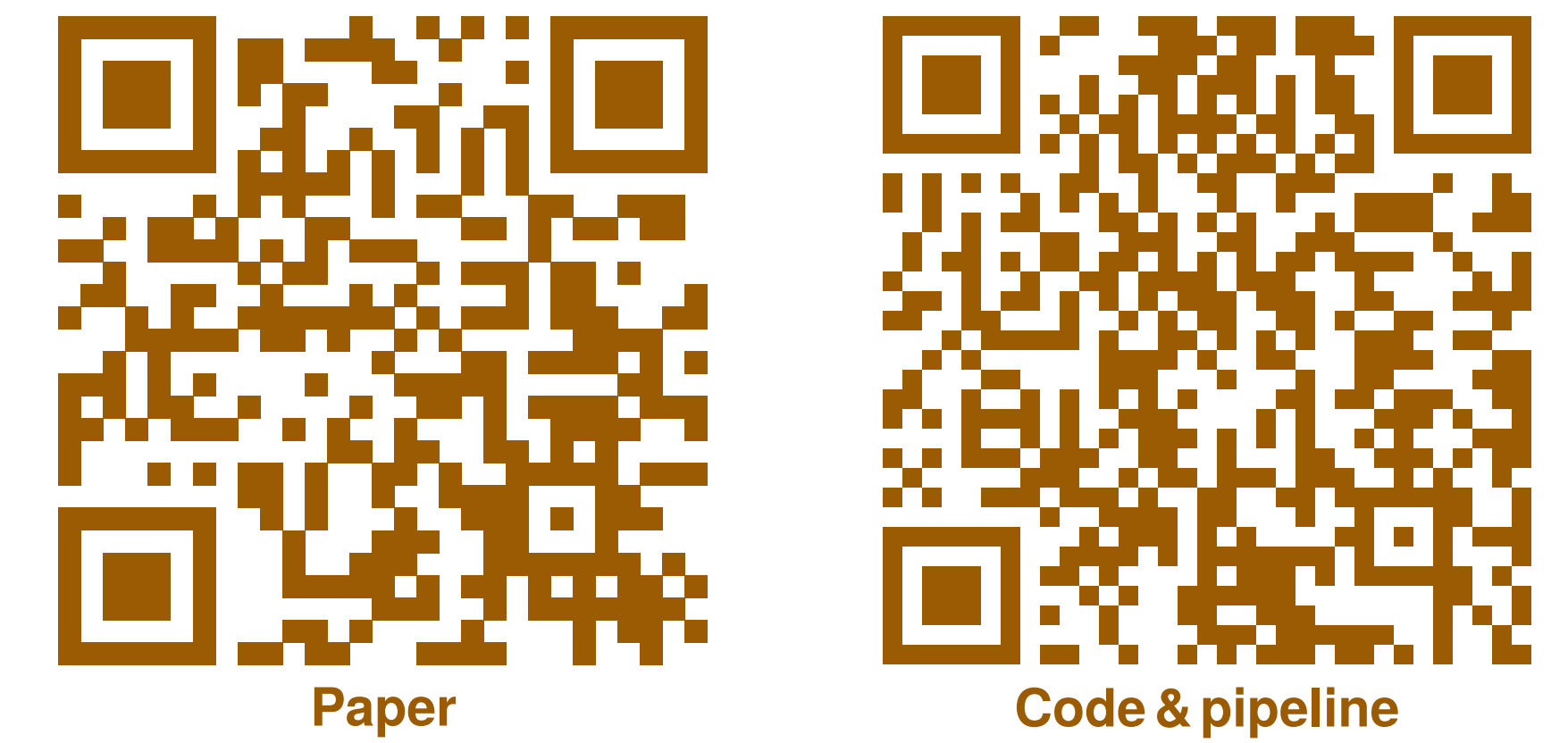


# A Pipeline for Chamber-Resolved Analysis of Pore Traits in Foraminiferal $\mu$ CT Volumes

Hanqing Wu<sup>1</sup>, Constance Choquel<sup>2,4</sup>, Sha Ni<sup>3</sup>, Helena L. Filipsson<sup>4</sup>, Behnaz Pirzamanbin<sup>1</sup>

<sup>1</sup>Department of Statistics, Lund University   <sup>2</sup>the Laboratory of Planetology and Geosciences, University of Angers   <sup>3</sup>Department of Geoscience, Aarhus University

<sup>4</sup>Department of Earth and Environmental Sciences, Lund University



## Background & Motivation

- Foraminiferal pore traits, such as pore number, pore size, pore density, porosity, and shell thickness, are promising proxies for paleoceanographic reconstructions<sup>[1, 2, 3]</sup>.
- Foraminiferal shells exhibit complex 3D morphologies, which are blurred by conventional analysis based on 2D slices and whole-shell averages<sup>[4]</sup>.
- Deep learning has been widely adopted and proven to be effective for micro-computed tomography ( $\mu$ CT) scans, particularly for 3D applications in medical settings<sup>[5]</sup>.
- No previous workflow assigns individual pores to individual chambers, so chamber-resolved variations have never been measured.

## Dataset

We analysed a dataset comprising Synchrotron Radiation X-ray  $\mu$ CT volumes of *Elphidium clavatum* specimens. The CT scans were acquired at the SPring-8 synchrotron facility (beamline BL47XU, Hyogo Prefecture, Japan).

### Quick facts about the dataset

|                   |                                               |
|-------------------|-----------------------------------------------|
| <b>122</b>        | $\mu$ CT volumes of <i>Elphidium clavatum</i> |
| <b>375–500 nm</b> | isotropic voxel size                          |
| <b>211</b>        | expert-annotated slices with 3 classes        |
| <b>0.61 %</b>     | of annotated pixels per slice are pores       |

## 1 Voxel classification

A multi-planar 2D U-Net model<sup>[6]</sup> with a pretrained MiT-B0 encoder<sup>[7]</sup> is trained for classification. The network takes normalised grayscale slices as input. The training uses a **class-wise Tversky loss**<sup>[8]</sup> to address the extreme class imbalance:

$$Tl_c = \frac{TP_c}{TP_c + \alpha_c FP_c + \beta_c FN_c},$$

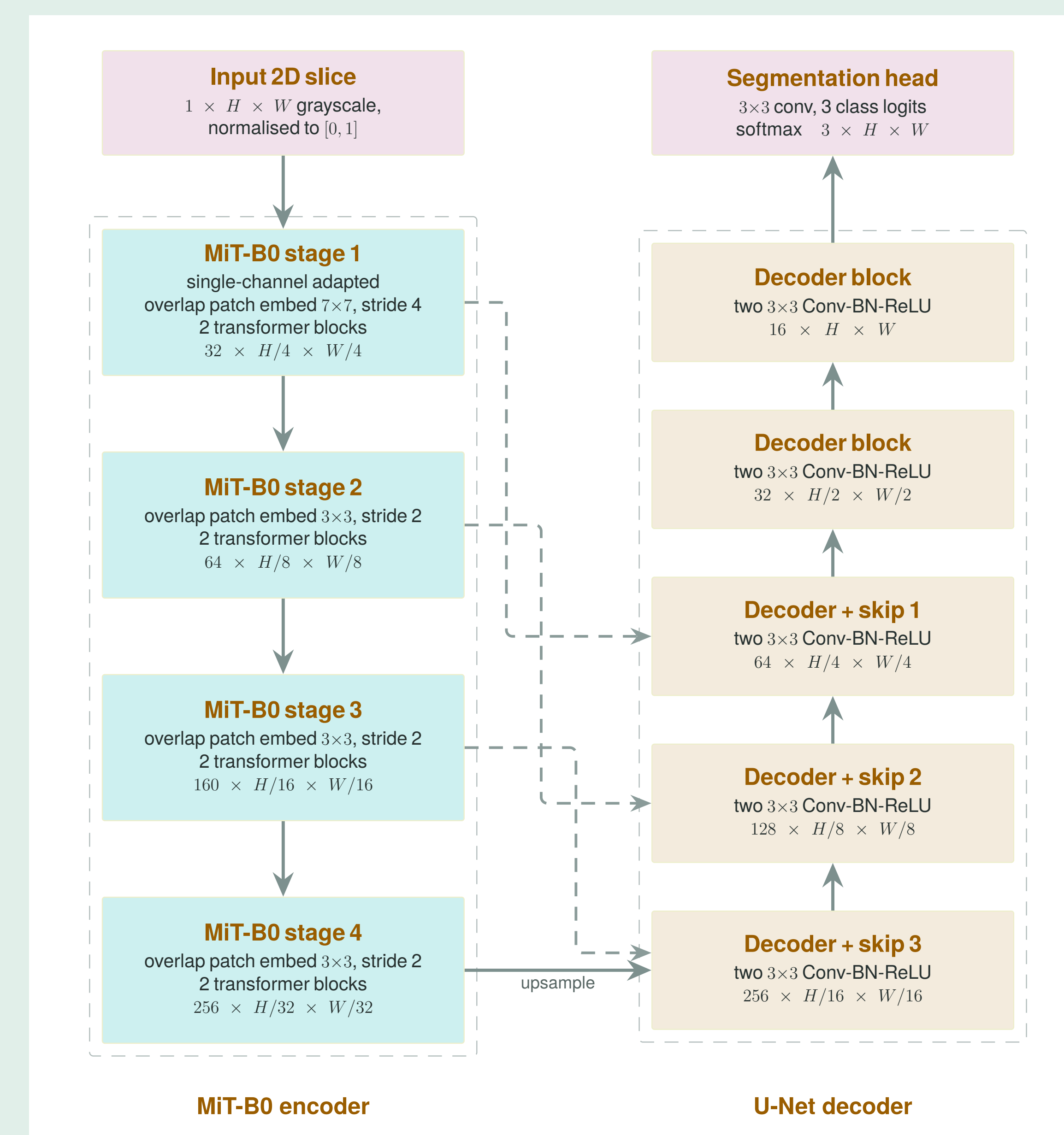
$$\mathcal{L} = 1 - \frac{1}{|C|} \sum_{c \in C} Tl_c$$

where  $TP_c$ ,  $FP_c$  and  $FN_c$  are soft counts over voxels. For pores we set  $\alpha_c = 0.3$ ,  $\beta_c = 0.7$  to penalise false negatives more.

## References

- [1] A. E. Rathburn et al. A New Biological Proxy for Deep-Sea Paleo-Oxygen: Pores of Epifaunal Benthic Foraminifera. *Scientific Reports* 8.1 (2018), p. 9456.  
 [2] C. Choquel et al. 3D Morphological Variability in Foraminifera Unravel Environmental Changes in the Baltic Sea Entrance over the Last 200 Years. *Frontiers in Earth Science* 11 (2023), p. 1120170.  
 [3] B. A. A. Hoogakker et al. Reviews and Syntheses: Review of Proxies for Low-Oxygen Paleoceanographic Reconstructions. *Biogeosciences (Online)* 22.4 (2025), pp. 863–957.  
 [4] S. Ni et al. Morphological Insights From Benthic Foraminifera for Environmental Conditions in the Baltic Sea During the Last Interglacial. *Paleoceanography and Paleoclimatology* 40.3 (2025), e2024PA005063.

### Multi-planar 2D U-Net with an MiT-B0 encoder



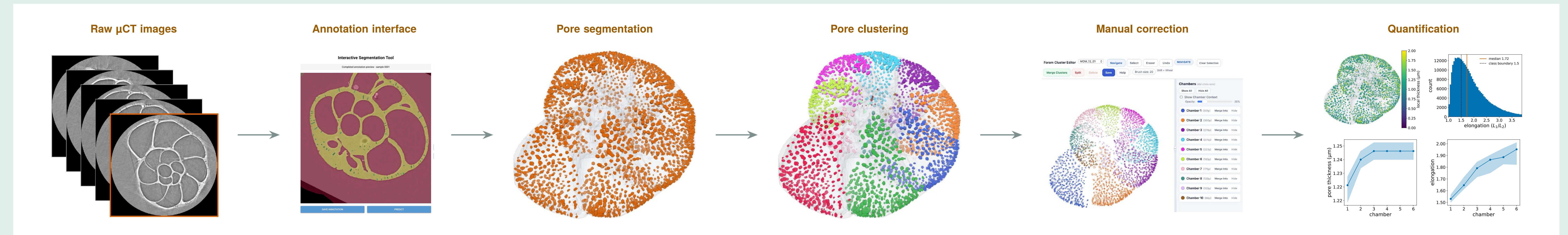
### A multi-view test-time augmentation scheme<sup>[9]</sup>

At test time every volume is segmented in 12 ways: 3 orthogonal planes  $\times$  4 in-plane rotations. The final prediction is the class with the largest summed softmax probability.

### Held-out accuracy

|              |              |              |              |
|--------------|--------------|--------------|--------------|
| <b>0.835</b> | <b>0.750</b> | <b>0.811</b> | <b>0.856</b> |
| Dice         | IoU          | precision    | recall       |

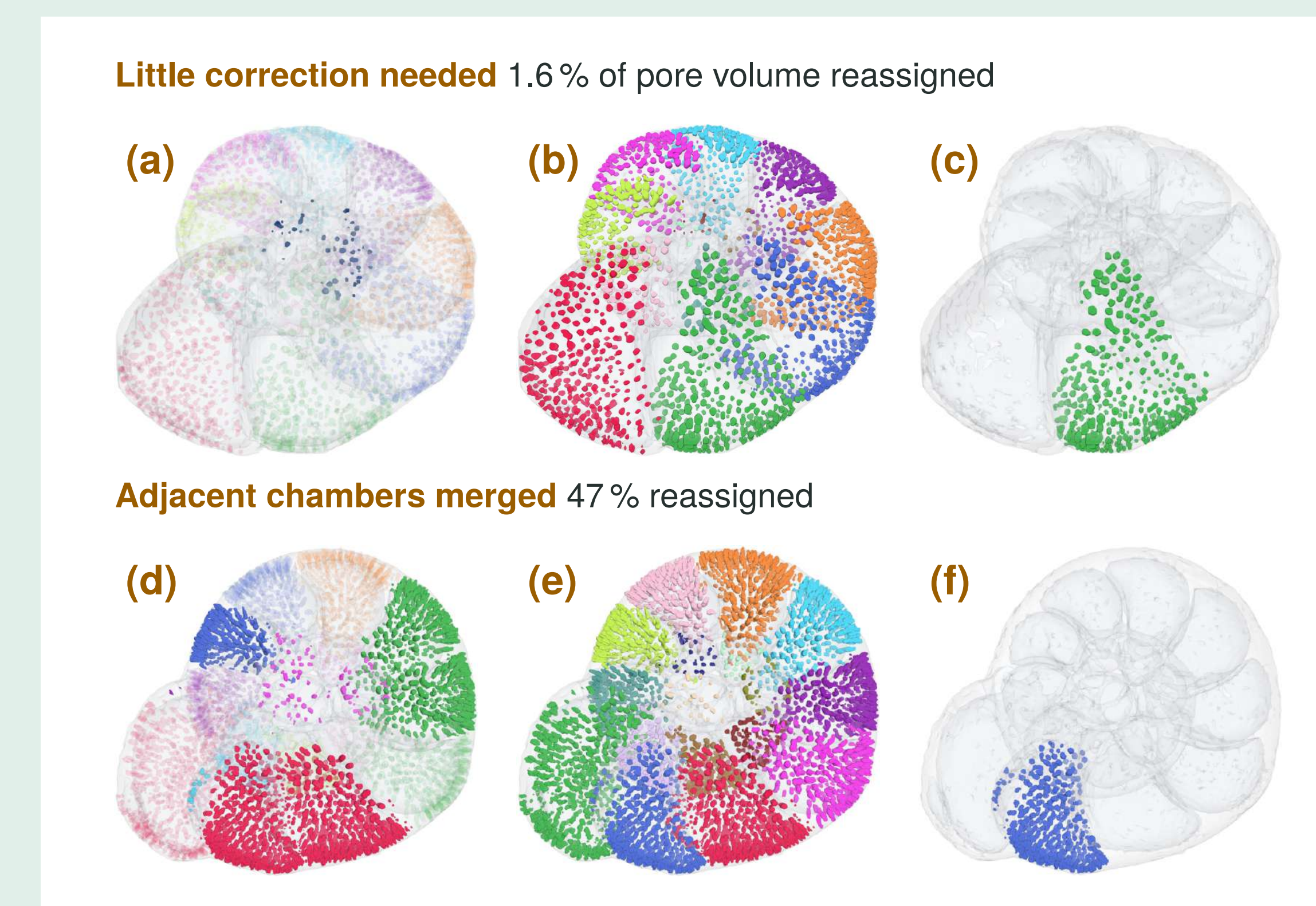
## The chamber-resolved pipeline for foraminiferal pore-trait analysis



## 2 Chamber assignment of pores

Each pore is reduced to its 3D centroid, embedded in 2D with t-SNE<sup>[10]</sup> to extract simpler group patterns. The embedded centroids are then clustered by HDBSCAN<sup>[11]</sup>. Small pores originally screened out by an Otsu threshold, which facilitates clustering, are recovered with inverse-distance  $k$ -NN ( $k = 3$ ). Practitioners can use a browser-based editor to merge, split and reassign clusters.

### (a, d) automated • (b, e) corrected (c, f) penultimate chamber isolated



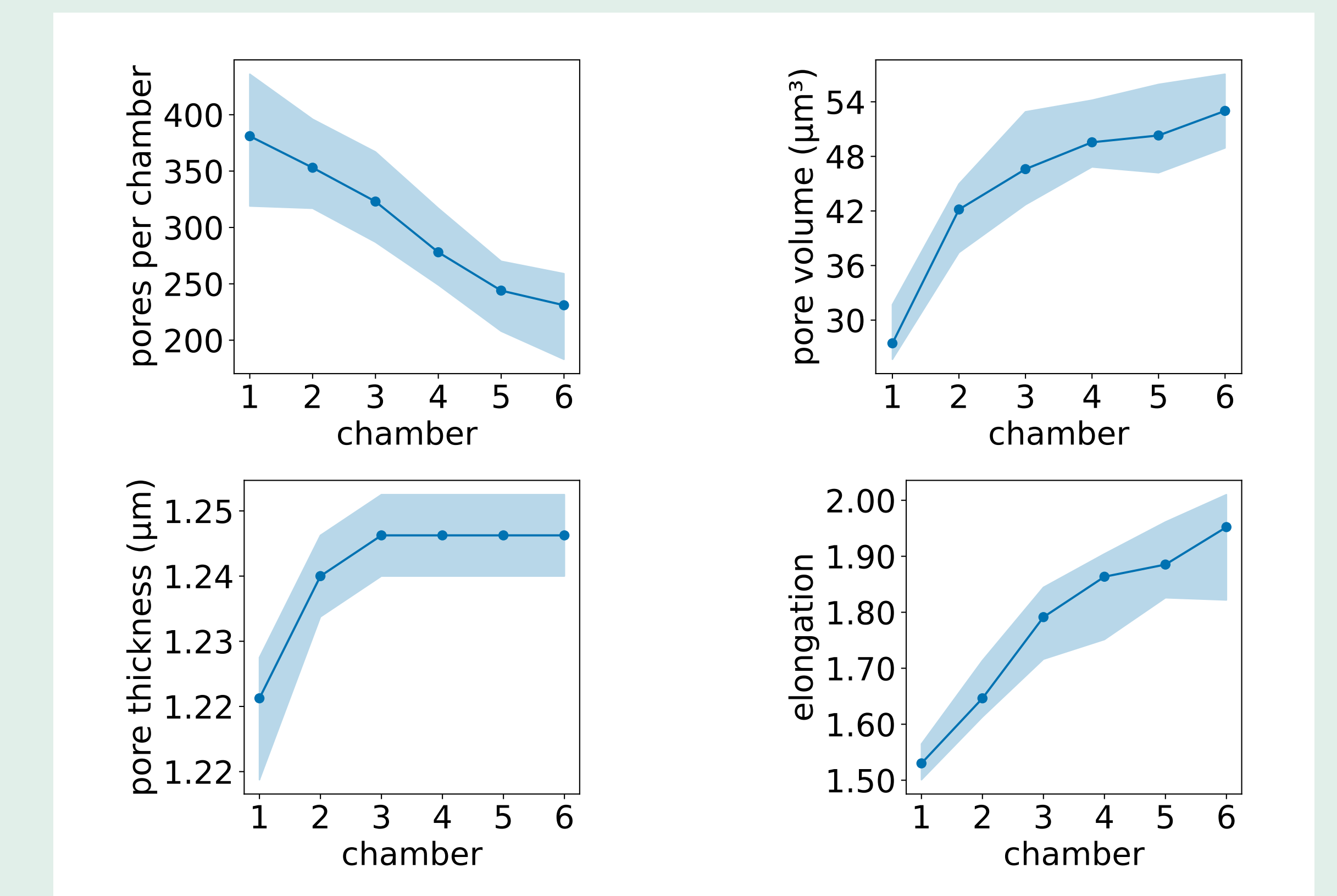
### Correction in numbers

|                |                                       |
|----------------|---------------------------------------|
| <b>319,807</b> | pores measured across 107 specimens   |
| <b>+3.0</b>    | more chambers recovered per specimen  |
| <b>90/107</b>  | specimens gained at least one chamber |

## 3 Insights from quantification

When resolved by chamber, a consistent gradient emerged across the final whorl: the last-formed, outermost chamber contained many small pores, whereas progressively older chambers contained fewer but larger pores. Pore thickness and elongation also increased toward older chambers.

### Lines are medians, bands bootstrap 95 % CI



## Conclusions

**Our semi-automated pipeline obtains chamber-resolved assignment of foraminiferal pores. Applied to *Elphidium clavatum*, it captures chamber-resolved measurements that conventional 2D analyses and whole-shell summaries cannot provide. This opens the way to more reliable paleoenvironmental reconstruction.**

Contact hanqing.wu@stat.lu.se

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- [5] W. M. Laprade et al. "Deep Learning for Resolving 3D Microstructural Changes in the Fibrotic Liver". In: *Applications of Medical Artificial Intelligence*. Ed. by S. Wu, B. Shabestari, and L. Xing. Vol. 15384. Cham: Springer Nature Switzerland, 2025, pp. 74–84.  
 [6] 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*. Vol. 9351. Lecture Notes in Computer Science. Springer, 2015, pp. 234–241.  
 [7] E. Xie et al. SegFormer: Simple and Efficient Design for Semantic Segmentation with Transformers. In: *Advances in Neural Information Processing Systems*. Vol. 34. Curran Associates, Inc., 2021, pp. 12077–12090.  
 [8] S. S. M. Salehi, D. Erdogmus, and A. Gholipour. Tversky Loss Function for Image Segmentation Using 3D Fully Convolutional Deep Networks. In: *Machine Learning in Medical Imaging*. Cham: Springer International Publishing, 2017, pp. 379–387.  
 [9] K. Matsunaga et al. *Image Classification of Melanoma, Nevus and Seborrheic Keratosis by Deep Neural Network Ensemble*. 2017.  
 [10] L. van der Maaten and G. Hinton. Visualizing Data using t-SNE. *Journal of Machine Learning Research* 9.86 (2008), pp. 2579–2605.  
 [11] R. J. G. B. Campello, D. Moulavi, and J. Sander. Density-Based Clustering Based on Hierarchical Density Estimates. In: *Advances in Knowledge Discovery and Data Mining*. Ed. by J. Pei et al. Berlin, Heidelberg: Springer, 2013, pp. 160–172.