Delta T1 Method: An Automatic Post-contrast ROI Selection Technique for Brain Tumors

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Introduction: The primary approach to monitoring patients with brain tumors is to obtain pre and post-contrast T1-weighted images. Bright areas on the pre-contrast images are suggestive of blood products, which may be a result or treatment, and are therefore not to be considered as enhancing lesions on the post-contrast images. However, the difference between the brightness that exists on both the post and pre-contrast images can be quite subtle, a condition that is occurring more frequently now with the increasing use of anti-angiogenic agents. Therefore it is becoming increasingly difficult to monitor patients with brain tumors simply by visually comparing differences in enhancement. As a solution in this report we propose an automatic method, the delta T1 method (dTM), which is capable of detecting even subtle enhancing tumor free of blood products, thereby enabling the automatic creation of ROIs in a fast and reliable manner that avoids subjective variability.

Data Acquisition: All MRI studies were performed on either a 1.5T GE CV or LX Scanner. Pre- and post-contrast T1 images were acquired (SE, TE/TR = 14-24ms/667 ms) before and after a 0.10 mmole/kg dose of Gadodiamide (Omniscan; Nycomed Amersham, Princeton, NJ). In addition, we obtained dynamic susceptibility contrast (DSC) MR datasets to validate the ability of dTM to distinguish tumor tissue from blood products. Specifically, GE EPI images were acquired for 1 minute before and 2 minutes after a 0.1 mmole/kg bolus injection (twelve, 5 mm thick slices were acquired with TE/TR = 30ms/1100ms) to confirm that the selected voxels in the ROI are perfused while the un-perfused blood product regions are not included in the ROI.

Data Analysis: The delta T1 method (dTM) for automatic post-contrast ROI is based on segmentation of standardized pre- (T1) and post-contrast (T1+C) anatomic images as described by the following listing of steps.

- Pre- and post- contrast T1-weighted images are standardized using the technique developed by Nyul et. al. [1] to obtain standardized T1 (stdT1) and standardized T1+C (stdT1+C) datasets.
- The stdT1 is subtracted from stdT1+C dataset to generate delta T1 maps.
- An empirically determined threshold of 3500 was applied to the dTM maps to obtain an enhancing tumor ROI.
- Finally, the noisy voxels mainly around skull and eyes area are manually removed.

We applied and validated this technique using DSC RAW data on 18 dates (number of brain tumor patients=15).

Results and Discussion: Example results from two patients are given in Figures 1 and 2. Figure 1 demonstrates the utility of dTM maps in accurately distinguishing between tumor and blood products in a 59 y/o patient, after resection of an anaplastic oligoastrocytoma and subsequent radiation therapy. These maps confirmed the existence of residual tumor. Figure 2. shows the of dTM for a case with no tumor (all blood products). This is a 51 y/o patient with an initial diagnosis of glioblastoma multiforme during treatment with bevacizumab (Avastin, Genentech South San Francisco, CA).

Figure 1. A) T1+C B) T1 C) T1+Cs D) T1s E) Delta T1 Map F) ROI G) representative voxel ignored from the ROI and corresponding DSC RAW time-series H) representative voxel included in the ROI and corresponding DSC RAW time-series

Figure 2. A) T1+C B) T1 C) stdT1+C D) stdT1 E) Delta T1 Map with value = 717 below threshold
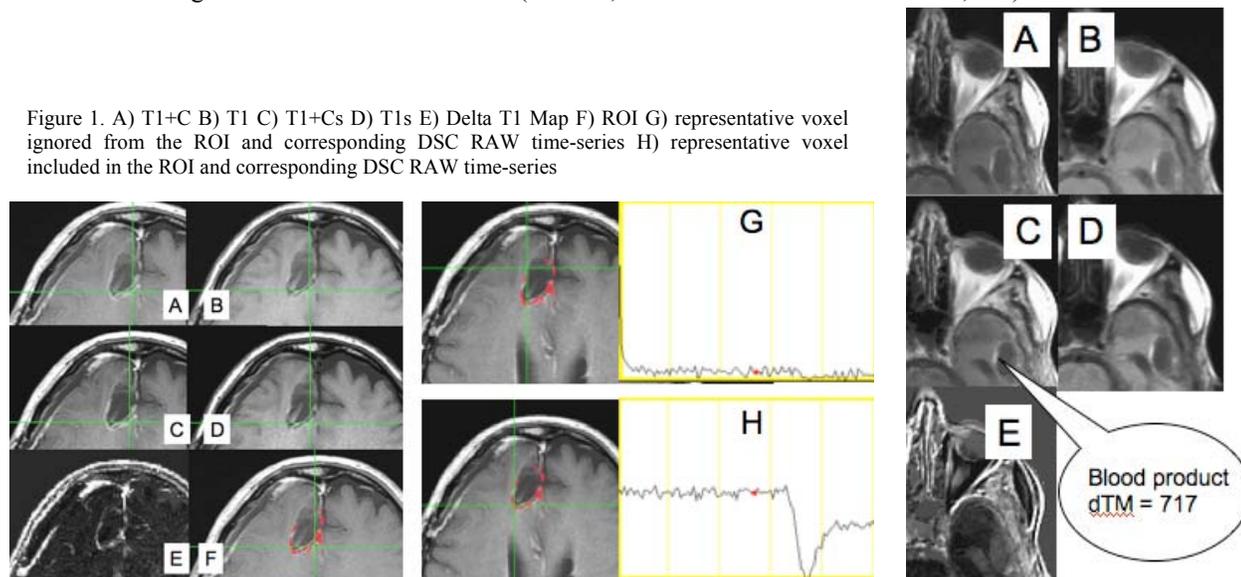
In this study we conclude that the delta T1 method reliably selects only the perfused tumor regions and ignores blood products for the ROI. We validated the resulting automatic post-contrast tumor ROI technique by visually evaluating the RAW DSC time series for voxels included and excluded from the ROI. Figure 2 shows that this technique is accurately and successfully able to ignore blood products (unperfused regions) from the ROI, thus leading to more accurate evaluation of tumor progression and treatment planning.