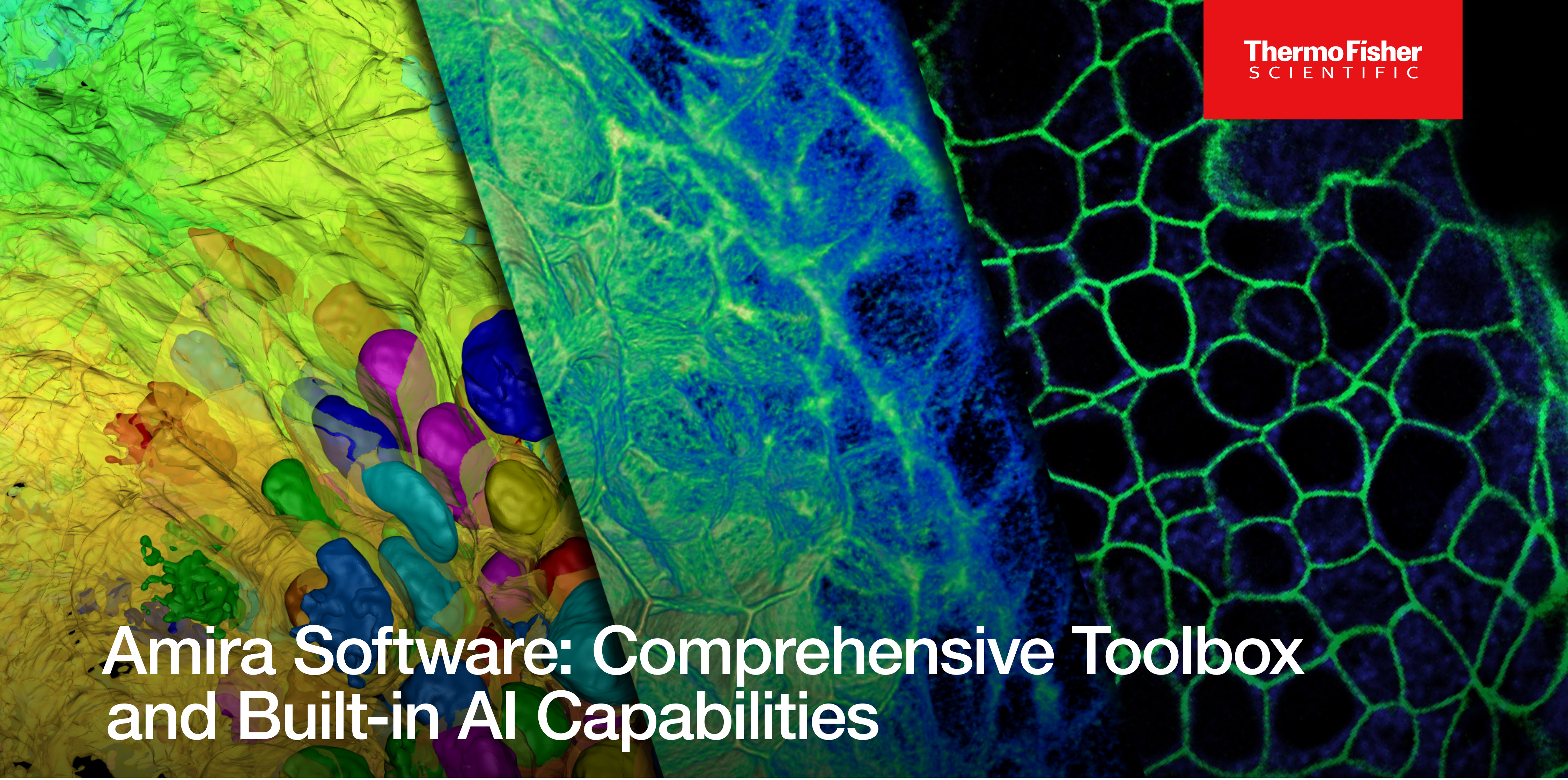


Amira Software: Comprehensive Toolbox and Built-in AI Capabilities

Accelerate your time to data and time to market

Modern life science research operates across a variety of formats, using a broad range of instrumentation. These variations can cause challenges in the compilation and analysis of relevant data that come from different sources. Thermo Scientific™ Amira™ Software is a powerful, multifaceted 2D-5D platform designed to process this abundance of disparate data across multiple file formats. Amira Software has an intuitive interface that reduces the learning curve for even the most novice users. It also makes use of powerful, trainable deep learning neural network models to accelerate and improve the segmentation and interpretation of complex data sets while reducing chances for error. Amira Software supports research processes for visualizing, manipulating, and understanding life science research data from multiple image modalities.

Empower your lab with a comprehensive imaging data toolbox

From straightforward visualization to advanced image processing, quantification, segmentation, and analysis, Amira Software provides a comprehensive, multimodal toolbox for advanced 2D-5D biological characterization and drug discovery.

Amira Software: From imaging data to insight

Data acquisition*

- Computed tomography (CT)
- Confocal microscopy
- Cryo-tomography
- Focused ion beam-scanning electron microscopy (FIB-SEM)
- High content screening
- Magnetic resonance imaging (MRI)
- Light microscopy
- Serial block face-scanning electron microscopy (SBF-SEM)

Imports

- Raw imaging data
- Imports from multiple imaging modalities
- Very large data
- BioFormats

Filtering and pre-processing

- Noise reduction of sample images
- Image artifact reduction
- Background correction

Visualization

- Interactive, high-quality 2D-5D visualization
- Direct manipulating of objects

Segmentation

- Thresholding and auto-segmentation
- Automatic labeling of objects

Measurement/Analysis

- Built-in measurements such as counts, volumes, areas, perimeters, aspect ratios and orientations
- Custom, user-defined measurements

Animation/Presentation

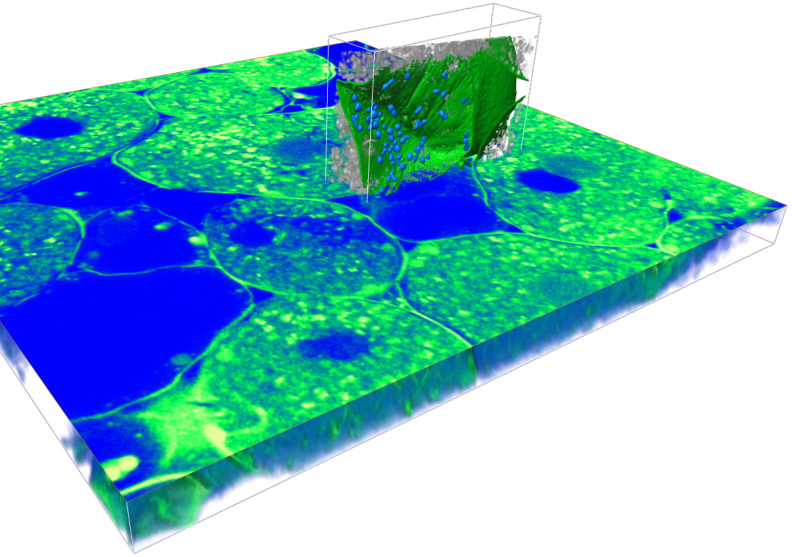
- Advanced video animations
- Charts, spreadsheets, and reports

** Amira Software is not an acquisition software*

A comprehensive set of techniques to serve multiple applications

Correlative imaging

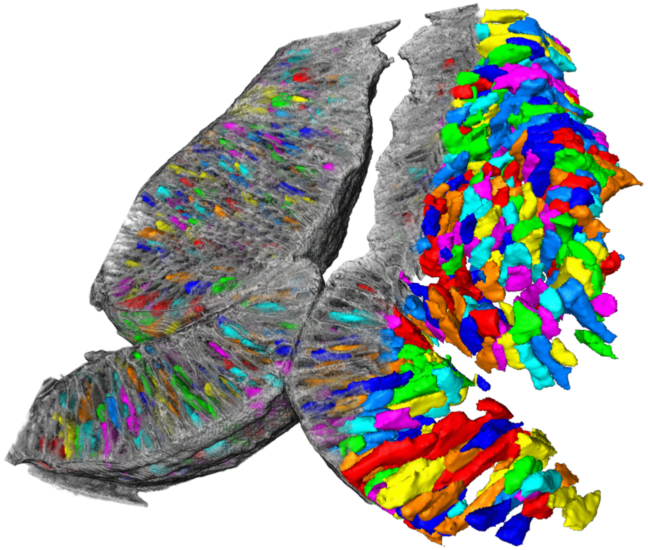
Amira Software supports multi-volume data processing and visualization paired with multiple imaging modalities simultaneously. The automatic registration tools with the Multi-Planar Workroom offer the most commonly used automated registration metrics and allow for adjustable registration parameters to meet users' data imaging and analysis needs.



Sample of Mung bean root nodule colonized by nitrogen-fixing bacteria imaged with CLSM and FIB-SEM. *Data courtesy of Dr. Miriam Lukas, EMEZ, ETHZ Zürich.*

Membrane detection

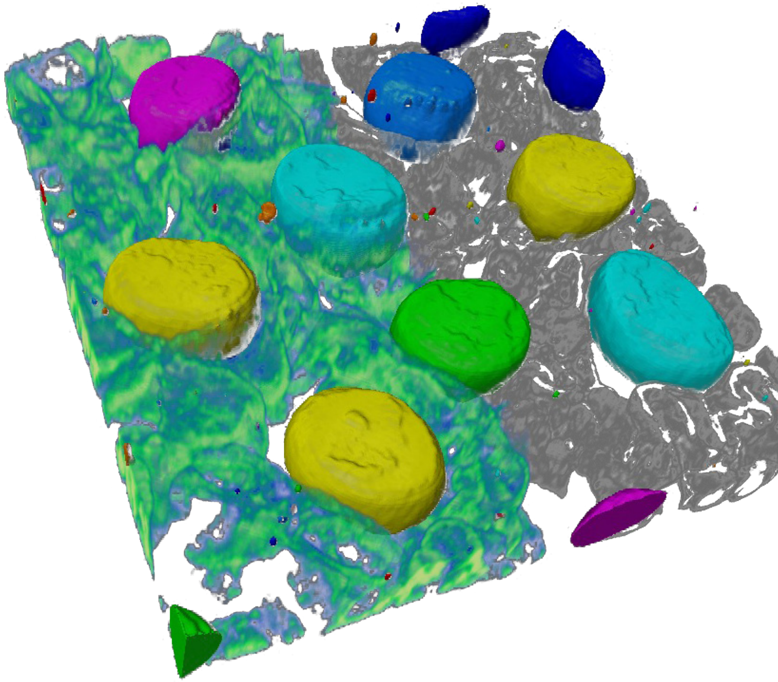
Users can accelerate segmentation with automated detection of cellular features such as membranes and filaments. Amira Software's advanced imaging analysis and combination capabilities allow it to average out noise and sharpen contrast to create a composite model with a higher resolution.



Light-sheet microscope data of Zebra Fish tissue sample. As this is a living sample – only fluorescence staining of the cell membranes was possible. *Data courtesy of Biophysical Fluorescence Laboratory, Center For Bioimaging Sciences, Departments of Biological Sciences & Chemistry, National University Of Singapore.*

Cell detection

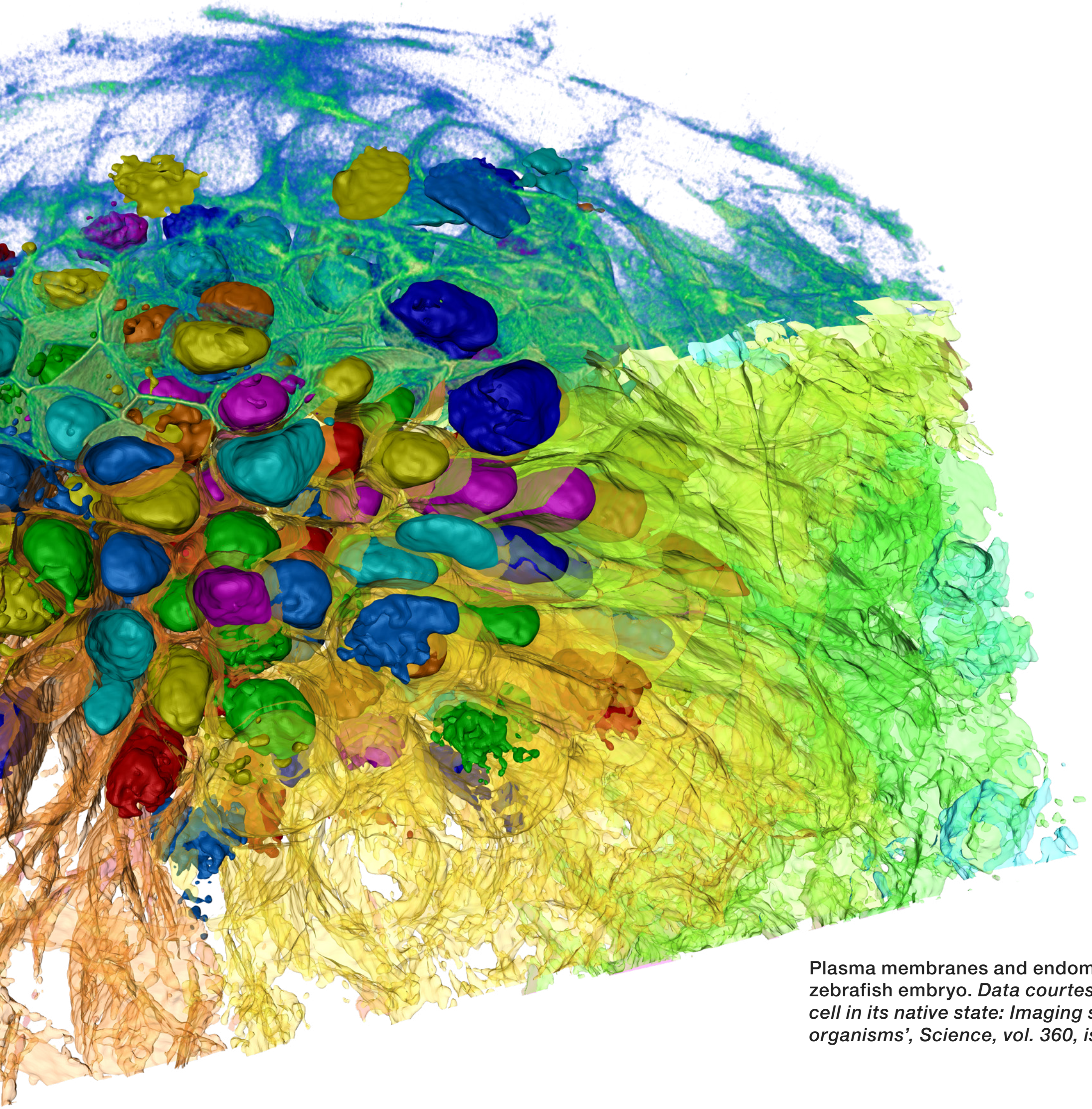
From 3D imaging data on cellular spheroids, Amira Software can automatically identify individual cells and subsequently collect 3D imaging data concerning volumetric, morphometric, and intensity measurements on those individual cells and their nuclei. The potential benefits of analyzing 3D cellular spheroids extend to studying cancers, researching diabetes mellitus, and investigating stem cells—all without destroying the samples in question.



Human corneal endothelial cell. *Zhiguo He, Laboratory "Biology, Engineering, and Imaging of Corneal Graft", BiiGC, EA2521, Faculty of Medicine, University of Saint Etienne, Saint Etienne, France.*

Multi-channel and time-series analysis

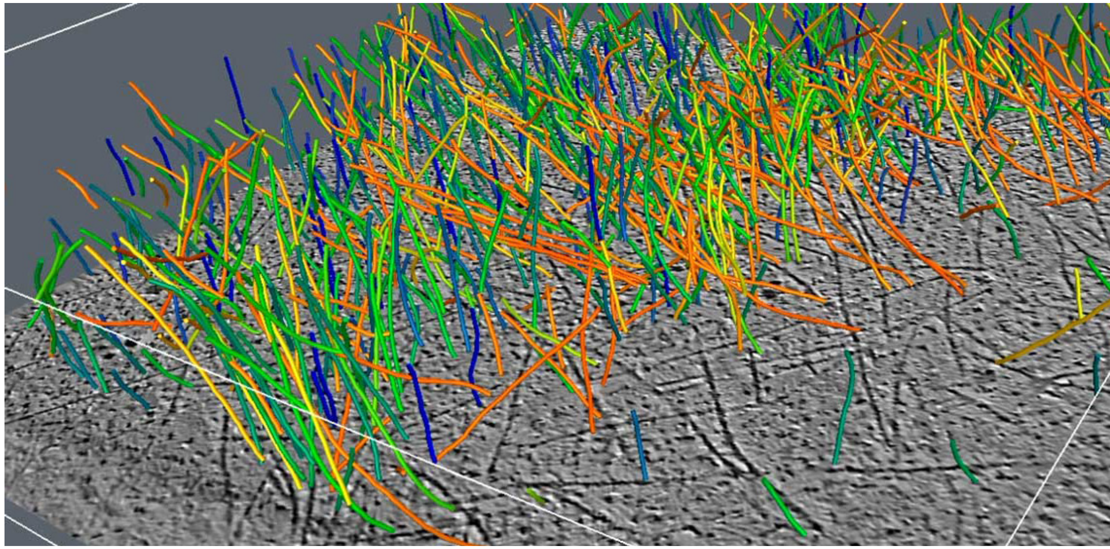
Amira Software allows for easy visualization, correlation, and processing of large multi-channel and time-series data in one platform without worrying about image size or memory limits. With its smart file format, Amira Software can compress all imaging data without losing precious information collected during acquisition. Amira Software with the Xplore5D extension offers you easy lossless data compression with immediate visual feedback, allowing you to quickly interact with and analyze large 3–5D data.



Plasma membranes and endomembranes within the eye of a zebrafish embryo. *Data courtesy of Liu, TL, 2018, 'Observing the cell in its native state: Imaging subcellular dynamics in multicellular organisms', Science, vol. 360, issue 6386.*

Filament tracing

Using a template-matching algorithm, Amira Software can automatically detect and trace noisy cryo-EM or DualBeam data. It can also reconstruct filamentous networks and edit the resulting graphs to remove features erroneously identified as filaments, or it can add the missing parts of a network.



Zooming in on cell migration: 3D architecture of a traveling actin wave from Dictyostelium discoideum. The cryo-electron tomography data set of an in-situ actin network shows that waves propagate by de novo nucleation of filaments instead of elongation of pre-existing filaments along the membrane. This type of visualization of subcellular structures in the native environment of cells has become possible by combining correlative cryo-fluorescence microscopy, cryo-focused ion beam milling and cryo-electron tomography. *Data courtesy of Dr. Marion Jasnin, Department of Molecular Structural Biology, Max Planck Institute for Biochemistry, Martinsried, Germany. Original publication of data: Jasnin et al. 2019. Structure. DOI: https://doi.org/10.1016/j.str.2019.05.009*

Compatible imaging modalities

Amira Software can process imaging data at any scale, from an abundance of imaging modalities, and into a variety of file formats. With over eight compatible imaging modalities and an array of exportable file formats, Amira Software offers pre-clinical trial flexibility in data acquisition.

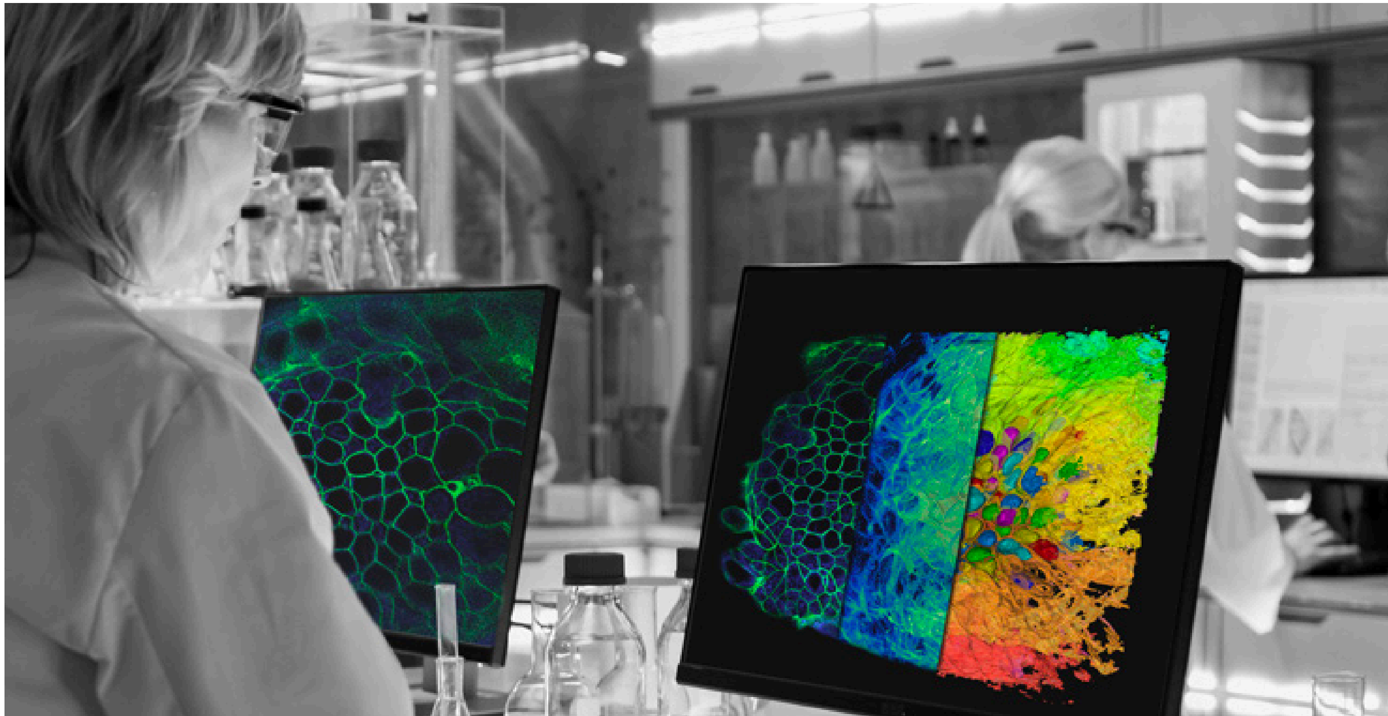
Imaging modalities compatible with Amira Software:

- Light microscopy
    - Including confocal, fluorescence, and serial sections
- Electron microscopy
    - Including transmission-electron microscopy (TEM), TEM-tomography, and focused ion beam (FIB) and scanning electron microscopy (SEM)
- Computed tomography
    - Including micro-computed tomography (μ-CT) and synchrotron-CT
- Magnetic resonance imaging (MRI)
    - Including diffusion tension imaging (DTI)
- Positron emission tomography (PET)
- 3D ultrasound
- Optical coherence tomography (OTC)

Compatible file formats

Amira Software supports the file formats below, and the XBioFormats Extension allows access to the Open Microscopy Environment's Java library, which then provides 140 additional file readers/importers.

- Bitmap formats
- Computer-aided design (CAD)
- Electron and optical microscopy
- Finite element modeling
- Geometric modeling
- Medical and neuroimage formats
- Molecular formats
- Multi-channel
- Multi-data/multi-view
- Time series
- Very large data



Accelerate your time to data and time to market with deep learning capabilities

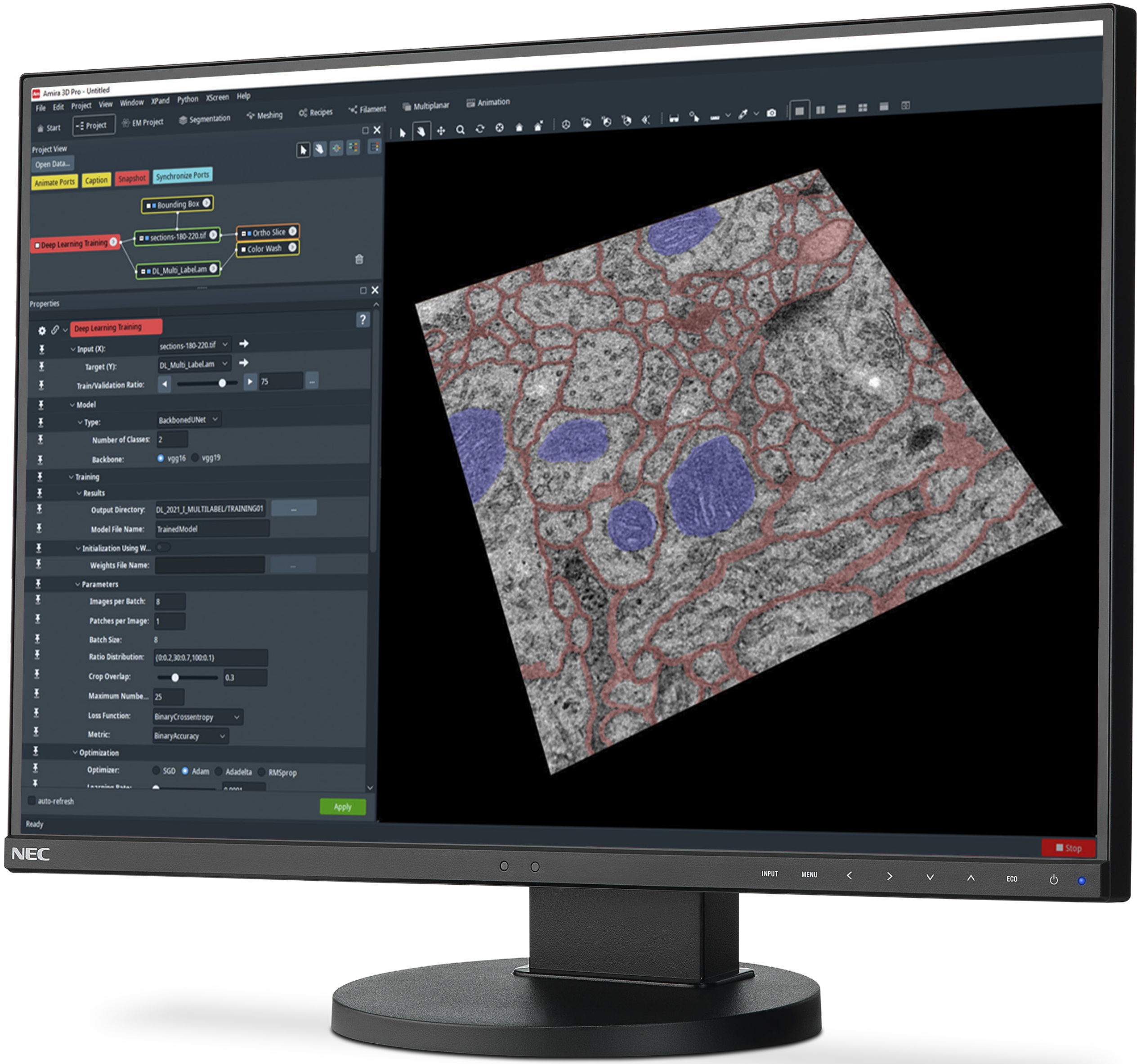
How does deep learning work?

Amira Software's deep learning capabilities allow you to train neural network models, and then apply the trained networks to solve complex or tedious segmentation problems. Its deep learning interface can work with neural networks based on the U-Net architecture.

In the [deep learning training module](), the neural network is nurtured with an example data set that has patterns. The data set is linked to the segmented ground truth data set that has been previously segmented manually. The "train" parameters are then set and refined further during an ongoing training session, commonly referred to as an iterative process.

This trained neural network model gets saved for further use in the prediction module. Having been trained, the model is able to recognize patterns in the deep learning prediction module. A region of interest could be extracted, on which segmentation would be automatically performed thanks to the trained deep learning model.

The output is called a "probability map" and can be visualized using volume rendering. This approach also guarantees that analysis is repeatable across specimens, meaning future image segmentation can be independent of manual processing or the user-based variability often seen in manual annotation tasks.

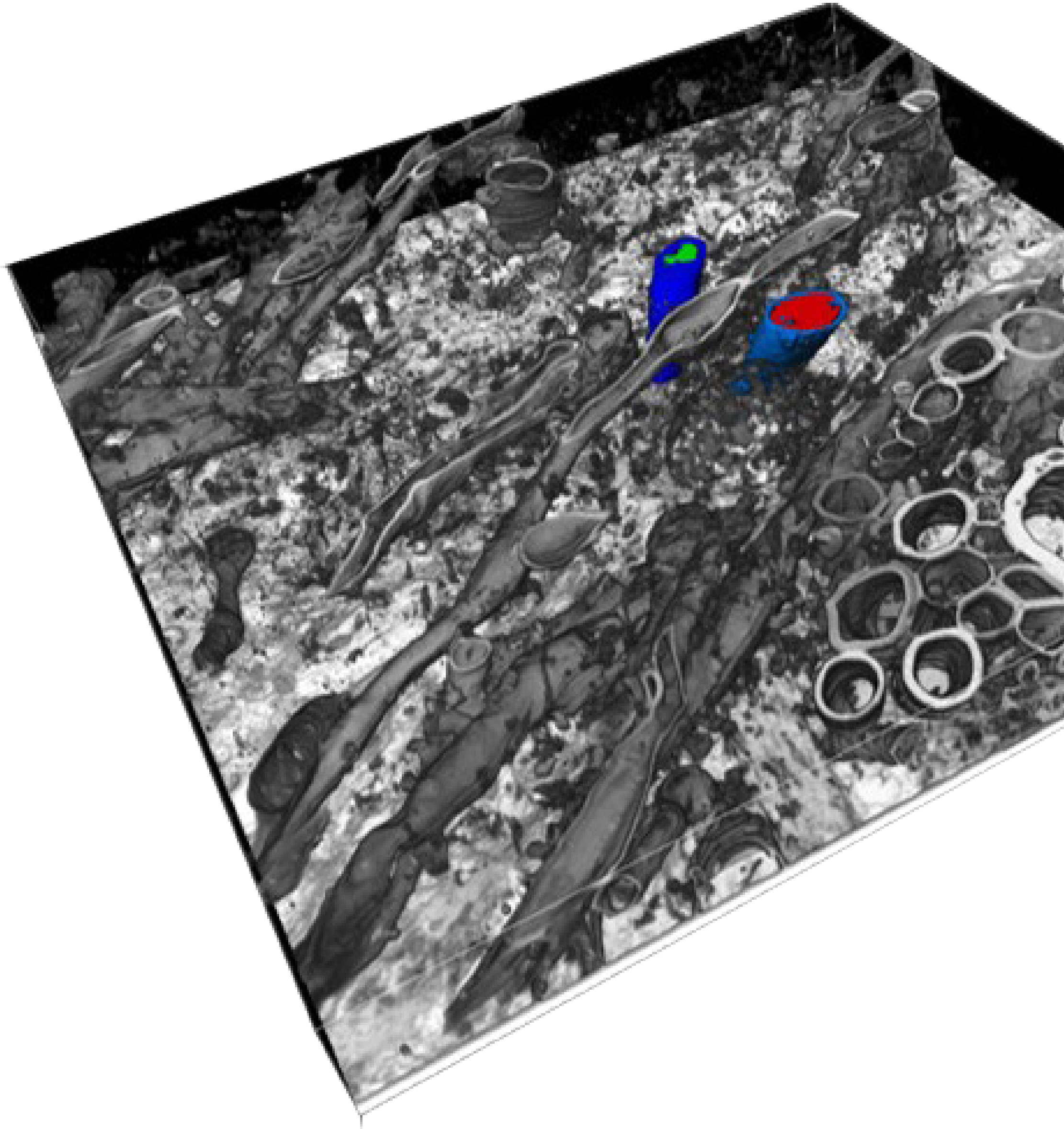


Input (X): sections-180-220.tif
Target (Y): DL_Multi_Label.am
Train/Validation Ratio: 75
Model
Type: BackbonedUNet
Number of Classes: 2
Backbone: ● vgg16 ○ vgg19
Training
Results
Output Directory: DL_2021_I_MULTILABEL/TRAINING01
Model File Name: TrainedModel
Initialization Using W...
Weights File Name:
Parameters
Images per Batch: 8
Patches per Image: 1
Batch Size: 8
Ratio Distribution: {0:0.2,30:0.7,100:0.1}
Crop Overlap: 0.3
Maximum Numbe... 25
Loss Function: BinaryCrossentropy
Metric: BinaryAccuracy
Optimization
Optimizer: ○ SGD ● Adam ○ Adadelta ○ RMSprop
☐ auto-refresh

In summary

Thermo Scientific Amira Software is a comprehensive imaging analysis toolbox for pharmaceutical and life science researchers who wish to **push the limits** of their data imaging and analysis. Amira Software allows researchers to visualize data acquired in 3D and analyze those images, from multiple file formats, at almost any scale.

The powerful, trainable **deep learning** neural network models embedded in the Amira Software environment supports the research process by reducing the number of manual, error-prone steps, thereby generating faster image analysis and enhancing **reproducibility**. Amira Software and other technological advances from Thermo Fisher Scientific help accelerate breakthrough drug discoveries and propel pharmaceutical research to new heights.



Learn more at **thermofisher.com/AmiraDrugDiscovery**