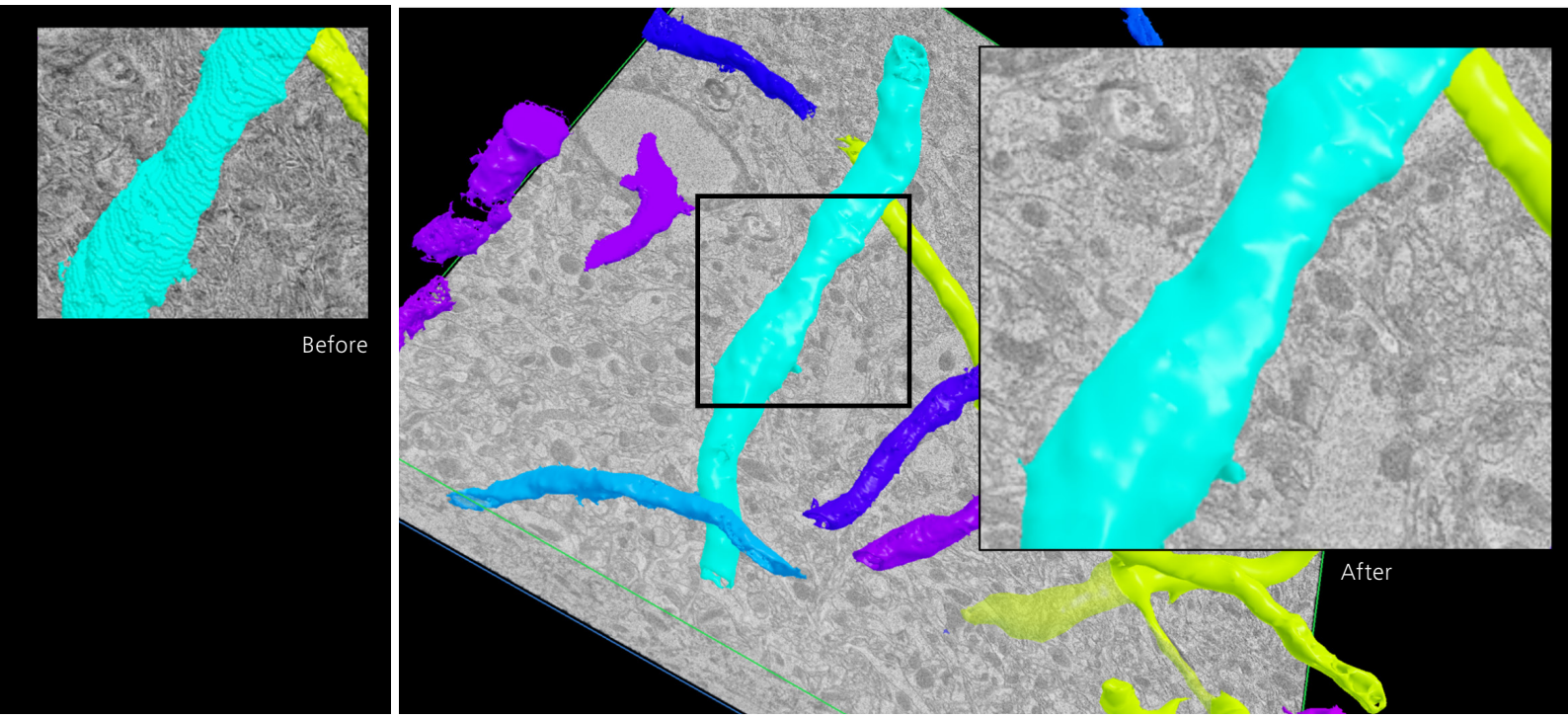
White Paper

Overcoming 3D Visualization Artifacts in Deep Learning-Based Bioimage Analysis



ZEISS

Seeing beyond

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Deep Learning Advances in Bioimage Segmentation and Analysis

The advent of deep learning has transformed how we analyze biological microscopy data, particularly for automated image segmentation. While these technological advances have made it possible to analyze vast datasets with unprecedented speed and accuracy, they have also introduced unique challenges in three-dimensional visualization and interpretation. This article explores one such challenge: the visualization artifacts that emerge when reconstructing 3D volumes from two-dimensional segmentation.

Recent years have witnessed remarkable progress in automated image analysis through deep learning. Pre-trained models such as Cellpose and Stardist have democratized access to sophisticated segmentation tools, allowing researchers to identify and analyze cellular structures without extensive computational expertise. The accessibility of cloud-based platforms such as ZEISS arivis Cloud has further expanded these capabilities, enabling researchers to annotate ground truth data and train custom models for their specific needs.

Despite these advances, practical constraints continue to shape how we approach three-dimensional analysis. While 3D segmentation algorithms and annotation tools exist, practical constraints remain. Notably, the computational resources required for training and running 3D models are still substantial. This resource intensity, combined with researchers' preference for local workstation processing in routine analysis, has led many to adopt a pragmatic approach: segmenting biological structures in 2D slices and subsequently combining these segmentations to reconstruct 3D volumes.

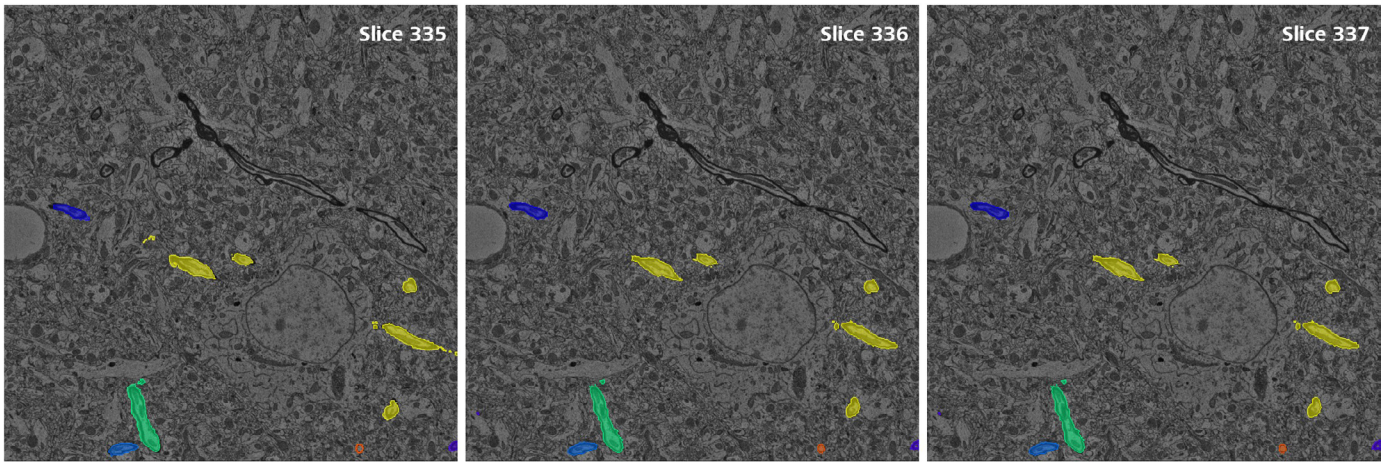

Figure 1: *Segmented neurons in consecutive 2D slices. Three sequential slices from an electron microscopy volume showing neuronal structures segmented and highlighted in different colors. The consistent coloring across slices helps track individual structures through the volume.*

Segmentation Artifacts: The Challenge of 3D Reconstruction

The challenge of this approach becomes apparent in the visualization stage, particularly when examining elongated objects such as neurons. Figure 1 shows three consecutive 2D slices from an electron microscopy volume dataset, where neuronal structures have been segmented and highlighted in different colors. These slices demonstrate how individual structures are identified and marked consistently across sequential planes in the volume.

The stacked reconstruction of these 2D segmentations creates what is known as the 'pancake effect,' as shown in Figure 2. This effect manifests as a series of discrete, disc-like structures rather than the smooth, continuous forms we expect in biological systems. The inset clearly demonstrates these discontinuous, pancake-like artifacts that result from stacking 2D segmentations. The discontinuous nature of these visualizations can impact our interpretation of cellular architecture and spatial relationships. For instance, when examining neuronal networks in electron microscopy data, the pancake effect can obscure the true connectivity and morphology of these dynamic cellular structures.

Advanced 3D Visualization: Solutions for Bio-Image Analysis

Modern visualization techniques can help bridge the gap between computational necessity and biological reality. Figure 3 demonstrates how ZEISS arivis Pro's advanced surface reconstruction approach can transform the same segmentation data into a more naturalistic representation. The inset in Figure 3 provides a direct comparison with Figure 2, showing how the discontinuous, pancake-like artifacts have been replaced with smooth, continuous surfaces. This enhancement isn't merely cosmetic; it helps researchers better interpret their data by presenting cellular structures in a form that more closely matches their biological nature. Through its powerful and state-of-the-art surface reconstruction capabilities, ZEISS arivis Pro efficiently handles large datasets with numerous objects while implementing new methods to remove artifacts that could impede interpretation, enabling researchers to better understand the three-dimensional organization of their biological samples.

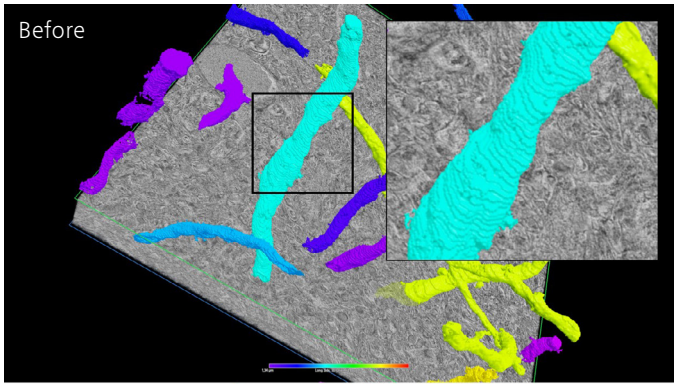

Figure 2: *Visualization artifacts in 3D reconstruction. Three-dimensional visualization of stacked 2D segmentations showing the 'pancake effect.' The inset highlights the discontinuous, disc-like appearance of neuronal structures that results from simple stacking of 2D segmentations.*

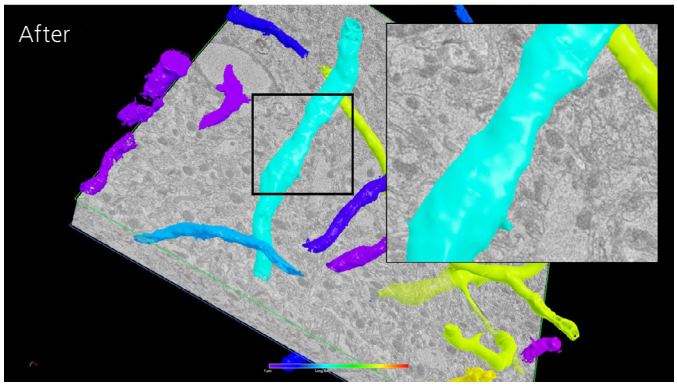

Figure 3: *Enhanced 3D visualization in ZEISS arivis Pro. The same segmented neuronal structures shown with advanced surface reconstruction approach. The inset shows the same region as Figure 2, demonstrating how the discontinuous artifacts have been replaced with smooth, biologically realistic surfaces.*

Conclusion

The challenge of visualizing 3D biological structures reconstructed from 2D segmentations reflects an ongoing balance between technological capabilities and practical constraints in scientific research. While computational limitations often necessitate a slice-by-slice approach to segmentation, advanced visualization solutions like ZEISS arivis Pro enable researchers to overcome the resulting artifacts. By transforming discontinuous stack reconstructions into smooth, naturalistic 3D visualizations, these tools help ensure that researchers can accurately interpret and understand the complex spatial relationships within their biological samples. This convergence of practical workflows with sophisticated visualization capabilities represents an important step forward in biological imaging analysis, making complex structural data more accessible and interpretable for the research community.

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