Null Point Imaging

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Introduction. A first step in the quantification and mapping of morphometric changes in the brain, tissue classification remains challenging due to the limited contrast differentiation obtainable using traditional volume sequences. Typically used for this purpose are T1 3D inversion recovery prepared SPGR or MPRAGE volume type sequences. Indeed, these display suitable grey matter (GM), white matter (WM), and cerebrospinal fluid (CSF) differentiation, good spatial resolution (1 mm^3 isotropic on 1.5T scanners), and can be performed within an acceptable time period [1]. Another standard approach, the multispectral technique, consists in leveraging the combined power of 2 or more different sequences (usually a T1-weighted sequence with a T2-weighted and a proton density sequence) [2].

Optimizing a T1 3D volume sequence for tissue classification conventionally entails fine tuning the imaging parameters to produce the best possible contrast between the aforementioned tissue types. Indeed, automated classification algorithms rely on this contrast to adequately segment the tissues. Similarly, in the multispectral approach, the combination of 2 or 3 contrast differences is used as a basis for classification.

Unfortunately, the often subtle intensity differences between GM and WM make the task of the classification algorithm particularly difficult and sensitive to noise and bias fields. This is particularly true of partial volume effect (PVE) voxels resulting from the mix of 2 or more tissue types within the same voxel, which present intermediate intensities between grey and white and abound along the boundary between GM and WM, and between GM and CSF.

Here, we propose an acquisition-time alternative to the conventional computational approach. By imaging at the mid point between the GM and WM null points, we introduce a nulled boundary layer between GM and WM tissues, *at the acquisition stage*. This boundary layer therefore coincides with the PVE voxels, thereby alleviating the main difficulty of image analysis approaches. Our Null Point Imaging (NPI) technique also has the potential to increase the robustness and accuracy of registration algorithms as we briefly report thereafter, and to help with structure segmentation.

Method. Imaging was performed on a 1.5T Philips Achieva scanner. Four healthy male subjects (mean age: 32) had their brain scanned using an 8 channel SENSE head coil. Two acquisitions were performed: a classical 3D T1 sequence (160 sagital slices with FOV=256^2, Matrix=256^2, flip angle=9°, TE=4.6ms, TR=9.9ms and TI=960ms) and the Null Point Imaging sequence (160 sagital slices with FOV=256^2, Matrix=256^2, flip angle=9°, TE=3.7ms, TR=8.1ms and TI=450ms).

Our tissue classification approach consists of 3 consecutive steps. First, we extract the brain from the T1 MR image and apply the brain mask to the NPI image [3]. Then, we segment the combined set of GM and CSF voxels using the simplex mesh deformable model approach [4]. The model was initialized as a sphere around the brain and subjected to inverted balloon pressure forces to force it towards the dark boundary layer whose gradient acted as the image coupling force. We let the initial model iteratively deformed into the brain until it reaches an equilibrium. The brain voxels which do not belong to the deformed model are then labelled as white matter. Finally, we use a simple thresholding technique with hysteris to segment the CSF voxels, which are highly contrasted in NPI .

As another application of this technique, we used the GM/WM boundary layer to increase the robustness of brain registration. Given two input T1-weighted scans and their associated NPI images, two sets of 500 points were randomly uniformly extracted from a thresholding of the boundary layers. We then used the soft-assign algorithm [5] to register these two point clouds in a non-linear fashion, with thin-plate splines as a deformation model. The resulting transformations were applied to the T1-weighted images. Comparison against a standard intensity-based thin-plate spline algorithm (we used mutual information as a similarity measure) showed an average 22% increase in accuracy over our 4 sample brains, where the accuracy is computed as the sum of square distances between 50 corresponding anatomical landmarks picked across the brain.

Results. Figure 1 illustrates the ability of our approach to separate GM and WM. (a) and (c) show 2 slices through a standard T1 volume scan. (b) and (d) show the corresponding slices with our NPI technique. Note that even though the contrast between GM and WM is reduced, the null boundary layer clearly indicates the GM/WM separation. Figure 1(e) displays a slice cut through the 3D deformation model as it is evolving inside the brain during the segmentation process (in orange and green) and the final segmentation (in orange and red).

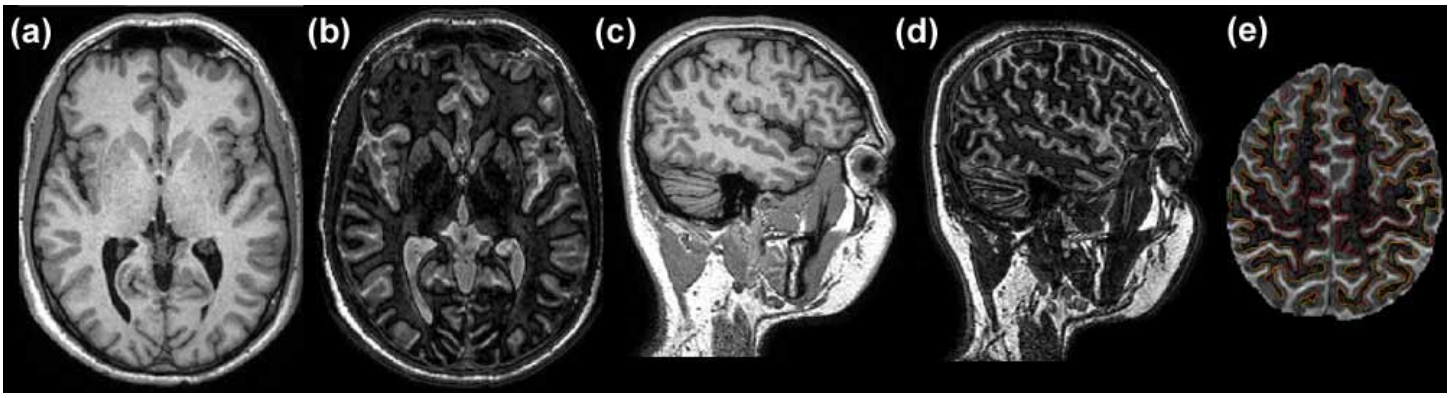

Figure 1: Null Point Imaging illustrated on a few coronal, sagital and axial slices.

Future Work. We are currently quantifying the performance of our classification technique on a variety of test cases, and applying null point imaging to other tasks, such as deep grey nuclei segmentation and cortical thickness map computation.

References:

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