

LinAlign: X-Ray Image Alignment before and after Total Hip Arthroplasty

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ABSTRACT

In this paper, we propose LinAlign: a computer vision algorithm for aligning X-ray images before and after surgery, providing a system for surgeons to compare images before and after surgery more efficiently and replace manually aligning procedure. LinAlign allows only align specific area when aligning images, and solve the problem that linear transformation cannot be performed on non-rigid objects. Therefore, it is suitable for comparing the position of bones during the hip replacement surgery, allowing orthopedic surgeons to make sure that implants have been installed correctly.

In our experiment, we took the X-ray images of the pelvis as our experimental data: each set of images contains the X-ray photographs of the same patient taken at different times. We experiment with different methods. By comparing similar features between images and calculating the displacement of these feature points, the images can be aligned.

We evaluate the performance of the algorithm by the error of pre-defined landmarks after alignment. These landmarks are anatomically important features of the skeletal system. The goal of our experiment is to minimize the distance of landmarks between image pair. We take the mean square error of these landmark distances as the performance metric to our algorithm.

Keywords: *LinAlign, Medical Image Processing, Feature Matching, Semantic Segmentation, Image Alignment*

1. INTRODUCTION

In orthopedic surgery, surgeons will take X-ray image and compare it with the image taken before surgery to ensure the surgery is accurate. We aim to develop a system to align these images. When surgeons need to compare the current image with the image taken before surgery, our system can align the previous one with current one automatically. Therefore, they are no longer

need to print the hardcopy of radiographs and compare them manually.

Our research focuses on the radiograph taken from Total Hip Arthroplasty (THA), which is a surgical procedure where the hip joint is replaced by a prosthetic implant. Fig. 1 shows the radiographs taken before and after THA, and Fig. 2. shows the components of the implant used in THA.



Fig. 1. An X-ray image showing a left hip has been replaced with prosthetic implant due to advanced femoral head collapse. [11]

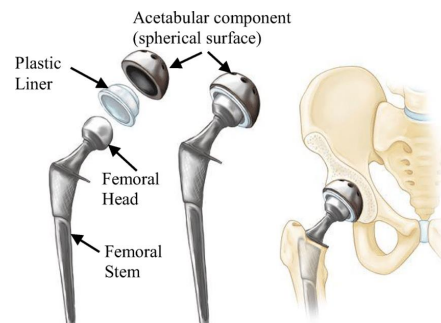


Fig. 2. The components of prosthetic implant for total hip replacement. [10]

Total hip arthroplasty is a major surgery that carries certain risks. Including: Infection, dislocation, limb

length inequality, fracture, etc. Dislocation is the most common complication in this surgery. For example, the ball coming out of the socket. It may be caused by misalignment of the prosthetic implant and hip joint, which can be reduced by ensuring the location of them are correct during the surgery. Our system is designed to reduce these risks.

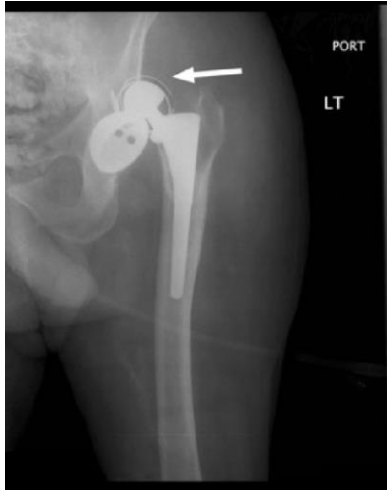


Fig. 3. The dislocation of the femoral head. [2]

2. RELATED WORK

2.1. Feature Matching

Feature matching in computer vision is the process of identifying and comparing the same or similar features in two or more images. Often, the matching result contains several wrong correspondences, which can easily affect our application. To prevent the effect of outlying data, a noise removal phase such as RANSAC (RANDOM SAmple Consensus) [6] is usually applied at the end. With this process, the noisy matching can be almost removed.

Depending on the approach, feature matching methods can be categorized into two types: detector-based feature matching and detector-free feature matching. Detector-based methods require a feature detector to extract and describe local features, and then match these feature points. As for detector-free methods, they remove the feature detector phase and directly produce dense descriptors or dense feature matches instead.

Feature matching can be used in various computer vision tasks, such as image registration, object recognition, Simultaneous Localization And Mapping (SLAM), and Structure-from-Motion (SfM).

2.2. Homography Estimation

Homography estimation is a computer vision task that finds a mathematical relationship (i.e. a homography matrix) between multiple images taken from different perspectives. The homography matrix estimation is based on corresponding points between two images and can be computed mathematically such as direct linear transformation, normalizing direct linear transform. Homography estimation can be used in computer vision tasks such as image alignment, image stitching, image mosaicing, and object recognition.

2.3. Semantic Segmentation

Semantic segmentation is a computer vision task assigning the semantic label to each pixel in the image. The goal is to categorize each pixel in the image into one of several predefined classes. The result of semantic segmentation is a dense prediction, where every pixel in the image is assigned with a color-coded class label. Semantic segmentation is a crucial task for various applications such as self-driving cars which can make the decisions informed by its fine-grained prediction of the environment.

Recently, deep neural networks achieve successful performance in semantic segmentation, such as Fully Convolutional Networks (FCN) [8], SegNet [1], U-Net [12], DeepLab [3], and so on. The networks take an image as input and outputs a corresponding segmentation mask where each pixel is assigned a class label.

2.4. Image Alignment

Image alignment is the process of matching and adjusting the relative positions of images to align them with each other. By the matching of common features between multiple images, we can align the images so that the same feature in different images correspond to the same real-world location.

There are two common methods for image alignment: feature point-based alignment and optical flow alignment. Feature point-based alignment aims to align the feature point correspondences in multiple images by calculating the global transformation matrices between them. Since it is a linear transformation, it can only perform the translation, rotation, and scaling on rigid body. In other words, the motion in images is restricted to be globally uniform. As for optical flow alignment, it aligns images by remapping with dense correspondences. Since it is an one-to-one correspondence between pixels, images can be aligned accordingly, but its result is often unstable.

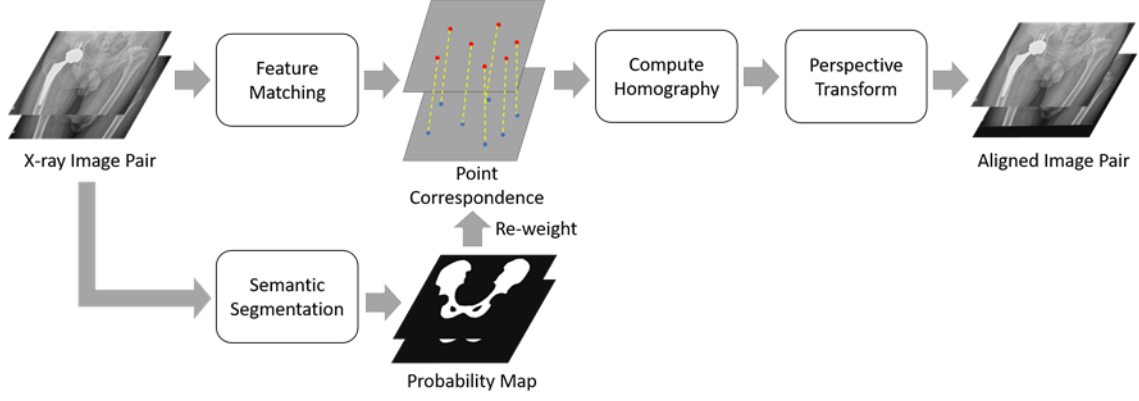


Fig. 4. The pipeline of LinAlign algorithm.

3. METHODOLOGY

We propose LinAlign for aligning X-ray images before and after surgery. Since the pose in X-ray images may be different and cannot be aligned linearly, we propose a new strategy to compute homography to deal with this issue.

For an X-ray image pair, we first perform the feature matching to compute the point correspondences between both images. Simultaneously, we compute the probability map of pelvis with a semantic segmentation model, which results in images with pixel-wise class prediction. Then, we assign the weight to each point correspondence with the product of class confidence on both images, and perform the homography estimation using weighted normalized Direct Linear Transform (DLT) on these correspondences. Finally, we align both images with perspective transformation. Fig. 4. shows the pipeline of LinAlign algorithm.

3.1. Feature Matching

We use LoFTR [14] to match the feature points from two images. LoFTR predicts thousands of dense point correspondences, and it works even in low-texture area. These correspondences are accurate and robust, so they give us good information for image alignment.

Our LoFTR model was pre-trained on MegaDepth [7] dataset, which contains large amount of outdoor scene images collected from Internet with depth map annotations. LoFTR learns how to match the dense features directly, so it can be easily adapted to other domains, even the scene is very different from training datasets. Thus, it achieves good performance in our application.

After feature matching, some outlying correspondences may exist. Since our goal is to align the images, these outlying data can seriously affect our results, even with only small number of outliers. To prevent this effect, we apply a noise removal phase using RANSAC at the end. Thus, we can select the good matchings that are helpful to align the images. Fig. 5.

shows the feature matching prediction of LoFTR tested on our data. Applying the RANSAC can remove the correspondences that are outlying to the linear transform.

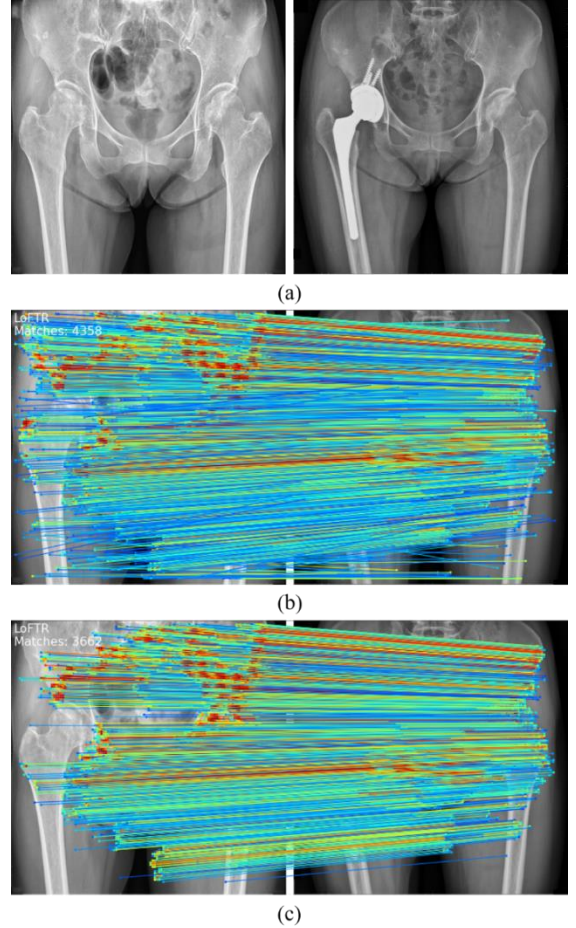


Fig. 5. The feature matching results with LoFTR [14].

(a) Original image pair; (b) matching result; (c) Matching result with outlier removal using RANSAC.

3.2. Pelvis Segmentation

In our application, we aim to compare the location of the hip joint before and after surgery. Since the human body is non-rigid, it may have pose difference and cannot align

the whole body with linear transformation. However, in this application, we only need to align the pelvis part well, which is the rigid part. Therefore, in this procedure, we segment the pelvis part from images, and use it to improve the alignment.

We segment the pelvis part with U-Net++ [16], which is an improved version of U-Net [12]. We use X-ray images of the pelvis to train our model, with 191 images as training data, and 33 images as validation data. Pixels in each image are labeled with two classes, where label 0 is background, and label 1 is pelvis.

The model outputs a probability map with the size (N, H, W) , where N is the number of classes; H and W are the height and width of input image. Each pixel represents the class prediction. We take the probability prediction of pelvis as our result to support our image alignment. Fig. 6. shows the probability map prediction on our dataset using our U-Net++ model. The pelvis area can be segmented perfectly so is helpful to our algorithm.

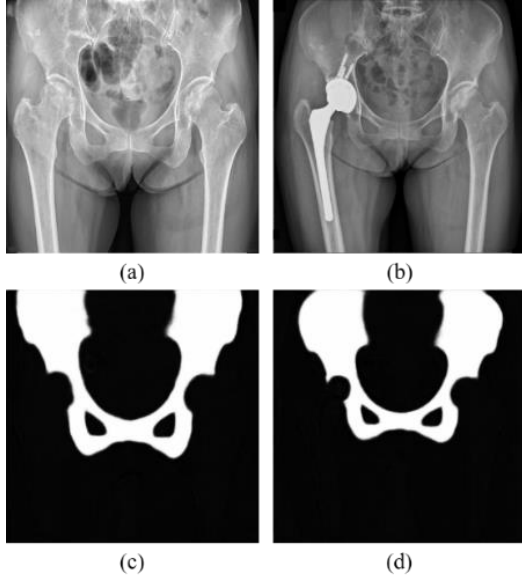


Fig. 6. The probability map prediction result of our data.

3.3. Weighted Normalized DLT

We propose a new method to estimate homography from point correspondences: weighted normalized DLT (Direct Linear Transform). Since the goal of our algorithm is to compare two images taken before and after surgery, it would be more suitable for comparison if we align the pelvis area better. Therefore, we modify the previous homography estimation methods to fit our requirement.

Our method is done by assigning the weight on each correspondence while computing the normalized DLT. Therefore, the correspondence with higher weight can be more likely to be aligned.

3.3.1. DLT

Assume that we are given N correspondence key point pairs, where the point correspondences are $\{(u_i, v_i), (u'_i, v'_i) | i = 1, \dots, N\}$, λ_i is a point-dependent scale factor, we have

$$\lambda_i \begin{bmatrix} h_1 & h_2 & h_3 \\ h_4 & h_5 & h_6 \\ h_7 & h_8 & h_9 \end{bmatrix} \begin{bmatrix} u_i \\ v_i \\ 1 \end{bmatrix} = \begin{bmatrix} u'_i \\ v'_i \\ 1 \end{bmatrix}$$

Then, we find the homography matrix H by replacing the equation into matrix form.

$$\begin{bmatrix} u_1 & v_1 & 1 & 0 & 0 & 0 & -u'_1 u_1 & -u'_1 v_1 & -u'_1 \\ 0 & 0 & 0 & u_1 & v_1 & 1 & -v'_1 u_1 & -v'_1 v_1 & -v'_1 \\ u_2 & v_2 & 1 & 0 & 0 & 0 & -u'_2 u_2 & -u'_2 v_2 & -u'_2 \\ 0 & 0 & 0 & u_2 & v_2 & 1 & -v'_2 u_2 & -v'_2 v_2 & -v'_2 \\ & & & & & \vdots & & & \\ & & & & & \vdots & & & \end{bmatrix} \begin{bmatrix} h_1 \\ h_2 \\ h_3 \\ h_4 \\ h_5 \\ h_6 \\ h_7 \\ h_8 \\ h_9 \end{bmatrix} = 0$$

$\rightarrow A\mathbf{h} = 0$

Since the Degree of Freedom (DoF) for perspective transformation is 8, we need at least 4 correspondences to find the non-trivial solution to this equation. We thus solve the least-squared-error solution:

$$\min_{\mathbf{h}} \|\mathbf{A}\mathbf{h}\|^2, \quad \text{s.t.} \quad \|\mathbf{h}\|^2 = 1$$

The solution is equivalent to

$$\operatorname{argmin}_{\mathbf{h}} \frac{\|\mathbf{A}\mathbf{h}\|^2}{\|\mathbf{h}\|^2} = \frac{\mathbf{h}^T \mathbf{A}^T \mathbf{A} \mathbf{h}}{\|\mathbf{h}\|^2}$$

According to the principle of Rayleigh quotient, the solution of \mathbf{h} is the eigenvector corresponding to the smallest eigenvalue of matrix $\mathbf{A}^T \mathbf{A}$. Thus, the solution can be obtained by performing the Singular Value Decomposition (SVD) on \mathbf{A} , so we get $\mathbf{A} = \mathbf{U}\mathbf{\Sigma}\mathbf{V}^T$, where the singular values in $\mathbf{\Sigma}$ are arranged in descending order. The solution is then the last column of \mathbf{V} .

3.3.2 Normalized DLT

There is a shortcoming in DLT. When we compute the linear transform, the x, y coordinate on the image is typically much larger than z coordinate since z is always equal to 1. The different order of coordinate results in an ill-conditioning number of matrix \mathbf{A} and numerically unstable solutions. To get more stable results, we can normalize on every point before direct linear transformation. Assume T, T' are the transformation matrices that normalize the points $(u_i, v_i), (u'_i, v'_i)$ respectively,

$$T = \begin{bmatrix} s & 0 & m_x \\ 0 & s & m_y \\ 0 & 0 & 1 \end{bmatrix}^{-1}$$

where s is standard deviation of coordinate, and m_x, m_y are the mean of x -axis and y -axis. After performing the direct linear transformation on normalized correspondences point, we get \hat{H} . The transformation

matrix between (u_i, v_i) and (u'_i, v'_i) will be $H = T'^{-1}\hat{H}T$. Thus,

$$\lambda_i \begin{bmatrix} h_1 & h_2 & h_3 \\ h_4 & h_5 & h_6 \\ h_7 & h_8 & h_9 \end{bmatrix} \begin{bmatrix} u_i \\ v_i \\ 1 \end{bmatrix} \approx \begin{bmatrix} u'_i \\ v'_i \\ 1 \end{bmatrix}$$

3.3.3 Weighted Normalized DLT

In previous methods, point correspondences have the same weight during the homography estimation. However, in our application, we want our interested area (i.e., pelvis area) more likely to be aligned, so we can compare the images better. Weighted Normalized DLT is done by modifying the equation of Normalized DLT. We re-weight the rows in A , so we get

$$\begin{bmatrix} w_1 \begin{bmatrix} u_1 & v_1 & 1 & 0 & 0 & 0 & -u'_1 u_1 & -u'_1 v_1 & -u'_1 \\ 0 & 0 & 0 & u_1 & v_1 & 1 & -v'_1 u_1 & -v'_1 v_1 & -v'_1 \end{bmatrix} \\ w_2 \begin{bmatrix} u_2 & v_2 & 1 & 0 & 0 & 0 & -u'_2 u_2 & -u'_2 v_2 & -u'_2 \\ 0 & 0 & 0 & u_2 & v_2 & 1 & -v'_2 u_2 & -v'_2 v_2 & -v'_2 \end{bmatrix} \\ \vdots \\ \vdots \end{bmatrix} \begin{bmatrix} h_1 \\ h_2 \\ h_3 \\ h_4 \\ h_5 \\ h_6 \\ h_7 \\ h_8 \\ h_9 \end{bmatrix} = 0$$

$$\rightarrow A'\hat{h} = 0$$

We solve $A'\hat{h} = 0$ in the same approach as we described in Section 3.3.1, we get \hat{H} . Then, we denormalize it to get the homography matrix $H = T'^{-1}\hat{H}T$. Thus, we have

$$\lambda_i H \begin{bmatrix} u_i \\ v_i \\ 1 \end{bmatrix} \approx \begin{bmatrix} u'_i \\ v'_i \\ 1 \end{bmatrix}$$

3.4. Image Alignment

We align the images using perspective transformation. For given point correspondences and the probability map of pelvis area determined by segmentation model, we tried two methods to compute the homography matrix.

Let P_c^1, P_c^2 be the probability map prediction of class c from semantic segmentation model; and

$$M = \{(u_i, v_i), (u'_i, v'_i) | i = 1, \dots, N\}$$

be our keypoint correspondences. In Method 1, we filter the keypoints with the label prediction, and compute the normalized DLT with the keypoints within pelvis area only. Take

$$\{(u_i, v_i), (u'_i, v'_i) | P_{pelvis}^1(u_i, v_i) \geq 0.5 \text{ and } P_{pelvis}^2(u'_i, v'_i) \geq 0.5\}$$

to compute normalized DLT; As for Method 2, we assign the weight with the product of the confidence score of pelvis from both images to compute weighted normalized DLT. i.e., $w_i = P_{pelvis}^1(u_i, v_i) \times P_{pelvis}^2(u'_i, v'_i)$. Tested these methods on our datasets and compare them with normalized DLT method, we finally take Method 2 because it has better performance.

3.5. Result Visualization

In order to make surgeons easier to compare the images using alignment result, we visualize the alignment using CDM (Color Difference Map), implemented based on YCbCr color space, where Y is the luminance, and Cb and Cr are the blue-difference and red-difference chroma components.

Assume that I_1, I_2 is our image pair, where I_2 is our target image. These images are grayscale images. We align I_1 with I_2 , so we get a transformed image I'_1 . The CDM is determined by assigning overlapping image to Y , and color difference to Cr and Cb . i.e., $Y = (I'_1 + I_2)/2$; $Cr = (I_2 - I'_1)/2$; $Cb = (I_2 - I'_1)/2$ in Fig. 7.

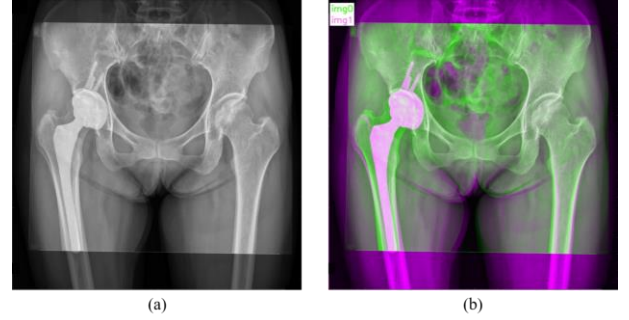


Fig. 7. The visualization of our aligning results. (a) The overlapping image. (b) The Color Difference Map (CDM).

4. EXPERIMENTAL RESULTS

4.1. Datasets

We experiment with a dataset of pelvis radiographs which contains 224 radiographs collected from 49 patients.

In our application, we require semantic segmentation dataset for model training, and pelvic landmarks dataset for performance evaluation. We create these by labeling our first dataset with pelvis mask and landmark point set. To test the repeatability, we experiment our algorithm on both datasets. Fig. 8. shows a part of our segmentation dataset. Fig. 9. shows the definition of landmarks

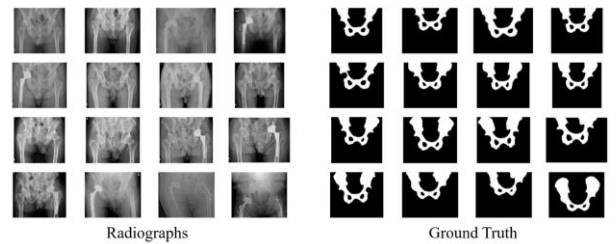


Fig. 8. Samples of our segmentation dataset containing pelvis radiographs and the mask annotations. Some of them are taken after THA surgery.

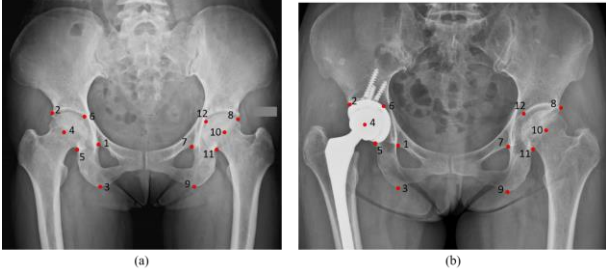


Fig. 9. Definition of the landmarks. (a) Normal. (b) With implants.

4.2. Feature Matching Experiment

Feature matching is a crucial step in our application. To improve our alignment, we experiment with three feature matching methods, SIFT [9], SuperPoint [5] + SuperGlue [13], and LoFTR [14].

We evaluate the alignment performance using MRE (Mean Radial Error). Given keypoint correspondences $\{(u_i^1, v_i^1), (u_i^2, v_i^2) | i = 1, \dots, N\}$ as our ground truth, where $(u_i^1, v_i^1), (u_i^2, v_i^2)$ are the pre-defined landmarks on both images. For every keypoint pair, calculate the distance between $(u_i^1, v_i^1)'$ and (u_i^2, v_i^2) , where $(u_i^1, v_i^1)'$ is the projection of (u_i^1, v_i^1) . Thus, the error is defined to be

$$MRE = \frac{1}{N} \sum_{i=1}^N \|(u_i^1, v_i^1)' - (u_i^2, v_i^2)\|_2$$

We perform the homography test on our landmark dataset, by estimating the homography using RANSAC [6]. LoFTR gets the best result finally, so we select LoFTR in our LinAlign algorithm. Table 1. shows the homography estimation results.

Table 1. Homography estimation results. (\downarrow : The lower, the better.)

Methods	SIFT	SP+SG	LoFTR
MRE \downarrow	0.134639	0.015056	0.014456

4.3. Semantic Segmentation Experiment

We experiment with four state-of-the-art semantic segmentation models: U-Net [12], U-Net++ [16], DeepLabV3+ [4], and PSPNet [15], tested on our segmentation dataset.

These models are trained in the same conditions. They trained with 64 epochs, supervised with pixel-wise cross entropy loss, and the data augmentation strategies are random horizontal flip, random shift-scale-rotation, random brightness contrast, and random resized crop. We take the IoU (Intersection over Union) score of pelvis area as our performance, where

$$IoU = \frac{TP}{TP + FP + FN}$$

Table 2. shows the IoU score on our validation data. U-Net++ is the best model in our experiment.

Table 2. Semantic segmentation test on our validation set. (\uparrow : The higher, the better.)

Model	U-Net	U-Net++	DeepLab v3+	PSPNet
IoU Score \uparrow	0.9233	0.9314	0.9246	0.7236

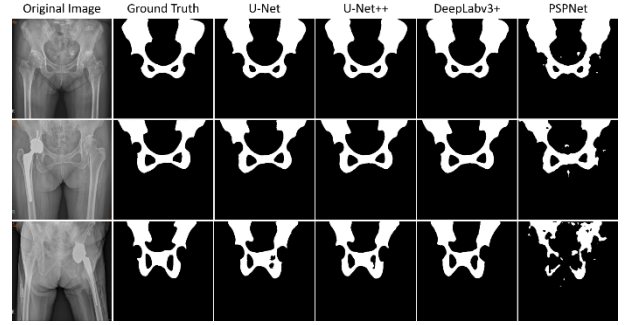


Fig. 10. Segmentation results on validation set.

4.4. Image Alignment Experiment

We experiment both proposed methods in section 3.3 and normalized DLT on our landmarks dataset to compare the performance, using MRE of landmarks as our evaluation protocol. Tested with i7-9770 and RTX 2080ti, the inference time for an image pair is 2.23 seconds. Table 3 shows the MRE scores of these methods. The following figures show the experimental results. In (d), red points are landmarks on the transformed image, and blue points are landmarks on the target image. Extensive experiments show that our algorithm can align most of the images well. However, due to the complexity of 3D structure of pelvis, it is difficult to handle the view difference, but we still can align the joint part as well as possible.

Table 3. Image alignment testing results. (\downarrow : The lower, the better.)

Method	Normalized DLT	Filtered	Re-weighted
MRE \downarrow	0.014470	0.014165	0.013985

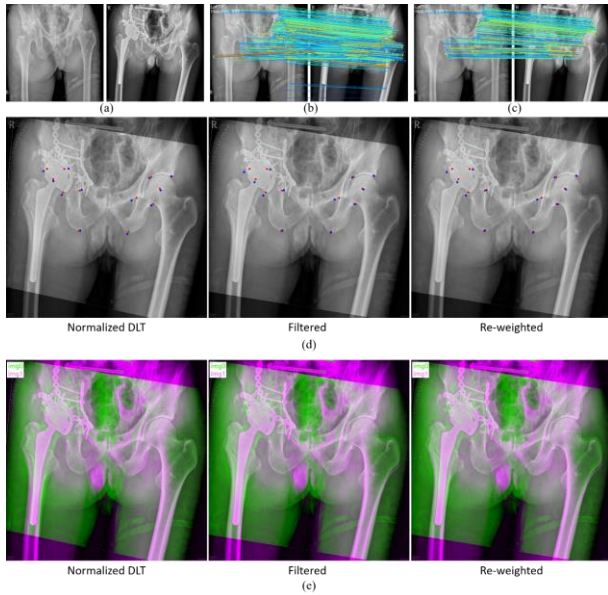


Fig. 11. Alignment result 1. (a) Original image pair. (b) Matching result. (c) Matches within pelvis area. (d) Alignment results with landmarks. (e) CDM. (The MRE are 0.013362, 0.012644, 0.012767 respectively.)

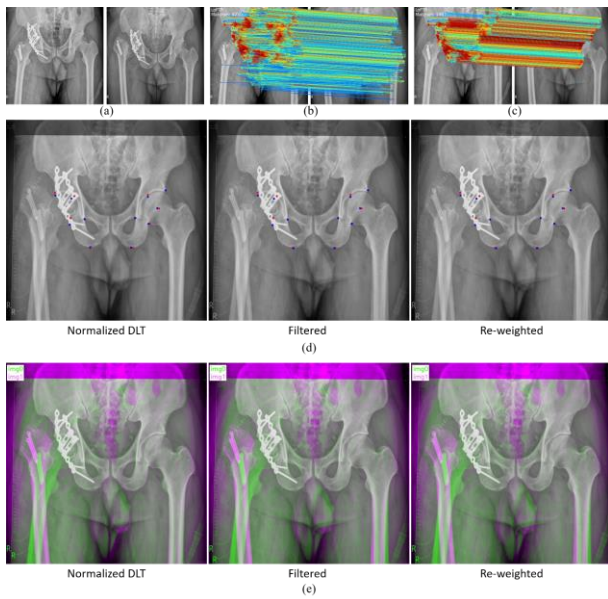


Fig. 12. Alignment result 2. (a) Original image pair. (b) Matching result. (c) Matches within pelvis area. (d) Alignment results with landmarks. (e) CDM. (The MRE are 0.01024, 0.009574, 0.009485 respectively.)

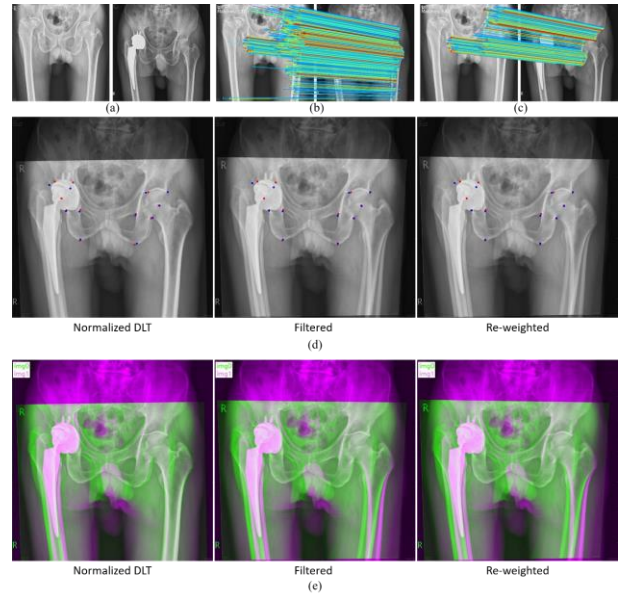


Fig. 13. Alignment result 3. (a) Original image pair. (b) Matching result. (c) Matches within pelvis area. (d) Alignment results with landmarks. (e) CDM. (The MRE are 0.011629, 0.009012, 0.008951 respectively.)

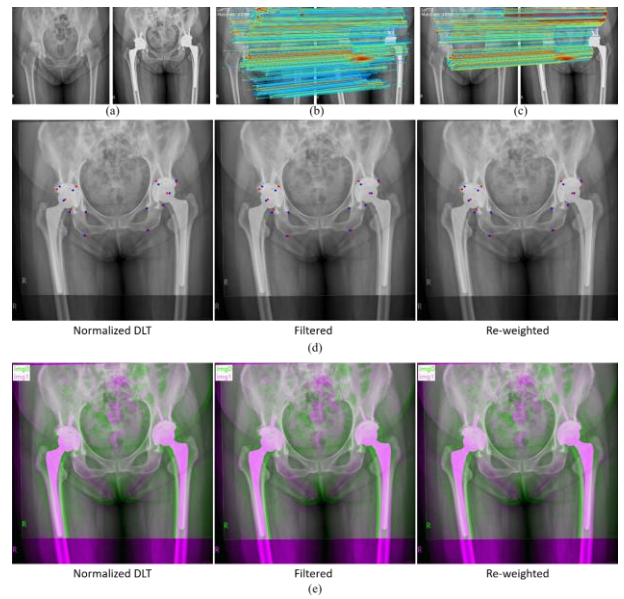


Fig. 14. Alignment result 4. (a) Original image pair. (b) Matching result. (c) Matches within pelvis area. (d) Alignment results with landmarks. (e) CDM. (The MRE are 0.011314, 0.011278, 0.011282 respectively.)

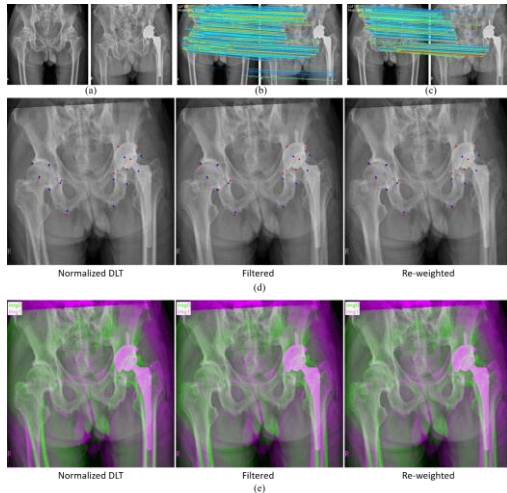


Fig. 15. Failure alignment result. (a) Original image pair. (b) Matching result. (c) Matches within pelvis area. (d) Alignment results with landmarks. (e) CDM. (The MRE are 0.034356, 0.032245, 0.03253 respectively.)

5. CONCLUSION

We propose LinAlign algorithm, which combines the results of semantic segmentation to homography estimation by weights assignment. LinAlign can successfully align the images of non-rigid bodies with partial differences by applying stricter alignment to our interested part. Tested on our dataset, our method has better performance compared with other alignment algorithm.

We also visualize the alignment results in CDM, which can obviously see the difference between two images. With this algorithm, surgeons can ensure the location of implants are correct during the surgery, and can prevent the risks such as dislocation after the surgery.

ACKNOWLEDGEMENT

This research was supported by National Science and Technology Council of Taiwan, R.O.C., under Grants NSTC 112-2221-E-002-189-MY2 and MOST 111-2221-E-002-174 and by MediCapture, Test Research, Jorjin Technologies, III, Chernerger, Jeilin Technology, D8AI, PSL, TSMC, FIH-Foxconn, and A-Top Health Biotech.

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