hMRI-vQC - A visualization Quality Control (vQC) toolbox for Multi-Parameter Mapping

#WTh854

S. Sherif[1], C. Bastin[1], P. Maquet[1,2], G. Vandewalle[1], E. Balteau[1], M. F. Callaghan[3] & C. Phillips[1,4]

1. GIGA Cyclotron Research Centre *in vivo* imaging, University of Liège, Liège, Belgium 2. Department of Neurology, University Hospital of Liège, Liège, Belgium 3. Wellcome Centre for Human Neuroimaging, UCL Queen Square Institute of Neurology, University College London, London, UK 4. GIGA *in silico* Medicine, University of Liège, Liège, Belgium

INTRODUCTION

Quantitative MRI (qMRI), such as the multi-parameter mapping (MPM) protocol, provides access to markers of biologically-relevant tissue features and offers a standardised approach to imaging that can improve comparability across sites and time points[1]. Image quality control (QC) is an integral preparatory step in the MRI data processing pipeline. QC tools are available for commonly used imaging modalities T1-weighting (T1w) and fMRI[2,3]. However, there is a lack of QC tools for qMRI

METHODS

The MPM protocol involves the combination of multiple images acquisitions (T1w/MTw/PDw/B1+/B0) with a signal model to generate parametric maps (MTsat, PD, R1, R2*). These maps represent physical tissue properties with (absolute) standardised units. Visual inspection and manual quality control of these data are time-consuming, subjective and error-prone since the MPM acquisition and output include multiple images. Hence, we developed a tool to visualize all maps and summarise objective QC measures in an easily accessible HTML format.

We used SPM12 and the hMRI-toolbox for processing the MPMs[4]. We estimated the following QC measures to assess inter-volume movement, which can invalidate model assumptions.

1. Coregistration parameters: MTw2PD and T1w2PD contain the co-registration parameters of MTw and T1w images to the PDw images respectively (3 translations in mm and 3 rotations in radians). We computed the Euclidean norm of the translation part to estimate the absolute distance. Next, intra-scan motion was quantified using a previously established metric, the motion degradation index[4-6].

2. Standard deviation in the white matter of the R_2* maps (SD-R2s), calculated from each individual multi-echo acquisition (PDw, T1w, MTw). An empirical heuristic of motion was extracted from the PD map.

3. **The ratio of standard deviation and mean** of the PD values in white matter. This value indicates the accuracy of the B1+ bias field correction[4,7]

4. GM, WM, CSF volumes and its ratio to the total intracranial volume (TIV) These values were estimated by multi-channel segmentation of MTw OLS fit and T1w OLS fit using SPM12 - unified segmentation[8]

5. Signal to Noise Ratio (SNR) for the GM and WM for the qMRI maps

6. Contrast to Noise Ratio (CNR) of GM and WM for the qMRI maps.

Figure 1 shows the image processing pipeline.

Figure 1 : Flowchart showing the steps involved in the hMRI-vQC tool for estimating the Quality assessment parameters and generating maps

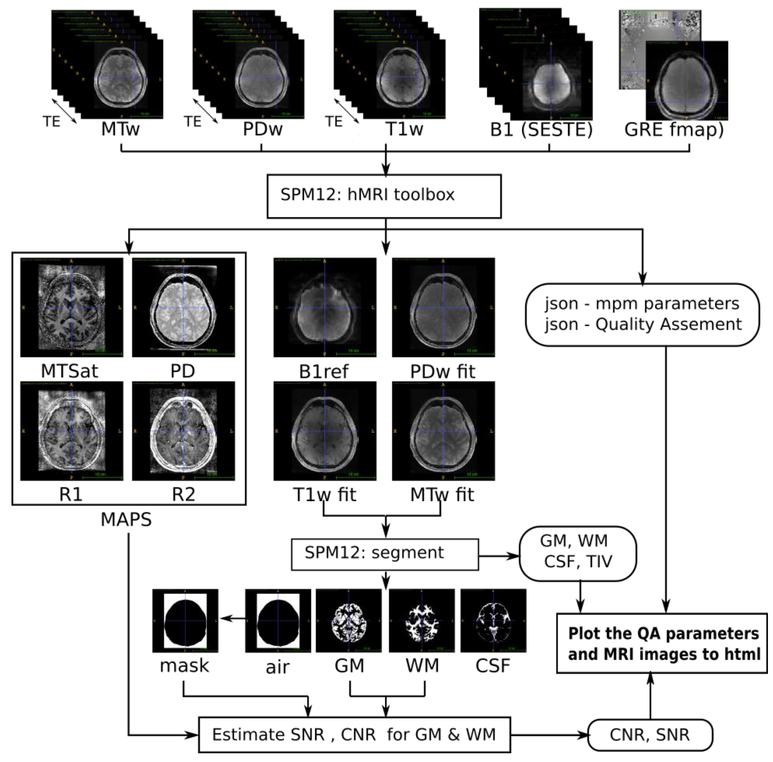
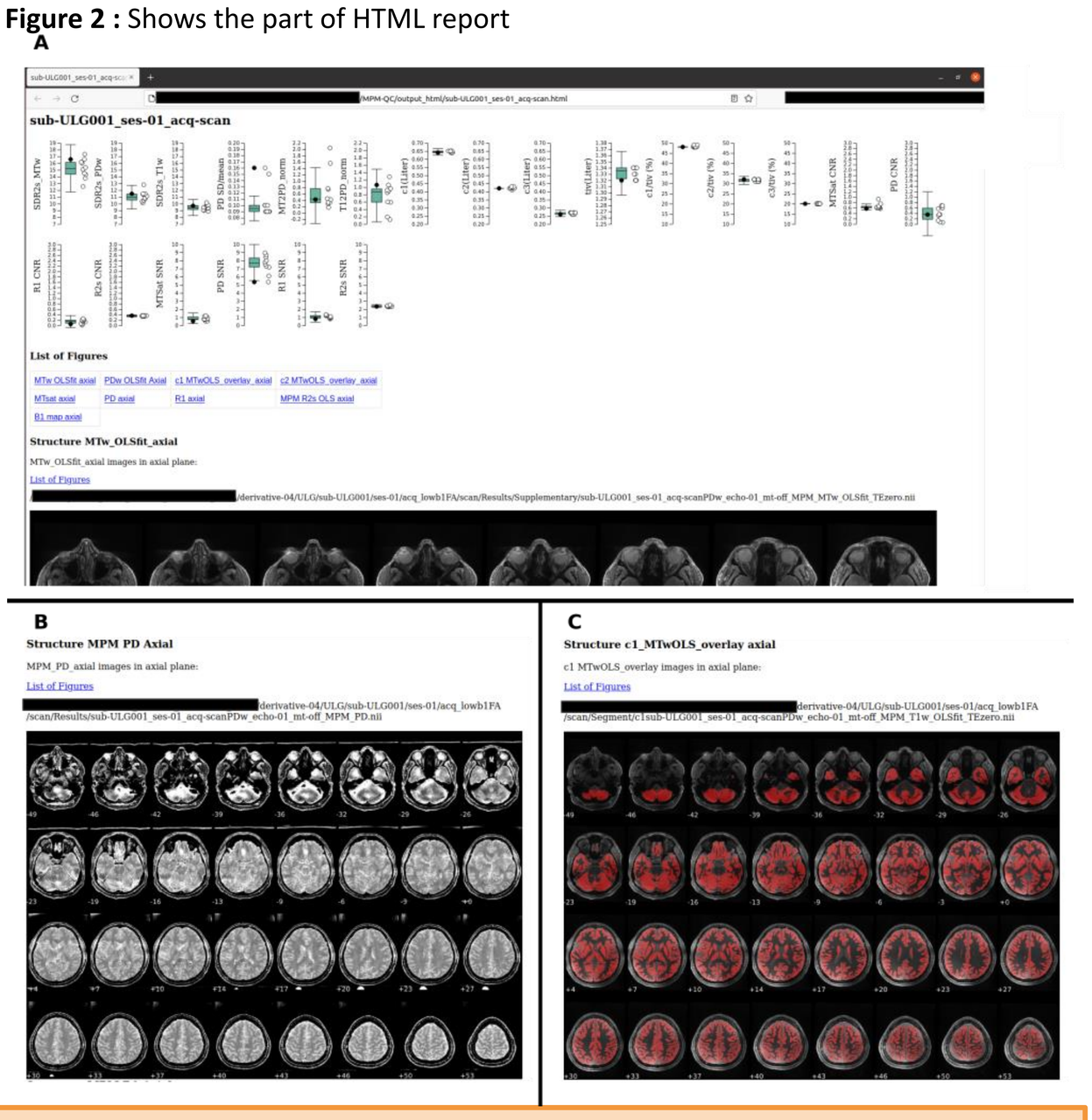


Figure 2 : Shows the part of HTML report



RESULTS

We used a subset of 7T multi-site MPM data acquired on a single subject and available in the lab to demonstrate the QC toolbox feature[9]. **Figure 2** shows the screenshots of different parts of the sample HTML report for the subject/session produced by the toolbox. The top part of the HTML shows the summary plots, side-by-side box plots and scatter plots of the QA parameters for data acquired for all subject data (**Fig. 2A**). The black dot in the box plot indicates the parameter's value for the particular subject/session within the sample range, which aids in quickly assessing the QA level of the specific subject/session. **Fig. 2B** shows the report's visualisation of the PDmap in the axial plane. This section is customizable, i.e. the user can determine the axis and number of images to display. Individual images can be zoomed in by clicking on them. **Fig. 2C** shows the segmentation-defined GM overlaid on the MTw signal extrapolated to a TE of zero, which was used as input to the segmentation. This output helps the rater to visually assess segmentation quality.

CONCLUSION

We present hMRI-vQC, a visual QC tool, which shows summary values in scatter/boxplots in an interpretable form to aid the rater. It also helps visualise multiple qMRI images/maps easily and flexibly in HTML. Further analyses of large MPM datasets are required to validate the quality assessment parameters and automatic image quality assessment. The source code is available on Github [10]**.** This tool is expected to add immense value to the assessment and quality control of large group studies by providing automatic, objective, quantitative assessment in an easy to use format.

SCAN ME

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