Automated quality control in MR-based brain morphometry

Bénédicte Maréchal[1], Tobias Kober[1], Tom Hilbert[2], Delphine Ribes[3], Nicolas Chevrey[4], Alexis Roche[1], Jean-Philippe Thiran[5], Reto Meuli[4], and Gunnar Krueger[1]
[1]*Advanced Clinical Imaging Technology, Siemens Healthcare Sector - CIBM, Renens, Switzerland,* [2]*Universität Heidelberg, Germany,* [3]*ARTORG Center for Computer Aided Surgery, Univ. of Bern, Switzerland,* [4]*Centre Hospitalier Universitaire Vaudois and Univ. of Lausanne,* [5]*Signal Processing Laboratory (LTS5) Ecole Polytechnique Fédérale de Lausanne*

Introduction: Computer-aided and quantitative analysis of structural MRI data show increasing promise for aiding clinicians in diagnosing a wide range of diseases. For instance, gray matter (GM) regional atrophy is an often used structural hallmark to diagnose Alzheimer's Disease (AD). It requires the detection of very subtle brain changes (e.g., annual GM loss rate of up to 5% [1]). Obtaining 3D structural scans with high SNR/spatial resolution requires long acquisition times, which make them susceptible to bulk head motion. Resulting artifacts may substantially degrade diagnostic confidence and automated MR-based quantification of brain tissue. Surprisingly, while motion is frequently encountered in routine MR scans, very few studies have shown how it affects automated image analysis [2,3]. Moreover, there is a lack of quality standards estimating confidence levels on resulting morphometry outcomes. Here, we explore the potential ability of an automated image quality assessment technique [4] to predict inaccurate morphometric measures and propose a model that allows customizing minimum quality criteria according to the required performance of a target application in brain morphometry.

Material & Methods: Raw data (i.e., k-space samples of all channels) from 5 healthy subjects ([25-68yo]) were analyzed. All images had been acquired on a 3T MAGNETOM Trio, A Tim system (Siemens Healthcare, Erlangen, Germany) equipped with 12- and 32-channel receive head matrix coils using a MPRAGE sequence with linear Cartesian sampling (TR-TI=2300-900ms, 1x1x1.2mm^3 resolution, 240x256x160 matrix size). Raw datasets were selected for their high-quality (i.e., assessed visually and quantitatively with an automated quality control algorithm [4]) and are referred to as *motion-free*. Synthetic rotational and translational motion was applied to each raw data sample using an in-house algorithm (Lanczos-based regridding method used for rotations) which was implemented as part of the scanner image reconstruction chain. 60 motion patterns (i.e., 10 degrees of translations and rotations ranging from 2 to 24mm and -10° to 10° respectively in each direction x,y,z) were applied at 9 different k-space locations using 30 seconds step functions, hence mimicking abrupt head movements. In total, 2700 *motion-corrupted* images were generated and underwent the following processing steps: 1) computing a quality index (QI) [4] which reflects the proportion of artifactual voxels in the background 2) pre-processing: B1 inhomogeneity, 3D gradient distortion and bias field corrections 3) tissue classification using a variational expectaction-maximization scheme [5] and atlas-based central nuclei segmentation (see example in Fig1). Focusing further analysis on GM classification, we assumed that the algorithm performs best on *motion-free* images and therefore considered the resulting GM a posteriori probability map (PPM) as our reference. Finally, motion-induced GM error was quantified by computing the fuzzy DICE coefficient ($fDICE_{GM}$ [6]) between *motion corrupted* GM PPM and the reference.

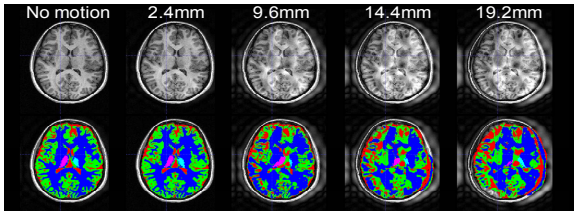

Fig1. Effects of abrupt head translations during k-space center sampling on brain tissue classification (CSF gray matter white matter) and thalamus segmentation (left- right)

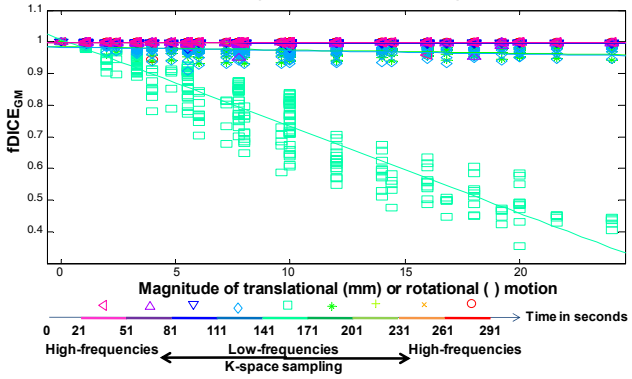

Fig2. Effects of motion severity and occurrence on GM error

Results: Our results suggest that the presence of motion artifacts may have a substantial impact on GM classification. As expected, motion produces more disturbances (i.e., larger GM error) if occuring during k-space low-frequencies sampling (cf. Fig2, 1.95% resulting error in GM volume estimation for 1mm or 1° motion halfway through the acquisition). The trend towards increased errors with motion severity is consistently captured by the quality index which is thus capable to predict errors (see Fig3). Based on 2700 data points obtained from 5 subjects, we demonstrate that QI and GM error are related by a four parameter power function when plotted on double-log coordinates. This function provides good description of the data except for four extreme outliers (pink dots) which turned out to be due to incomplete bias field correction.

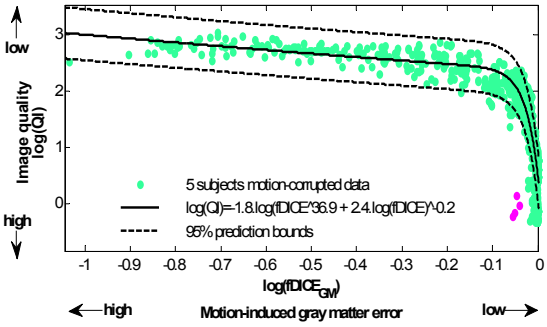

Fig3. Automated quality index is able to predict GM error

Discussion: This work demonstrates that an automated quality assessment is not only able to detect the presence of artifacts but also may predict the accuracy of subsequent algorithms for brain morphometry. Regression results in Fig2 suggest that a 2mm motion during traversal of k-space center would induce artifacts mimicking the annual dynamics of GM loss in AD (~5%). Such small movements are reliably caught by the automated quality index whose variation can be characterized by a simple power function of the error. This model allows determining whether an image is of sufficient quality to warrant further quantitative analysis and in other words, allows customizing quality cutoff levels with respect to the required performance of computer-aided brain morphometry. This will be increasingly needed for daily practice in the near future as the new diagnostic guidelines for AD recommend structural MRI to detect atrophic patterns [7]. Finally, this work underscores the importance of rigorous quality assessment prior to any computer-aided brain analysis in order to attribute tissue changes to a potential pathology rather than to image degradation.

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