# Automatic quantification of white matter hyperintensity volume

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## Abstract:

Hyperintensities in the neural white matter are areas of especially high contrast and are detectible by fluid attenuation magnetic resonance imaging(FLAIR). These hyperintense regions are associated with normal aging of the brain, but they can also indicate neurological diseases such as early dementia and Alzheimer’s. Building upon earlier work, we develop a Python based software tool to automatically quantify the volume of hyperintense regions, providing information that can be used to aid researchers by giving anatomical data that they can correlate to patient diagnoses. In order for our work to be more general and ported to other scanning hardware, we develop a semi-automatic calibration mechanism that leads to proper threshold values for a given scanner.

## Keywords: neuroimaging, MRI, Python

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## 1 Introduction:

## 1.1 White matter hyperintensities:

White Matter Hyperintensities(WMH) are artifacts from MRI scans appearing as voxels with extraordinarily high contrast in the white matter regions of the brain. They are most detectable with fluid attenuation inversion recovery(FLAIR) scans, and, while WMH regions correlate with the normal aging of the brain, they can also indicate, when appearing in excess, neurological and cognitive disorders.

Researchers involved in a study of patients with symptoms of dementia or other cognitive impairments would be interested in whether there was an anatomical correlation with the diagnosis. For this purpose, we have developed a software tool to automatically quantify the volume of WMH artifacts in an MR scan. Our tool gives the researchers the volume of the WMH for an entire three-dimensional scan.

## 1.2 Automatic Detection of WMH

Our software tool is based on previous work in the automatic detection of WMH regions developed by (Hulsey 2008) for a master’s thesis and provides an algorithm implemented with a bash based script, calibrated to a particular scanner, that calls programs from the FSL suite of software (Smith et. al, 2004; Woolrich et. al., 2009). This approach uses MPRAGE images to develop a set of binary masks towards the general goal of isolating the white matter of the brain. As MPRAGE MR scans are inadequate for delineating WMH, these generated masks are then coregistered to the FLAIR image space.

Using the transformation matrix generated by the FSL tool FLIRT (Jenkinson and Smith, 2004), it generates FLIRT based masks from the MPRAGE binary masks. Using the tool fslstats, again part of the FSL suite, it determines the mean and standard deviation of the contrast values for the peripheral cerebral white matter tissue.

Once these values are acquired, Hulsey’s algorithm adds the mean to the standard deviation multiplied by lower and upper thresholds, 3.0 and 3.5 in the original paper, giving two values. The upper threshold added to the mean multiplied by 3.5 is applied to the FLAIR cerebral tissue mask, and the lower threshold is likewise multiplied and applied to the entire FLAIR white matter mask generating two binary three dimensional images. Hulsey adds the two together generating a single binary three-dimensional scan containing the regions afflicted by WMH.

There are many limitations in Hulsey’s approach, the most prominent being that it is extremely time consuming as the tools used in the algorithm are computationally expensive and must be run sequentially in the order given by the bash script. Hulsey’s approach is also inadequate when applying it to new scanners. We found that Hulsey’s values for upper and lower thresholds dramatically underestimated the extent of the WMH. In fact, running the script with the default values detected no WMH in even cases with extraordinarily obvious effected regions. Furthermore, because of the computational cost of running the program, manually trying new threshold values to find the ideal for our scanning hardware was temporally prohibitive. Lastly, we found that when we applied Hulsey’s algorithms to our scans, it detected erroneous regions, i.e., areas known not to be white matter, as WMH.

## 1.3 Python approaches to neuroimaging

Python is a multi-paradigm programming language that is increasingly being used in the sciences. The primary attractions to Python are its power, brevity, ease of use, interactivity, the inclusiveness of its library, and the ease in which one can interact with third party modules. A Python based suite of software, NIPY, has been developed to aid in neuroimaging with especial emphasis on fMRI analysis. Nipype (Gorgolewski, 2011) was developed under this suite and specializes in interfacing with existing neuroimaging software tools such as FSL, SPM, and FreeSurfer.

Nipype allows one to create a workflow, linking nodes together with the output of one being the input to another. After a workflow is defined, it is run, and with each step, software artifacts are created and stored in the workflow directory, enabling one to easily debug and validate an algorithm if necessary.

We also make use of the tool NiBabel, also in the NIPY suite that allows one to easily import images of a variety of types, e.g., NIFTI, which we use in our volumetric analysis.

## 2 Methodology

## Figures:

See these guidelines for figures: more