

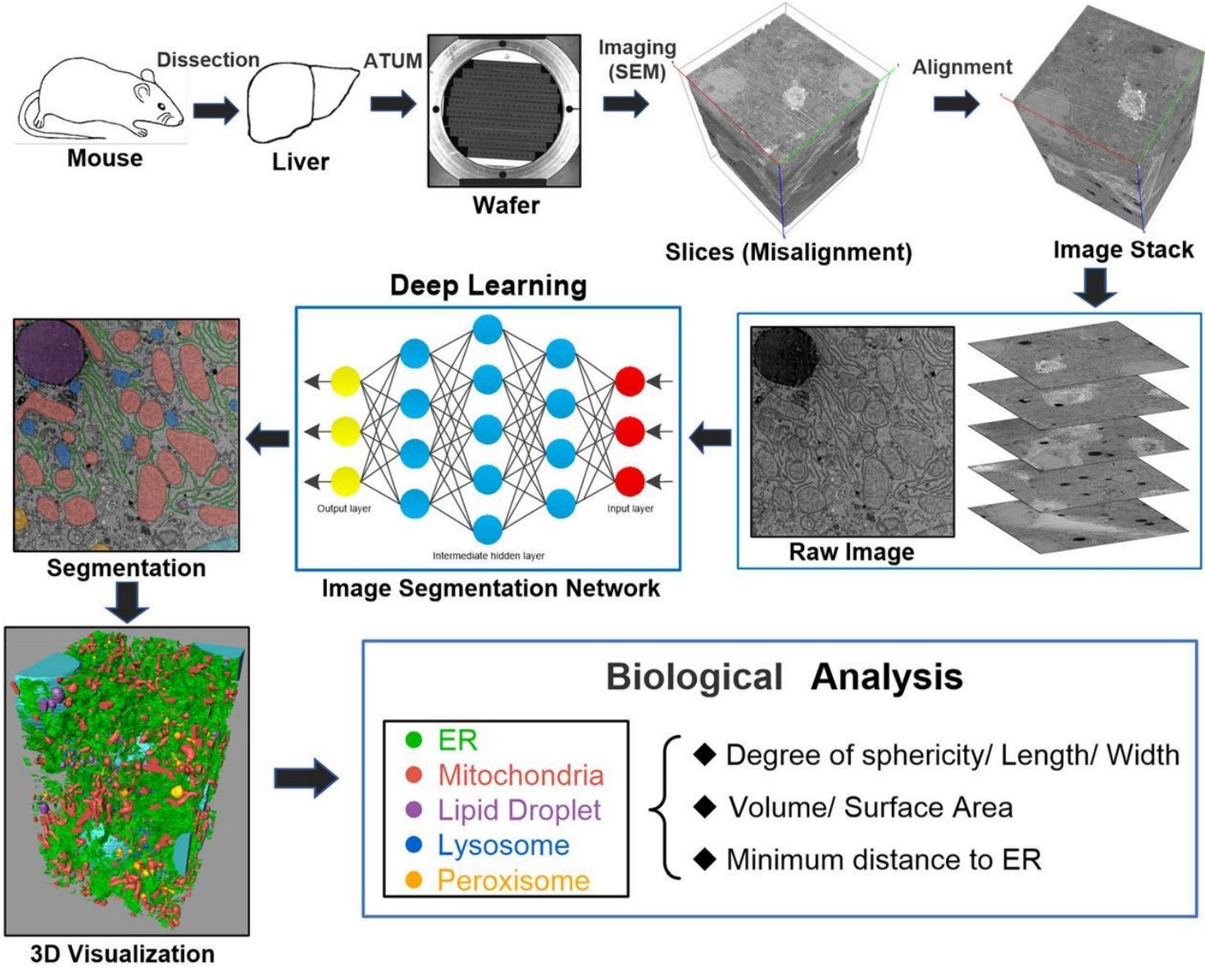
# Fast 3D Electron Microscopy Segmentation via Super-Resolution and Targeted Re-Imaging

Humza Iqbal

SickKids Nanoscale Biomedical Imaging Facility, University of Toronto

## Motivation

- 3D electron microscopy (EM) volumes let biologists study tissue ultrastructure in its true spatial context, revealing cellular and subcellular organization that is hard to capture otherwise.
- Creating these volumes is slow and costly: samples must be sectioned into thousands of slices, and faster low-resolution scans degrade segmentation quality.
- Our goal is to recover reliable segmentation maps by selectively re-imaging only the regions that need higher resolution, reducing microscope time while enabling more high-quality 3D volumes.



## Related Work

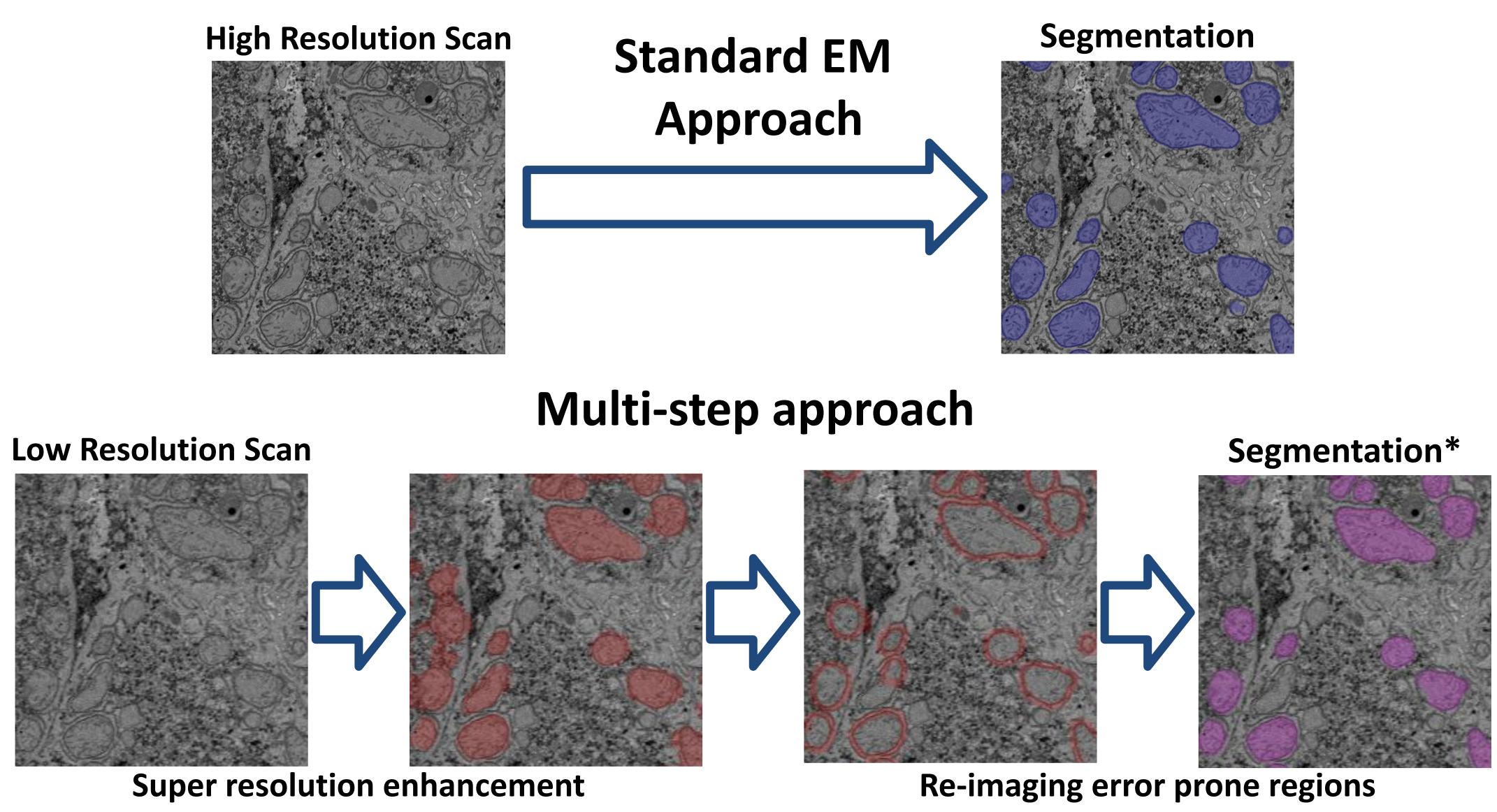
- **SmartEM** [1] integrates ML into real-time SEM acquisition by scanning quickly, then re-scanning only small subregions more slowly to guarantee “segmentability,” reporting large speedups.
- **EDSR** [2] proposes an optimized deep residual super-resolution (SR) network that improves SR quality by simplifying residual blocks and scaling model capacity/training.
- **RETINA** [3] improves EM segmentation generalization and downstream convergence by reconstruction-based pretraining on large unlabeled EM data (CEM500K) using a hybrid CNN+Transformer TransUNet backbone.

## References

- [1] Meirovitch et al., SmartEM: machine-learning guided electron microscopy, (preprint), 2023.
- [2] Lim et al., Enhanced Deep Residual Networks for Single Image Super-Resolution, arXiv, 2017.
- [3] Xing et al., RETINA: Reconstruction-based pre-trained enhanced TransUNet for electron microscopy segmentation on the CEM500K dataset, PLOS Computational Biology, 2025.
- [4] Kislinger et al., Multiscale ATUM-FIB Microscopy Enables Targeted Ultrastructural Analysis at Isotropic Resolution, iScience (Vol 23, Issue 7, 101290), 24 July 2020.

## Methods

- **Data:** Labelled Mouse liver data was used to finetune the segmentation model and train the error detection network. Collected human liver low and high resolution pairs to train the SR network and evaluate.



- Unlike SmartEM, we accelerate via lower pixel-count / lower-resolution imaging, rather than reducing dwell time.
- We aim for human liver deployment while training mainly on mouse liver labels.
- We employ a hybrid approach using both super resolution and reimaging.

## Results

- Classical baselines are too simple. SR consistently improves both image quality and segmentation metrics across the board. Selective re-imaging at 32 nm shows diminishing returns, suggesting the biggest payoff may come when starting from even lower-resolution scans.

Method	PSNR	SSIM	IoU	VI	Time Saved (%)
Bicubic	27.12	0.70	0.61	0.32	94
NLM + Linear	26.92	0.69	0.47	0.34	94
Super Resolution	27.76	0.73	<b>0.70</b>	0.22	94
Err Reimaging	<b>28.13</b>	<b>0.76</b>	0.6641	0.27	75
Super Resolution + Err Reimaging	28.059	0.75	0.65	<b>0.21</b>	88

Table 1: Average performance on 10 Human liver 32nm Patches

