

Part IV

Image Fusion

Chapter 15

Introduction

Image fusion is the process of combining information from different data sets (i.e. of different imaging modalities) into a single image. The advantages of each image are effectively added to increase the quality and information content of the final (3D) model.

In chapter 16, a short accuracy and precision review is made, summarizing, how well the final 3D knee joint model resembles that of an actual rat knee joint.

Chapter 17 describes the final steps taken to obtain the 3D joint model. The results will be presented and briefly discussed.

Chapter 16

Over-All Accuracy and Precision

In constructing a 3D model, the main concern is how accurately the model represents the original sample. Accuracy is a direct measure of the differences, while precision, on the other hand, shows how probable it is to obtain the same results again in future studies. Furthermore, in comparative studies, the relative change (precision) is often more important than the absolute error (accuracy).

Regardless of the type of study the scanner, registration- and segmentation-programs are used for, the user now has an idea of how large the induced error will be and whether the measurement will be an over or under estimation of the true value.

Based on the results from the acquisition accuracy and precision measurements in chapter 4, the following graphs in figure 16.1 are obtained.

Both acquisition methods underestimated the true thicknesses of the sample, however the CT scan was much closer to the real value. Thus, more accurate results can be achieved if the MR image is registered to the CT dataset (indicated with the green arrow). In addition, Maes [24] claims a better registration robustness for MRI to CT alignments than for the reversed case. However, in this case the registration program now uses the CT image size for re-sampling and alignment, and is therefore significantly slower and easily runs out of memory. A standard workstation with a 3.4GHz Pentium 4 processor with 2GB of memory is not capable of completing an MRI to CT Mattes MI based registration, with a CT dataset of 100MB, in less than 12 hours.

However, registration results in subchapter 4.4 have shown that when using down-sized images (from 100MB to 12MB), the registration quality remains excellent. This is due to the considerably larger voxel size in MR images. The CT dataset still has the higher resolution even after down-sampling by a factor of two.

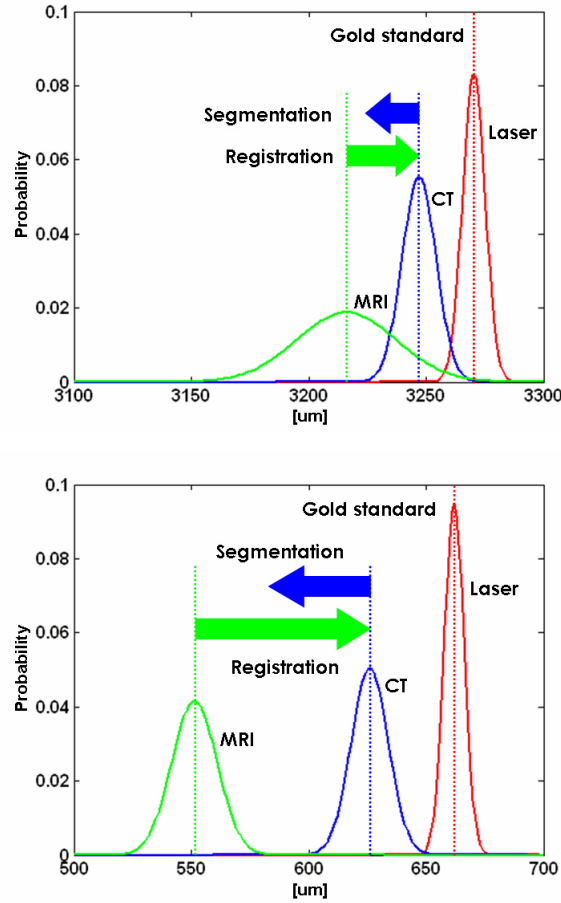


Figure 16.1: Accuracy and precision of the phantom trench (top) respectively drilling hole thickness measurements (bottom) for all three data acquisition methods.

Segmentation accuracy is strongly dependent on image quality. For high quality images ($CNR \geq 2$, $SNR \geq 2$, little intensity drift, noise and image artifacts), segmentation accuracies above 99% can be achieved. The induced error usually underestimates real tissue volumes as indicated by the blue arrow in figure 16.1.

All-in-all, the maximum accuracy (and precision) of the study is mostly limited by the image quality from the MRI and CT scans.

Better contrasts and less distortions automatically increase the accuracy of the registration and segmentation processes, whereas higher image resolutions increase acquisition accuracy.

Chapter 17

3D Model

17.1 Method

All segmentation results in mySNAP have been stored in separate AIM-files. Before all images are merged, the label of each partition must be changed to a unique number. For this purpose a separate relabeling application was implemented (see Appendix [I.1.17](#)). Tissue closer to the center was numbered higher, whereas tissue close to the surface has lower label values. The labels start at 1'000 and are increased by 1'000 for each partition. This is to preserve the option of smoothing tissue surfaces. For label values 1,2,3... edge smoothing would hardly be possible due to the small differences between labels and intensity levels. Table [G.1](#) in Appendix [G](#) lists all partitions and their corresponding label values.

Using the application "AppAIMMerge" (described in Appendix [I.1.14](#)), the relabeled segmentations can be added one-by-one to the final 3D model AIM-file. The program compares each voxel of the 3D model with the corresponding label of the segmentation file and writes the larger value back to the 3D image.

Finally the 3D knee joint model can be visualized using any 3D visualization program, like VIS or SHAPE.

17.2 Results

Four of the many possible display mutations are depicted below. Naturally, the quality of the result can be best observed if viewed in 3D. The final 3D knee joint model can be found on the enclosed DVD.

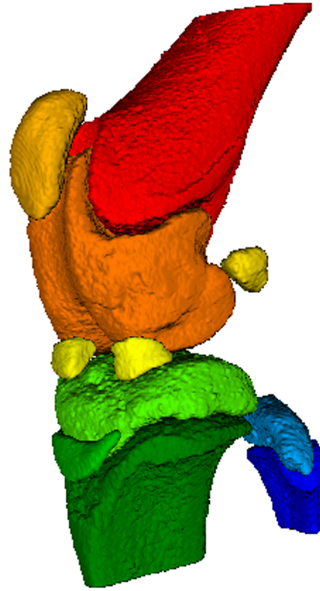


Figure 17.1: CT 3D knee joint model, where each bone is segmented and colored separately.

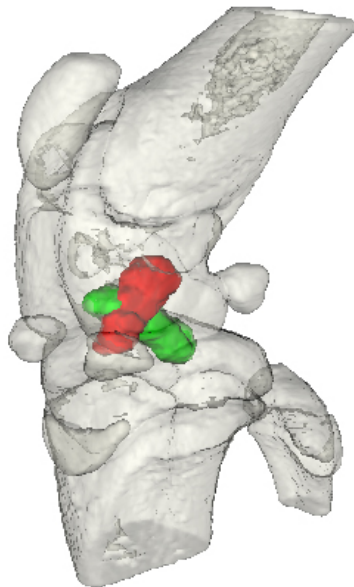


Figure 17.2: CT/MRI 3D knee joint model with femur, tibia and the cruciate ligaments (colored red and green).

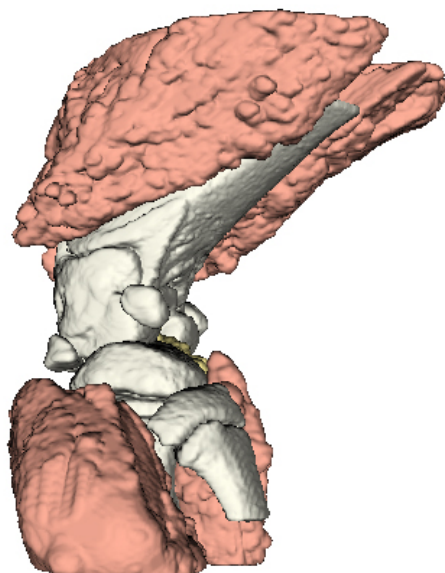


Figure 17.3: CT/MRI 3D knee joint model with all the 23 separately extracted components.

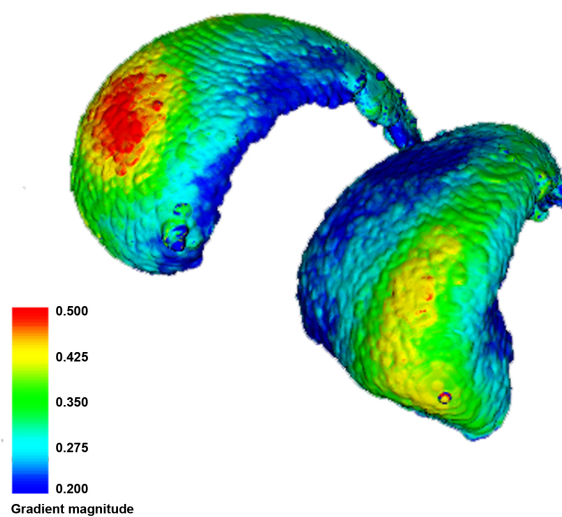


Figure 17.4: Contrast enhanced CT 3D knee joint model after a cartilage thickness measurement analysis. The color map is shown in the lower left corner. Blue resembles thin areas, red resembles thick areas.

17.3 Discussion

Due to possible further improvements previously mentioned and listed in the Outlook, not all of the over 40 individual rat knee joint tissue parts have been extracted.

However, the results presented show the potential of this method to model a complex structure such as a rat knee joint. Within a single image-modality, the information content can be improved significantly by separating the individual tissue structures, as illustrated in figure 17.1. Especially complex bone structures such as growth plates or vertebrae can be easily segmented with mySNAP and subsequently analyzed. Former, purely intensity-based segmentation methods failed to correctly partition the complex tissue structures.

Fusion of images with different modalities leads to a gain in advanced image information. Both datasets on their own are not capable of delivering as much information as a combined image does. The CT image contributes its high resolution information on bone structure, whereas with the MR image soft-tissue can be added to form the combined 3D model (see figure 17.2 and 17.3).

An example is given where cartilage was extracted from the contrast-enhanced CT scan and a thickness measurement analysis applied using the SiteSpecificThickness program. Figure 17.4 shows the potential of such 3D model analyzing methods.

In future FE analysis, different stiffness coefficients can be applied to bone and soft-tissue, and force dissipation (change) in the case of osteoarthritis or any other joint related diseases can be studied more accurately. This may lead to a increased understanding of the complex kinetics of (knee) joints, and hence, better treatments.

Conclusion

Every image acquisition method has its advantages and disadvantages. A CT scanner gives high resolution and high contrast images for bone structures, but can not visualize soft-tissues well. Whereas, MRI devices return good contrast for soft-tissue with the drawback of a lower image resolution and more distortions.

This study showed that the use of contrast agent increases MR image quality significantly. However, bone micro-structures are still only visible in μ CT scans. Hence, neither two modalities can replace the other without a loss in quality. Combining the advantages of both scan methods leads to the most accurate 3D models.

Movement of the sample is critical in multi-modality data acquisitions and the joint fixture requires improvement. However, under slight joint movement, the images can still be registered, provided the CT image is divided into two parts (separating upper leg bones from lower leg bones).

Cartilage distributes and dampens (impact) loads in a knee joint. It is highly important to have an accurate model of this "key role"-tissue. Due to the limited resolution of MRI, cartilage can not be accurately modeled. A scan of the growth plates immersed in non-diffusive contrast agent, made an accurate CT visualization possible. However, this is a destructive method and can not be used for eventual in-vivo experiments.

The best multi-modal registration results were achieved, with fiducial marker registration used as an initial guess for subsequent Mattes mutual information (MI) registration. The registration improvement due to the intensity-based method was small and hardly visible to the naked eye.

However, fiducial markers are inevitable for multi-modality registration. Due to significantly different intensity distributions in MR and CT images, there is no identical iso-surface and hence, no proper initial transformation can be found.

The fiducial markers have been improved during the study and are now leakage-free over long terms. This again increases the accuracy of point-based registration and may eliminate the need to perform the time and memory consuming MI registration.

Acquisition accuracy is directly linked with image resolution. Higher resolution leads to scan results closer to reality. Thus, a MR to CT registration returns more accurate results than a CT to MR alignment. The MR image loses information due to the transformation, but gains accuracy when registered to the more accurate CT dataset.

Normalized MI and Viola-Wells MI registrations are not leading to any improved result and are not recommended for large datasets. Kernel size and number of samples had to be significantly reduced to keep processing times within an acceptable range. This automatically incurs a loss in accuracy.

In this project, a semi-automatic segmentation program has been implemented. mySNAP is a graphical user interface based software which makes it simple to use, even for inexperienced users. Changes in filter or segmentation parameters are on-the-fly applied to the image. This significantly eases the segmentation process and leads to accurate partitioning results for bone and soft-tissue structures.

Segmentation strongly depends on image quality and voxel size. A voxel can only belong or not belong to a segmented region. There are no gray-levels in between. Hence, the segmentation accuracy increases with smaller voxel sizes.

On the other hand, with smaller voxel sizes the signal-to-noise ratio decreases, and image information is lost. Thus, the segmentation program can not find all edge features or intensity regions anymore.

The maximal segmentation accuracy is a trade-off between image information and resolution.

The final 3D model combines the advantages of both acquisition modalities. Each partition in the final 3D model can be visualized or analyzed individually or in groups. There is significant potential, to improve the understanding of the pathogenesis of joint diseases by analyzing 3D models as presented in this study.

However, the process of obtaining such a 3D model can still be improved. Some suggestions and ideas are outlined in the following chapter.

Outlook

There are several different approaches to improve the quality of 3D joint models. The experiments showed that the knee joint must be properly fixed. Femur and tibia could be fixated with screws at both bone ends, keeping the sample centered inside the tube. The sample should not touch any walls preserving the natural shape of the soft-tissue. The same holds for the fiducial markers. A simple system could be developed to place fiducials close to the surface, without actually touching the sample.

To minimize MRI surface distortions due to air/water interfaces, the tube should be filled with a liquid of low magnetization properties. The MR image information will further improve if the appropriate contrast agent concentration is found (see figure 5.8). The MRI gradients are soon to be replaced with stronger coils, and hence higher resolution and improved image quality can be achieved.

For CT scans, the voxel size can be further reduced to $10\mu\text{m}$. Although this would increase the data size by a factor of 8. Significantly longer registration and segmentation times would be expected. However, for 3D models, time is not a real issue - accuracy is.

Increased scan resolution would also help to more accurately extract cartilage. Newly developed techniques such as EPIC- μCT could be tried, to visualize cartilage.

A dataset of 100MB can not be processed by the registration and segmentation program on a regular 3.4GHz Pentium 4 computer with 2GB of memory. Thus, processing speed and memory efficiency of both programs should be improved.

Once the improved 3D model is created, extensive numerical analysis can be performed on the dataset. Different "stiffness" coefficients could be assigned to different segmented tissue-types. The subsequent FE analysis may clarify the highly complex force distribution in a healthy or injured joint.

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