INTERNATIONAL SCIENTIFIC CONFERENCE
20-22 November 2025, GABROVO

# NEURAL NETWORKS IN THE ANALYSIS OF 3D MEDICAL MODELS

**Olga Piščević, Tatjana Lazović, Mihailo Knežević*, Vanja Luković, Sanja Antić**

*University of Kragujevac, Faculty of Technical Sciences, Čačak, Serbia*
**Corresponding author: mihailo.knezevic@ftn.kg.ac.rs*

**Abstract**
*Accurate segmentation of medical images is essential for diagnosis and treatment planning. Traditional manual methods in platforms such as 3D Slicer are precise but time-consuming and dependent on the operator's expertise. With the development of deep learning, neural networks (particularly U-Net) have enabled automatic segmentation with improved efficiency and precision. This paper compares manual and automatic segmentation on MRI spleen scans. Manual methods included thresholding, painting, and tracing techniques, while automatic segmentation was performed using the MONAI Label framework integrated with U-Net. Evaluation with the Dice coefficient showed high overlap between methods, with values above 0.9 in most cases. Results confirm that deep learning - based segmentation provides faster and reliable outcomes, supporting its application in clinical practice.*

**Keywords:** medical image segmentation, neural networks, 3D Slicer, MONAI Label, U-Net, deep learning.

## INTRODUCTION

Medical image segmentation is a fundamental step in modern diagnostic and therapeutic procedures, as it enables the isolation of relevant anatomical structures and pathological regions. Conventional approaches, including thresholding and manual contour tracing, require significant human involvement and expertise, which makes them both time-consuming and prone to inter-operator variability [1].

Recent advances in machine learning and deep learning have enabled automated methods that can improve accuracy and reproducibility. Among these, convolutional neural networks (CNNs), and in particular the U-Net architecture, have achieved state-of-the-art performance in biomedical image segmentation. [3,6]. In this context, the MONAI Label framework, designed for clinical and research applications, offers a practical solution for interactive and automated annotation directly within platforms such as 3D Slicer [2].

The main objective of this paper is to compare manual segmentation of medical scans with automated methods based on neural networks, in order to evaluate their performance and applicability in medical practice. The dataset used in this study consisted of seven anonymized abdominal MRI scans obtained from the Embodi3D public repository, which provides de-identified medical imaging data for research and educational purposes. Voxel spacing varied between cases but was resampled to an isotropic resolution prior to segmentation. All data were preprocessed in 3D Slicer to ensure consistent orientation and image quality before further analysis.

## EXPOSITION

### OVERVIEW

This section describes the experimental workflow implemented to compare manual and automated segmentation of abdominal MRI (spleen) volumes [1,8,9]. The aim was to produce precise, volumetric ground-truth


*ISSN 2603-378X*


*doi: www.doi.org/10.70456/..........................*

masks by applying standard manual and semi-automatic tools in 3D Slicer, and then to evaluate the performance of an automated pipeline based on MONAI Label with a U-Net segmentation model[2,3,5]. Quantitative comparison was performed using the Dice similarity coefficient, supported by visual inspection of 2D overlays and 3D renderings.

## EXPERIMENTAL WORKFLOW (SUMMARY)

The experiment followed three main stages: (1) preparation and visual inspection of source volumes; (2) generation of reference masks via manual and semi-automatic segmentation tools in 3D Slicer [1,8,9]; (3) automated inference with MONAI Label and quantitative/qualitative evaluation of the resulting masks against the manual references using Dice. All masks and original volumes were archived to enable re-use for additional training or retrospective analysis.

## MANUAL SEGMENTATION - GENERAL PROCEDURE

Manual segmentation aimed to create high-quality reference masks while keeping the process practical for a clinical/research setting. For each volume the general approach was:

- perform an initial visual assessment of the volume (choose imaging plane(s) and representative slices for inspection),
- generate a coarse mask using intensity-based methods (thresholding) or contouring tools to limit the working region,
- refine boundaries on representative slices using painting and contour tools (e.g., level tracing), and
- interpolate across slices with the "Fill Between Slices" functionality to build a continuous 3D segment.

Where appropriate, semi-automatic algorithms (for example, region-growing / Fast Marching) were used to accelerate segmentation by expanding from user-placed seed points; however, these outputs were always reviewed and corrected manually when needed [9]. Intentionally, no global smoothing or aggressive post-interpolation smoothing was applied so that the resulting volumes retained the original image texture and anatomical detail - a decision that facilitates direct, voxel-wise comparison with automated masks. Finalized masks were saved alongside the original volumes in standard volumetric formats to preserve provenance.

## AUTOMATED SEGMENTATION WITH MONAI LABEL - GENERAL WORKFLOW

Automated processing employed MONAI Label as a server-based inference and annotation framework integrated with 3D Slicer as the client. In practice this workflow consisted of starting a MONAI Label service (server) hosting a pre-trained U-Net model for spleen segmentation, connecting 3D Slicer to that service via the MONAI Label extension, and submitting anonymized volumetric data for inference. The service responded with segmentation masks that were imported automatically into the Slicer Segment Editor for visualization.
Crucially, the interaction model used in the study combined fully automated inference with optional interactive correction: the user could accept the returned mask as-is, perform minor manual edits (Paint / Erase) inside Slicer, and then submit corrected labels back to the server to enrich the dataset for subsequent training cycles (active-learning loop). [10] All produced segmentation masks were stored as separate files, leaving the original volumes unmodified. This architecture enabled rapid mask generation while preserving the possibility of iterative improvement.

## MODEL ARCHITECTURE (U-NET)

The automated pipeline relied on a U-Net family architecture, chosen for its proven balance between contextual feature


*ISSN 2603-378X*

*doi: www.doi.org/10.70456/.........................*

extraction and spatial localization [2]. The U-Net encoder-decoder design with skip connections preserves fine spatial information while aggregating high-level context, which is particularly beneficial for organ segmentation where boundaries can be subtle. [7]. For volumetric data, a 3D variant of U-Net (using 3D convolutions and up/down-sampling) allows the model to exploit inter-slice continuity directly, improving consistency in the axial direction and reducing slice-wise artifacts. MONAI provides ready configurations and pre-trained variants of these networks, facilitating deployment within the Label framework. The MONAI Label framework employed a pre-trained 3D U-Net model optimized for spleen segmentation. The model was trained by the MONAI development team using standard configurations (Dice loss, Adam optimizer) as described in the MONAI documentation, and was used here only for inference.

## EVALUATION METHODOLOGY AND ANALYSIS

Segmentation agreement was quantified using the Dice similarity coefficient (DSC), defined as

$$DICE(A,B) = \frac{2|A \cap B|}{|A| + |B|}$$

Where A and B are voxel sets from manual and automated masks respectively. In addition to a global Dice score per volume, visual overlays of manual (ground truth) and predicted masks were inspected on representative slices and in 3D to identify common failure modes (e.g., under-segmentation at low-contrast boundaries, small false positives). A reproducible evaluation script based on SimpleITK / NumPy was used to compute metrics across the dataset. Although Dice score is used as main metric, Hausdorff Distance and Jacard score were used for back proofing of results. The observed Dice scores ranged across the cases in the study; most volumes showed high overlap (Dice $\gtrsim 0.9$), indicating strong agreement between MONAI Label's U-Net predictions and manual segmentation [7]. A minority of cases exhibited substantially lower Dice values, which were associated with reduced soft-tissue contrast, atypical organ morphology, or imaging artifacts; these cases highlight where model generalization is limited and where targeted additional annotation or model fine-tuning is beneficial. Incorporating active learning, where corrected segmentations are used to iteratively retrain the model, could enhance its adaptability to diverse anatomical variations

## POST-PROCESSING, QUALITY CONTROL AND REPRODUCIBILITY NOTES

To improve final mask quality for downstream use, standard post-processing steps are recommended: connected-component analysis to remove small spurious clusters, morphological operations to close small holes or remove speckle, and volume-based filtering to enforce physiologically plausible size ranges. Parameter choices (e.g., threshold values or Fast Marching limits) materially affect outcomes and should be documented; datasets and masks must be stored with clear filenames and versioning to guarantee reproducibility. When integrating into clinical pipelines, MONAI Label's support for DICOM-based protocols and PACS integration can be leveraged, but privacy-preserving data handling (anonymization and minimal metadata transfer) must be enforced.

## DISCUSSION — PRACTICAL IMPLICATIONS AND LIMITATIONS

The combined manual/automatic workflow demonstrated that modern deep-learning tools can substantially reduce annotation time while producing clinically acceptable segmentations for many routine cases. Nevertheless, automated methods are not uniformly robust: cases with low contrast, unusual anatomy or imaging artifacts require human oversight and,



*doi: www.doi.org/10.70456/.........................*

ideally, targeted retraining via submitted corrected labels [10]. In practice, manual segmentation of each case required between 20 and 30 minutes depending on image quality and organ delineation complexity. In contrast, automated segmentation using MONAI Label produced results within 15–30 seconds per case. This substantial reduction in processing time demonstrates a clear practical advantage of the automated approach, particularly for large-scale or time-sensitive clinical applications.

For future work, expanding the training corpus, applying stronger data augmentation, and incorporating active-learning strategies are recommended steps to improve generalization and reduce failure cases.

To quantitatively evaluate the agreement between manual and automated segmentation, the Dice similarity coefficient was calculated for all cases. The results are summarized in Table 1, where higher values indicate a better overlap between reference (manual) and predicted (automatic) masks.

***Tab. 1.*** *Dice similarity coefficients between manual and automated spleen segmentation*

| **Case** | **Dice coefficient** | **Manual segmentation method** |
|---|---|---|
| Spleen1 | 0.9423 | Threshold + Paint + Fill Between Slices |
| Spleen2 | 0.9165 | Level Tracing |
| Spleen3 | 0.9216 | Level Tracing |
| Spleen4 | 0.8845 | Level Tracing |
| Spleen5 | 0.5213 | Fast Marching |
| Spleen6 | 0.9052 | Threshold + Paint + Fill Between Slices |
| Spleen7 | 0.9153 | Threshold + Paint + Fill Between Slices |

As shown in Table 1, the majority of cases achieved Dice coefficients above 0.9, which indicates a high degree of agreement between manual and automated segmentation. The only exception is case *spleen5*, where the Fast Marching method resulted in a less accurate ground-truth mask, leading to a significantly lower Dice score (0.52). This highlights how certain manual techniques and image characteristics may influence the comparability with automated results.

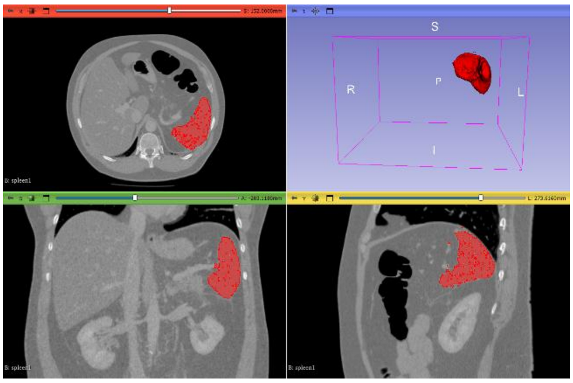

***Fig. 1.*** *3D model of the spleen obtained by manual segmentation in 3D Slicer.*

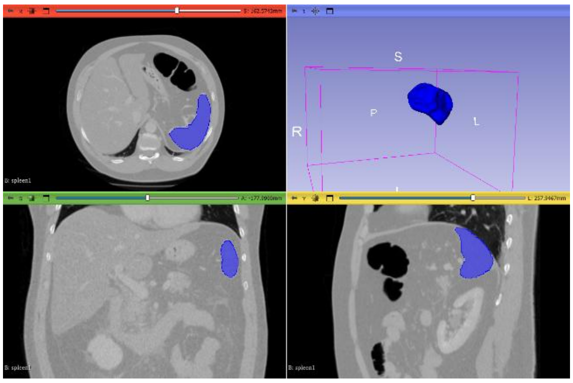

***Fig. 2.*** *3D model of the spleen obtained by automated segmentation using the MONAI Label framework*

In addition to the numerical results, visual representations of the obtained segmentations are provided for better illustration.

Figure 1 shows the 3D model of the spleen generated through manual segmentation in 3D Slicer. The contours were defined slice by slice using thresholding, painting, and tracing tools, and the final volumetric reconstruction was created by interpolating between the segmented slices. Figure 2 presents the spleen segmentation obtained by applying the automated MONAI Label workflow with a U-Net model. Unlike the manual process, this approach produced the 3D model in a fully automated manner, significantly reducing the time required for segmentation.

*"UNITECH – SELECTED PAPERS" vol. 2025*
*Published by Technical University of Gabrovo*
*ISSN 2603-378X*

*doi: www.doi.org/10.70456/.........................*

The visual comparison of the two figures highlights the high degree of similarity between the manually and automatically generated models, confirming the quantitative Dice scores reported in Table 1.

## CONCLUSION

This study demonstrated that neural networks, implemented through the MONAI Label framework, represent an effective and practical solution for medical image segmentation. Compared to traditional manual methods, automatic segmentation achieved comparable or superior results in significantly less time, thus reducing the burden on clinical experts.

The findings confirm the potential of deep learning models, particularly U-Net, in improving the efficiency and reproducibility of medical image analysis [2,7]. Future research should focus on testing larger datasets, evaluating performance across different imaging modalities, and integrating advanced models to further enhance clinical applicability [4]. Before clinical deployment, rigorous multi-center validation and data anonymization protocols are necessary to ensure robustness, reproducibility, and patient privacy. Integrating such systems into hospital PACS environments could further accelerate radiological workflows.

## REFERENCE


[1] A. Fedorov, R. Beichel, J. Kalpathy-Cramer, et al., “3D Slicer as an image computing platform for the Quantitative Imaging Network,” Magnetic Resonance Imaging, vol. 30, no. 9, pp. 1323–1341, 2012. DOI: 10.1016/j.mri.2012.05.001

[2] O. Ronneberger, P. Fischer, and T. Brox, “U-Net: Convolutional Networks for Biomedical Image Segmentation,” in Medical Image Computing and Computer-Assisted Intervention (MICCAI), 2015. DOI: 10.1007/978-3-319-24574-4_28

[3] A. Diaz-Pinto, O. Oktay, et al., “MONAI Label: A framework for AI-assisted interactive labeling of 3D medical images,” Medical Image Analysis, vol. 97, 102162, 2024.

[4] C. Cardoso, W. Li, H. Chen, et al., “MONAI: An open-source framework for deep learning in healthcare,” arXiv preprint arXiv:2211.02701, 2022.

[5] F. Isensee, P. Kickingereder, W. Wick, M. Bendszus, and K. H. Maier-Hein, “nnU-Net: Automated design of deep learning methods for biomedical image segmentation,” Nature Methods, vol. 18, pp. 203–211, 2021. DOI: 10.1038/s41592-020-01008-z

[6] J. Egger, T. Kapur, C. Nimsky, and R. Kikinis, “Pituitary adenoma volumetry with 3D Slicer,” arXiv preprint arXiv:1212.2860, 2012.

[7] A. Essamlali, V. Millot-Maysounabe, et al., “Bile duct segmentation methods under 3D Slicer applied to ERCP: advantages and disadvantages,” arXiv preprint arXiv:2312.03356, 2023.

[8] Y. Gao, X. Chen, Q. Yang, A. Lasso, I. Kolesov, S. Pieper, R. Kikinis, A. Tannenbaum, L. Zhu, et al., “An effective and open-source interactive 3D medical image segmentation solution,” Frontiers in Neuroinformatics, vol. 18, 2024.

[9] Sun, J., Chen, K., He, Z., et al. “Medical image analysis using improved SAM-Med2D: segmentation and classification perspectives.” *BMC Medical Imaging*, 2024, vol. 24, article no. 241. DOI: 10.1186/s12880-024-01401-6Y. You, Y. Niu, F. Sun, and W. Sheng, “Three-dimensional printing and 3D Slicer: powerful tools in understanding and treating neurosurgical diseases,” Frontiers in Neuroscience, vol. 14, 2020.







*doi: www.doi.org/10.70456/.........................*