

A novel deep learning model for enhanced segmentation of internal mammary artery, aorta and their perivascular regions

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Background: A prior study demonstrated that the novel radiotranscriptomic signature, C19RS, holds prognostic significance for clinical outcomes (Figure 1a). The automated segmentation of vascular structures, including the internal mammary artery (IMA), the aorta, and their surrounding perivascular areas from contrast-enhanced CT angiography (CCTA), would facilitate the high-throughput extraction of radiomic profiles.

Purpose: Our goal is to create an innovative deep learning (DL) model for the IMA and aorta that facilitates the automated calculation of C19RS in extensive cohort analyses.

Methods: The model utilises a distinct architecture that combines a CNN (squeeze-and-excitation block) and a transformer (Swin block) to improve segmentation by alternating between these blocks, which helps in capturing discriminative features (Figure 1b). The model was built using the CCTA (n = 227) dataset from the OxHVF study conducted in the UK, applying standardised preprocessing techniques such as resampling, clipping, and intensity normalisation. An iterative refinement process occurred three times (n = 140), resulting in a robust model (see Figure 1c). An external validation cohort (n = 751) from an international site in the United States was utilised, with all segmentations subjected to manual expert review for quality assessment. Lastly, a publicly available dataset (ASOCA) was also validated externally (n = 318).

Results: The model achieved a mean Dice similarity score (DSC) of 0.7876 ± 0.0176 for IMA/peri-IMA segmentation and 0.9207 ± 0.0057 for aorta/periaortic region segmentation (See figure). After refinement, it achieved a DSC of 0.947 for IMA/peri-IMA segmentation (Figure 1c,d). In the external cohort, 679 out of 751 cases (90.4%) were considered clinically acceptable for both regions; the remaining cases were excluded because the CCTAs' narrow field of view did not capture the IMA/aorta. In the ASOCA cohort, the model consistently performed at 0.961 ± 0.039 . These results underscore the model's generalizability and scalability for large-scale clinical applications.

Conclusion: This study presents a powerful and clinically flexible DL model designed for the automatic segmentation of vascular structures, specifically the IMA, aorta, and their surrounding perivascular space. Its use in radiotranscriptomic biomarker analysis presents an exciting opportunity for non-invasive prediction of patient outcomes, making it a significant resource for cardiovascular research and clinical applications.

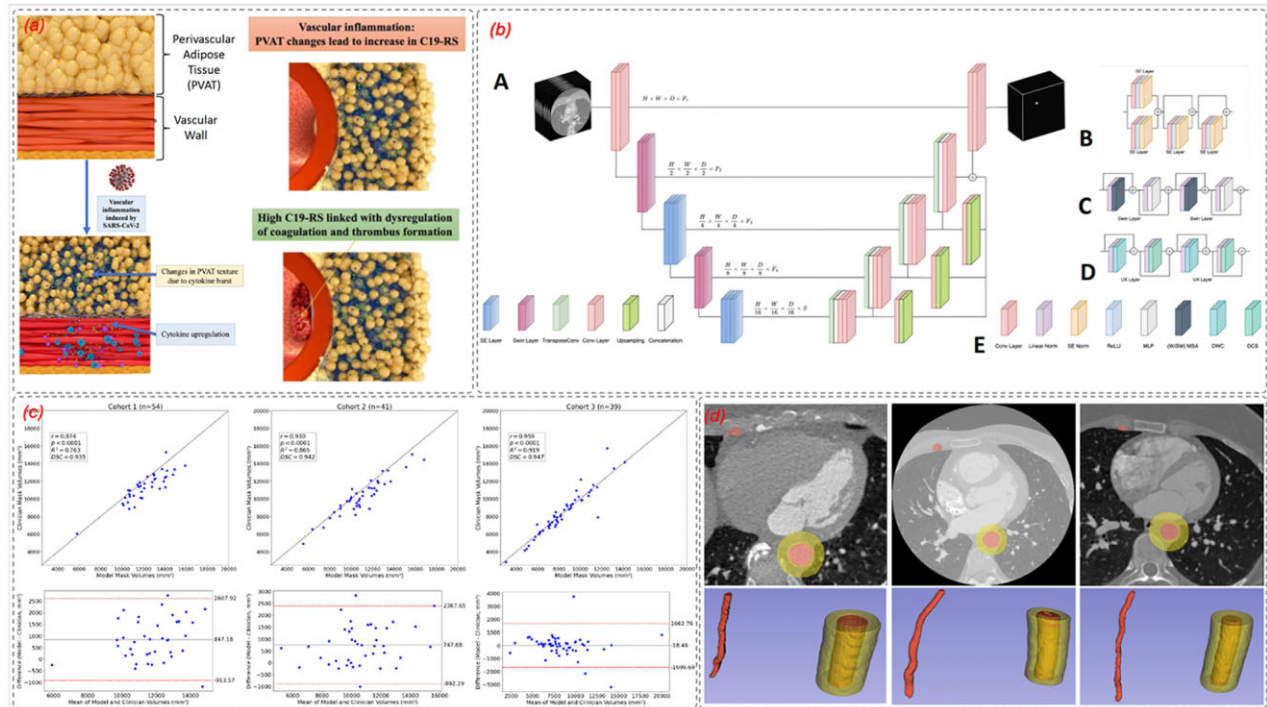


Figure 1. (a) The cytokine inflammation drives changes in the PVAT region, which leads to increased C19RS. **(b)** The proposed model alternates CNN and ViT blocks effectively to capture local and global features. **(c)** Iterative model improvement over three cohorts. **(d)** Qualitative results of IMA and aorta, along with their PVAT regions.