# Deep Learning-Based Multi-Organelle Segmentation in Human Liver Electron Microscopy Images

**Atheer Alwuthaynani[1], Cheng Xing[2], Gary D. Bader[2]**

[1] SUDS Summer Scholar, Data Science Institute, University of Toronto
[2] Bader Lab, Department of Molecular Genetics, University of Toronto

## Background

- Segmentation of cell organelles in electron microscopy (EM) images is essential for understanding cellular structure and function.
- Manual annotation is time-consuming and requires expert knowledge.
- Existing open source datasets mainly focus on animal liver tissue, limiting their use for human.
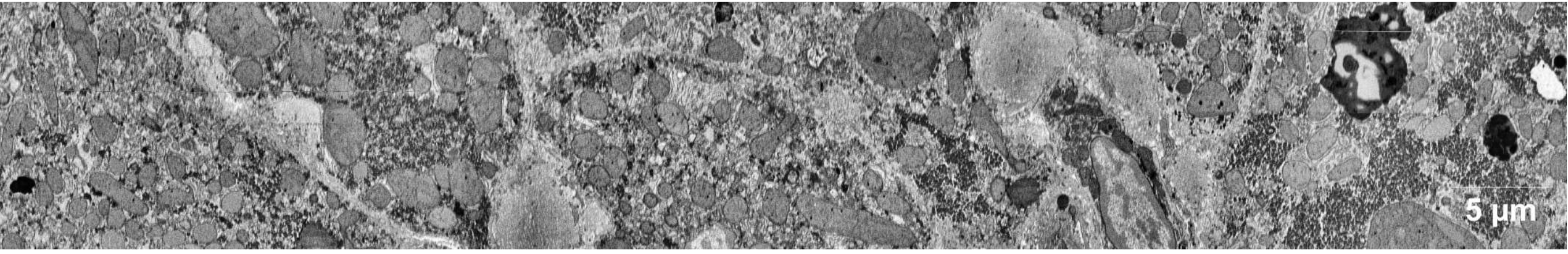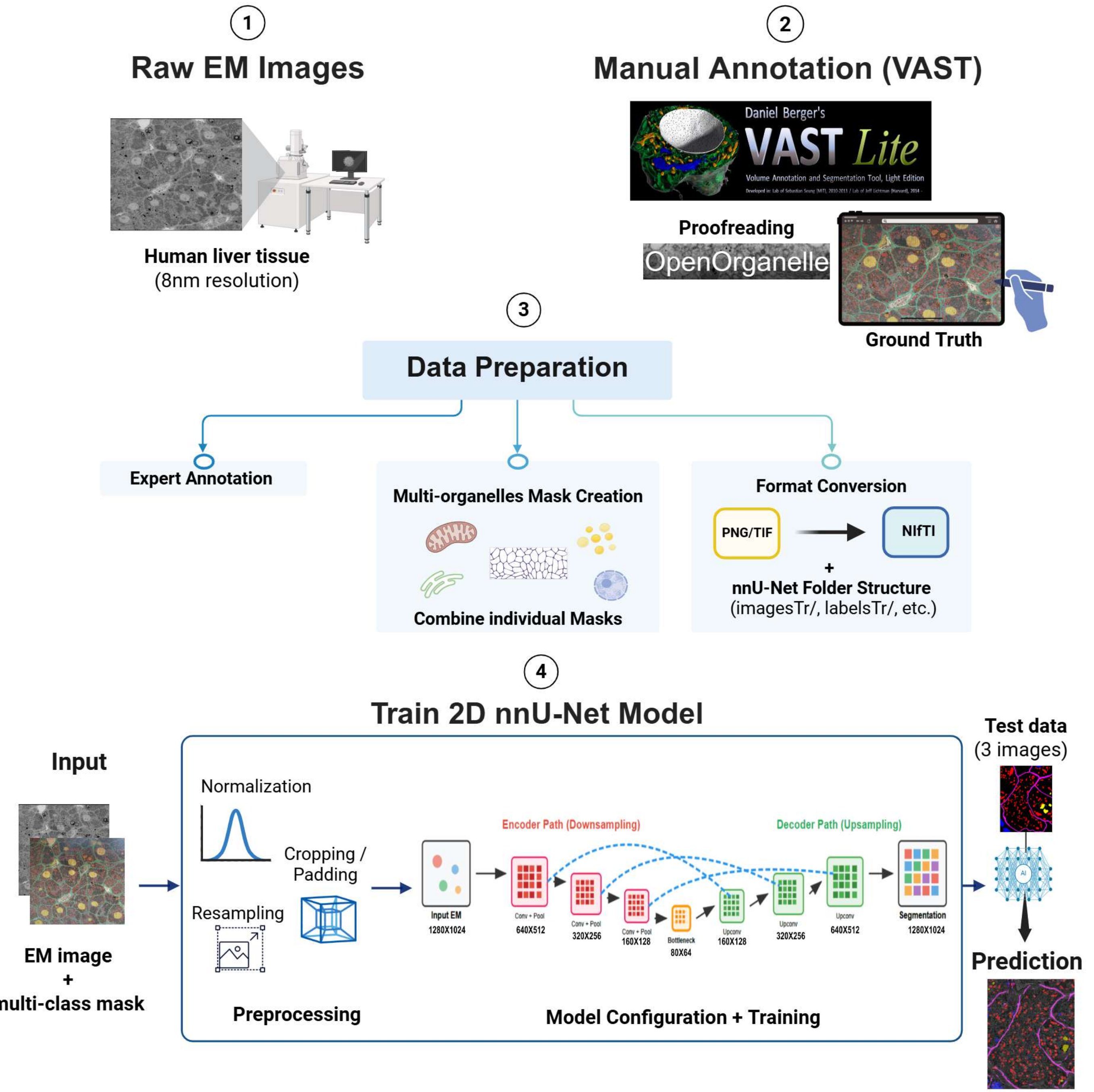


**Figure 1.** Raw electron microscopy (EM) image of human liver tissue showing complex cellular structures.

**This project** automates multi-class segmentation of five organelles in human liver EM images using a 2D nnU-Net model, with performance evaluated via Dice, IoU, and F1 score metrics.

## Methodology



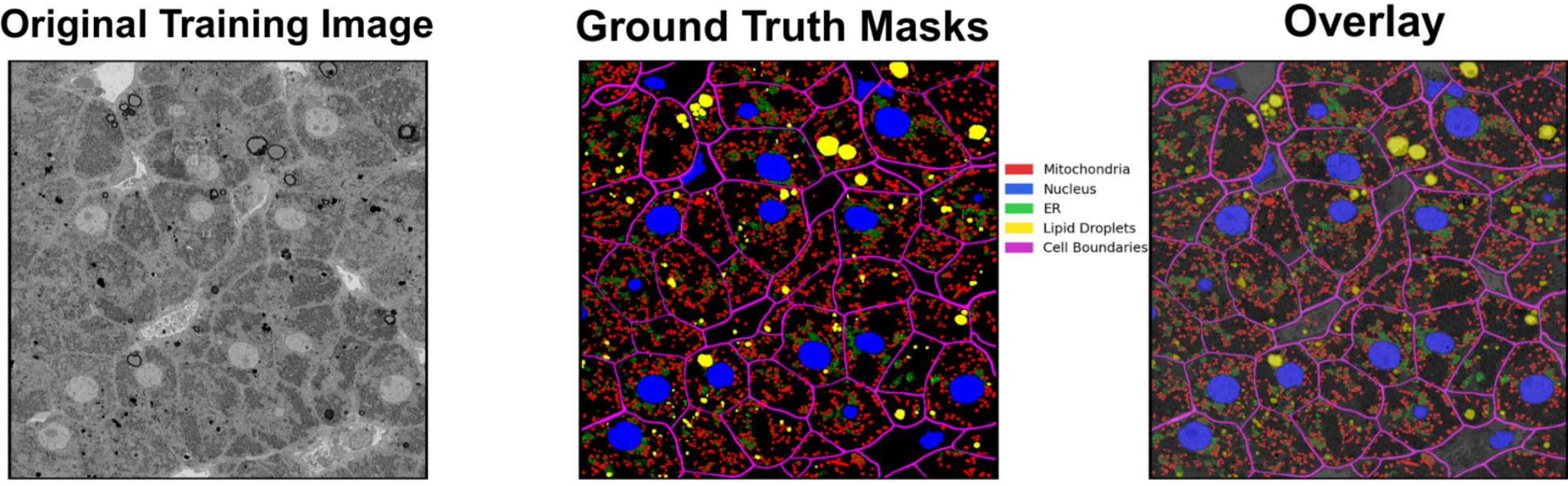① Raw EM Images — Human liver tissue (8nm resolution)

② Manual Annotation (VAST) — Proofreading OpenOrganelle — Ground Truth

③ Data Preparation — Expert Annotation — Multi-organelles Mask Creation — Combine individual Masks — Format Conversion PNG/TIF → NIfTI + nnU-Net Folder Structure (imagesTr/, labelsTr/, etc.)

④ Train 2D nnU-Net Model

Input: EM image + multi-class mask

Preprocessing: Normalization, Cropping / Padding, Resampling

Model Configuration + Training: Encoder Path (Downsampling), Decoder Path (Upsampling)

Test data (3 images) — Prediction

## Results



**Figure 2.** Single manually annotated EM image used for training with ground truth masks and overlay for all five organelle classes.

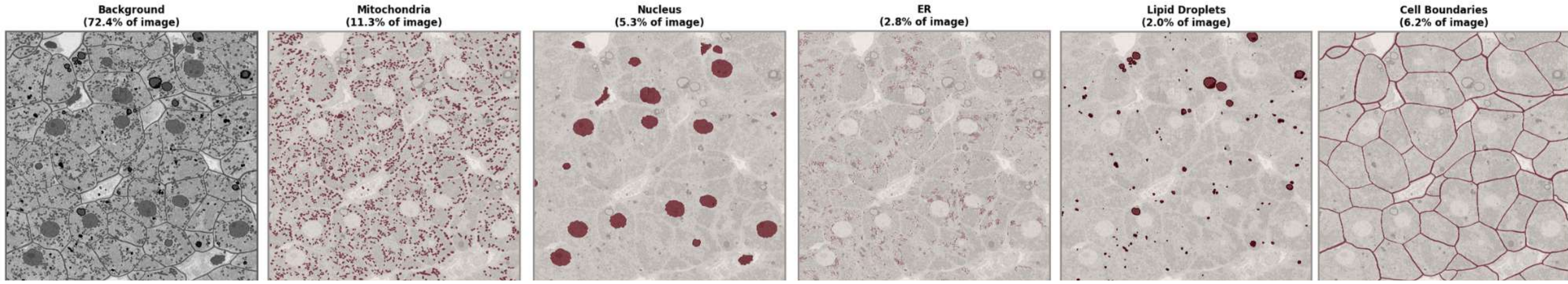Legend: Mitochondria, Nucleus, ER, Lipid Droplets, Cell Boundaries



**Figure 3.** Overlayed organelle masks with pixel-wise coverage.

Background (72.4% of image), Mitochondria (11.3% of image), Nucleus (5.3% of image), ER (2.8% of image), Lipid Droplets (2.0% of image), Cell Boundaries (6.2% of image)
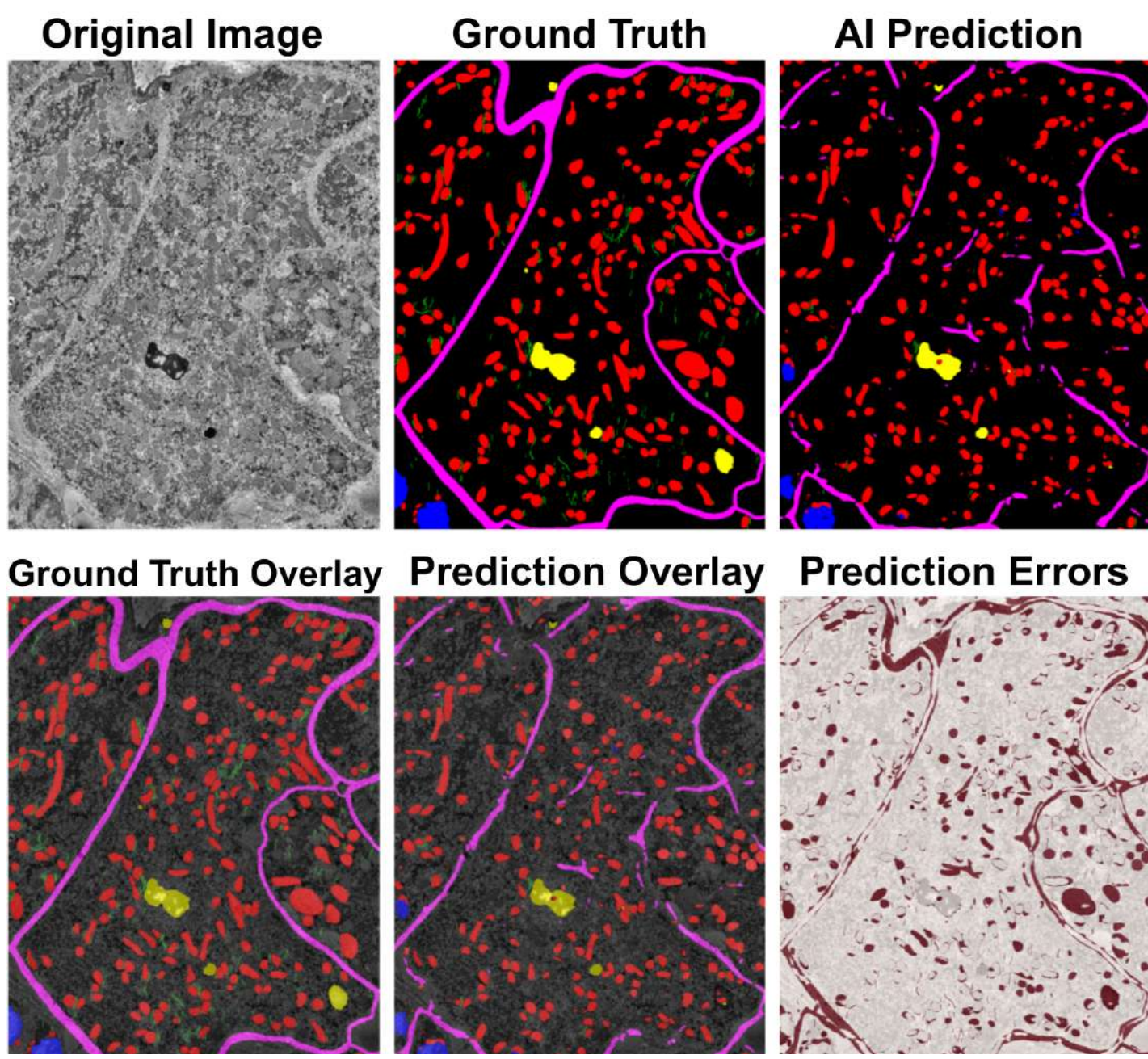


**Figure 4.** Test Set Results: Representative EM images, ground truth, predictions, and error overlays from a 3-image test set.
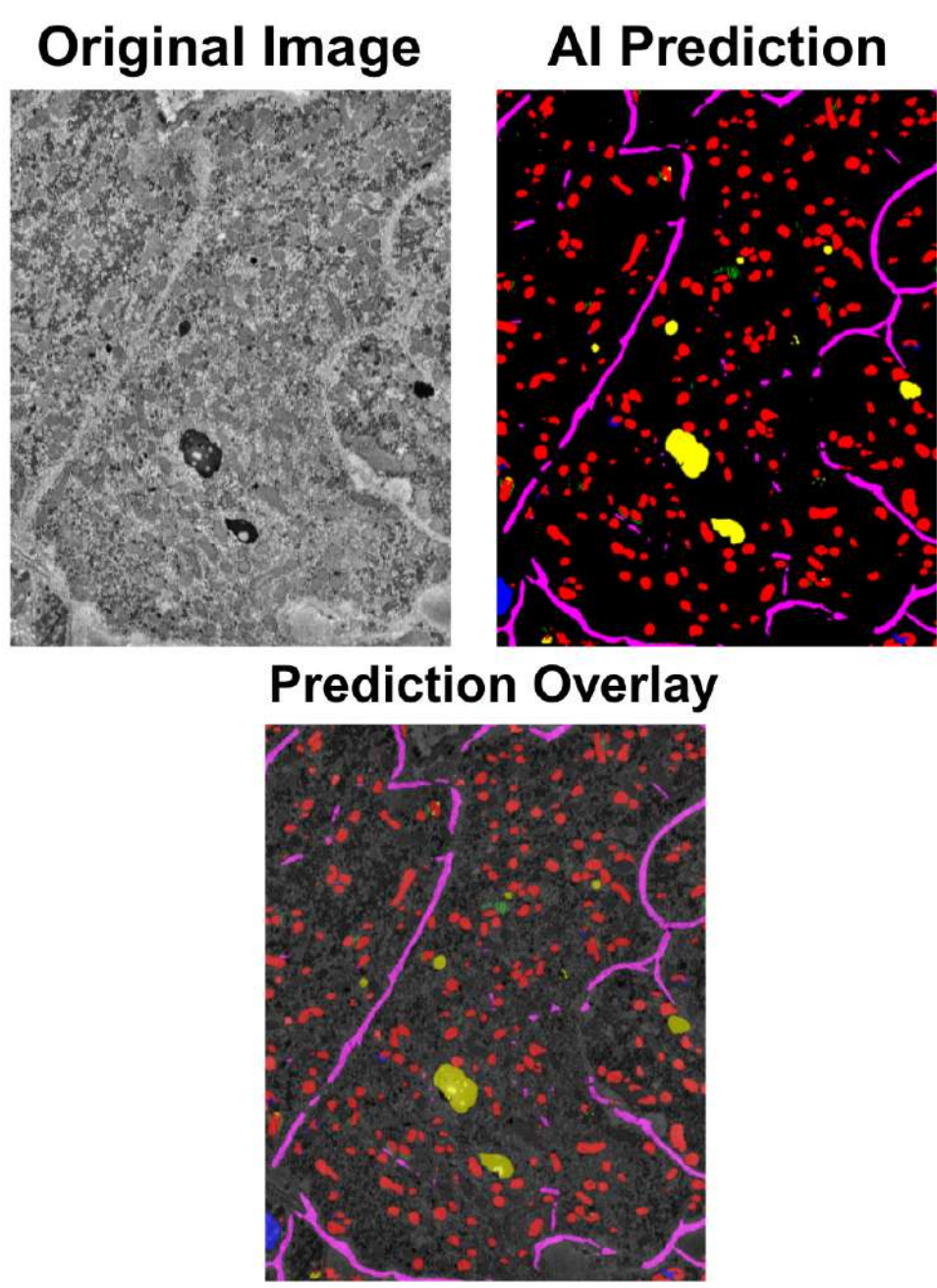


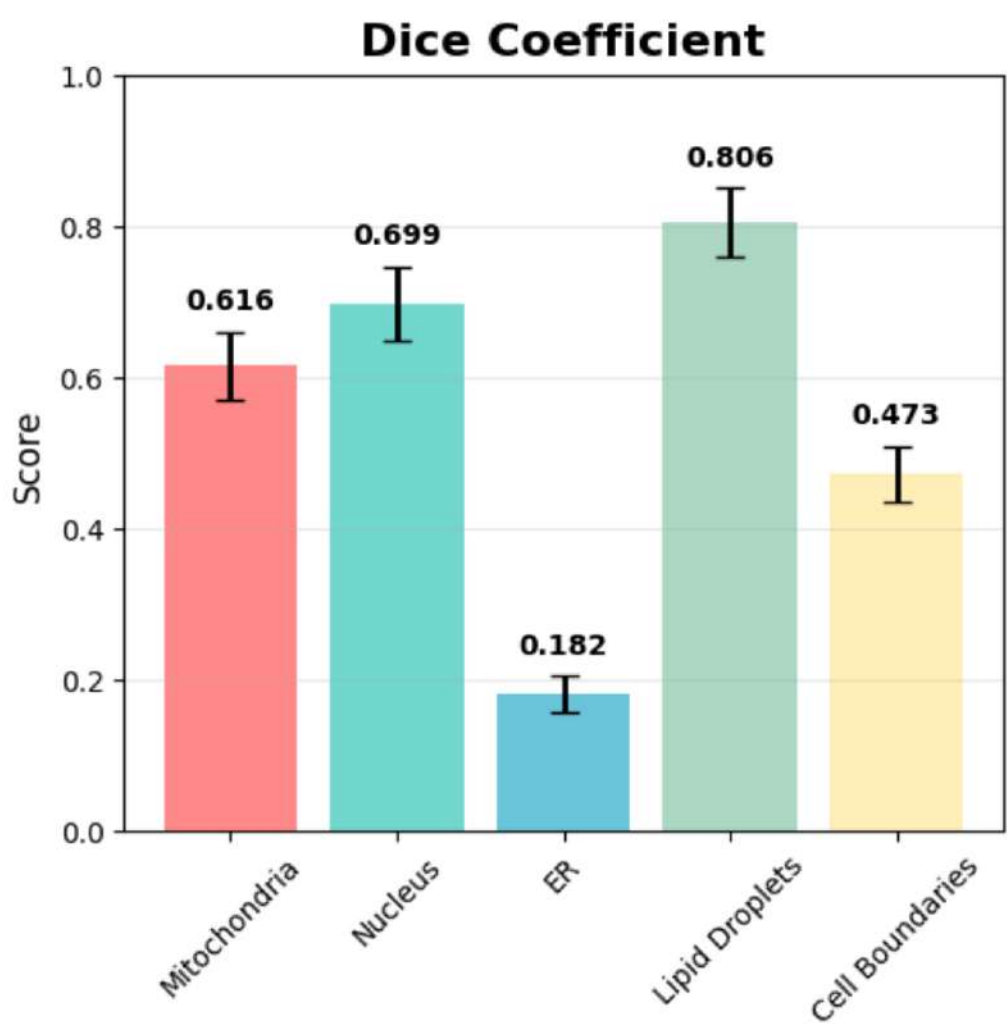**Figure 5.** Model prediction on unseen EM image.



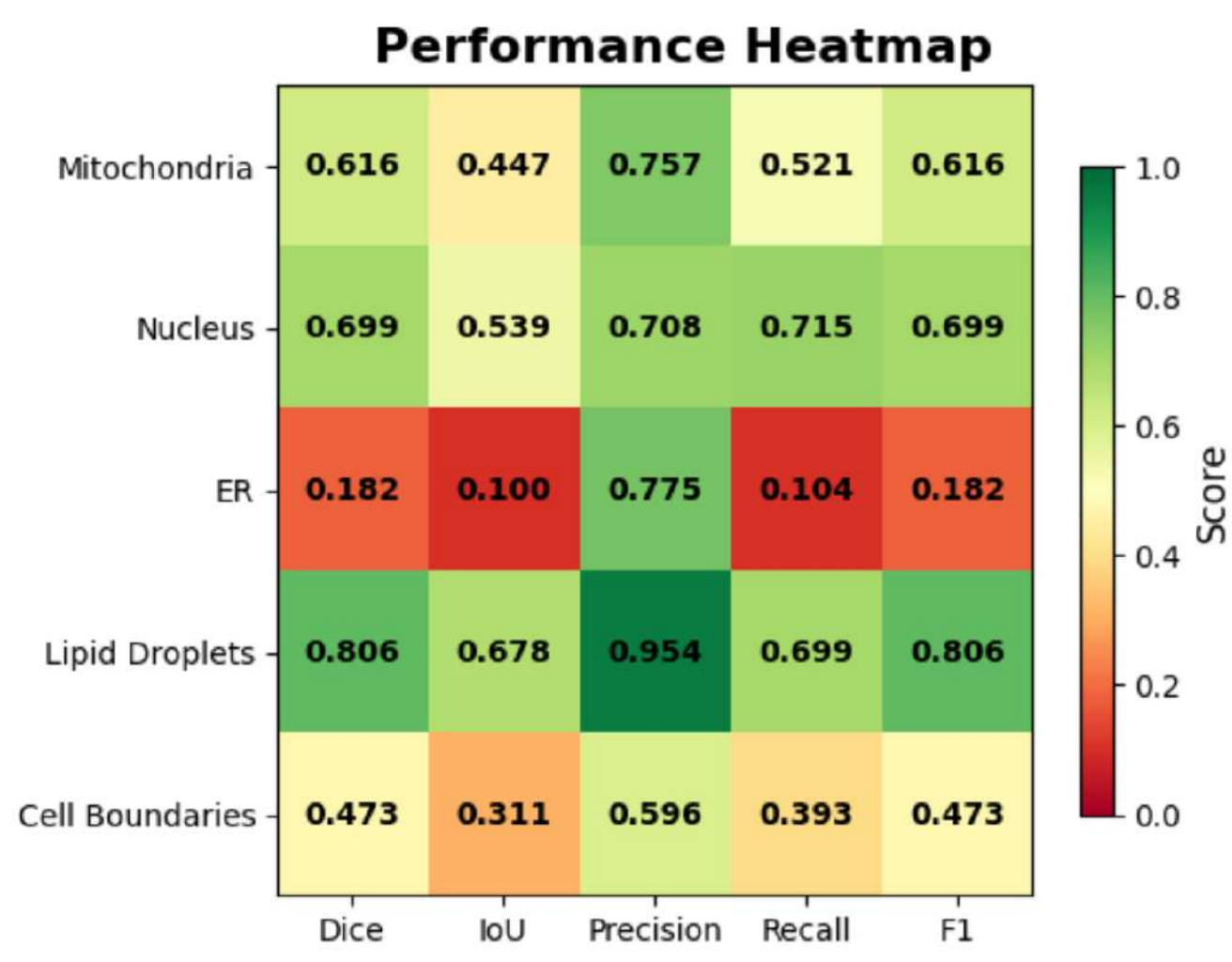**Figure 6.** Dice coefficient for organelle segmentation accuracy.



**Figure 7.** Performance heatmap of model metrics across organelles.

| | Dice | IoU | Precision | Recall | F1 |
|---|---|---|---|---|---|
| Mitochondria | 0.616 | 0.447 | 0.757 | 0.521 | 0.616 |
| Nucleus | 0.699 | 0.539 | 0.708 | 0.715 | 0.699 |
| ER | 0.182 | 0.100 | 0.775 | 0.104 | 0.182 |
| Lipid Droplets | 0.806 | 0.678 | 0.954 | 0.699 | 0.806 |
| Cell Boundaries | 0.473 | 0.311 | 0.596 | 0.393 | 0.473 |

## Discussion

**Segmentation performance varied by organelle:**

- Lipid droplets and nuclei showed the highest accuracy due to their distinct shapes and well-defined boundaries.
- The endoplasmic reticulum (ER) had low recall despite high precision, likely due to its complex, branched morphology and low contrast in EM images.
- Mitochondria and cell boundaries showed moderate results, affected by crowded cellular regions and unclear edges between organelles and surrounding structures.
- These observations suggest a potential influence of organelle morphology and annotation quality on segmentation accuracy.

**Future work** will include expanding annotated datasets and using human-in-the-loop methods to enhance segmentation, especially for difficult organelles like the ER.

## Conclusion

This work shows that high-quality manual annotations from a small dataset can effectively train deep learning models for EM organelle segmentation. The nnU-Net framework adapts well across organelle types, providing a promising approach for automated cellular analysis.

## Acknowledgements

References        Code & Notebooks