Segmentation of Prostate MRI Volumes Using 3D Shape Model Constrained Tissue Classification

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INTRODUCTION:
Benign Prostatic Hyperplasia (BPH) is a non-cancerous enlargement of the prostate which can cause constriction of the urethra and therefore obstruction of urinary flow. It affects 70% of men between the ages of 61 and 70, rising to 80% for men over 80. In 25% of men aged 80 symptoms are sufficiently severe to require surgical transurethral resection of the prostate (TURP), however this treatment has a high cost, morbidity (16%) and mortality (2.01%) and so alternative treatments are sought. From a Magnetic Resonance Imaging (MRI) perspective the prostate can be anatomically divided into two zones; the inner Central Gland (CG) which is partly surrounded by the Peripheral Zone (PZ) (figure 1). BPH primarily affects the CG causing it to enlarge and compress the surrounding PZ, thus progress of the disease and/or evaluation of treatment effectiveness can be assessed by measuring the ratio of CG to PZ. The current standard is Transrectal Ultrasound (TRUS) in which three orthogonal dimensions are measured and the volume is estimated using the formula for a prostate ellipsoid. Inter-observer variability in volume measurement using TRUS has been shown to be approximately 20% [1].

MRI is an attractive alternative to TRUS as it offers better definition of the prostate and is non invasive. MRI offers the possibility of accurately segmenting the prostate rather than assuming its volume from three orthogonal measurements. However, manual segmentation is time consuming, error prone and subjective, and so the goal of this project is to investigate the possibility of automatic segmentation of the appropriate regions of the prostate.

For this study we have used T2 weighted fat suppressed (T2FS) images as the CG/PZ contrast is enhanced in comparison with T2 or T1 weighting, and there is clearer separation of the prostate from surrounding tissue. The data were collected using a 1.5T Philips Gyroscan ACS MR scanner (software version NT5.3, Power Track 600, synergy body coil) from 22 patients with BPH. For each patient there are 50 axial slices with a thickness of 2mm and an in-plane resolution of 1.56mm. Figure 1 shows an axial MRI slice of a prostate – signal intensity is generally higher in the PZ than the CG and in non-disease cases differentiating the two based purely on image grey-level is relatively straightforward. However in BPH cases the compression of the PZ can darken its appearance in places reducing the definition of the PZ/CG border. Also bright BPH nodules can appear within the CG that are as bright as the PZ. From the manual segmentation of figure 1 it is clear that a two stage process is employed by the user in which an initial coarse segmentation is made based on image grey-level, followed by a smoothing of the boundary based on anatomical knowledge.

METHODS:
To develop a computer based prostate segmentation we have formalized this two stage process, using grey-level tissue classification followed by a coherent 3D shape constraint. Tissue classification is achieved by fitting a 3 Gaussian model to the grey-level histogram of each image volume giving a class conditional probability for each voxel of being either PZ, CG, or background (B) [2]. In cases whose appearance is close to that of a normal patient, i.e. the PZ and CG are clearly defined, segmentation can be achieved through tissue classification alone. However in the cases of more advanced BPH misclassification of PZ as CG and visa versa occurs, and a further smooth spatial constraint is required.

From the manually annotated data set a 3D Point Distribution Model (PDM) [3] can be trained – briefly this is a mechanism by which new examples of the CG and total prostate (TP) surfaces can be generated (figure 2), the shape and pose of which are controlled by just a few parameters. This model can be limited to produce only ‘credible’ prostate shapes and so can be used as a smooth shape constraint on the tissue classified data. The PDM is fitted to the tissue classified data for each patient by searching model shape and pose via a genetic algorithm until the best fit is found. The best fit is defined as that which maximizes the number voxels within the surface to which they have been classified.

RESULTS: The method was evaluated on the data set using a leave-one-out methodology and the resulting model fits were compared with the manual annotation in two ways: mean point distance, and percentage volume difference. The results of this are shown in the results table. Definition of the prostate is particularly poor in the superior and inferior portions where the CG/PZ becomes indistinct, and the PZ becomes difficult to distinguish from the seminal vesicles in the superior portion. Thus model fit accuracy can be improved by considering only the mid-third of the prostate (TPm, CGm), of course individual surface volumes for this region are meaningless in themselves, however the CGm/TPm ratio from manual annotation correlates strongly with CG/TP ($r = 0.97$), suggesting this ratio may be measured from the more clearly defined mid-section of the prostate.

CONCLUSIONS: In the majority of cases automatic segmentation results in Total Prostate and Central Gland surfaces that correspond accurately to the manual segmentation ‘ground truth’. The key measure in this case is volume and even in cases where there is the greatest difference between automatic and manual segmentation these are comparable with the variation in volume estimates using TRUS. Automatic segmentation from MR images clearly has the potential to deliver precise estimates of volume change. Much of the discrepancy between manual and automatic segmentation arises in places where the boundary location is genuinely unclear, and the absolute nature of the ground truth is questionable. We intend to investigate the variability in manual measurement in these regions.

References: