

Medical Image Analysis Assignment 2: Registration.

1 Introduction

The purpose of this assignment is to perform *landmark-based image registration*. Both rigid registration, using Euclidean transformations, and Procrustes alignment, using similarity transformations, are considered. The landmarks will be generated automatically using SIFT and RANSAC, and are therefore to be considered as *mathematical landmarks*. Landmark-based methods are especially interesting when dealing with image pairs having different modalities. This is illustrated clearly in the second part of the assignment.

Each assignment in the course is given a grade. Assignment 2 has three tasks three tasks (stated in the gray frames below) and if you complete the first task you'll pass and the assignment gets the grade 3. Completing the two first tasks gives grade 4. Completion of all three tasks results in the highest grade, 5. The teachers will correct and comment your solution and if you fail to pass the first time around we will ask you to improve and complement your report.

2 The Rules

The assignment is published on the course's Canvas page **Friday 13 November**. The deadline is on **Sunday 29 November** (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 with others. You may also ask your teachers and the course assistants for advice, if needed.

The report. Present your work in a report written in English or Swedish. The report should (at least) contain an introduction, a description of the theory and methods used, a section with the results, including necessary tables and a few images illustrating obtained results, and a conclusion where your results and findings are discussed. In particular, make sure to describe all essential choices made in the implementation of your algorithm, preprocessing steps included.

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.

Supervision sessions. There will be four opportunities get help with the assignment; see TimeEdit. All sessions take place online (see Canvas) and the assistants are PhD-studentes *David Gillsjö* and *Linn Öström*.

3 The data

Two data sets (both of them collections of image pairs) are provided for the assignment. They can be downloaded from the course webpage.

Collection 1. This data consists of 29 pairs of microscopy ($20\times$) images of histopathological material obtained from radical prostatectomy (surgically removed prostates). There are two folders, each containing one image from each pair. The images were created in the following manner. Cylindrical cores of 1mm in diameter were punched out from the specimens, arranged in tissue microarrays (TMAs), and embedded in paraffine. Each image pair consists of two consecutive sections of thickness $4\mu m$ from these cores. One slice was stained with hematoxolin-eosin (H&E), which looks red or pink, and the other slice with p63AMACR, which appears blue or purple. The tissue samples in the image pair will therefore appear to have similar, but not identical, shapes. Since the images were acquired with the same magnification our assumption is that they may be aligned using a Euclidean transformation (translation+rotation).

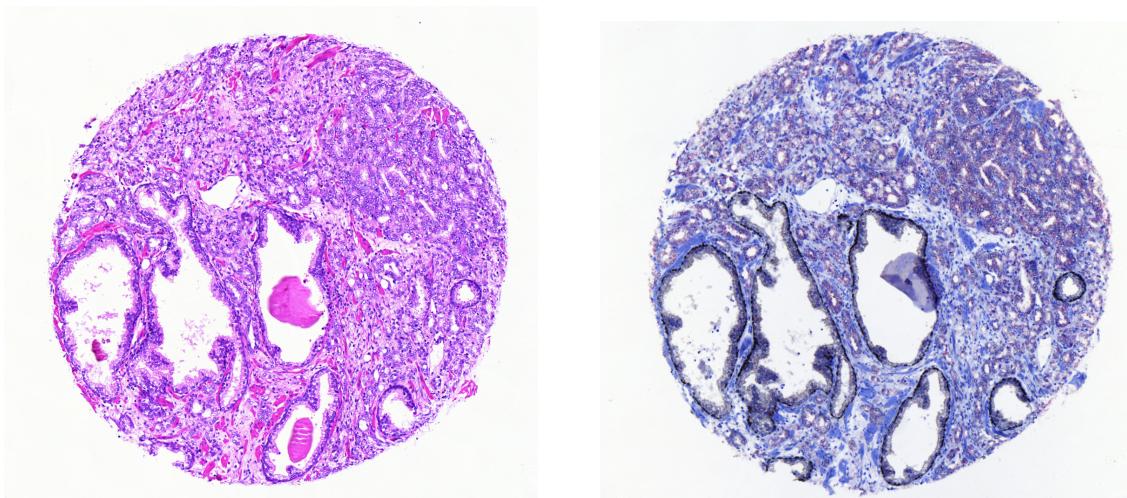
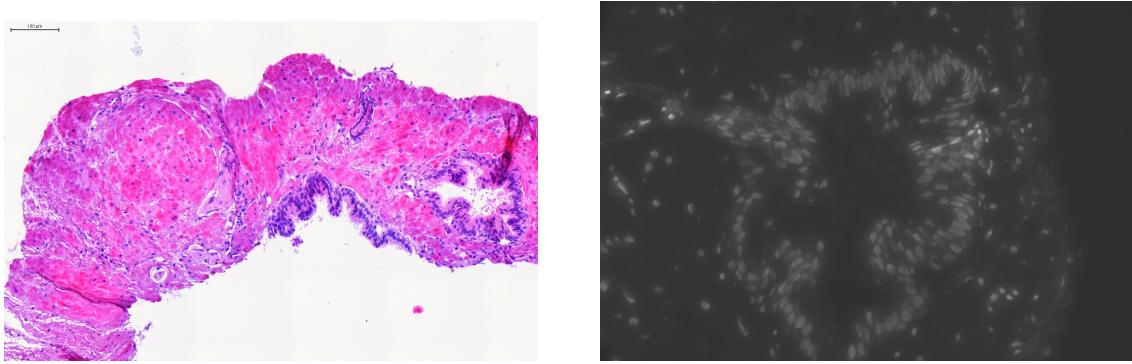


Figure 1: An image pair from Collection, prostate tissue cores. The two tissue samples are adjacent slices from the same core. The sample to the left is stained with H&E, the one to the right with p63AMACR.

For the report: Perform rigid registration of the image pairs. Record the *magnitudes* of the translation vectors and the rotation angles. Perform visual assessment of the performance of the method for each image pair. Describe the required theory adequately. This is the minimum requirement for the grade 3 (pass).

Collection 2. Here 12 pairs of images are provided. Each pair consists of an image ($10\times$) stained with H&E and another ($40\times$) stained with a fluorescent marker and acquired using time-resolved fluorescence microscopy (TRF), which looks a faint nebulous signal on a dark background. Both images come from the same slice, where the fluorescent staining was applied and the TRF image acquired first. Then the fluorescent staining was washed off, the H&E staining was applied subsequently and the corresponding image acquired. Due to the difference in magnification, the TRF image shows only a detail of the H&E image. The alignment should therefore use a similarity transformation (translation+rotation+scale).



Figur 2: An image pair form Collection 2. The tissue is from a prostate biopsy. The images are obtained from the same slice. The left one with a H&E-staining and $10\times$ magnification, the right one with an fluorescent staining and $40\times$ magnification and amplified.

More information about the images can be found in Lippolis et al. [1].

For the report: Perform image registration using similarity transformations. Record the magnitudes of the translations, scale factors and the rotation angels. Assess performance visually for each image pair. Describe the required theory adequately. (Minimum requirement for the grade 4.)

4 VLFeat

Download the open source computer vision toolbox VLFeat (release 0.9.19) for MATLAB from <http://www.vlfeat.org/>. We will use the MATLAB-command $[F, D] = VL_SIFT(I)$, which computes SIFT-keypoints (F) and SIFT-descriptors (D). A description of the features of the toolbox can be found in [3].

5 Landmark Generation

In both parts of the assignment the given images should be converted to gray scale images. In the case of the TRF images, it may be an advantage to make an histogram equalization as well. It may even be advisable to downscale the images to half the size (a quarter of the number of pixels) to reduce runtimes.

5.1 Keypoints and descriptors – SIFT

The first step in the landmark-generation is to find salient points in the images (keypoints) which are tagged with “fingerprints” (descriptors) which will allow us to find corresponding keypoints in pairs of images showing the same scene. To do this we use D. Lowe’s SIFT-algorithm [2], in particular the command $[F, D] = VL_SIFT(I)$, referred to above.

5.2 Generating landmarks from the keypoints – Lowe’s criterion and RANSAC

We first generate a set of preliminary matchings using Lowe’s criterion. We give a brief explanation here. Let $(\mathbf{x}_i, \mathbf{f}_i)_{i=1}^N$ denote the N pairs of keypoints $\mathbf{x}_i \in \mathbf{R}^2$ and corresponding descriptors $\mathbf{f}_i \in \mathbf{R}^{128}$ found by SIFT in the first image. Let similarly $(\mathbf{x}'_j, \mathbf{f}'_j)_{j=1}^M$ denote keypoint-descriptor pairs detected in the second image. Then we first compute the $N \times M$ -matrix $\mathbf{D} = [d_{ij}]$ where the entries $d_{ij} = \|\mathbf{f}_i - \mathbf{f}'_j\|$ are the euclidean distances between all pairs of descriptors, one from each image. Next, for each index i we find the index j^* such that

$$d_{ij^*} = \min_{1 \leq j \leq M} d_{ij}.$$

The keypoint \mathbf{x}'_{j^*} in image two is preliminarily matched to the keypoint \mathbf{x}_i in image one if Lowe’s criterion is fulfilled:

$$\frac{\min_j d_{ij}}{\min_{j:j \neq j^*} d_{ij}} < 0.77.$$

This criterion states that $(\mathbf{x}_i, \mathbf{x}'_{j^*})$ is a preliminary match only if the corresponding descriptors \mathbf{f}_i and \mathbf{f}'_{j^*} have a mutual distance d_{ij^*} which is *significantly* shorter than that from \mathbf{f}_i to any other descriptor \mathbf{f}'_j from the second image. The number 0.77 is a heuristically chosen. The parameter may be chosen to be any number between zero and one.

Among these matches we find real pairs of matching keypoints using RANSAC [4]. When RANSAC is used, it is necessary to compute the registration models (rigid or similarity referred to below) on minimal or near-minimal sets of preliminary keypoint correspondences. The result of this step is to obtain a maximal set of inliers, i.e. a maximal set of keypoint-pairs which are consistent with the registration model used. This set of inliers will be our landmarks. The final registration is estimated from these landmarks.

5.3 Rigid alignment

The landmarks should be aligned using a transformation $T : \mathbf{R}^2 \rightarrow \mathbf{R}^2$ of the following type,

$$T(\mathbf{x}) = \mathbf{t} + Q\mathbf{x} \quad (1)$$

where $\mathbf{t} \in \mathbf{R}^2$ is a translation vector and Q is a 2×2 orthogonal matrix, i.e. satisfying $Q^T Q = I$. An algorithm for computing \mathbf{t} and Q , based on singular value decomposition of a correlation matrix for the data, is presented in the lectures. This algorithm is formulated for the three-dimensional case, but is easily modified to suit our purpose.

5.4 Alignment using similarity transformation.

The landmarks should be aligned using a transformation $T : \mathbf{R}^2 \rightarrow \mathbf{R}^2$ of the following type,

$$T(\mathbf{x}) = \mathbf{t} + sQ\mathbf{x} \quad (2)$$

where $\mathbf{t} \in \mathbf{R}^2$ is a translation vector and Q is a 2×2 orthogonal matrix, and $s > 0$ is a scale factor. Again, \mathbf{t} , Q and s may be computed using an algorithm presented in the lectures. Alternatively one may use the method employed in Lippolis et al. [1].

5.5 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: This is the minimum requirement for the highest grade (5): Make an objective assessment of the performance of the two algorithms used above. Use manually recorded landmarks (5 to 10 correspondences for each image pair) and follow the evaluation method outlined in the paper Giuseppe et al. [1].

6 Suggested Pipeline

This short section provides a brief outline of the steps needed in landmark-based registration using landmarks provided by distinctive image features from scale-invariant keypoints (SIFT), see [2].

1. Load the images in corresponding pairs and rescale (possibly). Convert to grayvalue and single precision. The Matlab commands `imread`, `imresize`, `rgb2gray` and `single` may be used, but the step can be completed in different ways.
2. Compute SIFT keypoints and descriptors in both images using the VLFeat command `[k,d] = vl_sift(Im)`.
3. Find preliminary matchings of pairs of keypoints using the descriptors. Either you employ the VLFeat command `vl_ubcmatch` or you make your own implementation of Lowe's criterion (as outline briefly in the assignment instructions.)
4. Find the “true” matches among all preliminary matchings using RANSAC. This step requires the implementation of the alignment model - orthogonal Procrustes for the rigid registration and Procrustes for the similarity transformations. The “true” matches are defined to be the maximal inlier set found from the RANSAC procedure.
5. Align the images using the alignment model (rigid or similarity) using the maximal inlier set as landmarks. An image may be transformed and overlayed on top of another image using the Matlab script similar to the following:

```
T = [s*R, t ;
      0, 0, 1];
tform = affine2d(T');
```

```

I1_warp = imwarp(I1, tform, 'OutputView', imref2d(size(I2)));

figure; clf;
imshow(imfuse(I2, I1_warp, 'blend'));

```

6. Evaluate the result on both image collections and write the report.

Referenser

- [1] G. Lippolis, A. Edsjö, L. Helczynski and N. Chr Overgaard: *Automatic registration of multi-modal microscopy images for integrative analysis of prostate tissue sections*, BMC Cancer, **13**:408, 2013 (Open Access).
- [2] D. G. Lowe: *Distinctive Image Features from Scale-Invariant Keypoints*, International J. Comp. Vis. **60**:2, 91–110, 2004.
- [3] A. Vidaldi and B. Fulkerson: *VLFeat - An open portable library of computer vision algorithms*, MM'10, October 25–29, 2010, Firenze, Italy.
- [4] M.A. Fischler and R.C. Bolles: *Random sample consensus - a paradigm for model-fitting with applications to image-analysis and automated cartography*, Comm. of the AMC **24**(6), 381–395, 1981.