Acquisition of *a priori* Information from Groupwise Registration of Inter-Patient Prostate Boundaries in MR

Jonathan Francis Roscoe[1]
jjr6@aber.ac.uk
Hannah M. Dee[1]
hmd1@aber.ac.uk
Paul Malcolm[2]
paul.malcolm@nnuh.nhs.uk
Reyer Zwiggelaar[1]
rrz@aber.ac.uk

[1] Department of Computer Science
Aberystwyth University
Aberystwyth
SY23 3DB

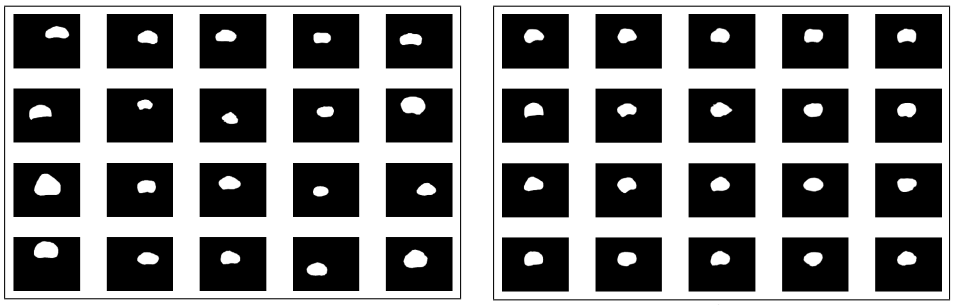
[2] Norfolk and Norwich University Hospital
Colney Lane
Norwich
NR4 7UY

Abstract

Registration is a complex computer vision issue that can be simplified with the aid of prior knowledge. In this paper we present the application of the groupwise method known as congealing with prostate boundaries to derive a series of transforms that can be applied to other foci for registration. Congealing provides us with transformation vectors for each image that we apply to known tumour boundaries in order to obtain a probability distribution for use as prior knowledge in future work. In this way we are able to visualise tumour locations on an mean prostate representation and provide a 'cancer prior' for future prostate work. The results of our initial experiment demonstrate a reliable set of affine transforms for use with prostate MR.

1 Introduction

Prostate cancer is one of the most common cancers and treatment plans can be hampered by issues in initial diagnosis and staging. An increasingly popular means of enhancing guided biopsy for improved diagnosis is to utilise TRUS/MR fusion for targeting and enhanced visualisation [6]. Current methods typically depend on manual intervention, fiducial markers and/or 3D tracking systems. We are concerned with enhancing registration and working towards a fully automatic process. We have investigated groupwise methods for combining images from multiple patients, namely congealing, which involves the simultaneous alignment of multiple images towards a common mean with no dependence on prior knowledge. Prior information on probability distribution of prostate regions, including the prostate capsule and known tumours can be usefully employed to both fit data and evaluate registration methodologies is examined in the work of Ashburner *et al*. [1]. If a segmentation is significantly different from the *a priori* distribution it is sensible to assume that the fit is poor. The output from the congealing process used in this paper can serve as a prior for further analysis.



(a) (b)

Figure 1: Prostate boundaries in MRIs of 20 different patients (a) prior to congealing (b) after being congealed towards a common mean

2 Method

Our work uses the congealing method [7] which has been used with a wide collection of data for non-specific alignment, including but not limited to datasets with spatial and brightness variability. In this instance we are interested in the most common spatial alignment problem. As we used binary images that were known to have no noise for our input, we settled on the conventional entropy measure. But many different similarity metrics exist for all manner of image registration tasks.

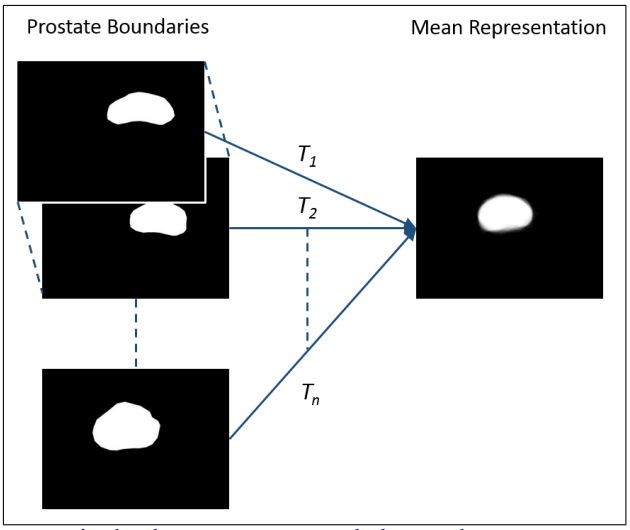


Figure 2: Each prostate in the data set was congealed towards a mean representation through entropy minimisation. The final output was a transformation ($T_1..T_n$) for each boundary.

The congealing process iteratively performs affine transformations on each image in a stack, simultaneously, in an entropy minimisation effort. Congealing's simultaneous registration towards a *common* mean can be superior in preventing bias when compared to those methods which work towards a single input template. The result is a mean representation of the object in question and the transformations $T_1..T_n$ which will convert each of the input objects to that mean.

We performed congealing on a collection of prostate boundaries obtained from the Nor-

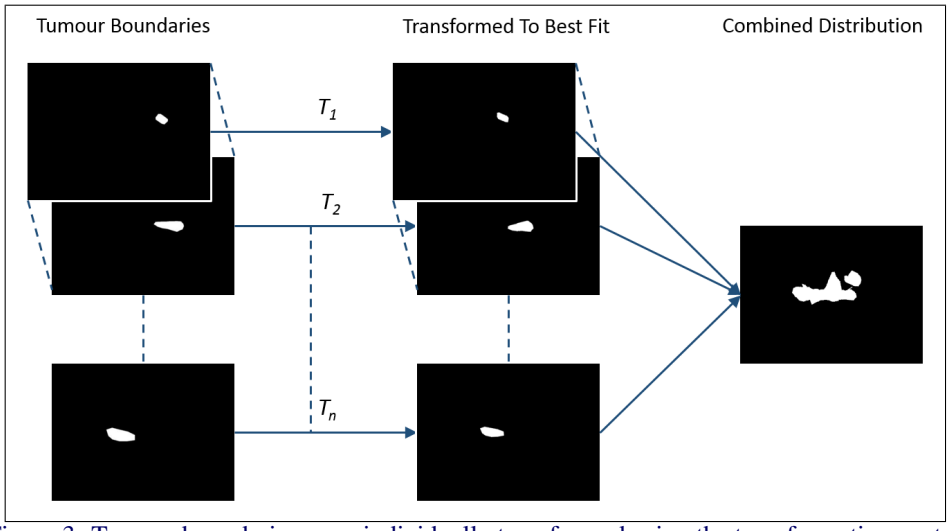


Figure 3: Tumour boundaries were individually transformed using the transformation vector (T_1..T_n) derived from the appropriate prostate boundary. The images were then combined into a single image to visualise the relative location of tumours.

folk and Norwich University Hospital. The images were each annotated by multiple experts and detail the boundaries of the prostate capsule, central zone and tumour(s). The axial slice most intersecting with the prostate centre in each MR volume was selected from 20 patients. These 20 images were treated as a single stack and the congealing method performed on all of them. The result of this process was a transformation vector for each image to reach an appropriate best fit to the mean, which is illustrated in Figure 2.

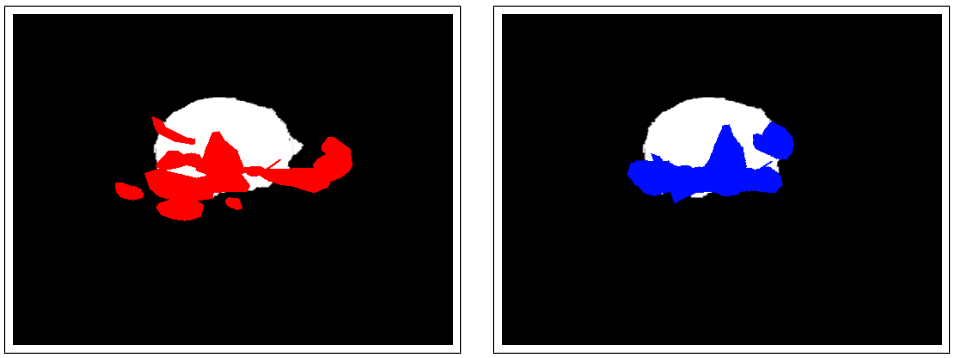
The resulting mean image provides a reliable model derived from multiple cases that further tools can use as a basis for boundary alignment. Those cases which do not conform to this model may be indicative of poor data quality or highly abnormal cases. In addition, we can expect earlier stage cancers to be constrained within the prostate capsule. As cancer progresses we would expect to see extracapsular extension (beyond the prostate boundary) leading to metastatic disease. Thus this mean model provides us with an ability to make estimates for staging.

Once the congealing process was complete, a unique transformation vector was available for each MR slice. The transformation vectors were applied individually to the ground truth tumour boundary for that particular slice as shown in Figure 3. Figure 4 provides an example of the transformation of tumour boundaries to fit the mean.

The final output of the method allows us to evaluate the typical and ideal distribution of tumour pixels. This is visualised in Figure 5 which shows an overlay of prostate capsule and tumour boundaries as heatmaps. This visualisation demonstrates the consistent location of the prostate boundaries and the majority of cancers.

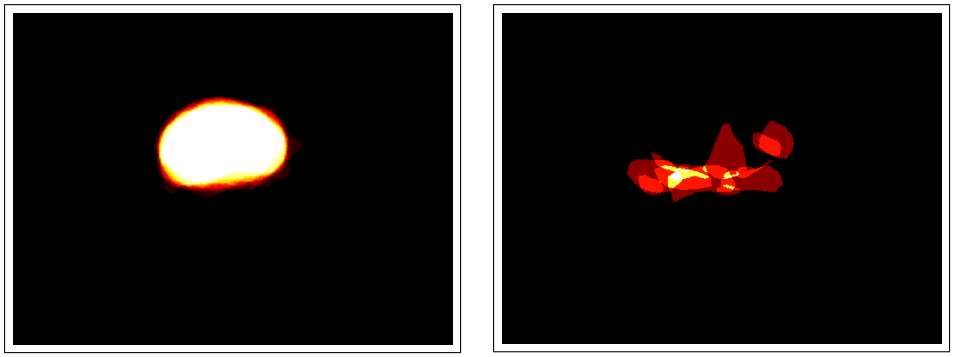
3 Results & Discussion

With the tumour boundaries transformed to the mean prostate representation we can make some observations about the typical distribution of prostate cancer. For example, we can see that cancerous regions are more common in certain regions of the prostate. The distribution



(a) (b)

Figure 4: Superimposition of all tumour boundaries with mean prostate boundary. Mean prostate boundaries are shown as white with (a) original tumour boundaries in red and (b) transformed tumour boundaries in blue.

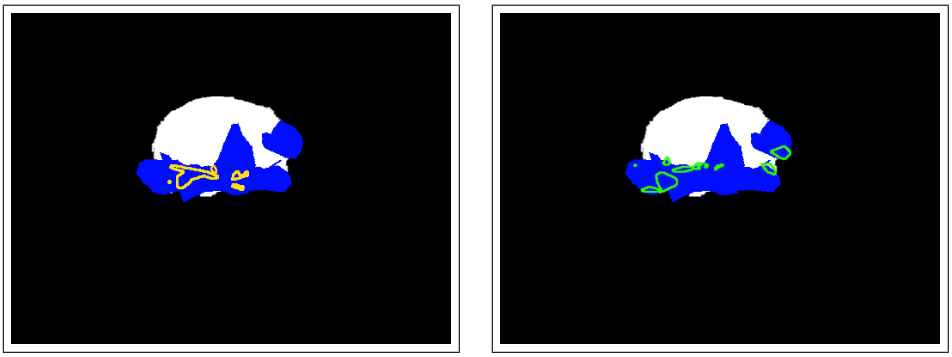


(a) (b)

Figure 5: Heatmaps for multiple patient cases depicting (a) congealed prostate boundaries and (b) transformed tumour boundaries. In (a) pixel colour represents number of cases covering that region ranging from black (0) to orange (10) to white (20). In (b) the same colour map is used but ranges from 0-4 as the tumour boundaries are sparser.

of transformed tumour boundaries, as well as the heatmap in Figure 5 (b) coincide with the peripheral zone, which contains three quarters of the prostate's glands and is subsequently the most common region of tumour incidence[3]. Looking at the progression of cancer from a pathological viewpoint, the primary focal point is the peripheral zone (80-85% of cases) [5]. Tumours extending beyond the prostatic capsule are considered more severe (as classified in pathological tumour grading) and central zone tumours are known to be more aggressive [4]. For initial prostate cancer diagnosis, guided biopsy is usually performed following a basic protocol to achieve even sampling, false negatives are not uncommon and repeat biopsies are often required. Our data could be particularly beneficial in the context of repeat biopsy. For example, at initial biopsy we could target the regions of statistically high incidence, if negative, recommend for the average incidence areas and if negative again, then areas of least occurrence - progressively moving from statistically likely to unlikely regions rather than sampling across an even spread.

In summary, the information gathered could be used to assess how well a suspected tumour region conforms to the expected distribution and thus automatically detect if regis-



(a) (b)

Figure 6: Superimposition of all tumour boundaries with mean prostate boundary. Mean prostate boundaries are shown as white and the congealed tumour boundaries are blue.(a) shows the boundaries of high incidence tumour regions in yellow and (b) shows the boundaries of medium incidence of tumour in green.

tration or other classification processes perform within expectations. Furthermore, analysis of conformity with the model distribution could indicate cases of meaningful abnormality.

4 Future Work & Conclusions

We executed the method on 20 cases as an initial trial; we intend to continue the work by using the additional (30) cases in our data set as well as trialling it with data from other sources in order to create a more comprehensive collection of prior knowledge. Visualisation of data from a variety of cases is an interesting problem and a useful clinical tool based on a larger data set might be in the form of a Voronoi tesselation or similar, in order to highlight regions of significant tumour incidence.

Groupwise techniques have had little application to multi-modality imaging, we believe improved similarity metrics would be of considerable benefit to achieving more accurate and reliable registration. Congealing makes use of pixelwise entropy; calculating local region entropy across a group may provided a clearer indicator of alignment in the case of greyscale images.

Issues of scalability due to broadening parameter space for metrics beyond pairwise registration has been highlighted by Bhatia *et al*. [2]. Various optimisation techniques exist for all stages of registration. For example, Wachinger and Navab [9] reported the successful use of multivariate metrics; highlighting that metrics are application dependent. In order to tackle the issues of scalability, they also present work on similarity measure and transformation optimisation, notably using accumulated pairwise estimates (APE). There are a number of methods that can be utilised to evaluate a group of images. One such example is STAPLE[10] though it is tailored to evaluation of segmentation results and has dependence on input parameters. It would of interest to investigate automatic parameter adjustment for STAPLE. Other variations of groupwise registration employ a variety or combination of fitness metrics and more complex transforms to suit data.

Groupwise registration of multi-modal [8] and 3D data[11] has been previously demonstrated. However, our research has a focus on 2D ultrasound and 3D MR registration. We hope to expand the groupwise methods to suit such a problematic dataset. In addition, ex-

tension of the method to generate volumetric prior models would be of particular use with MR data and might provide new insights into staging. We envisage that the incorporation of superior nonrigid transformations or locally restricted rigid transformations will enable an improved groupwise framework suited to multi-modal registration of real images with mixed dimensionality.

Joint alignment shows promising results for the registration of prostate boundaries in MR data. However, our approach used only affine transformations and the incorporation of nonrigid techniques would better preserve local data more effectively. Groupwise techniques such as congealing have been previously used for alignment of images from the same, such as slices from a single MR volume. Our application to inter-patient data is a novel use that our results demonstrate has applications to both multi-modal image registration and prostate cancer staging.

Acknowledgements

This work is funded by a Ph.D studentship from Prostate Cancer UK and the Hoover Foundation.

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