Tibial and femoral bones segmentation on CT-scans: a deep learning approach

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Abstract

Custom implants in Total Knee Arthroplasty (TKA) could improve prosthesis' durability and patient's comfort, but designing such personalized implants requires a simplified and thus automatic workflow to be easily integrated in the clinical routine. A good knowledge of the shape of the patient's femur and tibia is necessary to design it, but segmentation is still today a key issue. We present here an automatic segmentation approach of the three joints of the lower limb: hip, knee and ankle, using convolutional neural networks (CNNs) on successive transverse views from CT images. Our three 2D CNNs are built on the U-net model, and their specialization each on one joint allowed us to achieve promising results presented here. This could be integrated in a TKA planning software allowing the automatic design of TKA custom implants.

1 Introduction

Custom implants in Total Knee Arthroplasty (TKA) could improve prosthesis' durability and patient's comfort [1], but designing such personalized implants requires a simplified and thus automatic workflow to be easily integrated in the clinical routine. This challenging concept begins with the automatic processing of preoperative CT-scans to extract the anatomy of the patient's bones.

Deep learning has been shown to be effective at identifying patterns in medical imaging, especially with convolutional neural networks (CNNs). Some authors developed an original approach to segment both the knee bones and cartilages from magnetic resonance imaging by combining 2D and 3D CNNs

as well as statistical shape models (SSM) [2]. Some others [3] employed a CNN inspired by U-net [4] to extract and classify the entire human skeleton from CT images.

To obtain an accurate and fast enough segmentation usable during TKA planning for the design of a custom knee implant, we have created three 2D-only CNNs, i.e., one per joint, to extract (1) the hip joint, (2) both the distal femur and the proximal tibia on the knee joint, and (3) the ankle joint.

2 Material and Methods

2.1 Data

120 CT scans of lower limbs (right and/or left) from 71 patients were collected to train the deep learning models at the basis of the segmentation algorithm. These scans were acquired on 3 different machines at the Brest University Hospital during the years 2020-2021. The volumes were manually segmented and then cropped to create three separate datasets on the hip, knee, and ankle joints. Then they were split into training (100 scans from 59 patients) and test sets (20 scans from 12 patients).

2.2 Deep learning models

Three CNNs were trained separately to segment:
      - the femoral bone on the hip joint,
      - the tibial bone on the ankle joint,
      - the tibial and femoral bones on the knee joint.
These models were built based on the concept of 2D U-net [4] and take a series of transverse cross-sections as input. The number of input channels has been extended compared to the standard model to handle three different views of the image with one channel for the original image, one channel for the image normalized over a windowing of 200 HU to 1,900 HU (bone-centered), and one channel for the same second channel to which a Laplacian contour filter has been applied.

Models are composed of 5 down- and up-sampling levels, as shown in Figure 1. Each block consists of two convolutional layers using 3x3 filters and activated by a PreLU function. Down-sampling is performed through maxpooling, and up-sampling through transposed convolutional layers. A final convolution layer using 1x1 pixel filters and a Softmax activation function is applied at the output of the model to give the final segmentation map, on two or three output channels, depending on the number of different bones to classify (e.g. 1-background, 2-femur, 3-tibia for the knee).

Training was carried out using data augmentation, categorical cross-entropy as loss function and adaptative moment estimation (Adam) optimizer. The training was conducted on a Nvidia® Titan RTX GPU.
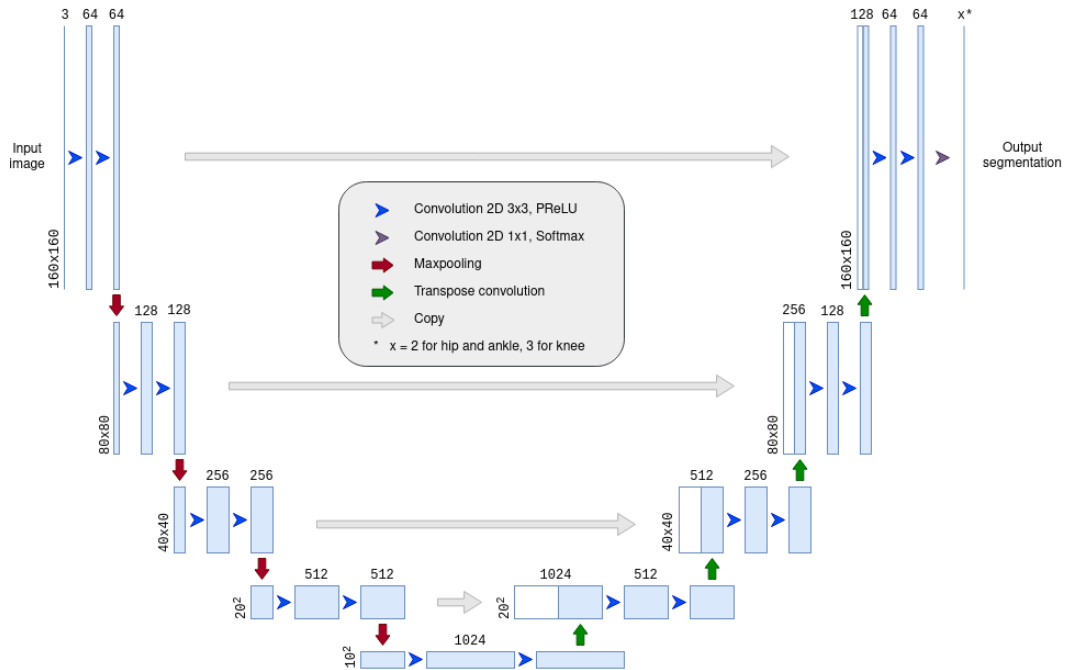
Figure 1: Architecture of the 2D U-net employed.

2.3 Evaluation metrics

Dice similarity coefficient (DICE), average symmetric surface distance (ASSD), and Hausdorff distance (HD) were computed for each volume of the test dataset, per bone and per joint.

3 Results

The results are detailed in the table 1.

	DICE (%)			ASSD (mm)			HD (mm)		
Ankle – Tibia	98,22 ± 0.66	min max	97,58 98,67	0,21 ± 0.15	min max	0,16 0,28	3,32 ± 2.40	min max	1,80 8,00
Knee – Tibia	98,46 ± 0.19	min max	98,06 98,71	0,26 ± 0.04	min max	0,20 0,34	4,36 ± 1.57	min max	2,10 8,97
Knee – Femur	98,62 ± 0.29	min max	97,57 98,91	0,24 ± 0.05	min max	0,19 0,40	3,36 ± 1.55	min max	1,66 6,55
Hip – Femur	98,56 ± 0.26	min max	97,57 98,81	0,23 ± 0.05	min max	0,18 0,37	3,75 ± 1.42	min max	2,28 8,79

Table 1: Mean DICE, ASSD and HD (± standard deviation) obtained on test dataset.

The computation time to fully segment all three joints of a patient's leg is about 3 to 4 minutes on CPU (Intel® Core™ i7-7820HQ, 2.90GHz), depending on volume depth.

4 Discussion

We presented a method for segmentation and classification of tibia and femur bones through the application of U-net-based 2D CNNs on successive transverse cross-sections of CT-scans of the leg.

Concerning the knee joint, our deep learning-based model shows better results than graph-cuts and shape prior combination reported in [5], or than region-based active contour segmentation used by the authors of [6]. In [7], authors used 3D U-net to segment the proximal tibia and distal femur and reached Dice scores comparable to ours.

Our initial results thus demonstrate the possibility of providing an accurate and fast enough segmentation step that can be integrated into a fully automatic workflow for custom implant design.

However, there are still some limitations. First, it would be relevant to test the algorithm with images coming from other imaging systems than the ones we used, to confirm its generalizability. In addition, at this time, our database does not include knees with very severe osteoarthritis and it will also be necessary to validate our results on such data.

References

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