Chapter 2

Domain Generalization and Multidimensional Approach for Brain MRI Segmentation Using Contrastive Representation Transfer Learning Algorithm

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ABSTRACT

Quantitative examination of human brain development when the individual is still in the womb is essential for aberrant characterisation. Therefore, the segmentation of magnetic resonance images (MRI) is a valuable asset for quantitative analysis. Conversely, there is little variation within cohorts of foetal brain MRI annotated datasets, which makes it difficult to create automatic segmentation methods. Within this framework, the authors suggest harnessing the potential of foetal brain MRI super-resolution (SR) reconstruction techniques to produce several re-creations of a one subject with varied parameters. As a data augmentation strategy, this would work well without requiring any tuning. In general, the latter makes a major improvement to the generalisation of segmentation approaches over pipelines. When it comes to the diagnosis and treatment of neurological illnesses, the accurate segmentation of brain magnetic resonance imaging (MRI) is absolutely necessary.

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INTRODUCTION

An abnormal mass of cells in or near the brain is known as a brain tumour. Brain tumours have the potential to be benign or malignant (non-cancerous). While some tumours progress slowly, others expand at a rapid pace (Yan et al., 2022). Brain tumours, whether malignant or not, are a major health concern (Zhu et al., 2019). Good news: if caught early enough, they are treatable. However, a brain tumour diagnosis might be complex and require the involvement of multiple doctors (Yamanakkanavar & Lee, 2020). However, while imaging for another medical condition can sometimes reveal a brain tumour, this is by no means uncommon (Zhu et al., 2019). Brain MRI segmentation is a crucial task in medical image analysis, which plays a vital role in the diagnosis and treatment of neurological disorders (Zhang et al., 2020). Accurate segmentation of MRI scans provides quantitative measurements of brain structures, which can aid in the detection of abnormalities and monitoring of disease progression (Ramzan et al., 2020). However, the performance of existing segmentation models often deteriorates when applied to data from different domains or modalities, which is known as the domain generalization problem (Alhassan & Zainon, 2020). In this paper, we propose a multidimensional approach that leverages a contrastive representation transfer learning (CRTL) algorithm for domain generalization in brain MRI segmentation (Jiang et al., 2021).

Even with state-of-the-art technology like MRI and U-Net, brain segmentation remains a challenging task (Chen et al., 2020). Therefore, we provide SEResU-Net, a hybrid of the deep residual network and the Squeeze-and-Excitation Network, as an enhanced variant of U-Net in this research (Minu et al., 2023). By preventing data loss and directing the network's attention to the relevant feature map, the Squeeze-and-Excitation Network addresses the issue of inadequate segmentation accuracy for small-scale brain tumours (Syazwany et al., 2021).

Most of the major brain development occurs when a person is still in the womb (Razzak et al., 2019). Serious issues including congenital illnesses, developmental delay, or cognitive impairment later in life can arise from aberrant development caused by prenatal disturbance of maturation processes (Wu et al., 2018). The clinical use of magnetic resonance imaging (MRI) for the evaluation of cerebral structures has made it an adjunct imaging modality for prenatal diagnosis. As a structural T-weighted (Tw) MRI provides an excellent soft-tissue contrast, it can be used to track the development of the foetal brain and other tissues (Aditya Komperla, 2023). Since the fetus's motion is highly unpredictable, rapid D acquisition approaches are employed to reduce motion inside the slices (Angeline et al., 2023). The low-resolution (LR) images produced by such an acquisition have significant anisotropy due to the residual inter-slice motion (Ansarullah et al., 2022a). Reconstructing a single HR motion-free isotropic volume from a series of LR orthogonal acquisitions has been a possibility for the past few decades thanks to super-resolution (SR) methods (Ansarullah et al., 2022b). These SR reconstruction (SRR) techniques estimate inter-slice inter-series motion by utilising the redundancy in LR images (Bala Kuta, & Bin Sulaiman, 2023). Next, a restoration of an HR image is achieved by resolving an inverse problem that takes into account a regularisation function with different weights (Bhoumik et al., 2020). The appearance of the reconstructed image can vary greatly depending on the reconstruction method, as we have already shown (Boopathy, 2023).

Clinical and research applications of magnetic resonance imaging (MRI) rely heavily on brain structure segmentation for evaluating and tracking brain morphology, volumetry, and connectivity in both healthy and diseased states (Elaiyaraja et al., 2023). There is an increasing demand for automated, quick, and dependable brain structure segmentation methods that can improve the accuracy, statistical

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