

# Medical Image Analysis, Assignment 2

## 1 Introduction

In this project you will do shape analysis and create a shape model which you will use to segment kidneys in renal scintigraphy images. The purpose of this assignment is to develop a shape model and use this model to improve the segmentation process. The assignment has two parts. In the first part you will develop a shape model based on a number of segmented kidneys. This model will be based on points sampled along the contour of the kidneys. In the second part you will use this model in order to improve the segmentation of further kidneys. In order to pass the assignment, only the first part is needed and then you will get grade 3. In order to get a higher grade, you should also do the second part.

## 2 The Rules

The assignment is available on the Canvas course page from **Friday November 14**. The deadline is on **Sunday November 30 (2025)** (23:59 CET). Each student should hand in his or her own individual solution and should, upon request, be able to present the details in all the steps of the used algorithm. You are, however, allowed to discuss the assignment-problem with others. You may also ask your teachers and the course assistants for advice, if needed. It is not allowed to use generative AI to produce text and/or solutions to the assignment.

**The report.** Present your work in a report of approximately four A4-pages, written in English or Swedish. The report should (at least) contain an introduction, a description of theory and the methods used, a section with results (including a few images, illustrating obtained results) and, finally, a conclusion, where the results are discussed.

You may submit your code along with the report, if you want to (see below). However, the teacher is going to judge your work based on the report alone. A well-written report will have a positive influence on the grade you obtain. Usually, the teacher will check the code only in very special cases, for instance when the results seem strange or if persistent problems remain with your implementation.

**Submitting your work.** Submit the report as a pdf-file with the name format `assignment_2_yourname.pdf` on the Canvas course page. Don't submit any code. Teachers usually do not check code since it is often hard to read (each person having its own style, structure and choice of variable names). Everything you wish to communicate should be written in the report. A well-written and well-structured report will have a positive influence on the grade you obtain.

### 3 Background

Scintigraphy is an imaging technique where the decay of a radioactive substance is measured with a gamma camera. In renal scintigraphy the radioactive substance is  $^{99m}\text{Tc}$ , Technetium. To get an image of the kidneys, this radioactive substance is attached to a biological molecule called dimercaptosuccinic acid (DMSA) which accumulates in the kidneys. This substance,  $^{99m}\text{Tc}$ -DMSA, is injected into the patient's blood flow and the images are acquired after 2–3 hours. Then you get an image as the one in Figure ?? where in most cases only the kidneys are visible (the urinary bladder can sometimes show up in the images too).



Figure 1: A renal scintigraphy image.

The images used in this project were acquired from children who have had repeated urinary tract infections which has lead to inflammation in the renal pelvis and left untreated this can cause scars in the kidneys. In the future these scars can lead to renal failure. The uptake of  $^{99m}\text{Tc}$ -DMSA is normally homogeneous but if the patient has scars, these can be seen as wedge-shaped regions with lower uptake. Because of this it is practical to use a shape model when segmenting the kidneys, since for example an edge detector might fail to include the scars if they are located close to the edge of the kidney (which is common).

### 4 Manual Segmentations

To create a shape model you need manual segmentations of organ of interest. These are preferably done by a physician who has great knowledge of the appearance of the organ. An example of such a segmentation can be found in `man_seg.mat`, where several landmarks has been placed around one of the kidneys of patient 1 in `dmsa_images.mat` (in `main_dmsa.m` code are provided to load the images correctly). Observe that the coordinates of the landmarks are represented as complex numbers in the variable `man_seg`. If you run the example code you will also obtain

the  $x$ -coordinates and the  $y$ -coordinates in the variables `Xmcoord` and `Ymcoord` respectively. However, it is not convenient to work with this many landmarks when creating a shape model.

For the report: Resample these landmarks to 14 equally spaced landmarks around the kidney, where landmark number 1 coincides with the given landmark number 1 for the first patient. Use linear interpolation to interpolate between the given landmarks.

## 5 Shape Model

You are now given manual segmentations of the kidneys in the first 20 images in `dmsa_images.mat`. They are stored in `models.mat` and should be used in the rest of the assignments. Observe that the coordinates of the landmarks are represented as complex numbers in the variable `models`. If you run the example code you will also obtain the  $x$ -coordinates and the  $y$ -coordinates in the variables `Xcoord` and `Ycoord` respectively. Since there are no consistent differences between left and right kidneys, the left sided manual segmentations has been mirrored and one shape model for both kidneys can be constructed. There are code in `main_dmsa.m` which can be used as a start to visualize the images and the manual segmentations. The manual segmentations are stored as: 14 (landmarks)  $\times$  40 (kidneys) in complex notation, where columns 1-20 are the right sided kidney of patient 1-20 and columns 21-40 are the mirrored left sided kidneys of patient 1-20, i.e. you do not need to mirror any segmentations.

Since we only want to model the shape of a kidney, the first step is to remove the scale, translation and rotation. This can be done using generalized Procrustes analysis, i.e.

1. Align each shape to the first
2. Calculate the mean of the transformed shapes (by calculating the mean value for each point)
3. Align the mean shape to the first (to guarantee convergence)
4. Align each shape to the mean shape
5. Update the mean shape
6. Iterate 3 to 5 until convergence (i.e. the mean shape does not change significantly from the previous iteration)

It is a good idea to plot the aligned shapes in the same figure before proceeding with the shape model in order to verify that the translation, rotation and scale are eliminated.

After aligning the shapes calculate the covariance function of the points and the corresponding eigen-values and eigen-vectors in order to obtain a shape model. Observe that the alignment should take care of different positions, orientations and scales of the kidneys in the data-set and the eigen-shapes should describe the shape variations and not variations in position, orientation and size.

For the report: Align the shapes using Procrustes analysis, calculate a shape model and visualize the different modes in the shape model. Describe what kind of shape variations the first principal modes describe. Plot the eigen-values and discuss how many modes that are suitable for your shape model.

## 6 Segmentation with a Shape Model (Optional - Only for higher grades)

Now use your shape model together with some segmentation algorithm and try to segment kidneys in the images that has not been used when constructing the shape model (e.g. the last five images). It is sufficient to be able to segment a right sided kidney since your model is a right sided kidney.

Start with an initial segmentation, e.g. based on thresholding, and use e.g. the matlab-function "bwboundaries" to find the coordinates of the edge of the segmented kidney. Use your solution to the first part of this assignment to resample the edge to only 14 landmarks, and make sure that the first landmark is at the bottom of the kidney.

Align your 14 landmarks to the mean shape (i.e. the coordinate system of the shape model), and save the pose parameters ( $s, R, t$ ). Determine new shape parameters ( $b$ ) and update your landmarks in the coordinate system of the shape model, before you use the saved pose parameters to transform your landmarks back to the coordinate system of the image. For each landmark, find the closest point on your edge, and use these as the new landmarks. Iterate until convergence.

For the report: Segment at least five images using the procedure above and your shape model and present the results.

## 7 Evaluation of results

Discuss how the registration results should be presented and the performance of the proposed algorithm can be adequately evaluated. In your report, only the simplest kind of evaluation is required. This could be simply a subjective visual assessment of the obtained results. However, this will not be enough in a scientific paper, and we therefore need to be aware of how we could proceed in order to get more objective assessments.

Extra assignment for even higher grade (5): Discuss how an objective and quantitative evaluation of your segmentation results could be made. Discuss in particular and examine the dependence on the number of principal modes used in the shape model and how an optimal number of modes could be determined.

## References

- [1] Dryden, I.L. and Mardia, K.V.: *Statistical Shape Analysis*, John Wiley & Sons, 1998.
- [2] Cootes T.F., Taylor C.J., Cooper D.H. and Graham J.: *Active Shape Models – their training and application*, Computer Vision and Image Understanding, 61(1), 38–59 (1995).
- [3] Cootes, T.F. and Taylor, C.J.: *Statistical Models of Appearance for Computer Vision*, March 2004.