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BRAIN TUMOUR DETECTION AND CLASSIFICATION

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ABSTRACT

With so much going on in the field of Deep Learning, categorization of brain tumours remains a source of worry. Brain tumour segmentation and classification using MRI images has piqued the interest of many researchers in the field of medical imaging. The focus remains on the development of automated computer-aided systems for early prediction and diagnosis. MRI of brain tumours not only changes in form but also provides less contrasting features at times. We introduce a FastAI-based Transfer Learning tumour classification method in which a pre-trained model with segmented characteristics identifies tumour based on its learning. The proposed Deep Learning model extracts characteristics from MRI brain images using ResNet152 as the basic model. Certain adjustments in the last three layers of ResNet152 result in 97% accuracy in Dataset-253, and 96% accuracy in Dataset-205. Resnet50, VGG16, ResNet34, and Basic CNN models are also tested. The model enhanced from ResNet152 produced better results. The observations imply that when the Dataset is restricted, Transfer Learning is successful. The produced model is useful and may be used in computer-aided brain MR imaging. Classification of tumours

INTRODUCTION

1.1 DETECTION AND CLASSIFICATION OF BRAIN AND TUMOR

It has been demonstrated that combining image detection and classification based on statistical classification with a geometric prior considerably improves robustness and repeatability. The use of a probabilistic geometric model of the desired structures and image registration allows to initialise probability density functions as well as define spatial limits. A large spatial prior, on the other hand, prevents the identification and categorization of structures that are not included in the model. In practise, we see either the appearance of new objects that cannot be represented with a spatial prior or regional intensity changes of existing structures that are not explained by the model. The identification and categorization of brain tissue and tumours using three-dimensional magnetic resonance imaging is our primary application (MRI). Our objective is to detect and classify healthy tissue with high accuracy, as well as to precisely delineate tumour borders. We offer an extension to an existing expectation maximisation (EM) detection and classification system that updates a probabilistic brain atlas with information on tumour location derived from post- and pre-contrast MRI subtraction for each individual patient. The innovative approach treats several sorts of disease, including space-occupying mass tumours and in-trade modifications such as enema. Preliminary findings from five examples showing tumour types with highly different event characteristics suggest the potential of the novel approach for clinical regular usage in neurosurgery, radiation oncology, and radiology for planning and monitoring. A geometric prior may be employed by atlas-based detection and classification, which considers detection and classification to be a registration issue in which a fully labelled template MR volume is registered to an unknown dataset. High-dimensional warping produces one-to-one correspondence between the template and subject pictures, resulting in a novel, automated detection and classification method. These approaches need elastic image registration to account for geometrical distortions caused by pathogenic processes. Such registration remains difficult and has not yet been addressed in the general situation. The registration of elastic atlases with statistical categorization. A brain atlas' elastic registration assisted in masking the brain from surrounding structures. A further phase employs "distance from brain border" as an extra feature to improve cluster separation in multidimensional feature space. The supervised selection of training zones is still required for the initialization of probability density functions. The basic idea of the novel technique given in this research is to complement statistical classification with spatial information to account for the overlap of distributions in intensity feature space.

Automatic identification and categorization of normal brain MR images utilising statistical classification, using an atlas prior for initialization and geometric restrictions. A new expansion detects brain lesions as outliers and has been used successfully to detect multiple sclerosis lesions. However, because of overlapping intensities with normal tissue and/or large size, brain tumours cannot be simply modelled as intensity outliers. We offer a fully automated technique for segmenting MR images with tumour and edoema, both of which are mass-effect infiltrating entities. Tumor and enema classifications have also been included to the

detection and categorization. The geographic atlas utilised as a prior in the classification is changed to incorporate tumour and edoema prior probability. To make the problem tractable, we focus on a subset of tumours, as previous researchers have done. Our technique differentiates brain tissue into white matter, grey matter, tumour, and edoema. Because the approach is totally automated, its dependability is excellent. We used our tumour detection and classification system to five distinct datasets, each of which had a diverse variety of tumour kinds and sizes. Figure 5 depicts the outcomes for two datasets. Because tumours have a high spatial prior, numerous tiny structures, primarily blood arteries, are diagnosed as tumours because they increase with contrast. To obtain a final detection and classification for the tumour, post processing employing level set evolution is required [shows the final spatial priors used for classification of the dataset with the extra tumour and edoema channels. We created a model-based detection and classification approach for segmenting tumours infiltrating edoema in head MR imaging datasets. This is accomplished by supplementing the spatial prior of a statistical normal human brain atlas with individual data from the patient's dataset. Thus, for both geometry of newly emerging objects and probability density functions for healthy tissue and disease, we mix the statistical geometric prior with image-specific information. Applications to five cancer patients with varying tumour appearance indicated that the process can manage a wide range of tumour size, internal texture, and location. The procedure produces high-quality images of healthy tissue architecture and pathology, which is required for surgical planning or image-guided surgery. As a result, it goes beyond earlier work that focuses just on tumour identification and categorization. We are now verifying the detection and classification system's validity in a validation research that compares the generated tumour shapes to repeated manual expert detection and classifications, both within and across many experts. A early machine versus human ratter evaluation revealed an average overlap ratio of more than 90% and an average MAD (mean average surface distance) of 0:8mm, both of which are less than the initial voxel resolution. In the future, we will investigate the issue of normal anatomy distortion in the presence of space-occupying tumours. The statistical atlas' soft bounds might accommodate spatial displacement throughout the range of tumours investigated thus far. However, in order to enhance the match between atlas and patient photos, we will create a technique for high-dimensional warping of multichannel probability data.

1,2 TUMOUR CLASS

We add a new class for tumour tissue to the three tissue classes assumed in EMS detection and classification (white matter, grey matter, and csf). Whereas the atlas defines the (spatial) prior probability for normal tissue classes, the spatial tumour prior is generated using the T1 pre- and post-contrast difference picture. We assume that the bias field (multiplicative) is the same in both the pre- and post-contrast photos. Because the bias fields (now additive) in the two pictures cancel out, using the log transform of the T1 pre- and post-contrast image intensities yields a bias-free difference image. Image Histogram of Difference: The difference image histogram reveals a peak around zero, due to noise and mild misregistration, and a positive response, corresponding to contrast enhancement. We want to find a weighting function, or soft threshold, that correlates to our judgement that a voxel is contrast enhanced. We fit a mixed model on the histogram. The normal difference image noise is modelled using two Gaussian distributions, while the enhanced tissue is modelled using a gamma distribution. The means of the Gaussian distributions and the gamma distribution's location parameter are bound to be identical. Priority Tumour Class Spatial: The gamma distribution's posterior probability representing contrast enhancements was utilised to translate the difference image to a spatial prior probability image for tumour. This option of spatial prior for tumour includes tissue that increases with contrast in the tumour class, preventing enhancing tissue from cluttering the normal tissue classes. We also keep the tumour class's base probability low over the whole brain area. In several of the cases we've looked at, the tumour voxel intensities in the T1 pre contrast and T2 channels are quite effectively separated from normal tissue. Even though the contrast agent only provides partial enhancement in the post-contrast picture, the tumour voxels in the other two images frequently have identical intensity values (see Fig. 2 left). By including a low base probability for the tumour class, non-enhancing tour can still be categorised as tumour as long as it is similar to enhancing tumour in the T1 and T2 channels. The normal tissue priors are correctly scaled to account for the additional tumour prior, such that the probabilities still add up to 1. B. Classification of Edema We also create a new class for edoema. There is no spatial precondition for edoema, unlike tumour formations. As a result, the probability density function for edoema cannot be automatically initialised. This is how we address the problem: To begin, we discovered that edoema, when present, is most visible in white matter. In addition, supervised classification experiments revealed that the edoema probability density seems to be around between and white matter in the T1/T2 intensity space. We develop an edoema class

prior that is a subset of the white matter spatial prior. The other atlas priors, like the tumour prior, are scaled to account for the edoema prior. The edoema and white matter classes occupy the same geographical area, but are represented by a bimodal probability density consisting of white matter and edoema. Using the updated atlas prior, we derive the estimates for grey matter, white matter, tumour, and edoema in a subject image during class parameter initialization. As a result, white matter and edoema would have identical probability density functions. Using existing knowledge about edoema qualities, the bimodal distribution is then started by altering the mean value for edoema to be between white matter and.

1.4 GREY LEVEL CO-OCCURRENCE MATRIX

A co-occurrence occurrence matrix, often known as a co, is defined over an image to represent the distribution of co-occurring values at a particular offset. Or Distance and angular spatial representation Represents the distance and angular spatial connection over an image sub-area of a given region of a specific size.

The GLCM is made up of grayscale images. A grayscale picture is used to produce the GLCM. The GLCM determines how frequently a pixel appears. The GLCM determines how frequently a pixel with gray-level (grayscale intensity or Tone) value I occurs either horizontally, vertically, or diagonally to neighbouring pixels with the value j.

1.4 ANALYTIC MODELING

Graphical modeming is a strong paradigm for multivariate probability distribution modelling and inference. It has been shown to be beneficial in a variety of stochastic modeming applications, including coding theory, computer vision, knowledge representation, Bayesian statistics, and natural-language processing. This factorization turns out to be closely related to certain conditional independence connections among variables, both of which may be simply described by a graph. Indeed, the relationship between factorization, conditional independence, and graph structure accounts for much of the graphical modeming framework's power: the conditional independence viewpoint is most useful for designing models, while the factorization viewpoint is most useful for designing inference algorithms. The rest of this part introduces graphical models from both the factorization and conditional independence perspectives, with a focus on models built on undirected graphs.

All of the approaches presented in this study presume that the model's structure has been determined in advance. It is natural to wonder if we can also learn the model's structure. This is a challenging challenge in graphical models in general. Indeed, Bradley and Guestrin highlight an intriguing difficulty that is unique to conditional models. Maximum likelihood structure learning for a generative model p(x) may be achieved effectively using the well-known Chow-Liu method if the model is confined to being tree-structured. When estimating the structure of p(y|x) in the conditional scenario, the similar approach is more challenging since it entails calculating marginal distributions of the type p(yu,yv|x), that is, we must estimate the effects of the complete input vector on each pair of output variables. Estimating these distributions is challenging without first knowing the structure of the model. Classification methods are well-established and effective approaches for predicting discrete events. However, in the applications considered in this study, we would want to predict more complicated objects, such as natural language phrase parse trees, alignments between sentences in various languages, and route planning in mobile robotics. Each of these complicated objects has internal structure, such as a parse's tree structure, and we should be able to exploit this structure to more efficiently describe our predictor. This is referred to as structured prediction. The topic of structured prediction generalises the classification issue to the challenge of predicting structured objects in the same way as the GREY LEVEL CO-OCCURRENCE MATRIX (GLCM) likelihood generalises logistic regression to predict arbitrary structures. Structured prediction approaches are basically a hybrid of classification and graphical modelling, combining the capacity to describe multivariate data compactly with the ability to predict using huge amounts of input characteristics. GREY LEVEL CO-OCCURRENCE MATRIXES (GLCMs) are one approach for doing this, as they generalise logistic regression, but other traditional classification methods can also be adapted to the structured prediction scenario. A recent collection of research articles provide detailed information on structured prediction algorithms. This section provides an overview and links to some of these approaches.

1.5 TIMES FASTER AI

You can use fatsia without installing it if you use Google Colab. In fact, every page of this manual is also accessible as an interactive notebook; simply click "Open in colab" at the top of any page to access it (be careful to set the Colab runtime to "GPU" to make it run quickly!) For further details, see the fast.ai guide on Using Colab. As long as you're running Linux or Windows, you may install fastai on your own PCs using conda (which is strongly recommended) (NB: Mac is not supported). Important notes for Windows can be found under "Running on Windows." fastai is a deep learning library

that gives practitioners with high-level components that can provide state-of-the-art results in conventional deep learning domains quickly and easily, as well as academics with low-level components that can be combined and matched to construct novel techniques. It seeks to accomplish both without sacrificing usability, flexibility, or performance. This is made feasible by a deliberately built design that describes several deep learning and data processing techniques' shared underlying patterns in terms of disconnected abstractions. By using the dynamic of the underlying Python language and the flexibility of the Porch library, these abstractions may be articulated elegantly and unambiguously. Fastai is based around two key design goals: being approachable and productive quickly, as well as being extensively hackable and flexible. It is built on a foundation of lower-level APIs that provide reusable building components. As a result, a user who wants to rewrite a portion of the high-level API or add specific behaviour to meet their needs does not need to learn how to utilise the lowest level. It is very simple to transition from plain Porch, Ignite, or any other Porch-based library, or to use fastai in conjunction with other libraries. In general, you will be able to use all of your existing data processing code, but you will be able to reduce the amount of code required for training and take advantage of modern best practises more easily. Python multiprocessing problems on Jupiter and Windows.

LITERATURE SURVEY

A system for estimation of brain tumor volume via mr imaging and fuzzy connectedness. The proposal was made by Liu J, Udupa JK, Odhner D, Hackney D, and Moonis G. This work describes a method for the exact, accurate, and efficient measurement of brain tumours (glioblastomas) using MRI that may be employed in the clinic on a regular basis. Tumor volume is thought to be beneficial in monitoring disease progression and response to therapy, as well as determining the need for treatment plan adjustments. To acquire information on the tumour and its surroundings, we employ a variety of MRI protocols, including FLAIR, T1, and T1 with Gd enhancement. Enhancing tissue, no enhancing tumour, edoema, and combinations of edoema and tumour are examples of these. In this study, we adopted the fuzzy connectedness framework for tumour identification and classification, and the system required minimal user intervention in everyday clinical use. Using 10 patient studies, the system was assessed for precision, accuracy, and efficiency. Most MRI techniques produce images with a bimodal histogram, with the first mode representing the background and the second representing the foreground item that we are interested in—in our case, the patient's head.[1]

A nonparametric method for automatic intensity non-uniformity correction in mri data Evans AC, Sled JG, and Zijdenbos AP have suggested A unique method for compensating for intensity non-uniformity in magnetic resonance (MR) data that achieves good performance without having a model of the tissue classes present is provided. The approach has the benefit of being able to be used early in an automated data analysis, before a tissue model is ready. Poor radio frequency (RF) coil uniformity, gradient-driven eddy currents, and patient anatomy both inside and outside the field of view are commonly blamed for this intensity non-uniformity. Although these 10%-20% intensity differences have minimal effect on visual diagnosis, automated detection and classification approaches that presume intensity homogeneity within each class might suffer dramatically. For such automatic processing systems to be accurate in labelling each voxel with a tissue type, a robust, automatic, and low-cost mechanism of compensating for this artefact is required. Furthermore, adjusting for non-uniform illumination may help quantitative measures utilised in tissue metabolite research.[2]

Existing methods and their validation in mri intensity non-uniformity correction et al[3]Belaroussi B, Milles J, Carme S, Zhu YM, Benoit-Cattin H suggested in this study We present an overview of available approaches in this work. We begin by categorising them based on where they are in the acquisition/processing cycle. Sorting is then improved depending on the assumptions upon which those approaches are founded. Following that, we discuss the validation methods that were utilised to evaluate these various correction systems both qualitatively and quantitatively. Finally, the accessibility and utility of the approaches offered are explored. Magnetic resonance imaging (MRI) is a powerful non-invasive imaging method used to research the architecture and characteristics of soft tissues. It is distinguished by the high overall quality of the datasets obtained. Such information is often in the form of a collection of two-dimensional (2-D) MR pictures or a whole three-dimensional (3-D) isotropic volume. Although MR data may be used for efficient qualitative or user-driven quantitative analysis, the current demand is for non-supervised, automated quantitative analysis tools. In this study, we looked at intensity non-uniformity correction as a worldwide challenge comprising numerous communities with varying goals. We offered an overview of all known approaches, as well as an innovative typology to group them based on how correction is accomplished and the assumptions made.

The impact of intensity standardization on inhomogeneity correction processing of inmarriage et in this work .al[4] Madabhushi A, Udupa JK suggested In terms of inhomogeneity correction, there is no

statistically significant difference in picture quality between the results of standardisation followed by correction and those of correction followed by standardisation. The corrective process is shown to skew the standardising effect. We illustrate this bias both qualitatively and statistically by employing two alternative inhomogeneity correcting approaches. We further demonstrate that this bias in standardisation is unaffected by the specific inhomogeneity correction approach adopted. The effect of this bias owing to correction was also apparent in magnetization transfer ratio (MTR) pictures, which have the standardless quality by nature. Standardization, on the other hand, appears to have little effect on the rectification operation. It has also been discovered that a lengthier series of repeated correction and standardisation procedures does not enhance image quality much. These findings were confirmed for clinical and phantom data sets, different MRI procedures, different degrees of artificial nonstandardless, different models, and varied levels of artificial in homogeneity.[4]

Prastawa M, Bullitt E, Ho S, Gerig G suggested in this paper et al[5]. The identification of edoema occurs concurrently with the detection and categorization of tumours, as information of the degree of edoema is critical for diagnosis, planning, and therapy. Many previous tumour identification and classification approaches rely on the intensity enhancement caused by the gadolinium contrast agent in the T1-weighted image, however the method provided here does not. The T2 MR image channel is the sole needed input for the detection and classification technique, although it can employ any additional non-enhanced image channels for improved tissue detection and classification. There are three steps to the detection and classification framework. First, we use a registered brain atlas as a model for healthy brains to discover abnormal areas. The robust estimations of the position and dispersion of the normal brain tissue intensity clusters are then used to identify the intensity attributes of the various tissue types. The second stage involves determining if edoema arises with tumour in the aberrant locations based on the T2 imaging intensity. Finally, we apply geometric and geographical limitations to the tumour and edoema sites that have been identified. The detection and classification approach was tested on three real-world datasets with varying tumour forms, locations, sizes, picture intensities, and enhancement.

EXISTING SYSTEM

The thorough assessment of existing tumour enhancement, detection, and classification approaches in the present system. Each method is categorised, analysed, and contrasted with others. The sensitivity and specificity of the methodologies are described and compared when applicable to test the accuracy of the tumour enhancement, detection, and classification strategies. Finally, this study gives a taxonomy for the existing methodologies and emphasises the best improvement, detection, and classification methods. It only divided tumour detection and classification approaches into two categories: mass detection with a single view and mass detection with multiple views. Model-based approaches, region-based methods, contour-based methods, and clustering methods are the four types of mass detection employing single view detection and classification.

PROPOSED SYSTEM

The notion of transfer learning is used in the proposed work by employing a pre-trained CNN with Resnet152. Furthermore, the Resnet152 is being improved for tumour classification. On Dataset-253, the suggested approach is verified for classifying tumorous and non-tumorous data. Similarly, Dataset-205 validates the categorization of High-Grade Glioma (HGG) and Low-Grade Glioma (LGG).

PREPROCESSING FOR MRI:

Typically, pre-processing photos include eliminating low frequency, background noise, adjusting the intensity of individual practical images, removing reflections, and masking portions of images. Prior to computer processing, image processing is the practise of improving data images. The appropriate fractal and intensity characteristics are retrieved after conventional pre-processing processes for brain MRI. Following that, several feature set combinations are used for tumour detection, classification, and classification. The feature values are then immediately input into the AdaBoost classifier for tumour and non-tumor classification. For supervised classifier training, tumour areas are manually labelled. The learned classifiers are then utilised to detect tumour or nontumor segments in previously unseen brain MRI. The Kaggle data collection Dataset-253[28] contains 98 non-tumorous photos and 155 tumorous data. Dataset-205, obtained from[11], comprises 172 High Grade Glioma (HGG) pictures and 56 Low Grade Glioma (LGG) images (LGG). Data Augmentation is used to increase the amount of data. 15 o Angle of rotation for each horizontal and vertical flip. The figure 4 and Figure Dataset-253 and Dataset-205 enhanced photos are shown in Figure 5.

CREATION OF A FASTAI MODEL

The ResNet152 [13, 24] architecture is used as the foundation model for classifying tumour and non-tumor brain pictures. ResNet152 architecture is a pre-trained

model on ImageNet that comes with the FastAI package. A callback fns method is used to assess model improvement using graphs. Accuracy is used as an output measure in function Metrics. Binary-cross entropy is used to train and verify the model. This is done for binary categorization of two classes. The layout model overview of ResNet152 following model training of the basic Convolutional architecture is shown in Fig. 6. The model represents the entire learned parameters using Adam Optimizer.

DETERMINING THE BEST LEARNING RATE

With the model's basic training, the best learning rate is discovered using the built-in learner object capabilities. It aids in determining learning rate ranges. This is done to train models. Fitting the model for a few epochs yields the best learning rate. When the loss begins to degrade, the learning rate is saved. The function learner.lr find() is used to find the learning rates, and the function learner.recorder.plot() is used to create the learning rate curve. The learning rate with the sharpest slope and the smallest loss curve is selected. Figure 7 depicts learning rate curves for brain MRI datasets 253 and 205, respectively. In our scenario, the starting learning rate is set at e-02. The learning rate gradually increases as the validation loss decreases. Model training is completed for a few epochs within one cycle. In our situation, we performed this for ten epochs. Following training, the learning rate is modified once again for the following learning cycle.

epoch	train loss	Valid loss	Accuracy	Time
0	0.572963	0.518684	0.730196	00:15
1	0.675802	054281	0.706348	00:15
2	0.541887	0.830186	0.658721	00:16
3	0.52735	0.518714	0.768942	00:16
4	0.540524	0.469857	0.809521	00:17
5	0.454532	0.433384	0.912689	00:18
6	0.457034	0.228426	0.968524	00:18
7	0.405162	0.163970	0.960371	00:18
8	0.335286	0.193147	0.961025	00:19
9	0.300564	0.153146	0.961025	00:20

Training and Validation Loss for each epoch before unfreeze for the Brain Datasets.

FINE-TUNE AND UNFREEZING FOR MODEL ENHANCEMENT

Finally, the model is re-trained in this stage. After unfreezing with the learner.unfreeze () function, the learner curve is shown. This assists in determining the new optimum learning rate. The figure below shows Dataset-253 and Dataset-205 of brain pictures being re-trained with new optimum learning rates. For both datasets, the learning rates are set to 1e-04 and 1e-05, respectively. The datasets are verified to 97% and 96% after re-training the model accuracy for both brain MR scans. The model does not cause over-fitting since the validation loss is less than the training loss at each epoch cycle. The validation accuracy and losses plot graph for Dataset-253 and Dataset-205 are depicted in Fig. 10. In addition, if the model is under-fitting, it may be improved by increasing the epoch count when training the model.

The Confusion Matrix establishes: True-Positive (TP) as: brain MR scan is tumorous and projected to be tumorous. True-Negative (TN) as: anticipated image is non-tumorous and identical. False-Positive (FP) is defined as the picture being tumorous but being expected to be non-tumorous.

False-Negative (FN) means that the picture is not tumorous but is projected to be tumorous. The total number of errors is used to calculate accuracy.

epoch	train loss	Valid loss	Accuracy	Time
0	0.223470	0.173160	0.9678245	00:20
1	0.237084	0.171897	0.9523487	00:21
2	0.385604	0.157545	0.976190	00:20
3	0.384724	0.118425	0.985126	00:20
4	0.286101	0.108415	0.954238	00:21
5	0.216819	0.153427	0.947619	00:21
6	0.254501	0.109394	0.967825	00:20
7	0.273091	0.110689	0.983125	00:21
8	0.245608	0.117646	0.984137	00:20
9	0.256968	0.114028	0.976280	00:20

Validation Accuracy and Losses Plot Table for dataset

Dataset-253		Dataset-205	
Confusion Matrix	46 0 3 77	Confusion Matrix	47 2
Accuracy	97.61	Accuracy	96.82
Precision	100	Precision	97.4
Sensitivity	96.25	Sensitivity	97.4

Performance evaluation of ResNet152 for both Datasets

CONCLUSION

The ResNet152 architecture, which is a pre-trained FastAI CNN model, is employed in this study. The ResNet152 architecture is used as a starting point and then enhanced by changing the last three layers. New layers improve the dense layer, followed by the SoftMax layer and the binary cross-entropy layers. The upgraded ResNet152 deep learning model was then trained on two separate brain datasets from Kaggle and BRATS2015. Model fine-tuning is carried out. When tested on Dataset-253 and Dataset-205, the improved model's accuracy percentage is 97% and 96%, respectively. When compared to other deep learning models, the upgraded model produces the best results with two separate brain MRI datasets. The accuracy % comparison is shown in Fig. 15. Data augmentation was used to increase the number of MR images in a brain dataset. The better model produced may be useful in detecting various brain disorders such as stroke, haemorrhage, Alzheimer's, and so on. Other pre-trained designs can also be enhanced by altering the network layers.

REFERENCES

1.Liu J, Udupa JK, Odhner D, Hackney D, Moonis G (2005) A method for estimating brain tumour volume using MRI and fuzzy connectedness. 29(1):21-34, Comput Med Imaging Graphics.

2.J.G. Sled, A.P. Zijdenbos, and A.C. Evans (1998) A nonparametric approach for automatically correcting MRI intensity nonuniformity. IEEE Transactions on Medical Imaging, 17(1), pp.87-97.

3.Belaroussi B, Milles J, Carme S, Zhu YM, Benoit-Cattin H (2006) Existing approaches and validation of intensity non-uniformity correction in MRI. Medical Image Analysis 10(2):234

4.Madabhushi A, Udupa JK (2005) Interaction between intensity standardisation and inhomogeneity correction in magnetic resonance imaging. IEEE Transactions on Medical Imaging, 24(5):561-576.

5.Prastawa M, Bullitt E, Ho S, Gerig G (2004) An outlier detection-based brain tumour detection and classification system. Medical Image Analysis 8(3):275-283