Automatic 3D Probe Localization and Iceball Segmentation for MRI-Guided Kidney Cryoablation

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Purpose

MRI-guided cryoablation provides direct visualization of the target tumor and iceball. However, qualitative visual assessment of therapy progress during the freezing cycle can be limited. To aid the interventionalist in better monitoring the progress of the therapy, there is a need of computer software for real-time quantitative assessment of ablation by, first, identifying the inserted probes, and, then, segmenting the ablated volume - the iceball - in a rapid, accurate and fully automatic manner. For this purpose, we sought to develop and validate a system containing novel methods for automatic localization of 3D cryoprobes and segmentation of the 3D iceball during 3T MRI-guided cryoablation of kidney tumors.

Methods

Our probe localization method automatically detects multiple 3D cryoprobes directly from MRI images taken during the pre-freeze probe placement phase of therapy. Noting that cryoprobes create a signal void (black) artifact in MRI with a bright cylindrical border, our localization method first locates an initial 2D line which approximates the position and direction of the 3D probes bundle. A region of interest (ROI) in the 3D image is then created according to the distances to the initial line, and feature points having higher probability of being probes are selected within the ROI. The directions of 3D probes are then sequentially determined by applying the 3D Hough Transform[1,2] to the feature points selected. The tip of each probe is then identified based on the continuity of feature points along the probe axis.

Guided by the labeled probes resulting from probe localization, the iceball segmentation method automatically extracts the 3D configuration of the iceball from MRI scanned periodically during the first 15 minute freezing cycle. Iceball segmentation is a challenging problem as the abdominal anatomy surrounding the iceball, the probe artifacts, and the iceball have similar intensity values. To overcome this difficulty, we incorporated shape prior information into the standard graph cut image segmentation framework.[3,4] Given the location of a probe and its tip, the shape of the iceball at a certain timepoint is modeled as a prolate ellipsoid with its major axis being the probe axis. The parameters of this modeling were derived experimentally by measuring single unperturbed iceball shape evolving in time from a set of x-ray CT images, acquired during freezing, with the probe inserted into an abdominal gel phantom. Determined by combining iceball shape of multiple probes, the shape prior is then used to initiate a graph cut segmentation of the iceball in the 3D 3T MRI at each timepoint in the periodic freeze cycle scanning.

Results

To assess feasibility and accuracy of the two methods, MR images (using breath-hold HASTE sequence) from 5 kidney tumor cryoablations were used retrospectively with mean tumor size 3.8 cm. We used the last scan taken in the probe placement phase to validate the probe localization method; the number of probes used for the 5 cases was 2, 3, 3, 3, 5, respectively, yielding a total 16 probes. During the first of two 15 minute freezing cycles, MRI monitoring was performed every 3 minutes in 4 cases and every 5 minutes in 1 case, yielding a total 23 iceball timepoints for validation of the iceball segmentation method. An experienced interventionalist manually labeled the 16 probes by dropping two fiducials (one for the tip and one for the end) for each probe in the 3D images. As the direction of a line in 3D space can be represented by two angles, the mean angle differences of these two angles between the manual results and results from our automatic probe localization method are 2.6° and 2.5°, respectively. The mean Euclidean distance between probe tips of the two approaches is 4.5 voxel (9 mm). We compared 3D iceball configuration resulting from our automatic iceball segmentation method to manually segmented iceball volumes at each time point using Dice similarity coefficient (DSC), and the mean DSC for 23 timepoints was 0.88. Based on published data, a DSC of > 0.7 was considered accurate segmentation. The iceball segmentation algorithm was implemented using C++ and the computational time is about 2 sec at a given timepoint.
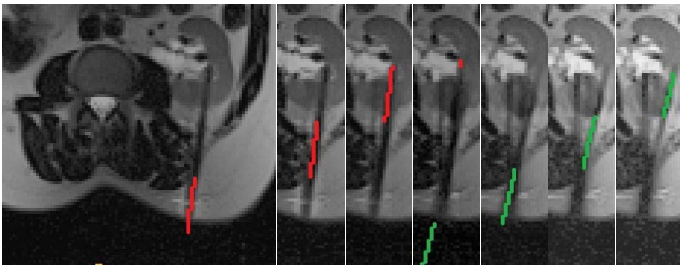

Fig.1. 7 consecutive slices show two 3D probes localized by our method
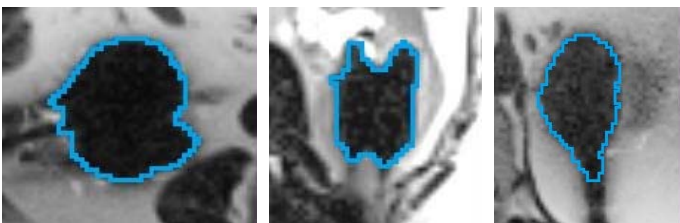

Fig.2. 3 examples of automatic iceball segmentation at 3 different timepoints.

Conclusion

We present a fully automatic system for MRI-guided cryoablation involving a localization method for multiple 3D probes inserted pre-freeze, and a 3D iceball segmentation method during the freezing cycle. Both methods showed good accuracy when applied to 5 ablation cases of kidney tumors. By comparing the segmented iceball to the ultimate planned therapy volume composed of tumor and a margin, real-time quantitative monitoring and automatic controlling of cryoablation can be possible during therapy.

References

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