Software Based Matching of X-ray Images and 3D Models of Knee Prostheses

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Abstract:

Revision joint replacements are challenging surgical tasks. The key factor for preoperative planning is to know the exact type of primary prosthesis to avoid long preoperative organisation, long operation times, and especially loss of bone and soft-tissue during operation. In daily routine there is often no information about the primary prosthesis. We are developing methods for identifying implanted prostheses from x-ray images by means of matching template images generated from prosthesis CAD data.

At the current stage of the project with only one prosthesis model we can already show promising matching qualities, so that further research in this area seems to be worthwhile. Improved segmentation algorithms as well as building up a larger prosthesis data base are our next steps.

Keywords: *Revision Joint Replacement – Identification of Implanted Prostheses – X-ray Image Analysis*

1 Problem

According to an analysis of the German Office for Quality Assurance approximately 33000 revisions of knee and hip arthroplasties were performed in 2008[1]. This corresponds to a burden rate of 10.2%. The number of primary joint replacements as well as the number of revisions in industrial nations like the US and Great Britain has constantly risen in the past decades[2,3]. Considering the aging of the population, this trend will continue and the number of revision operations will increase even stronger[4].

Revision joint replacement is an extraordinary challenge for the surgeon in terms of preoperative planning: knowing the exact type of the prosthesis that was implanted during primary replacement is a key factor. Only with this knowledge it is possible to provide suitable instruments, to ensure an acceptable duration of the procedure and to keep the damaging and loss of bone and soft-tissue to a minimum. Ensuring shorter operation times is especially important regarding the fact that a revision of total joint replacement is still associated with a higher rate of complications (such as deep vein thrombosis, bleeding and myocardial infarction amongst others) and costs nearly twice as much as primary arthroplasty[4,5,6].

The typical patient presenting for a revision joint replacement usually does not know the exact type of prosthesis that was used in primary replacement. Also a sufficient documentation of the primary prosthesis as well as prosthesis IDs are often not available. Therefore the organisation of several different operation instruments or a freestyle approach for prosthesis removal is sometimes necessary. Furthermore, knowing the exact type of prosthesis, when planning a replacement, could facilitate a revision of only the damaged components in some cases.

The development of a software application that is able to identify the prosthesis within a set of x-ray images, compare the found prosthesis with a database, and tell the exact type of prosthesis fast and accurately seems to be a promising approach.

2 Methods

The application is separated into three major components (see Figure 1): The first component "Template Image Generation" adds 3d models of endoprostheses to a database. The second component "X-ray Image Segmentation" extracts endoprostheses from provided sets of x-ray images. Finally the third component "Template Matching" finds the best matching prosthesis types in the data base.
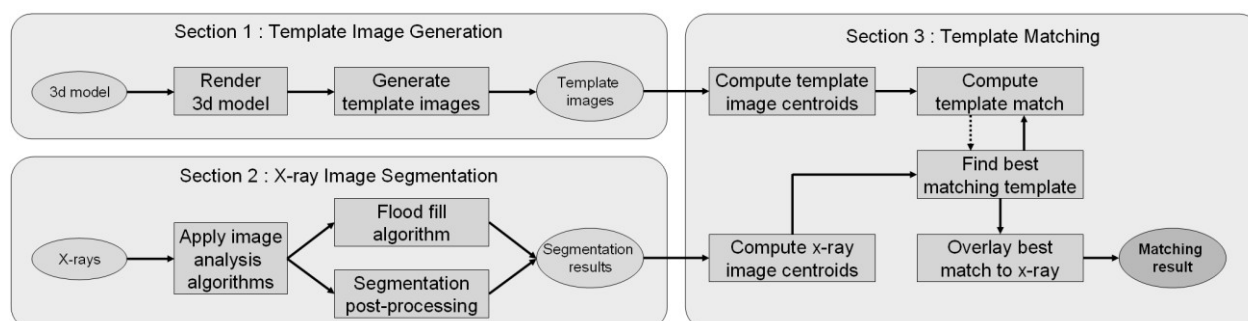
Figure 1: Flow chart and project structure of the developed application.

Template Image Generation

Since it is necessary to compare 3d objects with 2d x-rays, 2d template images of the 3d CAD endoprosthesis models are generated. These template images represent the 3d models in all possible orientations. Template images are generated using standard computer graphics image rendering methods with a virtual camera rotating around the centre of the 3d model in all three rotational degrees of freedom (DoF). Subsequently, thresholding is used to segment the silhouette of the endoprosthesis model in the projected image.

In order to reduce the number of template images and also to reduce the amount of time needed to generate those template images, the images are aligned vertically along the major axis of the segmented prosthesis region utilizing central image moments. With this image based alignment, one rotational DoF – namely the rotation about the view axis of the virtual camera – can be renounced. In doing so, the time and memory complexity can be decreased from $O(k^3)$ to $O(k\ )$ with k being the number steps in a complete 360° rotation about one axis.

X-ray Image Segmentation

Segmenting the endoprosthesis parts from given x-ray images is an important step in the prosthesis identification procedure. The following algorithm was implemented in order to extract the endoprosthesis part from x-rays given in DICOM format: First, a median filter is applied in order increase homogeneity in the area of the prosthesis while at the same time preserving the edges. Next, the Sobel operator is applied to highlight the edges around the prosthesis components. The third step requires some user interaction. The user has to select a seed point in the interior of the prosthesis components and also a colour similarity threshold value for a flood-fill algorithm, which follows. The final step is a Dilation algorithm, which is applied in order to fill small holes in the interior of the prosthesis area. Figure 2 illustrates the segmentation process and its results.
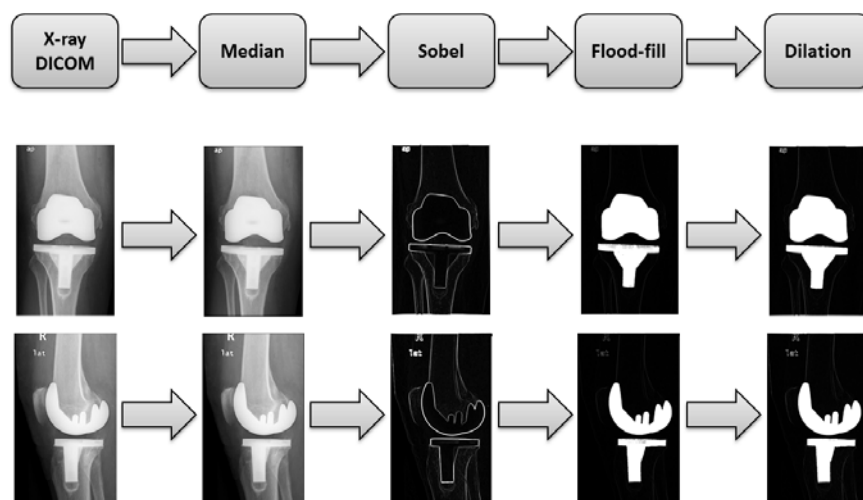

Figure 2: The implemented segmentation algorithm consisting of median filtering, Sobel operator application, flood-filling and Dilation (shown in the top row). The results achieved with an exemplary X-ray are shown in the AP (middle row) and lateral (bottom row) viewing direction.

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Template Matching

As a last step, the template images, which best match the segmented prosthesis silhouette from the provided x-ray images, is determined. The matching quality for a given combination of segmented silhouette and template image is computed in the following way: first, the centroids of both images are computed. Next, both images are layered, so that their centroids and major axes overlap. The matching quality is then determined as the number of pixels shared between template image and segmented X-ray image.

Since this method only calculates matching results for one pair of images, another algorithm is required to compare a set of results, so that a variety of different template images may be considered. The project implementation considers two cases: In the first case, only one x-ray is given as an input and the matching result is based on only one x-ray extraction. The second case provides two x-rays (lateral and frontal) as input. Therefore, matching results must be based on the segmentation results of both x-rays; meaning in particular that computed matching endoprostheses must guarantee satisfactory results for both images. The algorithm computes the degree of similarity by determining the amount of shared pixels, and then simply compares the degree of similarities of all pairs of extracted and template images. The Matching endoprostheses can be derived from the template image with the highest degree of similarity (see Figure 3).
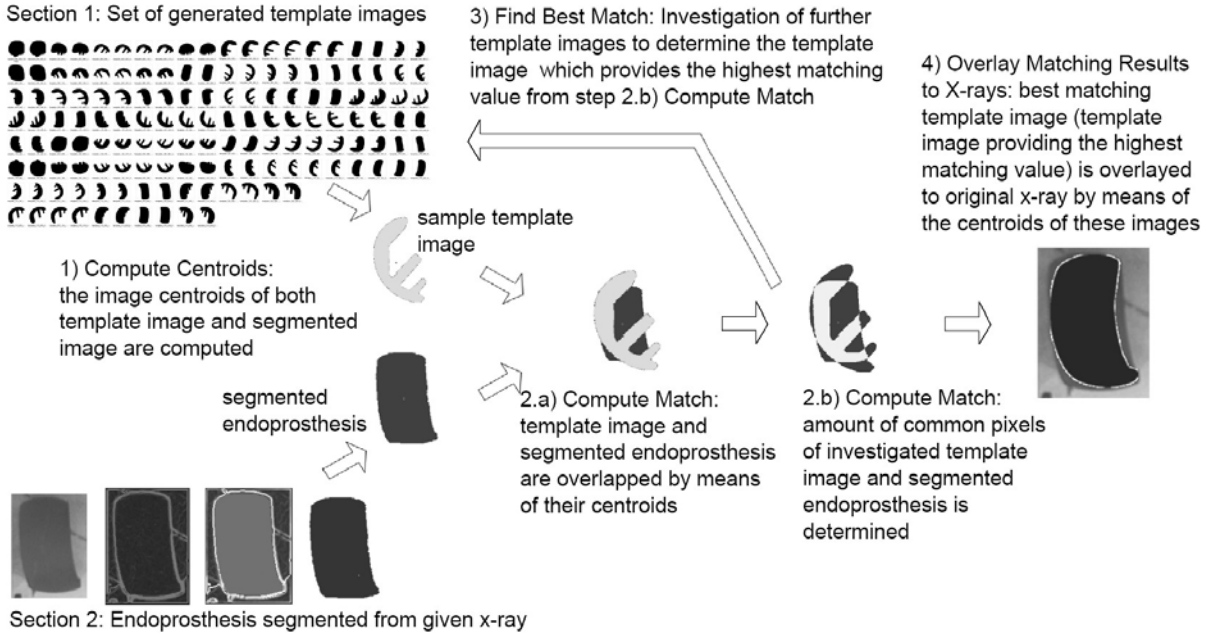
Section 1: Set of generated template images

3) Find Best Match: Investigation of further template images to determine the template image which provides the highest matching value from step 2.b) Compute Match

4) Overlay Matching Results to X-rays: best matching template image (template image providing the highest matching value) is overlayed to original x-ray by means of the centroids of these images

sample template image

1) Compute Centroids: the image centroids of both template image and segmented image are computed

segmented endoprosthesis

2.a) Compute Match: template image and segmented endoprosthesis are overlapped by means of their centroids

2.b) Compute Match: amount of common pixels of investigated template image and segmented endoprosthesis is determined

Section 2: Endoprosthesis segmented from given x-ray

Figure 3: The complete process of template image generation, endoprosthesis segmentation from given x-rays, and finally the matching of segmented endoprosthesis images to the template image database.

In order to find candidate template images more quickly Hu moments are used to pre-select templates with similar characteristics to those of the segmented X-ray images. The Hu moments are computed during the template image generation process and stored in a database together with the templates. When searching for possible candidate images in the database only those templates are considered, which have similar Hu moments as the endoprosthesis segmented from the x-rays. Utilizing Hu moments in this way the matching / identification process can be realized more efficiently as inappropriate matches (as illustrated in Figure 3) don't need to be considered.

3 Results

At the current stage of the project, only one prosthesis model (Fa. Corin, Knee Prothesis Uniglide) was available for evaluating the algorithms presented above.

To evaluate the template identification process, template images have been generated with different angle step sizes. Furthermore, template images were generated with and without alignment to their major axis in order to evaluate its effects on the resulting identification accuracies. It could be shown that a step size of 5° achieves very accurate identifications with accuracies of about 90% for lateral and over 70% for frontal images. With larger step sizes, the accuracies degrade, such that step sizes over 20° are no longer applicable. Furthermore it could be shown, that utilizing image central moments in order to renounce one rotational DoF, is applicable and achieves comparable accuracies while reducing memory and computation complexity (see Figure 4).
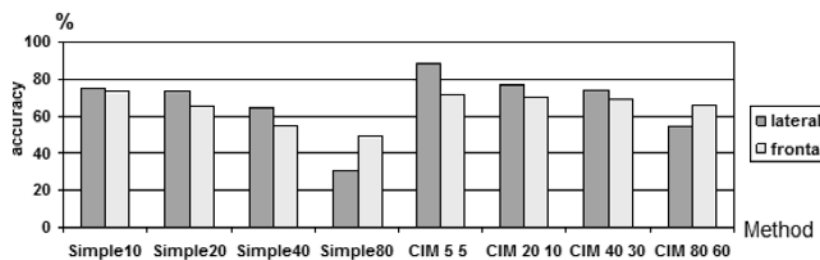
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Figure 4: Results of our prosthesis identification process, comparing the best matching template to a manually segmented x-ray of the prosthesis: *Simple x* = rotation about all three axes with a degree step size of *x*; *CIM x y* = rotation with image alignment to central moments using angle step sizes of *x* degrees around the x-axis and *y* degrees around the y-axis; accuracy is the number of pixels that the determined matching result has in common with the manual segmentation divided by the total amount of template image pixels

4 Discussion

The software based matching of X-ray images and 3D models of knee prostheses or prostheses in general can be very helpful for the surgeon to plan a challenging operation. Therefore it is necessary to achieve a high sensitivity and a high specificity.

The segmentation procedure in its current stage, utilizing common segmentation algorithms, does not always lead to optimal results. Advanced algorithms like Canny edge detection or region growing might improve the segmentation results and will be evaluated in our future work. Furthermore, problems like possibly overlapping prosthesis components in the X-ray or indistinct edges due to cemented prosthesis components will be addressed in our future work.

A weak point is the limited amount of currently available data. Due to lacking 3d models, the recent state of the application considers one type of endoprosthesis only. So until now, no conclusions about the discriminability between differ-

ent prosthesis types can be drawn. With the help of original CAD data and data obtained from CT-scans we hope to further optimize the speed and accuracy of matching of x-ray images and template images derived from 3d models. After including further 3d models as a next step, an analysis of discrimination can be performed for further evaluation of our approach.

Our current results at this stage of development are promising, so we are looking forward to the next steps to support the surgeon in future efficiently. The goal of a fast and accurate identification of prostheses when planning a revision operation could ultimately lead to a more cost-effective preparation, less complications due to shorter operation duration and less bone and soft-tissue damage.

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