi-automatic segmentation used as a “ground-truth”, (c) U-Net predicted probability map and (d) 3-dimensional display of the U-Net probability maps of all slices of a healthy subject (top) and patient with multiple myeloma (down)

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