

Image Registration by Model Criteria

R. S. Schestowitz, C. J. Twining, T. F. Cootes and C.J. Taylor

Imaging Science and Biomedical Engineering, University of Manchester
Stopford Building, Oxford Road, Manchester M13 9PT, United Kingdom

Abstract. The need to establish correspondence across groups of images has for long been recognised. This problem is referred to as registration. To enable comparative analysis of images depicting a similar object, analogous object structures must be identified and a practical way of doing so is by aligning these structures. In other words, an object in one image needs to fit inside a boundary that is common to other images so that they can all be analysed or processed in space that is neutral to changes in size, view-point, etc. The alignment is achieved by treating each image as a deformable object and transforming it to match another. One image is said to match another when it appears similar, i.e. objects within it overlap. A framework describing a registration scheme is specified by an objective function and it comprises measures of similarity. Similarity measures assign an evaluative score to a collection of images that are subjected to transformations. That score reflects how good the alignment is and when it can no longer improve, convergence (i.e. registration) is assumed.

There is no agreement in the literature on what to consider a powerful family of transformations. It is also unclear what correctly defines similarity and which images should be compared when measuring that similarity. Popular methods are based on heuristics and results are difficult to validate. Our work addresses these issues not by finding good registration schemes empirically, but by providing a well-founded approach to the problem. Since registration is known to reduce variation within groups of images, a model which represents these images will be accordingly affected. By looking at a model, we can derive similarity across the entire set, without needing to select a reference. In a sense, the model is used here as a global similarity measure. Moreover, when models are used in the process of registration, statistical models are created, whereupon variability in datasets is broken down into meaningful 'components'. These are in fact the principal modes of model variation and they can highlight attributes of interest. This functionality can aid identification of pathology symptoms in an autonomous manner. By registering raw sets of images of different groups, models can be built to find where greater variability lies.

The objective function presented in this work obtains similarity indirectly. It does so by calculating the complexity of a statistical model, namely by looking at the covariance matrix of that model. To efficiently

evaluate model complexity, we obtained $\sum_{i=1}^n \log(\lambda_i + \delta)$ where $\lambda_{1 < i < n}$ are the n Eigen-values of the covariance matrix whose magnitudes are the greatest. This essentially approximates

$$\det(\mathbf{M} + \delta) \equiv \prod_{i=1}^n (\lambda + \delta)_i \propto \sum_{i=1}^n \log(\lambda_i + \delta) \equiv \log(\det(\mathbf{M} + \delta)) \quad (1)$$

where \mathbf{M} is the covariance matrix under consideration. The algorithm makes the registration purely model-driven so that no choice of images is needed for comparison. The objective function leads to one distinct solution without dependence upon individual images. This resolves the recurring issue of having to select a reference image and treat the problem as if it relies primarily on that one image.

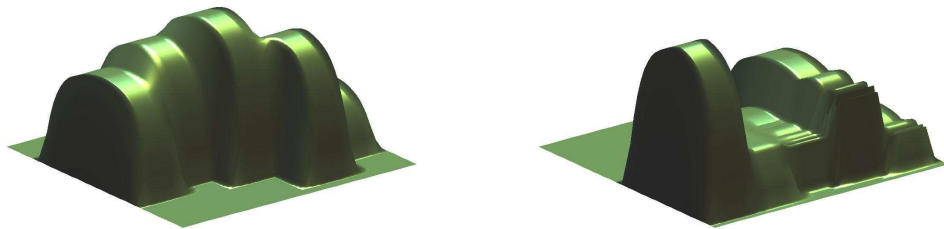


Figure 1. On the left: Example bump data is displayed in its initial form. Each bump on the surface represents a 1-D vector. On the right: Example of the result of registration. The edges of the bumps clearly begin to align.

To transform images, we chose to employ the clamped-plate splines because they address known flaws often encountered when thin-plate splines and the B-splines are used. The clamped-plate splines prevent

any of the regions in an images from being torn or folded, hence they preserve the existence and integrity of all image regions. Particularly in the bio-medical domain, visibility of all constituent structures becomes crucial.

To demonstrate the advantages gained by the model-based approach, we experimented with one dimensional synthetic data where the correct solution is known. Generated data depicted a bump, essentially an half-ellipse, which varied in its height, width and position (see Figure 1).

The sets were stochastically generated with significant difference in values. We describe a solution to be good when we observe proper alignment of the bumps and a resulting registered set that is distinct from any of the original images. At the same time, we are continuously delivered statistical models (as shown in Figure 3) of variable bumps and well-founded ways to visualise and evaluate models.

After only several minutes, good alignment amongst all bumps was obtained. Sets comprising dozens of bumps could be successfully handled by the algorithm and statistical model of their appearance emerged as a by-product of registration. Judging by the known correct solution, the quality of registration was high. It also successfully surpassed naïve implementations of some conventional algorithms.

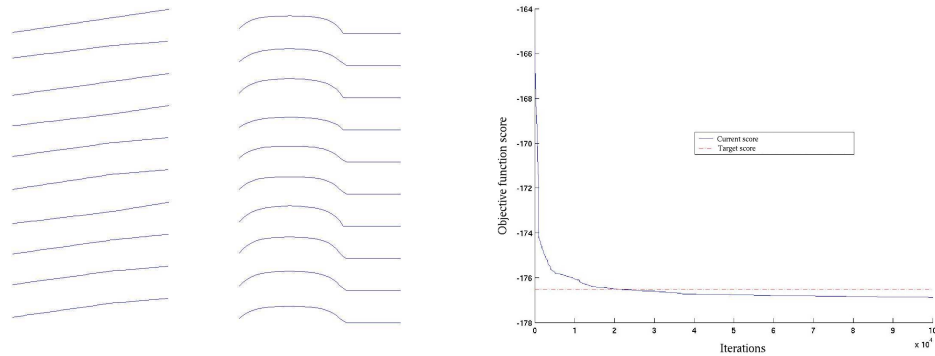


Figure 2. On the left: The correct warps that align given data and that same data with the warps applied. On the right: The value of the objective function as convergence is approached.

As well as a basic model-based objective function, we investigated the use of subsets to speed up the process. Subsets are chosen stochastically every 100 iterations, thereby the problem is simplified and the algorithm becomes more effective in dealing with large sets. It is worth adding that choice of warps was random at all stages so no data-bias or *a-priori* knowledge was involved.

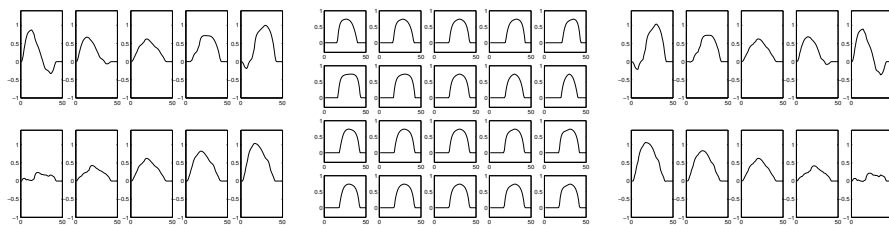


Figure 3. From left-to-right: Combined, shape and intensity models of 10 data instances at the start. The principal modes are shown with up to ± 2 standard deviations away from the mean.

The results we have seen thus far suggest that our approach works properly while addressing common difficulties. It can handle large sets and provide a solution that does not depend on any arbitrary selection of images. Future work will apply this approach in a real-world problem by treating 2-D images of the human brain. In the problem of inter-subject brain registration, where variability is much greater, the damaging effects of choosing individual images crop up. The great benefits of driving registration by models should then become even more apparent and models be generated without the need for any manual mark-up.