MRI Brain study simulation

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Introduction: Repetition studies has been presented to verify the precision of brain segmentation methods, while only subjective evaluations of accuracy, based on observation of segmented images or comparison with manual segmentation, have been possible. In fact, an a priori exact voxel classification of different tissues acquired by MRI scanners is necessary to measure and compare the performances of segmentation algorithms. Since is not possible to have this information from subjects, only a brain phantom simulating tissue morphology, topology, texture and MRI characteristics should be used. None of currently available physical phantoms meets these requirements. Current brain digital phantoms (e.g. Brainweb [1]) do not include thin structure and inhomogeneity of tissues, which represent a key challenge for segmentation methods. Aim of this work was the implementation of a software tool allowing the simulation of MRI studies of digital brain phantoms focused to validate segmentation algorithms.

Materials and methods: As in physical phantoms, the present digital simulation consists of a set of compartments representing the anatomical distribution of the different tissues and the "virtual chemical solutions" that fill the compartments and simulate the tissue characteristics detectable by the scanner. On the contrary of the case of a physical phantom the virtual solutions are not homogeneous, but simulate also the variability of the normal and pathological tissues in terms of the principal MR characteristics (relaxation times and proton density). Compartments and "solutions" compose the anatomical model, which is the base of the simulation of MRI studies.
The 3D anatomical model, consisting of seventeen tissue compartments, was derived from a normal volunteer MRI study, composed of 150, 1mm apart, 3mm thick slices obtained from 5 acquisition groups covering the entire brain. Each acquisition group was composed of a T1w and a PD-T2w spin-echo sequence. After an automatic classification of the voxels using a previous published segmentation program [2], a manual/semi-automated procedure was applied to improve the model quality. Relaxation rates R1 and R2, and proton density (PD) maps were derived and codified in multi-feature color images (QMCI) [3]. The five groups of 30 relaxation rate maps were then registered, resliced at 1mm and averaged, giving a low noise, isotropic voxel, three-dimensional multi-feature maps. The QMCI maps were divided into the compartments defined by the above refined segmentation. Each compartment was characterized by the mean value of R1, R2 and PD, and by three functions of spatial coordinates representing the variations of the above parameters around their mean values. As a result, in the multi-feature space (MFS), each tissue was described by a cluster with an own shape. As residual noise and partial volume effect in the NVS enlarge the clusters in the multi-feature space, while segmentation errors spread some voxels far from the core of their own tissue, creating artifactual inhomogeneities, to maintain the theoretical possibility of a correct classification, the tissues connected in the physical space has been separated in the feature space, confining the voxels of each tissue in an own closed surface. Tissue compartments and inhomogeneities, defined above, compose the anatomical model of the phantom to be "filled" by tissue mean values and to be virtually acquired. In order to obtain a further phantom family simulating multiple sclerosis (MS) patients, a new model with MS lesions was produced inserting in the original model some MS lesions, as a further compartment of abnormal White Matter (AWM).
The procedure simulating the MRI acquisitions uses real MRI studies (in DICOM format) as models. TR, TE, B0, matrix, slice thickness, and the other acquisition parameter are read from DICOM header, while the mean values of MR signal in T1w, T2w and PDw acquisitions are measured in the whole volume of non air voxels and in each tissue, using the 3D ROI resulting from the classification performed by our automatic segmentation procedure[2]. The noise level is measured in air. Values of tissues (e.g. some basal ganglia) not segmented by the software are obtained from the model rates. Z-RF inhomogeneity and reconstruction frequency filter are estimated for each series of the target study. From the mean signal values of target study, R1, R2 and PD mean values of each tissue are calculated[3], while parametric maps of scans to be simulated are calculated. From the QMCI map of the simulated scans, MR signals are calculated voxel by voxel for each sequence. The slices are averaged to obtain the desired slice thickness (multiple of 1mm). Finally, for each slice of each series, the FFT is calculated, complex Gaussian noise is added, the k-space sampling and the frequency filter are applied, inverse FFT is calculated and the unused part of the FOV is zeroed.

Results: T1w, PDw, T2w axial slices from a real scan and corresponding phantom images are shown in figure 1. Three different scanners (one at 1T and two at 1.5 T), with four different spin-echo sequences were simulated following the normal and the MS models.

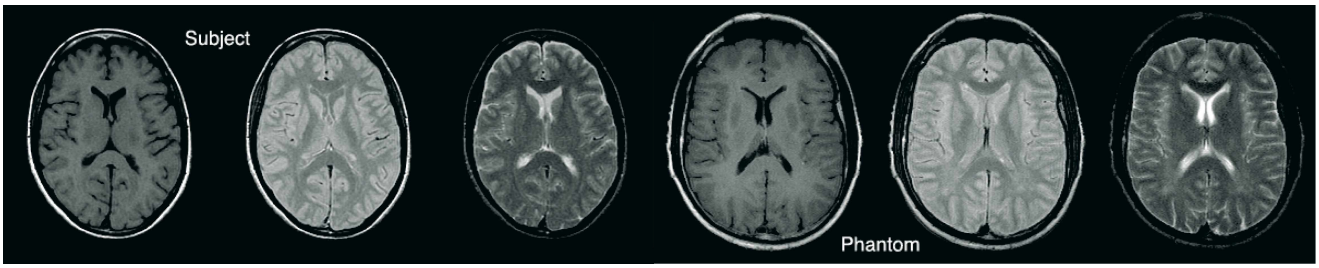

Fig. 1

Discussion: The described procedure used to build digital brain phantoms simulating spin-echo sequences has been successfully tested and could be extended to gradient-echo allowing validation and comparison among most segmentation algorithms.

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