Determining histology-MRI slice correspondences for mapping prostate cancer extent in vivo

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Introduction: We present an automated computerized system to automatically determine slice correspondence between images from histology and MRI. Mapping the spatial prostate cancer extent from *ex vivo* whole-mount histology to *in vivo* MRI to determine the MRI-based cancer signatures is important for (a) for constructing an MRI-based computer aided diagnosis (CAD) system for prostate cancer detection [1] and (b) training radiology residents. However, a prerequisite for this data mapping is the determination of slice correspondences (i.e. indices of each pair of corresponding image slices) between histological and MR images. The explicit determination of such slice correspondences is especially indispensable when an accurate 3D reconstruction of the histological volume cannot be achieved because of (a) the limited tissue slices with unknown inter-slice spacing, and (b) obvious histological image artifacts (tissue loss or distortion) [2] [3]. In the clinic practice, the histology-MRI slice correspondences are often determined visually by experienced radiologists and pathologists working together, but this procedure is laborious and time-consuming. The image slice correspondences obtained using our method were compared with the ground truth correspondences determined via consensus of multiple experts over a total of 23 patient studies. In most instances, the results of our method were very close to the results obtained via visual inspection by these experts.

Methods: We develop an iterative approach to determine the histology-MRI slice correspondences. It consists of 3 modules. In Module 1, we obtain an estimate of the slice correspondences through a group-wise comparison approach according to a specific image similarity measure (combined mutual information (CMI) [4]). We consider all the histology slices as a single group and all the MRI slices as another group. The goal is to find a sub-set of MRI slices that best matches the histology group. With this group-wise approach, the order of the image slices in each group is strictly maintained, thereby limiting the extent of the mismatch. In Module 2, based on the initial estimate obtained in Module 1, each histology slice is registered to its corresponding MRI slice in order to compensate for the image differences caused by possible histological artifacts and distortion to the prostate. In Module 3, using the estimate of the slice correspondences obtained in Module 1 and the registered histology slices obtained in Module 2, a 3D histological pseudo-volume is reconstructed through zero padding (i.e. inserting additional zero-value slices), so that the slice correspondences are further refined through 3D registration between the histology pseudo-volume and the MRI volume. The procedures in Modules 1-3 iterate until the slice correspondences no longer change.

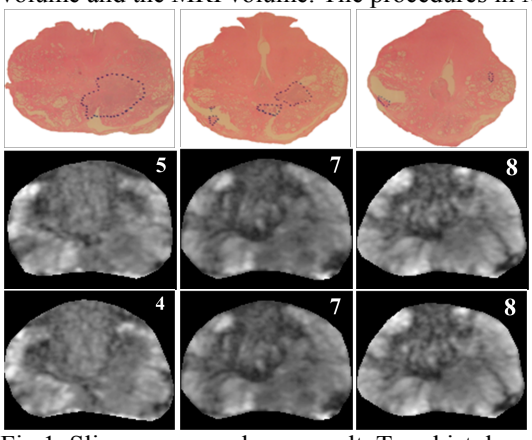

Fig 1. Slice correspondence result. Top: histology slices. Mid: corresponding MRI slices determined by our method. Bottom: expert determined ground truth. The number in the top right corner of each MR image is the index of each MRI slice.

Results: We tested our method using the histology and MRI slices for 23 patient studies. 3 Tesla endorectal, pre-operative, T2-w prostate MRI slices were obtained *in vivo* with resolution 0.27 mm/pixel and slice spacing 2.2 mm. The prostate region of interest was manually extracted in these images by an expert radiologist. Following radical prostatectomy, the prostate gland was sectioned into a number of blocks before one representative thin slice (approximately 5 μm thick) with relatively good imaging quality is selected from each block. The ground truth slice correspondences were determined by the radiologist and the pathologist using certain common fiducials visible in both modalities (BPH nodules, urethra, etc). Fig. 1 shows an example of the results. We also used the L1-norm of the difference between the vectors of slice indices to quantify the accuracy of our method. Across the 23 patient studies, the mean and standard deviation of the results are 1.34 and 0.78, respectively, which are very close to the ground truth correspondences determined by the experts.

Concluding remarks: We presented an automated computerized system to automatically determine slice correspondence between images from histology and MRI. Our method consists of three modules which are executed iteratively until there is no further change to the slice correspondence result. The prostate histology-MRI slice correspondences obtained using our method were compared with the ground truth slice correspondences determined by experts. The accuracy of our method was in most instances close to the ground truth.

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