

Neural Network Ensembles Will Enable Teravoxel Image Segmentation for Electron Microscopy



National Institute of
Biomedical Imaging
and Bioengineering

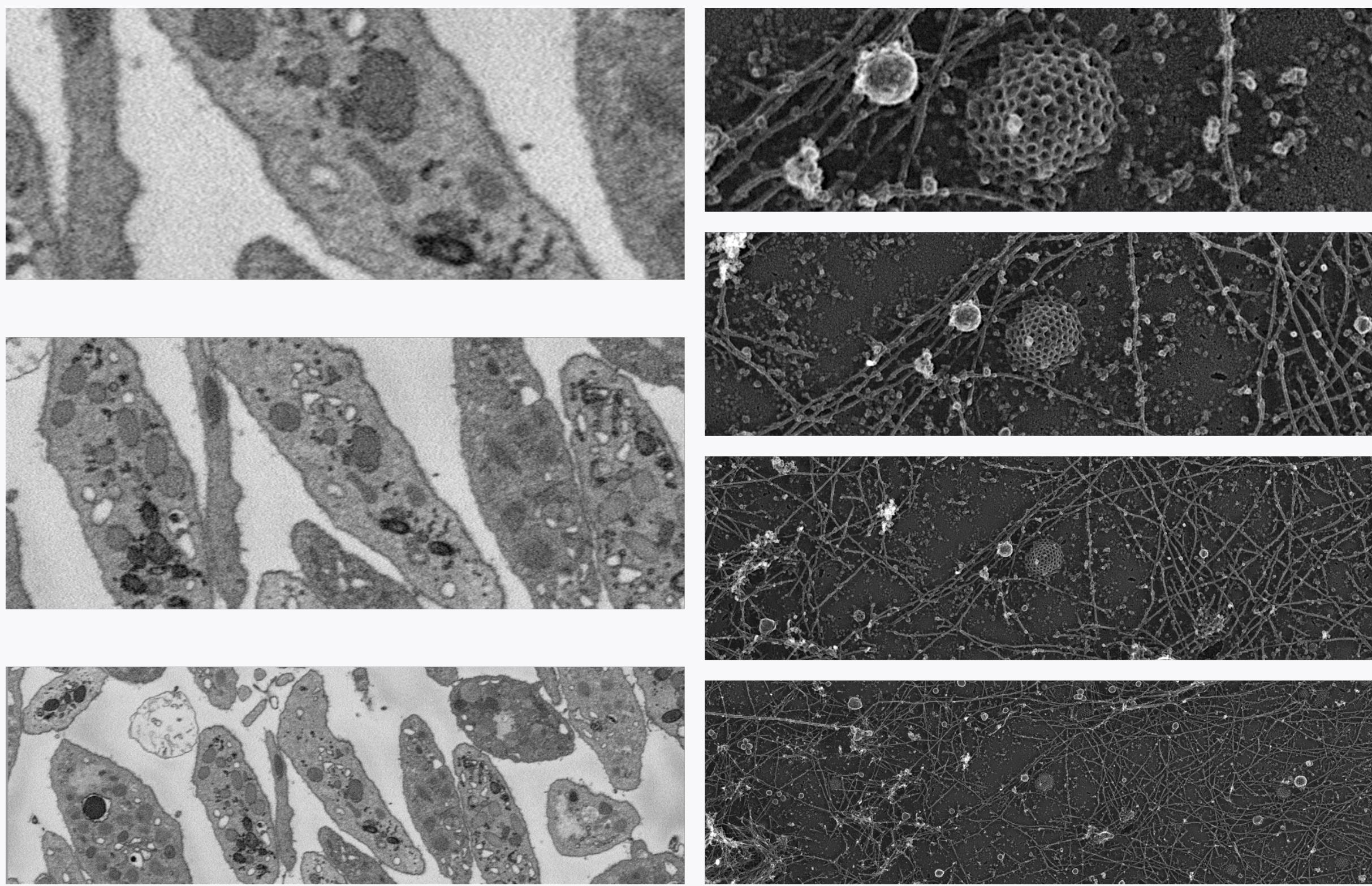
Matthew Guay*, Zeyad Emam, Adam Anderson, Richard Leapman
*matthew.guay@nih.gov



Laboratory of Cellular Imaging and Macromolecular Biophysics, NIBIB, NIH
AMSC Department, University of Maryland, College Park

Background

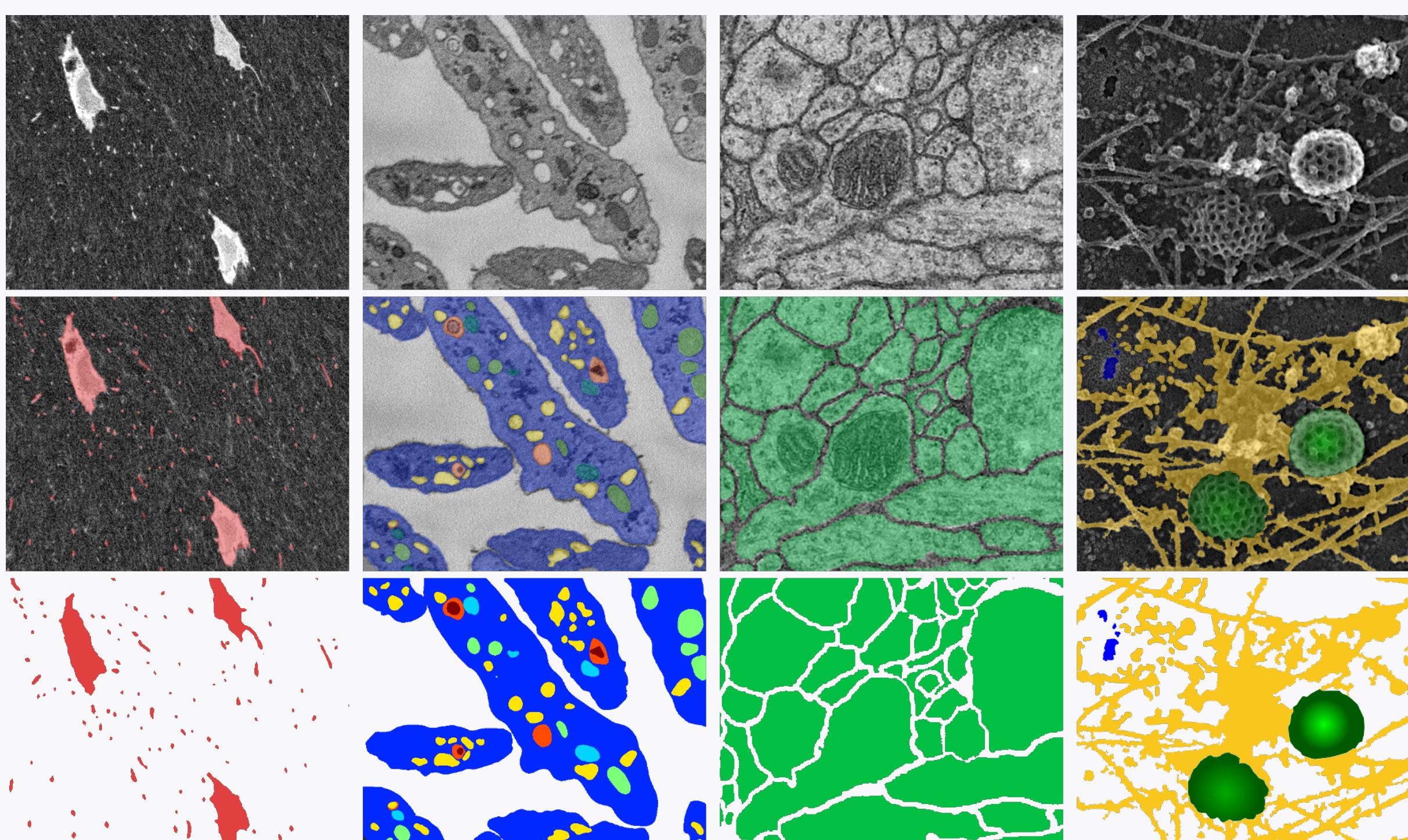
- Electron microscopy (EM) produces nanoscale images of matter.
- Biologists use EM to understand the organization of proteins and organelles in cells, and cells in tissues.
- Modern EM camera sensors can produce gigapixel images.
- Serial block-face scanning electron microscopy (SBF-SEM): Image big 3D samples by repeated cutting and scanning.
- SBF-SEM can generate teravoxel image volumes: 1 mm³ tissue samples with 20 nm lateral, 40 nm axial resolution.



Left: SBF-SEM images of platelet cells. Right: Platinum replica TEM images of HeLa cell membranes. Courtesy of Justin Taraska, NHLBI.

Challenge

- How do we make sense of all this data?
- Segmentation groups image voxels into labeled regions, corresponding to image content.
- Segmentation is fundamental to quantitative image analysis, but manual segmentation is slow.
- Systems biologists need automated segmentation tools to make full use of modern EM hardware.
- Extreme accuracy required for practical segmentation tools.



Examples of EM datasets and their segmentations. Left: SBF-SEM image of bone cells. Middle-left: SBF-SEM image of platelet cells. Middle-right: ssTEM image of Drosophila nervous tissue, courtesy of the ISBI 2012 2D EM segmentation challenge. Right: Platinum replica TEM images of HeLa cell membranes.

Aim

- Demonstrate the utility of neural network ensembles for EM segmentation algorithms.
- Highlight the role of our software library *genenet* for designing segmentation network ensembles.
- Describe a software pipeline for large-scale EM image segmentation on a computing cluster.

Methods

- Segmentation algorithm: classify each pixel in an image.
- Convolutional encoder-decoder neural networks “translate” image patches into segmentations.
- Ensembles: Train multiple segmentation networks, average their predictions.
- Ensembles of segmentation networks offer significantly improved generalization.

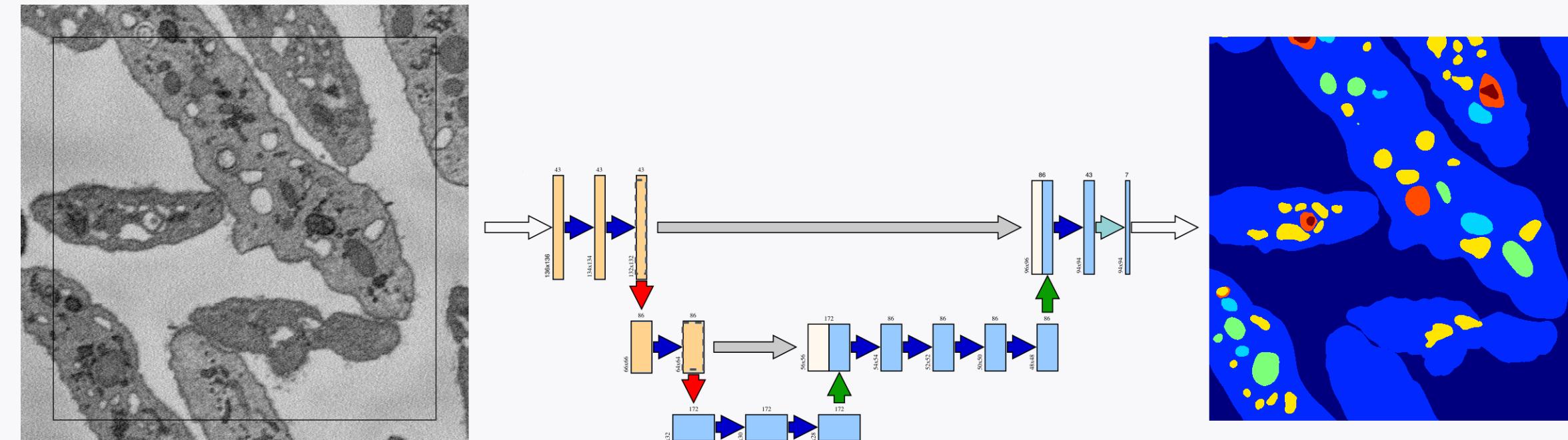
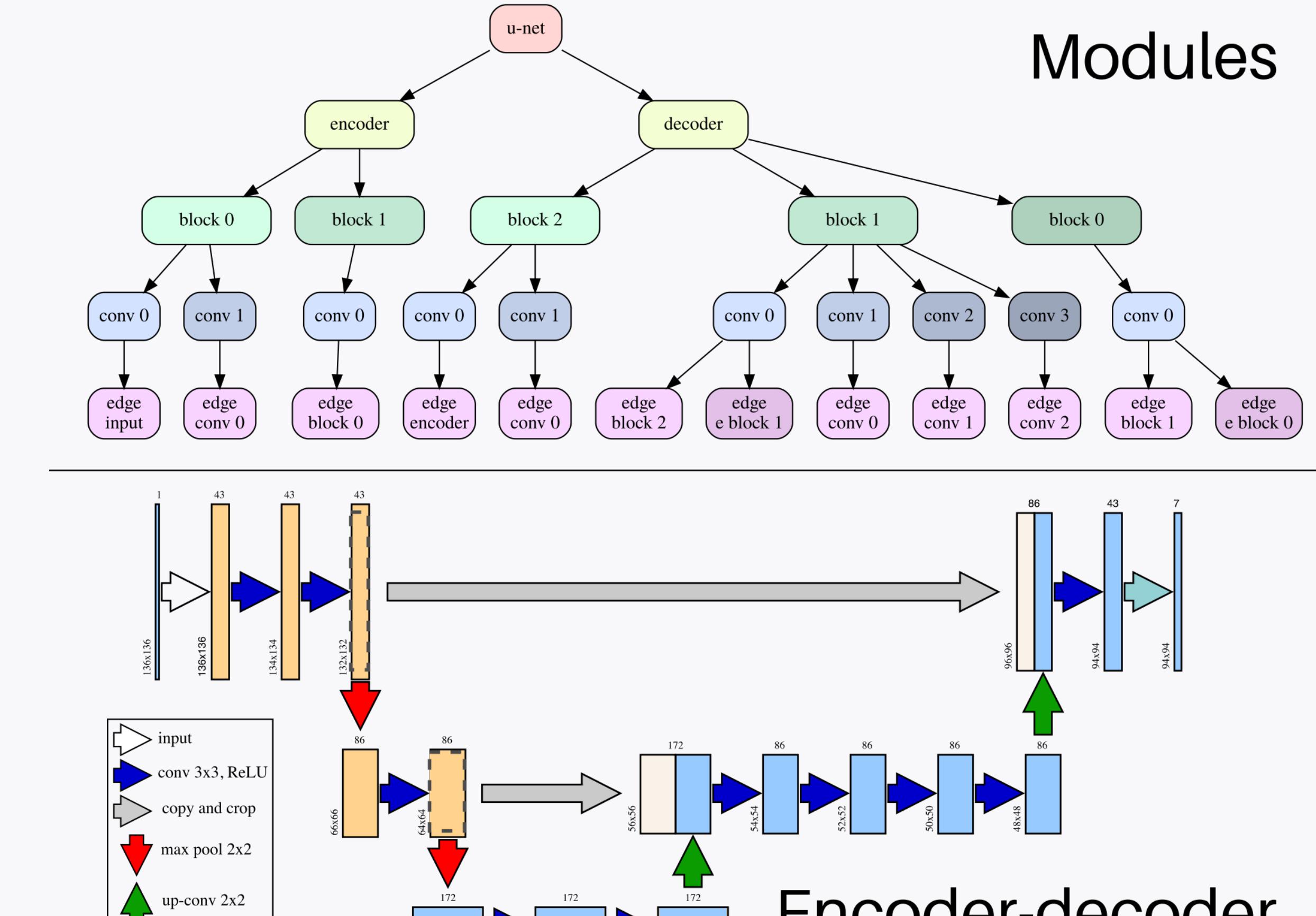


Image segmentation with a convolutional encoder-decoder network. An encoder module (orange) decomposes the input into a multiscale collection of features. A decoder module (blue) synthesizes those features into a segmentation.

- *genenet*: Build an encoder-decoder network as a hierarchy of network modules.
- Easy to randomly sample encoder-decoder network architectures for simple algorithmic neural network design.
- Train many random networks on Biowulf, NIH’s HPC system. Use the best ones together in an ensemble.
- Large volume segmentation: break volume into tiles, process on Biowulf, recombine.

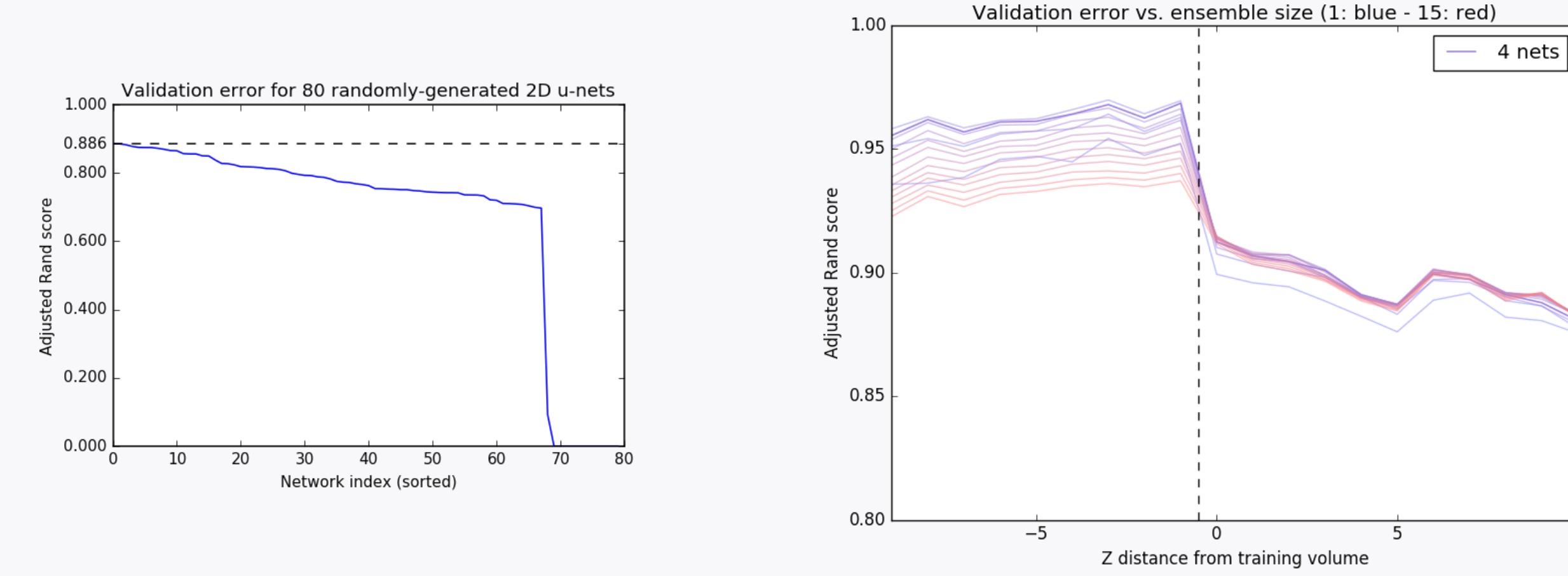
Modules



Comparison of a network module hierarchy and the corresponding encoder-decoder network. Encoder and decoder modules combine convolution block modules, which combine convolution modules, which combine edge modules.

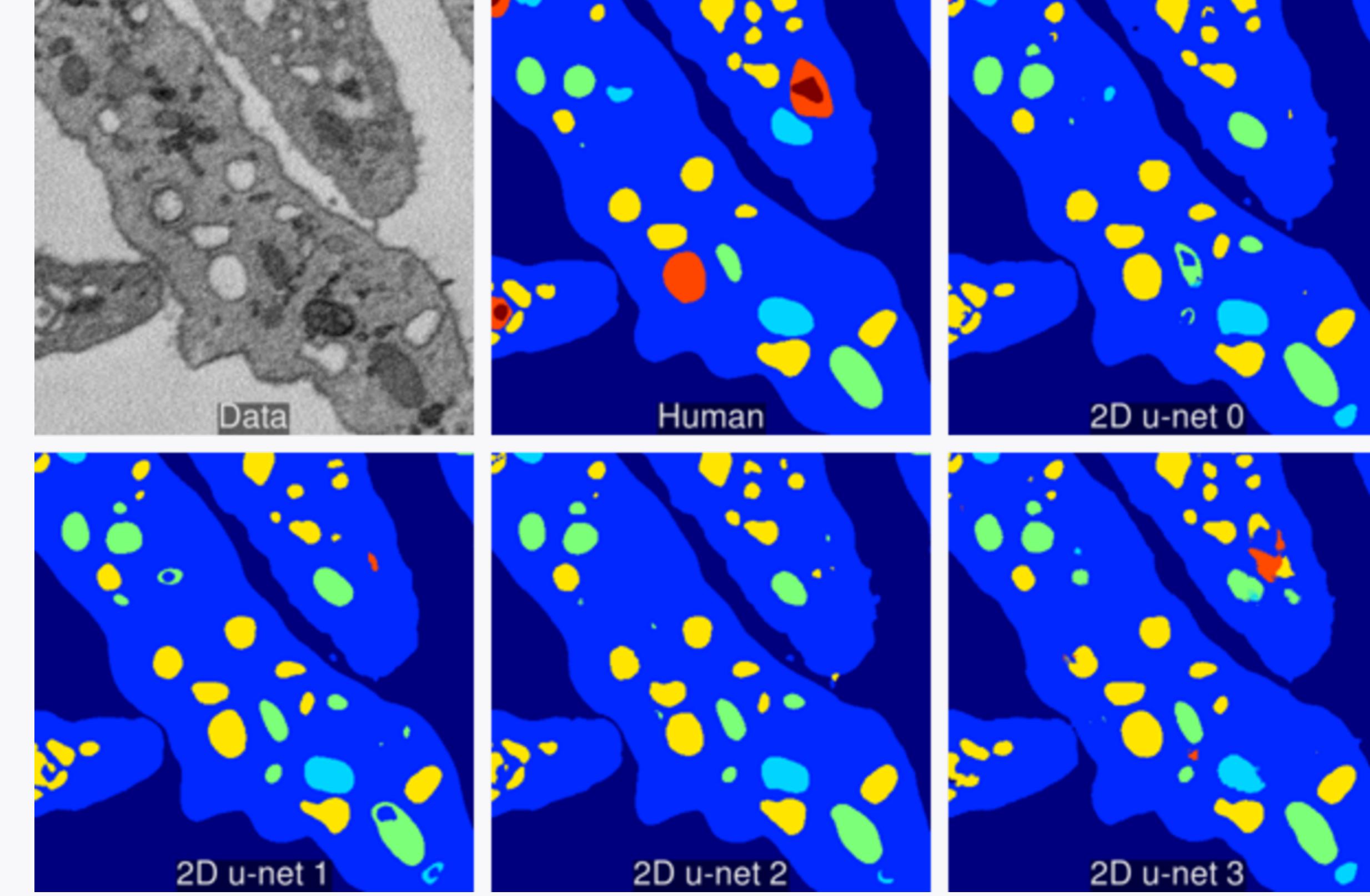
Results

- Trained 80 random encoder-decoder networks over 48 hours on Biowulf.
- Optimal performance found with an ensemble of the four best random networks.
- Timing: To determine if algorithmic segmentation is practical, compare manual segmentation time with computer segmentation + manual correction time.
- Right now, computer-aided segmentation is 3× faster.

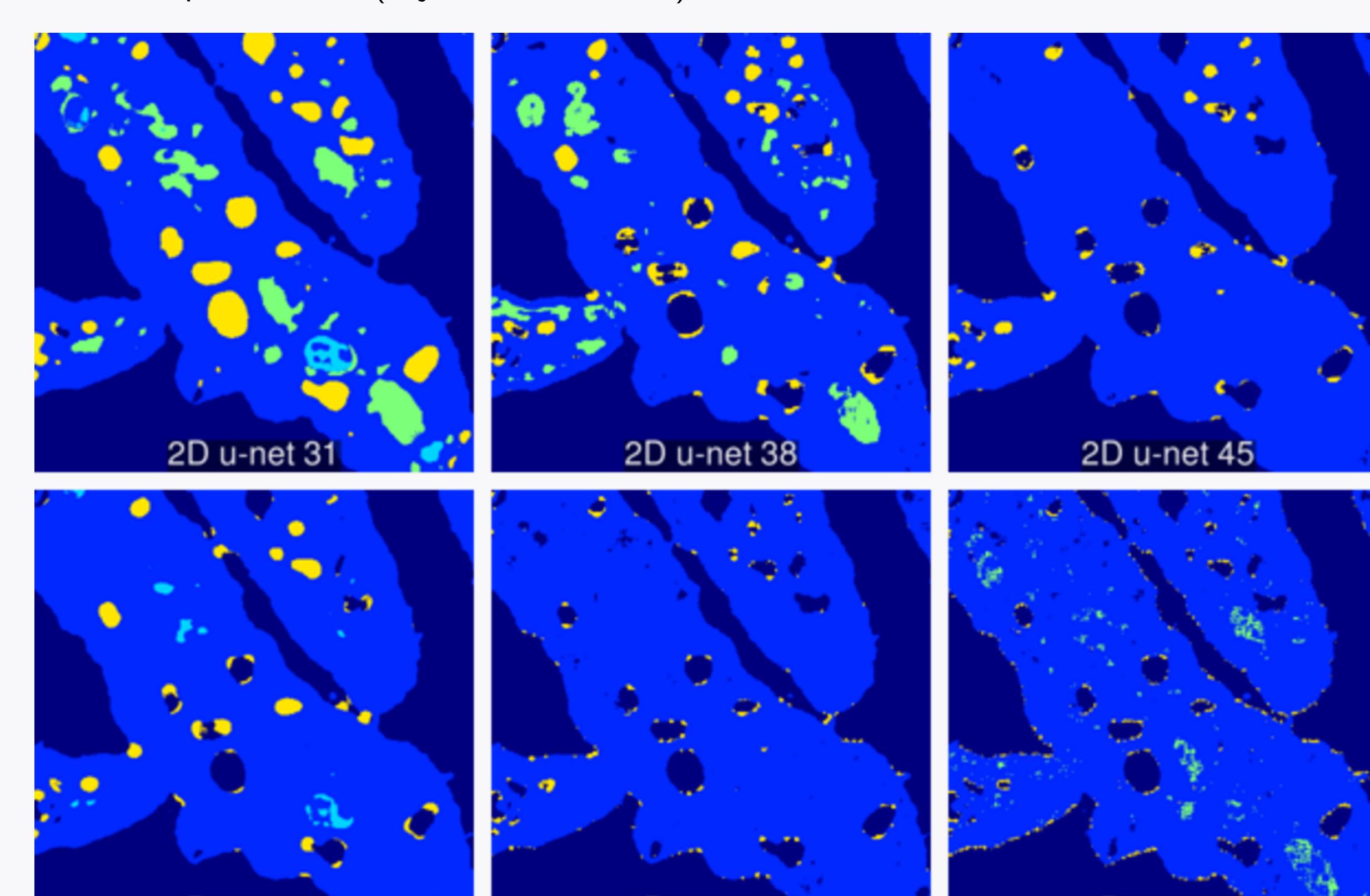


Left: Plot of the validation error (adjusted Rand score) for each of the 80 random encoder-decoder networks. Right: A comparison of the performance of n -best network ensembles for $n \in [1, 15]$. Data points to the left of the dotted line indicate evaluations on training data, data points to the right indicate evaluations on validation data. Ensembles perform significantly better on both training and validation data.

Individual networks

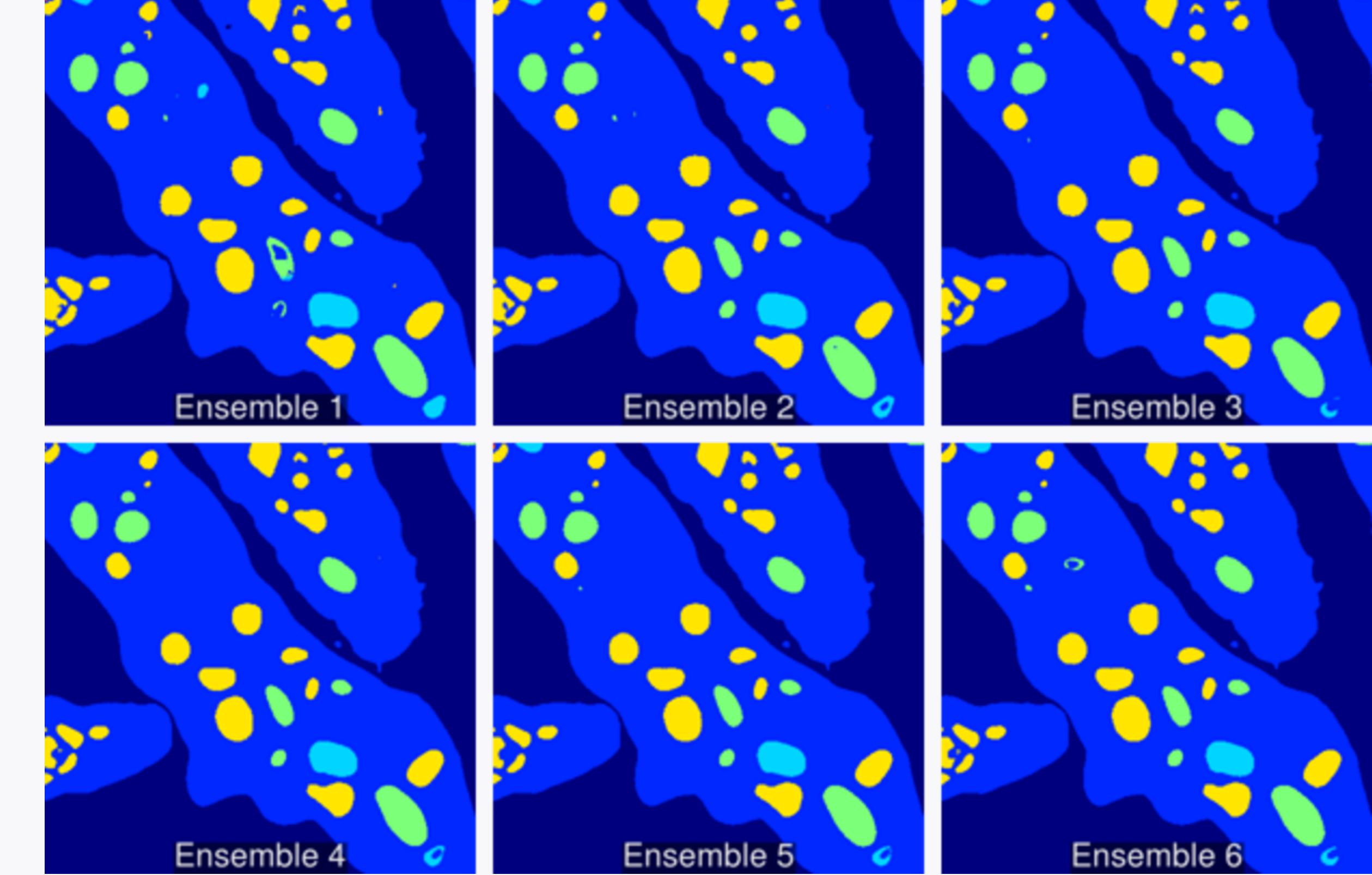


A comparison of a ground-truth segmentation with the four random networks with best validation performance (adjusted Rand score).



A comparison of the six worst-performing random networks. Several others failed to converge during training, and are not depicted here.

Network ensembles



A comparison of the n -best network ensembles for $n \in [1, 6]$. Ensemble 4 gives best performance on the validation data.

Discussion

- Easy to generate encoder-decoder network ensembles with *genenet*.
- Random network generation allows for architecture selection and training without deep learning expertise.
- Our best ensemble accelerates segmentation as-is, but not by enough.
- Computation time is negligible: 10 - 100 s for a 50 × 800 × 800 volume.
- Accelerate the workflow by reducing correction time.
- Ongoing correction challenges:
 - 2D segmentation lacks context for proper organelle identification, false positives on cellular debris.
 - Rare classes (dense granule, dense granule core) are frequently misidentified.

Future Work

- 3D segmentation: coming very soon!
- Generalized segmentation algorithms: Designing neural networks which may be used for multiple segmentation tasks.
- Network population evolution as a better alternative to random architecture sampling.

References

- [1] W. Denk and H. Horstmann. Serial block-face scanning electron microscopy to reconstruct three-dimensional tissue nanostructure. *PLoS biology*, 2(11):e329, 2004.
- [2] O. Ronneberger, P. Fischer, and T. Brox. U-net: Convolutional networks for biomedical image segmentation. *CoRR*, abs/1505.04597, 2015.

Acknowledgements

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