End-To-End Convolutional Neural Network for 3D Reconstruction of Knee Bones From Bi-Planar X-Ray Images

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Abstract. We present an end-to-end Convolutional Neural Network (CNN) approach for 3D reconstruction of knee bones directly from two bi-planar X-ray images. Clinically, capturing the 3D models of the bones is crucial for surgical planning, implant fitting, and postoperative evaluation. X-ray imaging significantly reduces the exposure of patients to ionizing radiation compared to Computer Tomography (CT) imaging, and is much more common and inexpensive compared to Magnetic Resonance Imaging (MRI) scanners. However, retrieving 3D models from such 2D scans is extremely challenging. In contrast to the common approach of statistically modeling the shape of each bone, our deep network learns the distribution of the bones’ shapes directly from the training images. We train our model with both supervised and unsupervised losses using Digitally Reconstructed Radiograph (DRR) images generated from CT scans. To apply our model to X-Ray data, we use style transfer to transform between X-Ray and DRR modalities. As a result, at test time, without further optimization, our solution directly outputs a 3D reconstruction from a pair of bi-planar X-ray images, while preserving geometric constraints. Our results indicate that our deep learning model is very efficient, generalizes well and produces high quality reconstructions.

Keywords: 3D reconstruction · X-ray imaging · Deep Learning · Patient specific planning

1 Introduction

3D reconstruction of knee bones is an important step for various clinical applications. It may be used for surgical planning, precise implant selection, patient specific implant manufacturing or intraoperative jig printing which perfectly fits the anatomy. X-ray images are often used due to their wide availability, lower price, short scanning time and lower levels of ionizing

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radiation compared to CT scanners. However, since X-ray images provide only 2D information, some prior knowledge must be incorporated in order to extract the missing dimension. Previous approaches use Statistical Shape Models (SSM) or Statistical Shape and Intensity Models (SSIM) for reconstructing bones from X-ray images. However, optimization for the deformable model parameters might be slow and needs a good initialization point to avoid local maxima.

In this paper, we present a novel end-to-end deep learning approach for 3D reconstruction of knee joints from two bi-planar X-ray images. The overall scheme is presented in Fig. 1. CNNs have recently proven very effective for various types of tasks, including image segmentation and classification. However, implementing 3D reconstruction from two or more 2D images using a deep learning approach remains a challenging task, due to the difficulty of representing a dimensional enlargement in multi-view settings with standard differentiable layers. Moreover, matching surface points between two or more images for dense reconstruction is extremely challenging compared to the standard multiview setting, due to the transparent nature of the X-ray images.

We address these challenges by introducing a dimensional enlargement approach that given two bi-planar X-rays back-projects each pair of corresponding epipolar lines into a two-channeled epipolar plane. This results in a 3D volume that contains all the information observed from the two X-ray images, while preserving the two-view geometric constraints. We combine this representation with a deep learning architecture that outputs 3D models of the different bones. The experiments show the utilization of our approach for 3D reconstruction of knee joint. We strongly believe that our method paves the way for future research in deep learning based 3D modeling of bones from X-ray scans. In contrast to SSM based methods, our method does not require an initialization and runs in 0.5 seconds while a standard SSM optimization for one knee bone takes about 5 seconds.
2 Related work

Deformable models Reconstruction of 3D bones from X-ray images is mostly done by SSM [3,15] for bones surface modeling, SSIM for further modeling the interior density of the bones [6,4]. We refer the readers to [20,7] for comprehensive overviews of the existing methods. The basic idea is to rigidly align a collection of 3D models and to characterize their non-rigid mutual principal components. Then, given one or more X-ray images, a 3D reconstruction of the bones is achieved by optimizing the model parameters to maximize the similarity between its rendered versions to the input X-ray images. Kim et al. [13] recently used a deep learning approach for detecting landmarks in X-ray images and triangulating them to 3D points. However, their network does not directly outputs a reconstruction of the bones, and the detected 3D landmarks are only used for initialization of the 3D deformable model parameters. As a result, an SSM optimization is still required and takes around 1 minute.

Reconstruction from multiple images While reconstruction of shape from a single image is a geometrically ill-posed problem, several recent methods [22,24,6] use deep learning approaches for reconstructing a shape from single image, for predefined objects [25]. Given two or more images it is possible to reconstruct the object surfaces by triangulating corresponding points, assuming the cameras’ relative positions are known [9]. The relative poses of the cameras can be computed by matching points [18] or lines [26,12,1] descriptors. Utilizing the geometric constraints in deep learning frameworks is challenging, and only few recent papers use deep learning approaches to reconstruct shapes from two and more images. 3D-R2N2 [2] and LSM [11] use RNNs to fuse feature from multiple images for reconstructing a binary voxels mask for representing 3D models. In contrast, [27] reconstructs a different volume from each image and then fuses them in a context-aware layer. [23] starts with initial mesh generated from a single image by [22] and refines it by iteratively applying graph convolutional layers on its 3D coordinates with learned 2D features sampled from the projections of the 3D points on the multiple images.

Computed Tomography from X-ray images Although mathematically, generation of computed tomography from few images is an ill-posed problem, a prior knowledge on the scanned objects can approximate the free parameters. X2CTGAN [28] uses an end-to-end deep learning approach for reconstructing a CT from X-ray images. [21] trained a patient-specific deep network to extract a CT volume from single X-ray image. [10] uses a deep network to reconstruct computed tomography of different mammalian species from single X-ray images. However, these approaches only estimate the CT volumes, and another challenging segmentation step is required for extracting the 3D reconstructions of the anatomical objects.
3 Method

3.1 Network Architecture

Given two bi-planar X-ray images of lateral and Anterior-Posterior (AP) views both of sizes $128 \times 128$, we assume orthogonal projection camera models. Furthermore, assuming that the two images are rectified, that is for $i = 1, \ldots, 128$ the $i^{th}$ rows of the two images are two corresponding epipolar lines, we generate a two channeled volume by replicating the AP and lateral X-ray 2D-scans over the 0 and 1 axes, respectively. This volume representation is geometrically consistent with the input images as follows: each input X-ray image forms a DRR from this volume through the corresponding axis and channel.

The rest of the architecture is inspired by [19] and presented in Fig. 2. We use 3D convolutions of size $3 \times 3 \times 3$, and skip connections between the encoding and the decoding layers. The last layer is a $1 \times 1 \times 1$ convolution block with 5 output channels, representing 5 output classes followed by a Softmax activation. Classes $0 - 4$ represent an anatomical partitioning of the knee bones as shown in Fig. 3(e).

3.2 Training

While CT images with ground truth 3D segmentation are available, pairs of X-ray images with associated ground truth 3D reconstructions are very rare. Moreover, geometrical alignment of each ground truth reconstruction with its X-ray images requires a 2D-3D registration process, which is itself challenging and error prone. Instead, we use CT scans annotated by doctors to create synthetic X-ray images by rendering DRRs. This way, each pair of synthetic X-ray images is associated with an aligned ground truth reconstruction.

For a supervised loss function, inspired by Fidel et al. [8] we spatially weight the cross-entropy loss to give more importance to the challenging near surface

![Diagram showing network architecture and loss functions as described in Sec. 3.](image-url)
For each training sample, we define a spatial 3D Distance Weight Map (DWM) that has a size of the ground truth volume where its value on voxel $i$ is defined by:

$$DWM(i) = 1 + \gamma \cdot \exp(-d(i)/\sigma)$$  \hspace{1cm} (1)

Where $d$ is a distance transform that specifies for each voxel its corresponding distance from any bone surface, and $\gamma, \sigma$ are constants which we set to 8,10 respectively for all the training samples. A visual example is presented in Fig. 3(d). The DWM is then applied for weighting the voxel-wised cross entropy loss as follows:

$$loss_{CE} = -\frac{1}{N} \sum_{i=1}^{N} \sum_{k=0}^{4} DWM(i) \cdot q_k(i) \cdot \log(p_k(i))$$  \hspace{1cm} (2)

where $i$ is the index of a voxel, $N$ is the total number of voxels, $k$ is the class label, $q_k(i) \in \{0,1\}$ and $p_k(i) \in (0,1)$ are respectively the ground truth and network prediction probabilities of voxel $i$ being labeled $k$.

We further define an unsupervised reconstruction loss to align the network prediction of bones probability map with the input X-ray images. Even though the input X-ray images contain bones together with additional anatomical elements, the image gradients of the bones are quite dominant. Therefore, the input X-rays are expected to have gradients that are relatively correlated with the DRRs from the predicted bones probability map. The reconstruction loss is defined by:

$$Loss_{reconst} = 1 - \frac{1}{2} (NGCC(I_{Lat}, DRR_{Lat}) + (NGCC(I_{AP}, DRR_{AP}))$$  \hspace{1cm} (3)

where NGCC is the Normalized Gradient Cross Correlation\footnote{The exact definition is given in the supplementary material} $I_{AP}, I_{Lat}$ are the input X-ray images from AP and lateral views respectively,
|          | Background | Femur     | Patella   | Tibia     | Fibula    | Bones average |
|----------|------------|-----------|-----------|-----------|-----------|---------------|
| Chamfer(mm) | -          | 0.87      | 0.769     | 0.822     | 0.966     | 0.86          |
| Dice     | 0.988      | 0.954     | 0.918     | 0.957     | 0.877     | 0.93          |

Table 1: Evaluation metrics for our results given inputs of bi-planar DRRs. The results are averaged over the test set.

\[ \text{DRR}_\text{AP}, \text{DRR}_\text{Lat} \] are DRRs applied on the maximum over the bones channels of the network prediction. This loss encourages the network to use the available information of the input images, that can actually be used in inference time, where no supervision is available. We observe that this loss improves the generalization of the network to unseen images (see Sec. 4.1).

Overall our loss function is:

\[ \text{Loss} = \frac{1}{2}(\text{Loss}_{\text{reconst}} + \text{Loss}_{\text{CE}}) \] (4)

For training the network, Adam optimizer was used with initial learning rate of \(10^{-2}\), reduced by a factor of 10 after every 10 epochs. We used training and validation sets created from of 236 knee joint CT scans. Each scan was augmented by rotating it randomly with random angles of range \((-5, 5)\) and projected into 2 bi-planar DRRs which are used as synthetic input X-rays. The validation set forms 5\% of the augmented dataset. The test data contains 12 original scans. We trained the network for 23 epochs.

### 3.3 Domain adaptation

X-ray images have a different appearance than DRRs. In order to apply our deep model on X-ray images, we trained a network that is based on CycleGAN [29] to transfer them to have a DRR-style appearance. During training, in each iteration the model uses two non aligned images \(I_{\text{Xray}}\) and \(I_{\text{DRR}}\) to generate two fake images: \(I_{\text{DRR}} \rightarrow I_{\text{Xray}}, I_{\text{Xray}} \rightarrow I_{\text{DRR}}\). In order to generate DRR-style images which are completely aligned with the input X-ray images we used the original CycleGAN with additional content preserving loss function:

\[ L_{\text{Cont}} = 1 - \frac{1}{2}(\text{ZNGCC}(I_{\text{Xray} \rightarrow \text{DRR}}, I_{\text{Xray}}) + (\text{ZNGCC}(I_{\text{DRR} \rightarrow \text{Xray}}, I_{\text{DRR}})) \] (5)

Where ZNGCC is the Zero Normalized Gradient Cross Correlation\(^2\) We trained the style transfer model with training/validation sets of 391/61 pairs of bi-planar X-ray images of the knee, for 30 epochs. In the supplementary material we show visual results of the style transfer process.

\(^2\) The exact definition is given in the supplementary material
Table 2: Ablation study. Measuring the importance of different components in our model. The results metrics are averaged over the 4 reconstructed bones.

| Component          | Full | Without DWM | Lateral only | No Loss reconstr |
|--------------------|------|-------------|--------------|-----------------|
| Chamfer (mm)       | 0.86 | 0.93        | 1.44         | 0.91            |
| Dice               | 0.93 | 0.92        | 0.87         | 0.92            |

Table 3: Quantitative evaluation of real X-rays inputs averaged over the test set, and comparisons with the Femur reconstructions of [14]. The Patella metrics computed only on the lateral view (GT annotations for the AP view are unavailable).

| Component          | Manual | Perturbed | Femur | Patella | Tibia | Fibula | Bones avg |
|--------------------|--------|-----------|-------|---------|-------|--------|-----------|
| Chamfer (mm)       | 7.581  | 10.503    | 1.881 | 1.691   | 1.923 | 1.999  | 1.873     |
| Dice               | 0.791  | 0.694     | 0.937 | 0.856   | 0.935 | 0.832  | 0.89      |

4 Experiments

4.1 DRR inputs

We tested our method on the testing set described in Sec. 3.2 and evaluated the results using the ground truth 3D segmentations. Each pair of bi-planar DRRs is used as an input to our deep network described in Sec. 3.1. For each testing sample we used the Marching Cubes algorithm [17] to extract a set of 3D bones meshes from the predicted volumetric labels. A qualitative result is presented in Fig. 3a-3c. Quantitative metrics are calculated for each bone type and presented in Table 1. Dice (higher is better) is computed over the predicted voxels maps and Chamfer (lower is better) is computed directly on the final reconstructions. We also show an ablation study in Table 2 of running the model without several of its components to evaluate their importance.

4.2 Real X-ray test cases

We evaluated 10 test cases of X-ray images. We applied domain adaptation procedure to transform their style as described in Sec. 3.3, and applied the network on the transformed X-ray images. In Fig. 4 we present a qualitative results of a 3D reconstruction given an input of bi-planar real X-ray images. Since 3D ground truth is not available for the X-ray images, we used 10 test pairs with 2D bi-planar ground truth multi-class masks annotated by doctors for evaluation. Each reconstructed 3D model is projected to the 2 X-ray views and the evaluation metrics computed relative to the ground truth annotations.
We compared our performance with the Femur SSIM model\(^3\) of \cite{14} in terms of accuracy and running time. We note that the SSIM method requires initialization. We first initialized this method manually to the best of our ability, and the optimization converged after 4.5 seconds while our method, without any initialization reconstructed 4 bone types in 0.5 seconds, and achieved better results. To demonstrate the initialization sensitivity of \cite{14}, for each test case we used a random perturbation of the manual initialization. We shifted the position parameters in a range of 5mm and we multiplied the scale parameters in a factor of range [0.985, 1.015], and evaluated the average results. The average running time for the perturbed initializations increased from 4.5 seconds to 9.8 seconds. The accuracy comparisons are presented in Table 3. We also performed an ablation study for running our method directly on the X-rays without style transfer. The Chamfer and Dice metrics averaged over the bones degraded significantly from 1.873mm and 0.89 to 9.33mm and 0.59 respectively.

4.3 Technical details

We performed all of our experiments on a computer with MS Windows 10 64bit OS, Intel i7 7700K CPU and Nvidia GeForce GTX 1070 graphic card. The data is provided by a third party who has obtained consent for use in research.

5 Conclusion

We present an effective end-to-end deep network for reconstructing 3D models of knee bones from two standard bi-planar X-ray scans. We use a novel deep neural network model, synthetic data creation and domain adaptation to achieve an efficient, robust and accurate 3D reconstruction model. In the future we would like to extend our method to more bones reconstruction setups, and to extend the geometric 2D-3D representation of our model for additional X-ray projection models.

\(^3\) Only their Femur model has an available code.
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A Supplementary Material

\[ NGCC(I_1, I_2) = \frac{1}{2} \left( \frac{G_x(I_1)}{\|G_x(I_1)\|} \cdot \frac{G_x(I_2)}{\|G_x(I_2)\|} + \frac{G_y(I_1)}{\|G_y(I_1)\|} \cdot \frac{G_y(I_2)}{\|G_y(I_2)\|} \right) \] (6)

\[ \overline{G_x(I)} = G_x(I) - \text{mean}(G_x(I)), \overline{G_y(I)} = G_y(I) - \text{mean}(G_y(I)) \] (7)

\[ ZNGCC(I_1, I_2) = \frac{1}{2} \left( \frac{\overline{G_x(I_1)}}{\|\overline{G_x(I_1)}\|} \cdot \frac{\overline{G_x(I_2)}}{\|\overline{G_x(I_2)}\|} + \frac{\overline{G_y(I_1)}}{\|\overline{G_y(I_1)}\|} \cdot \frac{\overline{G_y(I_2)}}{\|\overline{G_y(I_2)}\|} \right) \] (8)

Fig. 5: Visualization of the training data that we used for training CycleGAN.

Fig. 6: CycleGAN results: (a) X-ray inputs. (b) DRR-style outputs. (c) Inputs-outputs content comparisons.
Fig. 7: Supplementary qualitative results on test cases: left - inputs, right - outputs. (a) Real X-rays inputs. (b) Real X-rays inputs without Cycle-GAN, as ablation study. (c) DRRs inputs.