# MAGNETIC RESONANCE BRAIN IMAGE CLASSIFICATION USING HIDDEN MARKOV RANDOM FIELD FITTED WITH MODIFIED EXPECTATION-MAXIMISATION ALGORITHM

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# JULY, 2023 MAGNETIC RESONANCE BRAIN IMAGE CLASSIFICATION USING HIDDEN MARKOV RANDOM FIELD FITTED WITH MODIFIED EXPECTATION-

## MAXIMISATION ALGORITHM

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# A THESIS SUBMITTED TO THE POSTGRADUATE SCHOOL FEDERAL UNIVERSTY OF TECHNOLOGY, MINNA, NIGERIA IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF THE DEGREE MASTER OF TECHNOLOGY IN MEDICAL PHYSICS

#### ABSTRACT

The segmentation of brain tissues from magnetic resonance (MR) images is of primary importance for subsequent diagnosis, pathological analysis, prognosis assessment, and brain development monitoring. Accurate segmentation is quite challenging because of the tissue heterogeneity, which is caused by bias field, partial volume effects, noise and magnetic field non-uniformities. The algorithms based on Markov random field (MRF) have shown strong abilities in dealing with noisy image segmentation compared to other methods. In this study, a hidden Markov random field fitted with modified expectation maximisation algorithm (HMRFEM) was proposed for neighbourhood correlation (addressing partial volume effect) and signal non-uniformity (intensity inhomogeneity). The algorithm has been implemented on T1weigthed simulated brain web dataset using R programming's magnetic resonance image tissue classification (MRITC) package. The study obtained a good result for segmenting the three major brain tissue types; white matter (WM), gray matter (GM) and cerebrospinal fluid (CSF) in 18%, 47% and 35% respectively. The validation measures of our results showed average tissue mean square error of 0.02901258, misclassification rate of 0.08698863, and tissue volume error of 0.057795773, 0.02458168, and 0.006265323 for cerebrospinal fluid (CSF), gray matter (GM) and white matter (WM) respectively. Dice similarity measures were found to be 0.9244405, 0.9085912, and 0.9134111 for CSF, GM and WM respectively. These results demonstrated that the algorithms returned good performance for a brain tissue classification and can be considered to be reliable for clinical use.

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