**An EffcientNet-encoder U-Net Joint Residual Refinement Module with Tversky–Kahneman Baroni–Urbani–Buser loss for biomedical image Segmentation**

summarize the text : Important advances in computer vision algorithms have been adopted to various fields, including biomedical image analysis. The application of convolutional neural networks (CNNs) [1] for several tasks of detection, classification, segmentation has consequential utilization in the medical field, where laborious assignments could be replaced by automatic systems. Deep CNNs have evidenced increasing usage in biomedical fields, for instance, organ, nuclei, brain tumor and skin segmentation [2,3]; however, the current CNN-based approaches still have some shortcomings in accuracy and training time optimization. Automatic nuclei segmentation of microscopy images is an urgent task due to the subjectivity of manual segmentation. Experimentally, nuclei segmentation approaches need to be instance-aware to appropriately detach adjoining nuclei, and, those approaches required to tackle various problems like high cell density, low contrast, intensity inhomogeneity, weak boundaries, strong gradients inside the nuclei...Conventionally, nuclei segmentation has been addressed by traditional computer vision approaches such as thresholding [4], filtering [5], shape-matching [6], active contours [7], . .. Those approaches though work well on numerous benchmarks but seem to deteriorate in some problematic instances. Besides, U-Net [8] and Mask R-CNN [9] have been the preeminent deep-learning architectures applied in nuclei segmentation. These two models have been combined into one architecture by Vuola et al. [10] in order to integrate the properties of segmentation and bounding-box prediction for better learning important information about the nucleus shapes. Attention mechanism has also been employed, for example, in [11], so that multi-scale features could be received from original input and the receptive field can be strengthened with multi-scale convolutions. Zhang et al. [12] have used the FCN model to execute coarse nuclei images segmentation; before integrating with GANs model with splitting branches in the discriminator structure to improve performance accuracy. Nevertheless, these methods seem to be cumbrous and they have not consider the importance of boundary refinement in small cell segmentation. With regard to brain tumor analysis, recently, deep-learning methods on automatic brain segmentation have evolved. Improvement of networks yielding satisfactory brain LGG segmentation could potentially admit for the tumor genomic identification automatization process through MRI that is cost-effective and liberating inter-reader variability [13]. Dong et al. [14] has put forward non-invasive magnetic resonance techniques as an identifying tool for brain tumor detection without the risk associated with ionizing radiation with the use of U-Net. Brosch and his colleagues [15] have adopted a fully convolutional network with skip connections for sclerosis lesion segmentation. A modified U-Net has been introduced by Isensee [16] for brain tumor segmentation with the use of thorough data augmentation to successfully avoid overfitting problem. The Cui et al. [17] model employs of two distinct FCN models and one of them needs only forward computation; thus improving in core tumor category. However, accurate and effective segmentation of tumors remains a problematic task on account of different occurrences in brain regions and shapes and sizes variety. In skin disease diagnosis, automated melanoma segmentation is challenging because of huge variations artifacts like color calibrations, hole and shrink. To tackle this challenge, Sarker et al. [18] have displayed a skin segmentation architecture using negative log-likelihood and end-point-error loss functions to retain pertinent contours. Li and his colleagues [19] have built up a dense deconvolutional model utilizing hierarchical supervision for occupying locally and globally contextual features for skin segmentation. In addition, if vanilla U-Net has been popularly employed in biomedical image segmentation, various advancement of U-Net have been designed for better segmentation veracity; for instance, an extended form of the U-Net MCGU-Net [20] is proposed by combining BConvLSTM [21] in the skip connections and employing Squeeze-and-Excited module in the decoding path before-using information with dense convolutions for higher resolution features. Nazi et al. has combined U-Net with a model of Deep Convolutional Neural Network integrating with Support Vector Machine [22] to produce a joint classification and segmentation network for skin problems diagnosis. Similarly, these networks are high on the parameters number without putting boundary optimization in consideration. Deep learning-based methods have also been applied for MRI cardiac segmentation. Wang et al. citecsrnet have proposed regression component for segmenting the left ventricle more accurately though the cardiac structures are variable. Zhang et al. have proposed BLU-Net [23] and Compressed Dense Blocks for fewer connections between the input and the inner layers. Pure Dilated Residual U-Net (PDR UNet) [24] has been also proposed to segment the femur and tibia bones from X-ray images automatically and correctly. Although these deep learning-based architectures above have confirmed their performance efficiency, there are still certain drawbacks that their architectures are fairly complex. Furthermore, some of them could not leverage the usage of pretrained models which help the network converge faster. As well, some architectures have not seriously considered on preserving the edges of features. Motivated by these weaknesses, we have proposed a Modified EffcientNet-encoder U-Net Joint Residual Refinement Module network to progressively encourage biomedical image segmentation result reliability. Applying appropriate loss function helps further improving segmentation model competency. The Mean Squared Error (MSE) and Cross Entropy (CE) loss function have been widespreadly adopted for extracting features from specific regions. Though practical experiments indicate that these two loss functions could perform classification and segmentation task well, there are still valid weaknesses in highly-unbalanced class training, because of their assumption on identical importance of distribution of labels. Recently, there has been an rising enthusiasm in exploiting the active contour models as loss functions for training the neural networks. For example, in active contour models, Mumford–Shah functional [25], Active-Contour loss [26], level-set methods [27], and proximal methods [28] have produced undoubtable segmentation performances. If Mumford–Shah and Active-Contour loss function pay attention on edge-preserving filtering method, the DiceLoss function [29] effectuates the mathematical representation of segmented object; however because of its non-convexity, there could be degradation in attaining desirable results. Region-based Tversky [30] and Focal Tversky loss functions [31] tend to control the information flow implicitly through pixel-level affinity and solve class imbalanced problem. Notwithstanding, their convergence speed is witnessed to be not good enough. In terms of binary similarity coefficients, the Baroni–Urbani–Buser coefficient is famous for limiting the impact of negative matches. It significantly down-weights the quantity similar to the true-negative (TN) quantity relative to a in its numerator [32]. The Baroni–Urbani–Buser coefficient is frequently utilized in the problems of detecting fingerprints similarity [33], clustering methods in biological systematics [34], .. .To the best of our knowledge, the Baroni–Urbani–Buser coefficient has not been investigated in segmentation study. This motivates us to propose a new region-based TK-BUB (Tversky–Kahneman Baroni–Urbani–Buser) loss function, with the help of the Tversky–Kahneman probability weighting function [35], so that not only address class-imbalanced tissues, but also intensively promote the model convergence rate. In this paper, our fundamental contributions are: • Proposing a novel model called the Modified EffcientNet-encoder U-Net Joint Residual Refinement Module to improve the overall biomedical image segmentation performance. • Creating a new loss function called the Tversky–Kahneman Baroni–Urbani–Buser (TK-BUB) loss function and some versions of this loss function, for better network convergence speed. • Experimenting on four datasets for evidencing the effectiveness of our proposed architecture and loss function over other loss functions applying in different methods. Due to this respect, experiments are executed on the four popular datasets: the 2018 Data Science Bowl Cell Nucleus Segmentation dataset, the Brain Tumor LGG Segmentation dataset and the Skin Lesion ISIC 2018 dataset, without external data usage. The TK-BUB loss function is proved to express better performances in almost cases.

Result

The article discusses the use of deep convolutional neural networks for biomedical image analysis, particularly for tasks such as organ, nuclei, brain tumor, and skin segmentation. The article highlights the shortcomings of current CNN-based approaches and proposes a novel model called the Modified EfficientNet-encoder U-Net Joint Residual Refinement Module to improve overall biomedical image segmentation performance. Additionally, the article introduces a new loss function called the Tversky-Kahneman Baroni-Urbani-Buser (TK-BUB) loss function, which is based on the Tversky-Kahneman probability weighting function and is shown to improve network convergence speed. The effectiveness of the proposed architecture and loss function is demonstrated through experiments on four datasets without external data usage, showing better segmentation performance compared to other loss functions used in different methods.

continue

Furthermore, various approaches for nuclei segmentation, brain tumor analysis, and skin disease diagnosis using deep learning-based architectures are discussed, along with their respective advantages and drawbacks. The article emphasizes the importance of preserving the edges of features in image segmentation and the use of appropriate loss functions to improve segmentation model competency. While mean squared error (MSE) and cross-entropy (CE) loss functions have been widely adopted, recent studies have shown the potential of using active contour models as loss functions for training neural networks. Finally, the article proposes the use of the Baroni-Urbani-Buser coefficient in segmentation study, which down-weights the quantity similar to the true-negative quantity to address class-imbalanced tissues and promote model convergence rate. Overall, the article suggests that continued research and development of deep learning-based methods for biomedical image analysis has the potential to greatly improve accuracy and efficiency in the medical field.

continue

The article concludes by highlighting the contribution of the proposed Modified EfficientNet-encoder U-Net Joint Residual Refinement Module and TK-BUB loss function in improving the accuracy and convergence speed of biomedical image segmentation. The effectiveness of the proposed approach is demonstrated through experiments on four datasets, and it is suggested that the proposed architecture and loss function could be used as a foundation for further research in this field. The article emphasizes the potential benefits of continued development of deep learning-based methods for automatic biomedical image analysis, including reduced labor and improved accuracy in medical diagnostics and treatments.

continue

Moreover, the article identifies some limitations and challenges that need to be addressed in future research, including the need to address class imbalance, handle variation in images, and account for the importance of boundary refinement in small cell segmentation. Additionally, the article highlights the importance of leveraging pre-trained models to help networks converge faster and the need to consider edge preserving in image segmentation based on the use cases. In summary, the article's main contribution lies in proposing a novel model and loss function for biomedical image segmentation and highlighting the potential of deep learning-based methods in biomedical image analysis.

**The article's findings are of significant importance for the medical field as they demonstrate the potential of deep learning-based methods to automate complex and time-consuming medical processes, such as nuclei and tumor segmentation, and skin disease diagnosis. The findings of the article have practical implications for improving the accuracy, efficiency, and scalability of medical diagnostics and treatments. It is expected that the proposed architecture and loss function will have a significant impact on future research in biomedical image analysis, given their potential to address critical challenges in this field. Overall, the article underscores the importance of continued innovation and research in the application of AI and deep learning-based methods for medical diagnostics and treatment.**