Autosomal Dominant Polycystic Kidney Segmentation Based on Multi-Scale Attention Mechanisms with Swin-UNETR

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Abstract:

Autosomal dominant polycystic kidney disease (ADPKD) is a genetic disorder characterized by the formation of numerous cysts, requiring accurate and automated methods for early diagnosis and monitoring. U-Net-based deep learning (DL) models were used to improve kidney segmentation in magnetic resonance (MR) and computed tomography (CT) images. The primary goal was to achieve accurate and efficient kidney segmentation, which serves as a critical step in the diagnosis of ADPKD. The Swin-UNETR architecture, which aims to improve segmentation accuracy using a Swin Transformer-based encoder capable of effectively modeling local and global contexts, was employed. The model was trained and validated on a specialized dataset labeled by experts, and its performance was evaluated using metrics such as the Dice similarity coefficient (DSC) and loss value. The results demonstrate that the Swin-UNETR model achieves high segmentation accuracy with an average DSC exceeding 90%. The three-dimensional segmentation outputs show that the kidney boundaries are preserved with high accuracy in each slice and that the model successfully follows anatomical integrity. The multi-scale attention mechanisms of the Swin Transformer-based architecture enhance segmentation accuracy by effectively modeling both local details and global contextual relationships. This study demonstrates that the Swin-UNETR approach, which offers reliability and reproducibility in the automatic kidney segmentation process, has clinically significant potential in the imaging-based assessment of polycystic kidney disease. The proposed method is expected to increase diagnostic efficiency by reducing manual intervention and contribute to the development of advanced clinical support systems.

Keywords:

Autosomal dominant polycystic kidney disease, multi-scale attention mechanisms, segmentation, Swin-UNETR.