Supporting Drug Discovery with Amira Software

Empower your lab with a cutting-edge, comprehensive imaging analysis toolbox

thermo scientific

Pharmaceutical research and development firms face **immense competition** to be the first to release a drug to the market. To alleviate some of this intense pressure, pharmaceutical life science researchers need state-of-the-art, **repeatable**, and **automated** 2D/3D software for biological imaging analysis to **reduce manual steps** in the drug discovery process and **increase accuracy** as well as **time- and cost-efficiency**.

From **target discovery** and **compound identification** to **preclinical research**, the Thermo Scientific™ Amira™ Software is a powerful, multifaceted 2D-5D platform for **visualizing, manipulating, and understanding** life science research data from multiple image modalities, including light microscopy, high-content screening, electron microscopy, X-ray, CT, PECT, MRI, and other techniques.

Advanced research and development for breakthrough drug discoveries

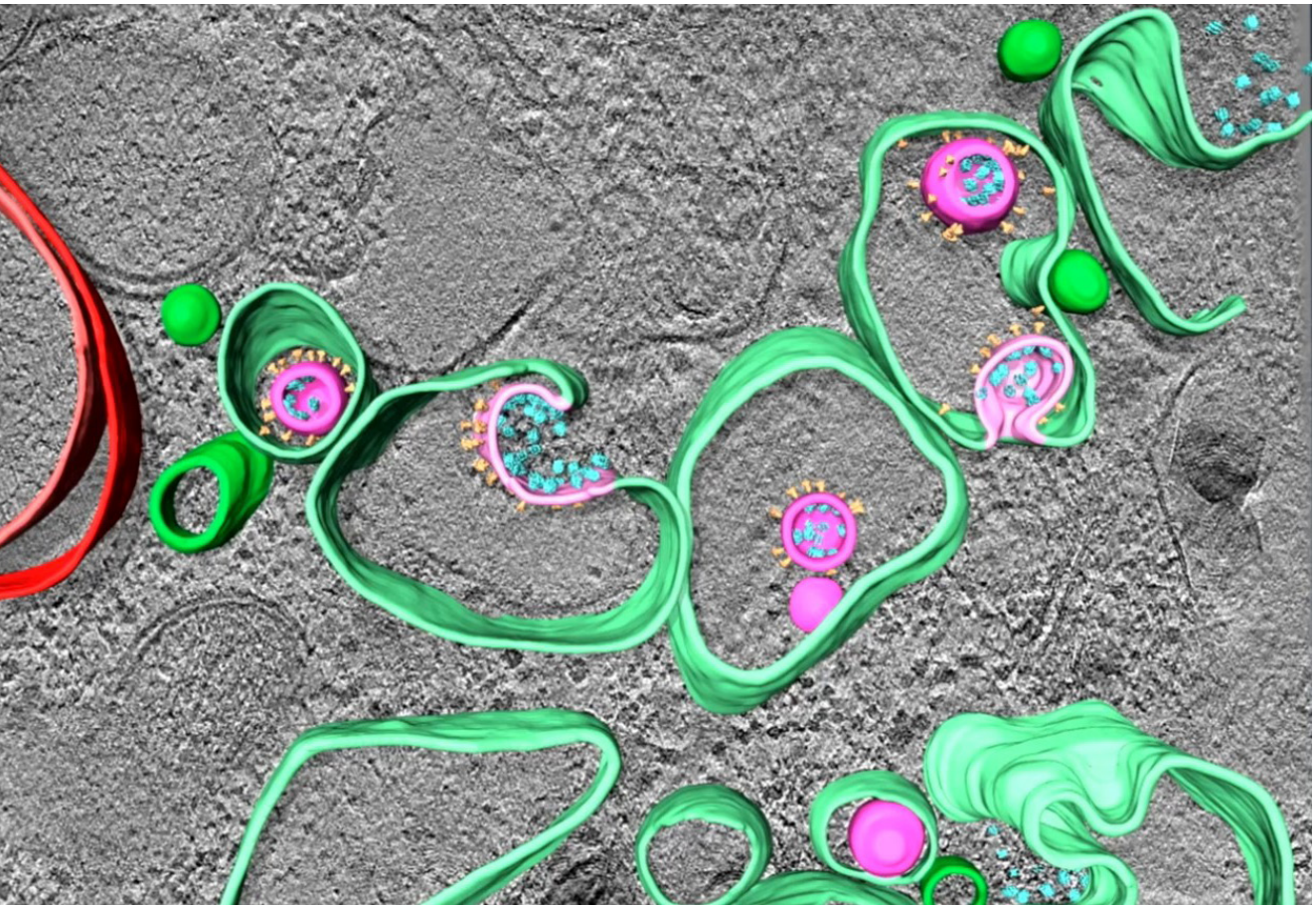
Amira Software can manage images at any scale or from multiple imaging modalities, supporting drug discovery screening and pharmaceutical research from a structural, sub-cellular level up to organ and anatomical biology. By pushing these limits of analysis, life science researchers can better understand how cells function or respond to disease or genetic variations, and then use these findings to advance research and development for breakthrough drug discoveries.

The applications that Amira Software offers are numerous. It has the computing power to accurately observe neuronal networks within a fully functioning brain, while its advanced imaging segmentation can sort and identify metastatic protein and cellular behaviors.

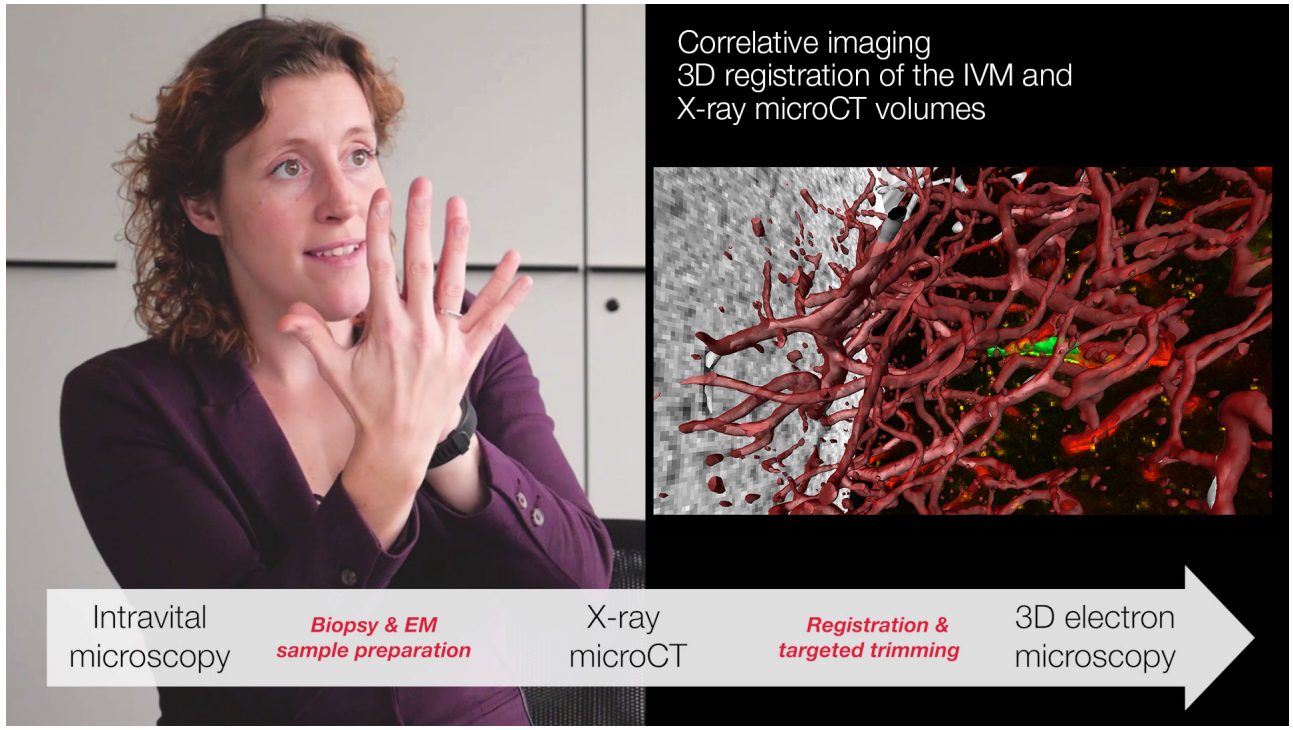
"Amira Software helps to set up complex data processing workflows. [...]
We particularly like the general idea of how Amira Software is organized in the project view. This helps to set up complex data processing workflows. The great variety of specialized image processing modules makes Amira Software particularly useful for EM data. The segmentation modules are very flexible, and it is easy to combine different tools enabling the segmentation of complex structures."

—Steffen Klein *(Chlanda lab, Department of Infectious Diseases, Virology, Heidelberg University, Heidelberg, Germany)*

Read more



SARS-CoV-2 structure and replication characterized by *in situ* cryo-electron tomography. *Data courtesy of Heidelberg University.*
https://doi.org/10.1038/s41467-020-19619-7



Intravital microscopy imaging is overlaid with microCT data, showing the location of blood vessels in a tissue sample. ***Data courtesy of Dr. Matthia A. Karreman (DKTK, DKFZ, Heidelberg, Germany), Dr. Yannick Schwab (EMBL, Heidelberg, Germany), and Prof. Dr. Frank Winkler (DKTK, DKFZ, Heidelberg, Germany).***

Amira Software is an established, trusted resource for life scientists. It has been cited in an increasing number of open-source peer-reviewed publications over the past decade, highlighted by some of the most prestigious names in life science research and development. Citations include **Heidelberg University** (Klein 2020), **National University of Singapore** (Devalla 2019), and the **Shanghai Institute of Materia Medica** (Sun 2021), to name a few[1,2,3]. These acknowledgments demonstrate that Amira Software's reliability in delivering high-quality imaging data analysis meets the ever-changing needs of life science research and the standards of stringent peer-reviewed publications.

Amira Software is not only a powerful imaging analysis toolbox; it is accompanied by a professional service team that is committed to helping pharmaceutical researchers reach their goals. With cutting-edge software updates and hotline support, as well as professional training, expert consulting, and custom development, Thermo Fisher Scientific will partner with your pharmaceutical team in all stages of assay development.

Watch testimonial

"It's very powerful software [that's] good for both electron microscopy and fluorescence microscopy, which is quite extraordinary, because typically software is focusing on either one of those. You can do so much with the software–I would really recommend Amira [Software]."

***—Matthia A. Karreman** MSc, PhD, EMBL, Heidelberg, Germany*

Current challenges in early research and development

The pharmaceutical industry is growing rapidly, investing more than $80 billion in research and development, or 10 times what the industry spent even 40 years ago, according to the **Congressional Budget Office** (Austin 2021)[4]. This exponential growth has resulted in 60% more drugs being approved annually by the Food and Drug Administration (FDA) compared to the previous decade. As life science research advances, so does the intricacy of imaging datasets.

Pharmaceutical research and development teams are under incredible pressure to deliver stable, efficient, and safe drugs. They must do this quickly, too: the average allotted time for preclinical trials is only about 31 months. Research and development conducted during this stage is crucial since preclinical development expenditures also account for as much as 31% of a company's total expenditures on drug research and development, equating to roughly $474 million per new drug.

Shepherding a prospective drug through clinical trials and FDA approval relies heavily on the detailed biological and chemical analyses performed during the research and development phase.

Condensed R&D timelines, the ever-increasing intricacy of datasets, and the need to reduce manual steps and automate the drug discovery process, all emphasize the need for cutting-edge, reliable, and automated 2D-5D software for biological imaging analysis: Amira Software. research and development. Therefore, a solution that reduces manual steps and automates the drug discovery process is imperative for accuracy as well as timeliness and cost-efficiency.

More investment in R&D

More drugs approved

Increased pressure to ensure accuracy, efficiency, and speed in development

Getting to clinical trials and, ultimately, FDA approval relies heavily on detailed biological and chemical analyses performed during R&D

How Amira Software supports pharmaceutical research and development

Empower your lab with a comprehensive imaging analysis toolbox

Amira Software is a powerful 2D to 5D platform for visualizing, segmenting, manipulating, and understanding life science imaging data. This multifaceted software solution offers native compatibility with an abundance of imaging modalities, customizable workflows, and deep learning capabilities.

Further reading from **"Protocols for Generating Surfaces and Measuring 3D Organelle Morphology Using Amira"** by E. Garza-Lopez et al.:

"Amira [Software] provides interactive high-quality volume visualization with orthogonal and oblique slices, volume, and surface rendering, and isolines and isosurfaces for more advanced customization [28]. Following segmentation, Amira [Software] provides post-image processing and analysis, including colocalization, photobleaching correction, and 3D visualization. While Amira [Software] is user-friendly, it allows advanced users to control the statistical analyses by customizing protocols through MATLAB scripts and by outputting data to Excel."

Accelerate your time to data and time to market

With ready-to-use recipes and Artificial Intelligence (AI)-powered automated processing tools, Amira Software supports faster image analysis by significantly reducing the number of manual steps and the overall amount of tedious manual labor. It can also execute challenging feature identification and improve the accuracy of the analysis.

From **"Supervoxel-Based Segmentation of Mitochondria in EM Image Stacks with Learned Shape Features"** by P. Fua et al.:

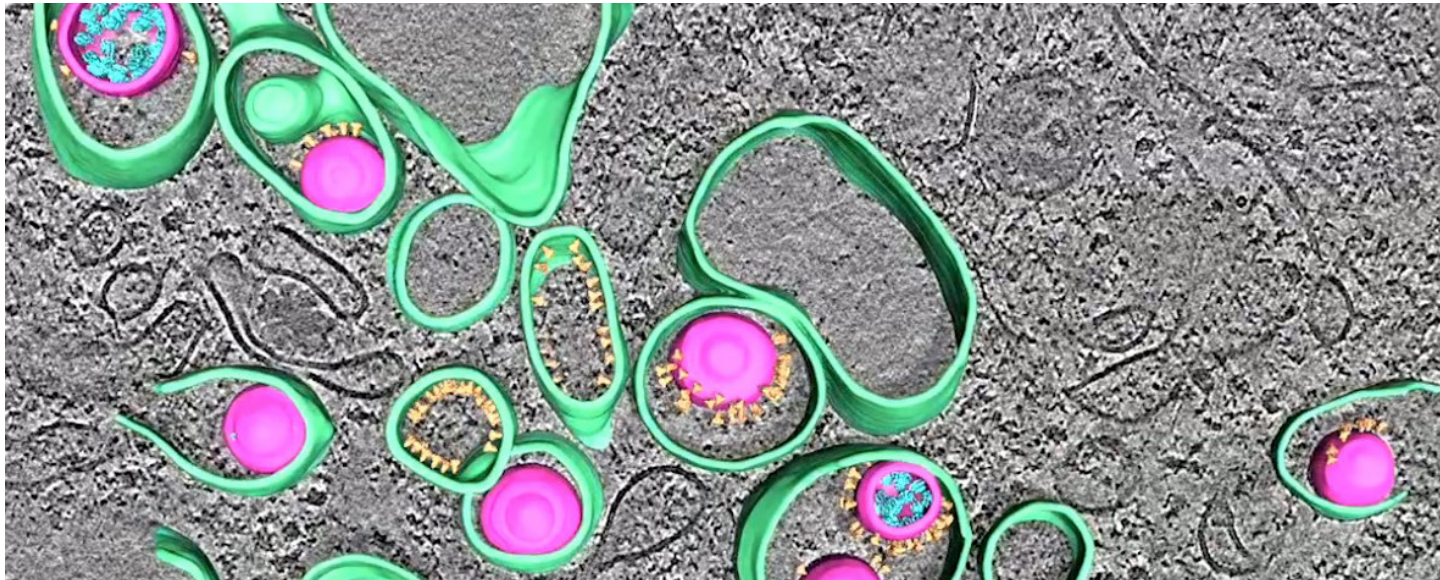
"Analyzing such an image stack by hand could require months of tedious manual labor and, without reliable automated image-segmentation tools, much of this high-quality data would go unused."

Deep learning to automate your image segmentation

Amira Software has built-in support for deep learning models and includes a ready-for-use Python environment. By creating automated workflows, Amira Software supports scientists with faster image analysis and reproducibility, reducing the number of manual steps and lowering the learning curve for non-experienced users. Deep learning models accelerate and improve the segmentation and the interpretation of complex or large datasets.

Deep learning uses for non-experts:
Easy access to a deep learning interface and modules, for which no Python skills are required.

Deep learning uses for experts:
A customizable and extensible platform.



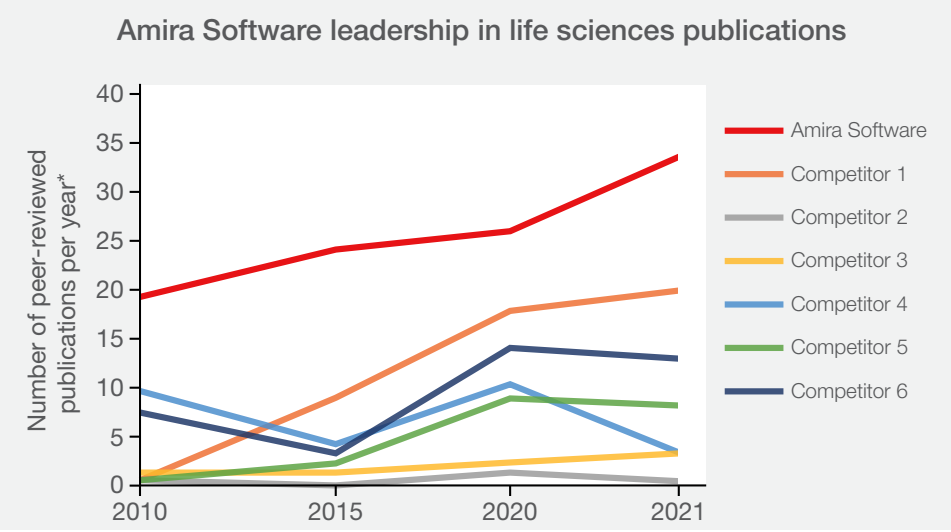
The Department of Infectious Diseases-Virology, Heidelberg University, Heidelberg, Germany used Amira Software deep learning tools for segmenting cell organelles after training on a subset of full volumes.

Amira Software's growing leadership in life sciences

Over the past two decades, Amira Software has been consistently ranked as one of the leading commercial solutions for life science applications, with mentions in more than 350 individual, open-source peer-reviewed publications*.

This number illustrates that Amira Software is regularly chosen as a preferred solution to support complex, innovative research questions in life science biomedical domains with a problem-solving mindset.

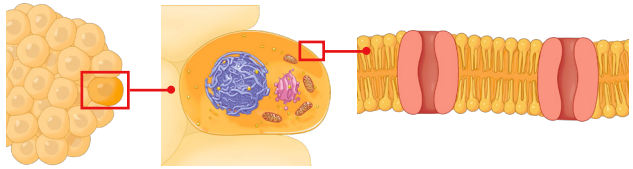
Life science literature provides a constantly refreshed source of validated, detailed examples of image analysis workflows and methodologies. The demonstrated range of Amira Software's applications can be leveraged by scientists across academia and pharma when developing their own research ideas for drug development.



Source: PubMed NCBI query search = (All times, "Amira AND Software," "Avizo AND software")

How Amira Software supports distinct stages of pharmaceutical research and development

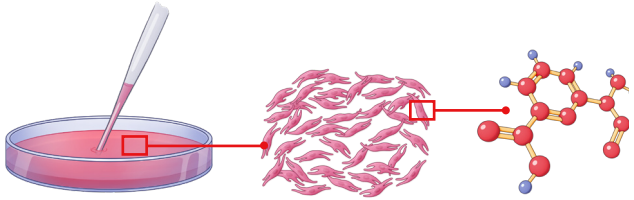
From organic molecules to tissues, Amira Software provides a broad range of segmentation and visualization of wide-ranging imaging data. Below are some categories and sub-categories of Amira Software's applications for life sciences.



Biological target discovery and validation

Where Amira Software can be used for target characterization and "druggability" validation:

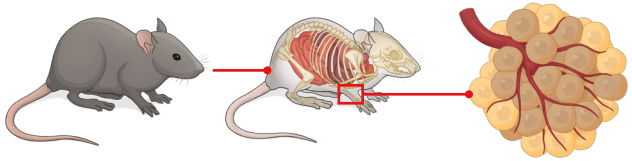
- **Cell morphology**
- **Cellular target localization**
- **Cell viability**
- **Cell dynamics**



Lead compound identification and optimization

How Amira Software is used for lead compound validation for safety and efficacy:

- **Analysis of drug characteristics**
- **Drug particle distribution**
- **Molecular structure visualization**
- **Toxicity studies through cell viability testing**



Preclinical development

How Amira Software can visualize data for *in vivo* and *ex vivo* testing in animal models:

- **Structural anatomy of small animal models**
- **Bone, skeleton structure analysis**
- **Soft tissue / tumor characterization**
- **Tumor localization, growth**

Biological target discovery and validation overview

Amira Software can be trained to evaluate the "druggability" validation of a specific disease and can target that disease during its segmentation and visualization. The software can be taught to sift out irrelevant samples, which then enables researchers to carry out more relevant analyses on a larger number of in vitro assays and perform imaging of 2D or 3D cell models.

At the intercellular level:

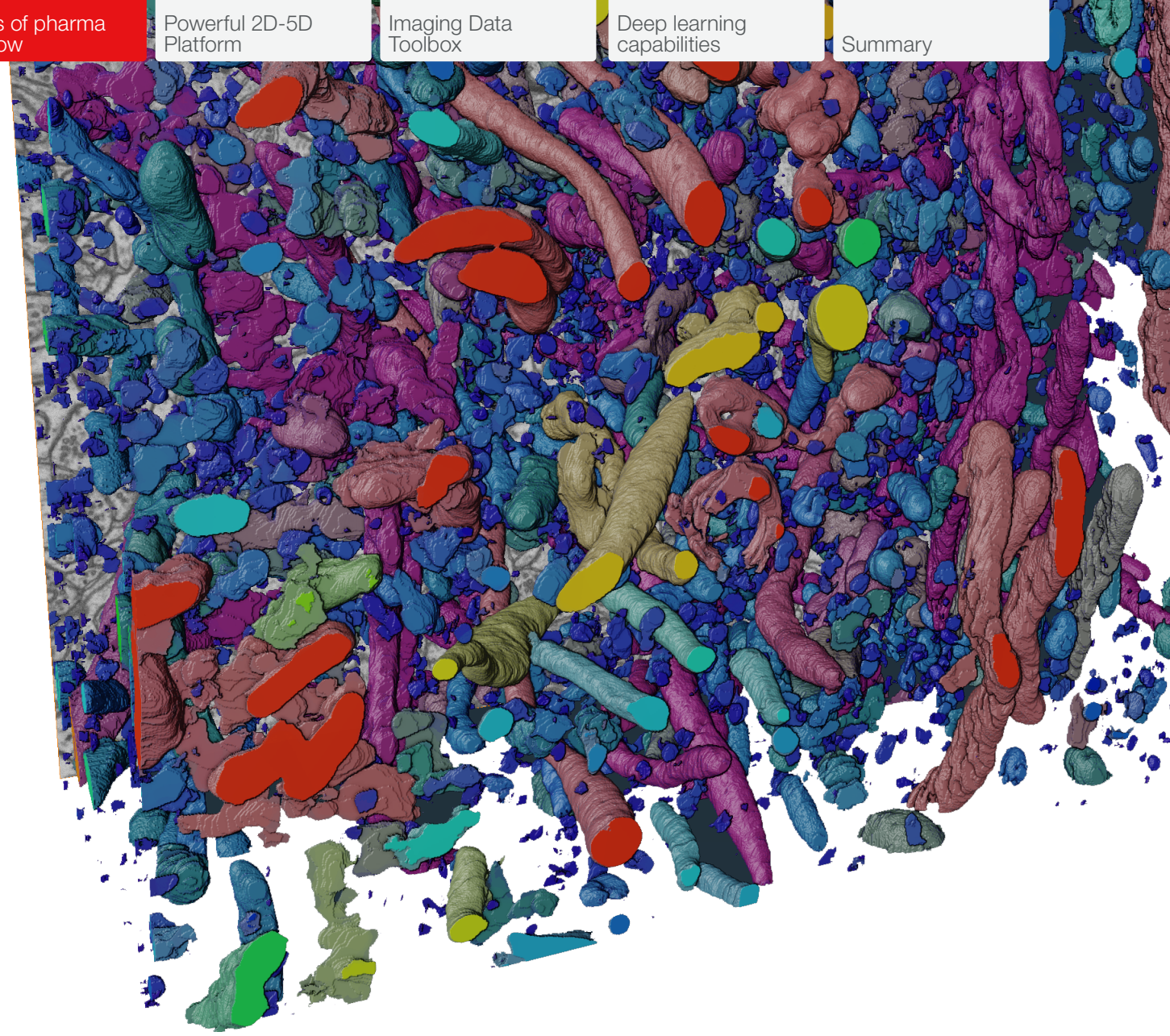
- Cell viability (or its apoptosis or cell count)
- Cell dynamics (their proliferation and migration)
- Spatial cell distribution

At the intracellular level:

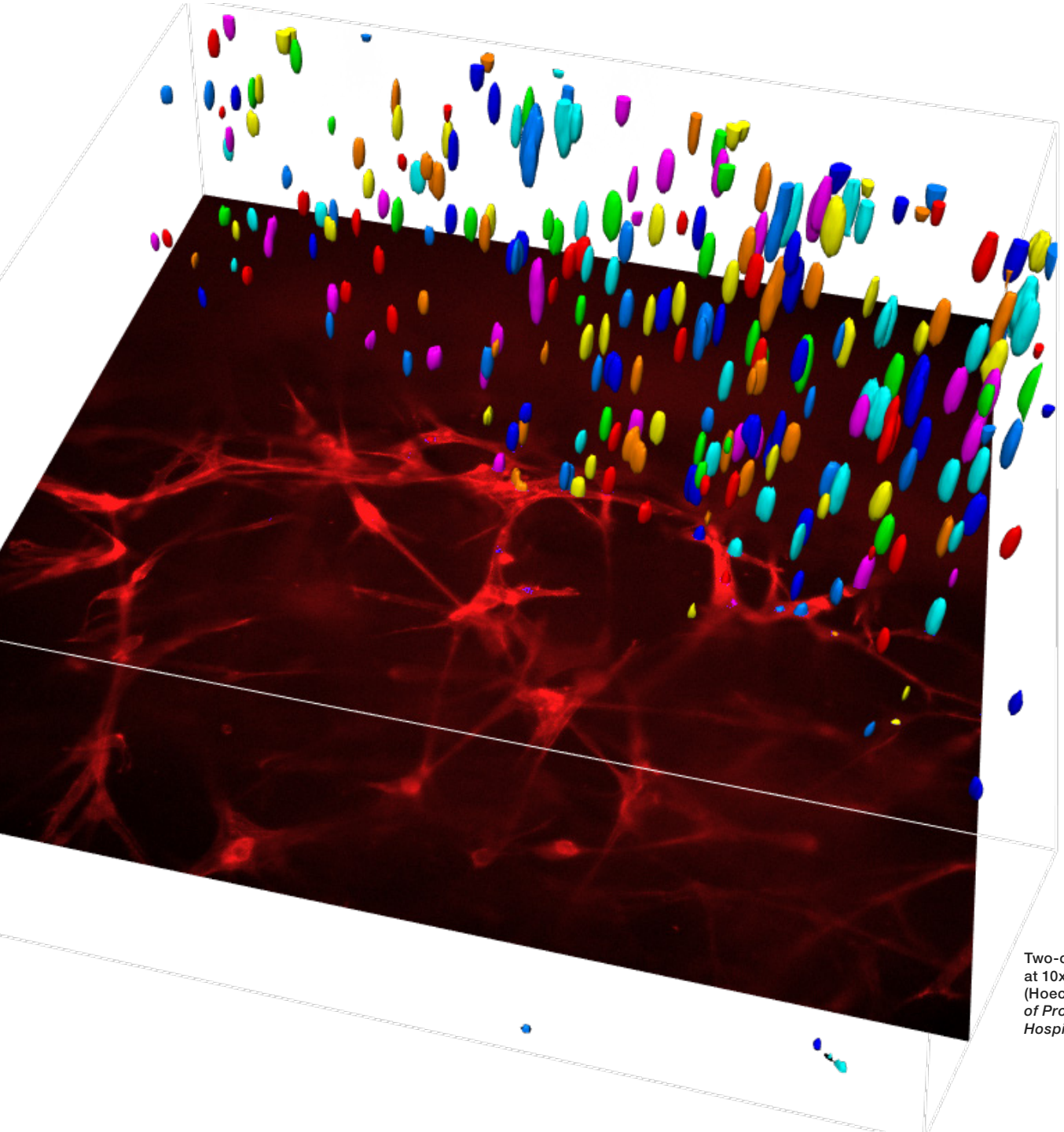
- Cell morphology (size, shape, volume)
- Organelle detection and count
- Cellular target localization (its biomarker expression)

At the molecular level:

- Molecular surface analysis of cells
- Membrane porosity



EPFL FIB-SEM dataset of a mouse brain imaged at 5nm^3. Image shows detection and segmentation of mitochondria using trained deep learning models within Amira 3D Pro. *Data courtesy of Graham Knott and Marco Cantoni at EPFL.*



Identifying and optimizing lead compounds

Identifying the lead compound's validation, optimization, and efficacy is imperative at the pre-clinical stage to assess a drug's effectiveness and potentially tweak a compound for any unintended side effects. Determining a drug's structure early on can ensure that it will act as intended on the tested animal model(s).

Capabilities of 2D-3D molecular analysis for compound characterization and validation:

- Analysis of drug characteristics (structure, stability, etc.)
- Drug particle distribution (in cell)
- Molecular structure and surface imaging
- Toxicity studies through cell viability testing (apoptosis, count)
- Cell dynamics (proliferation, migration, localization)
- Cell morphology (cytoskeleton)

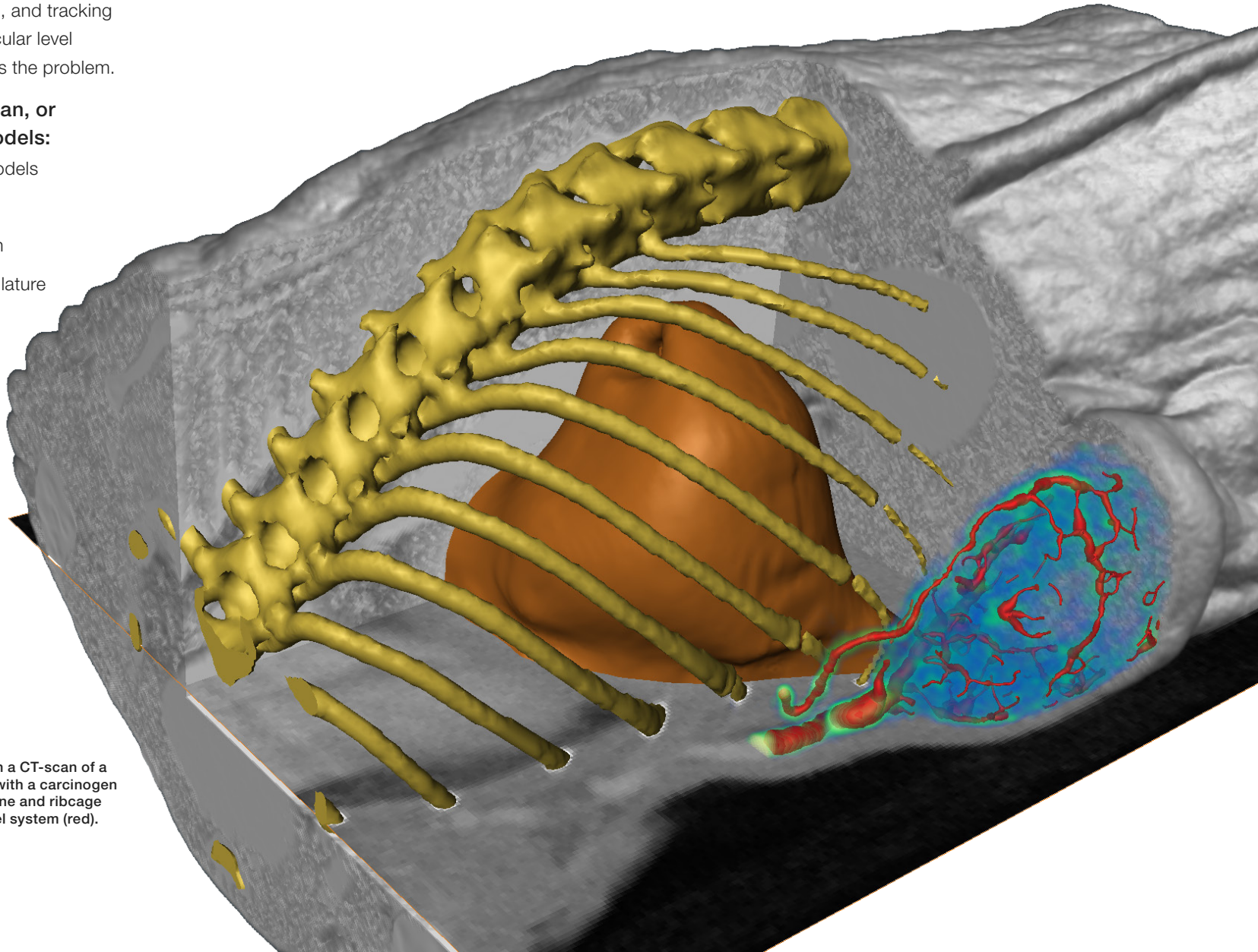
Two-channel sample imaged on a Thermo Scientific CellInsight CX7. Data captured at 10x magnification, 100 z-slices at 4 micron spacing. Two stains consist of DNA (Hoechst) stain and an Actin stain (Phalloidin) for the cytoskeleton. *Data courtesy of Prof. Dr. med. Caroline Ospelt, Center of Experimental Rheumatology, University Hospital of Zurich.*

Preclinical development

Observing the intended effects and potential side effects during the pre-clinical stage of drug development determines whether the tested drug is safe for human ingestion and performs as intended. Using the proper software to assist in mapping, monitoring, and tracking these effects from the tissue to the molecular level ensures that fixes in these stages address the problem.

2D-3D *in vivo* or *ex vivo* tissue, organ, or full organism analysis in animal models:

- Structural anatomy of small animal models
- Bone, skeleton structure analysis
- Soft tissue and tumor characterization
- Tumor localization, growth, and vasculature
- Bone, skeleton structure analysis
- 3D vascular microenvironment



Volume rendering of the reconstruction based on a CT-scan of a mouse which has been treated subcutaneously with a carcinogen agent to induce the growth of a tumor (gray). Spine and ribcage (yellow); liver (orange); Tumor (blue); Blood vessel system (red). *Data courtesy of Dr. Elizatea Stepina and Dr. Peter Hauff, Bayer Healthcare.*

A powerful, multifaceted 2D-5D platform for visualizing, manipulating, and understanding life science research data

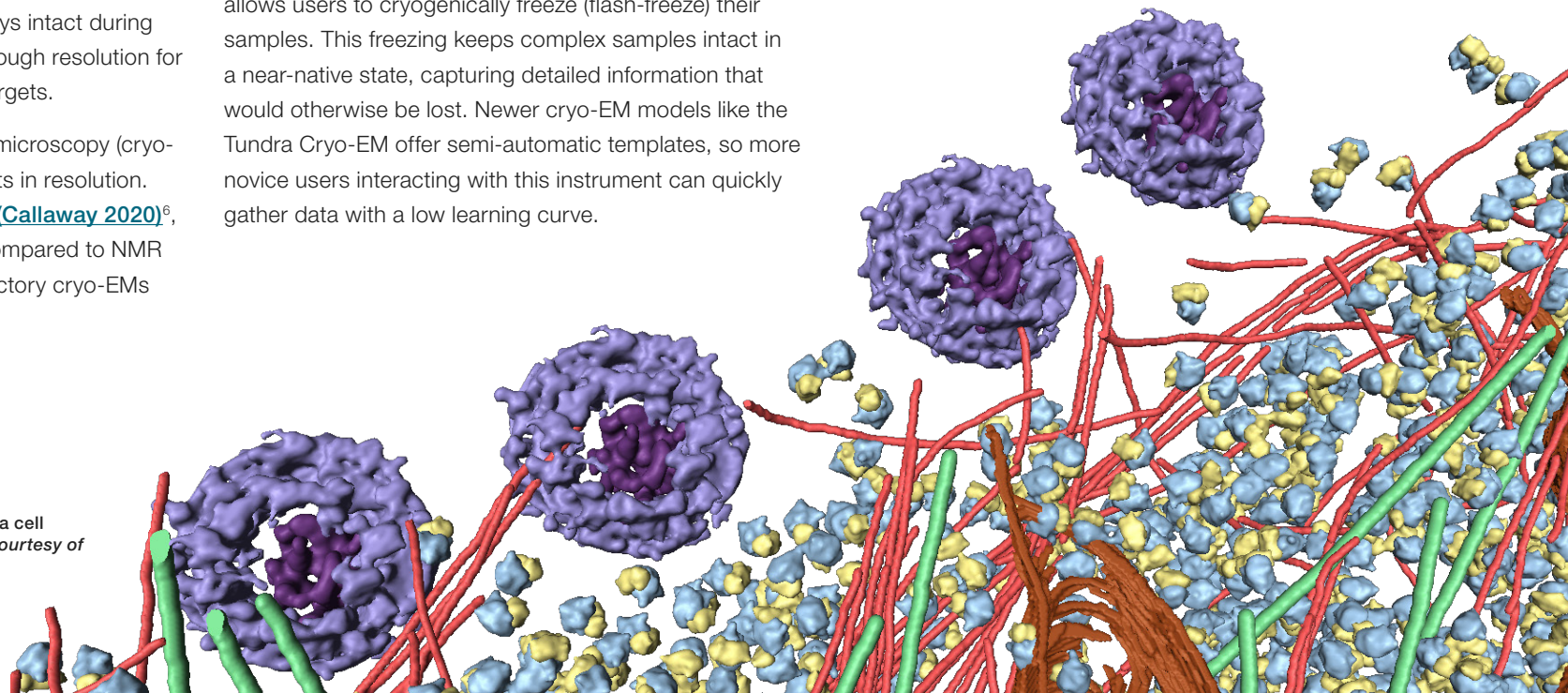
Studying membrane proteins with cryo-EM, cryo-ET, and Amira Software

Obtaining accurate sample images of membrane proteins is key to implementing accurate structure-based drug designs. Traditional methods such as nuclear magnetic resonance (NMR) and X-ray crystallography can provide incredible resolution but those methods require specific sample preparation to acquire data from membrane proteins. **Additionally, membrane proteins account for over 60% of drug targets but make up only 2% of existing crystal structures (Aguayo-Ortiz 2021)**.[5] This gap in imaging membrane protein data illustrates how pharmaceutical research needs imaging techniques that will ensure a membrane protein stays intact during sample preparation and have a high enough resolution for researchers to identify potential drug targets.

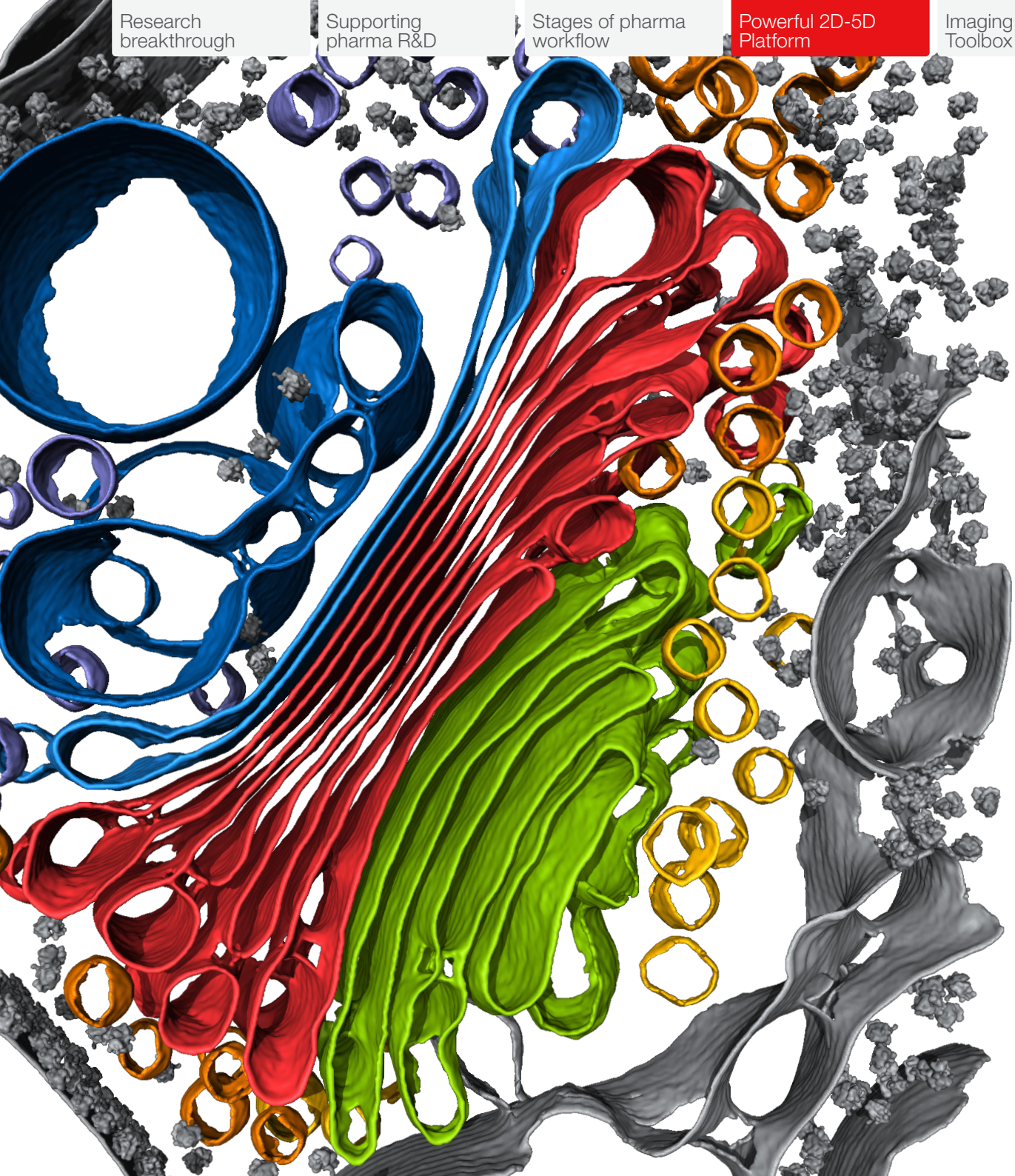
Recent developments in cryo-electron microscopy (cryo-EM) have led to significant improvements in resolution. Thanks to this **"resolution revolution" (Callaway 2020)**[6], cryo-EM is now a competitive option compared to NMR and X-ray crystallography. Even introductory cryo-EMs such as the **Thermo Scientific™ Tundra™ Cryo-TEM** offer competitive resolutions as fine as five angstroms. The Tundra Cryo-TEM's resolution is high enough to acquire membrane protein processes such as revealing binding sites and conformations, assisting with hit finding, and other day-to-day protein functions that unlock a meaningful observation of cell and protein function.

Another advantage of cryo-EM is that pharma researchers do not need to rely on the "perfect crystal" when preparing their samples. The cryo-EM analytical process allows users to cryogenically freeze (flash-freeze) their samples. This freezing keeps complex samples intact in a near-native state, capturing detailed information that would otherwise be lost. Newer cryo-EM models like the Tundra Cryo-EM offer semi-automatic templates, so more novice users interacting with this instrument can quickly gather data with a low learning curve.

For a broader view of cell functioning, cryo-electron tomography (cryo-ET) enables 3D visualizations and analysis of cellular structures. This clear overview gives researchers a better understanding of cellular processes and thus a better understanding of cell function. Cryo-ET samples are preserved in a native state through label-free cryogenic imaging, without the need for sample staining or chemical fixation. The structural and exact spatial arrangement of organelles and proteins remains intact.



Visualization of the nuclear periphery of a HeLa cell revealed by cryo-electron tomography. ***Data courtesy of Dr. J. Mahamid, EMBL.***



This generation of previously unseen, high-resolution imaging data with an abundance of information for pharma researchers means that manually analyzing imaging data gathered from cryo-ETs could take months. An imaging analysis toolbox such as Amira Software allows pharma users to define the search parameters in their imaging data, so automatic data segmentation can be reduced to mere days on large data sets.

Amira Software also allows for a multifaceted approach by enabling pharma research teams to process the same sample with multiple modalities. For example, a team could employ cryo-EM, confocal microscopy, and X-ray crystallography imaging on the same sample. No matter how many modalities a user may implement, Amira Software can automatically sort through the relevant information that the user has specified.

Especially when used with Amira Software, cryo-EM and cryo-ET offer pharma researchers the ability to analyze membrane proteins, cell processes, and cell functions. Using cryo-EM or cryo-ET with Amira Software also streamlines analysis so pharma researchers can make faster, more accurate, structure-based drug discoveries. These unique, cutting-edge imaging techniques hold enormous potential for imaging cell biology.

In situ* cryo-electron tomography reveals the molecular architecture of the Chlamydomonas Golgi apparatus with native morphology. *Data courtesy of Dr. Benjamin Engel, Helmholtz Zentrum München.
https://doi.org/10.1126/science.aaq1392

High-content screening and Amira Software

High-content screening (HCS) also known as High-content imaging, is a widespread technique employed in drug discovery and other biological research to identify inter- or intracellular morphology, key characteristics of cell migration, druggability, and drug safety especially within the fields of oncology, neuroscience, and toxicity studies (BCC Research Sep 2021)[7]. Because this technique must generate, test automatically, and segment thousands to millions of high-resolution samples, employing a variety of imaging modalities, such as fluorescence and confocal microscopy, helps illuminate specific aspects of cell functionality.

Additionally, having imaging analysis software with sufficient throughput and processing power to effectively sort through and automatically interact with these very large data sets is also imperative for streamlined High-Content screening campaigns. The **Thermo Scientific™ CellInsight™ CX7 Pro HCS Platform** offers imaging modalities of LED fluorescence illumination, widefield and brightfield modes, and confocal capabilities to enable high-resolution fluorescent 3D imaging.

Below are two application examples of how Amira Software offers seamless functionality with the CX7 Pro HCS Platform to deliver high-quality data sets to immuno-oncology and neuroscience studies.

HCS and Amira Software for immuno-oncology

Immuno-oncology, or the study of stimulating the body's natural immune response to preventing, halting, and eliminating cancers, is currently one of the most promising cancer therapy programs. This field of study requires HCS to target abnormal cell characteristics effectively. Immuno-oncology researchers use 3D tumor spheroid models to train the immune system to identify, target, and kill tumor-embedded metastatic cells.

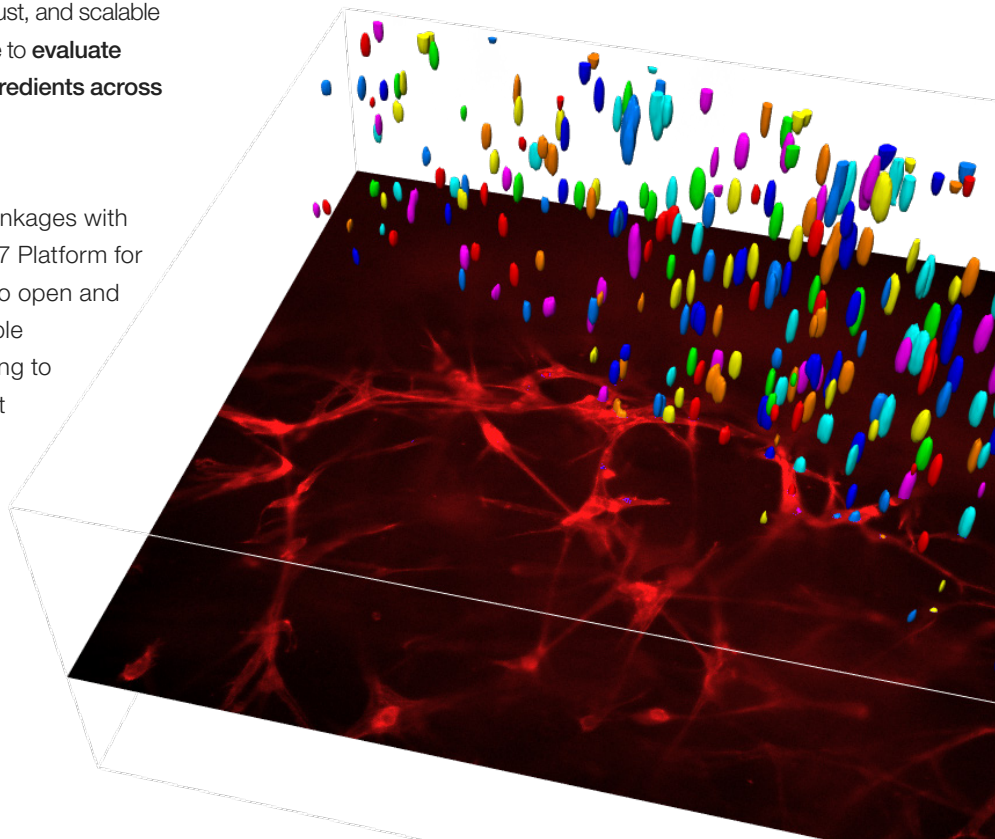
To create these accurate 3D tumor spheroid models, immuno-oncology researchers need an accurate, robust, and scalable 3D software solution such as Amira Software to **evaluate hundreds of potential pharmaceutical ingredients across dose-response curves.**

Key benefits:

Amira Software provides permanent file linkages with HCS Studio Analysis Software for the CX7 Platform for a secure imaging data channel. It can also open and process HCS Studio native files and enable multichannel 3D visualization and rendering to provide Amira Software users with almost immediately available imaging data.

In addition, users can implement time-course analysis capabilities to permit kinetic studies for "4D" measurements necessary for chemotaxis studies. Amira Software also offers 3D morphological evaluations necessary for more accurate immune cell activation studies. To ease the analysis of data from complex, cell-rich samples, Amira Software can evaluate co-localization statistical analysis in 3D samples including the co-localization of immune cells infiltrating a cancerous tumor model.

As noted in the examples above, Amira Software provides users with an extensive quantitative toolbox to tackle tasks such as cell count, morphology, and segmentation for more targeted cancer therapy studies.



HCS and Amira Software for neuroscience

Neuroscience research continues to evolve as new technologies are developed. Traditional *in vivo* animal testing, while very useful, has become both time- and resource-prohibitive. *In vitro* human-model neuroscience studies yield faster, more accurate models of neuronal networks than animal-based testing. Accordingly, the amount of *in vitro* neuroscience research in neurodegenerative, neurogenesis, and neurotoxicology applications has increased considerably.

Studies performed using human-derived 3D neuronal models generate even better outcomes than either monolayer cell culture models or animal-based models. Research using these 3D models is aimed at generating meaningful, realistic outcomes. Specifically, the studies aim to develop, within the models, healthy neurite growth and synaptogenesis that closely mimic *in vivo* results.

However, identifying—let alone targeting—neuronal outgrowth morphology is difficult, even *in vitro*. Neuroscience researchers have attempted to trace neurites and synaptogenic areas, but manual tracing could not keep up with the increased volume of compounds needing to be characterized. To address this issue, three-dimensional software toolboxes such as Amira Software were specifically developed.

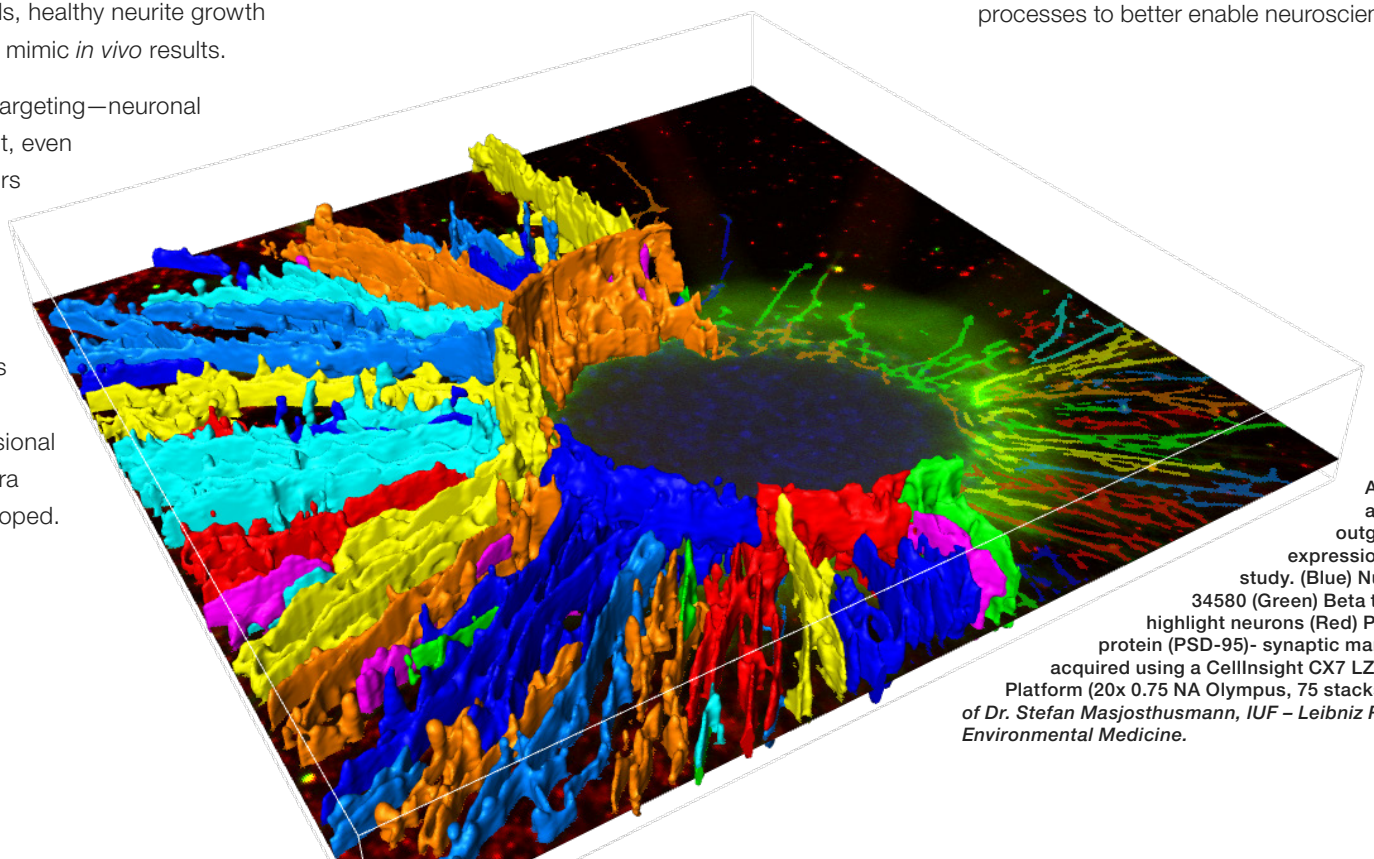
The software's 3D neuroscience abilities have been designed to quantify neuronal morphology accurately and efficiently, to facilitate the high throughput demands of the research. Amira Software offers overarching support in a neuroscience workflow by automating standardized imaging analysis, reducing the end-user learning curve, and improving model accuracy.

Key benefits:

Amira Software has built-in tools to detect primary and secondary neurite morphology and alignment in both 2D and 3D cell culture models. Amira Software also performs automatic detection and segmentation, allowing users to save time and automate their workflows in a way that supports accuracy and reproducibility of analysis.

The Amira Software toolbox can also be adapted to evaluate multi-channel fluorescent markers, allowing for the selective identification of both pre- and post-synaptic (puncta) fluorescent markers. This colocalization capability is imperative to understanding neurodevelopmental disorders such as Autism Spectrum Disorder or neurodegenerative disorders like Alzheimer's Disease. For a faster analysis of large data sets, users can scale Amira Software to enable high-throughput screening of multiple well plate formats, including 96-, 384-, and 1536-well plates.

These features can alleviate some of the pressure points in acquiring and accurately segmenting notoriously complex data sets from neurites while streamlining the associated processes to better enable neuroscience research.



Amira Software 3D analysis of neuronal outgrowth and synapse expression in a toxicological study. (Blue) Nuclear staining Hoechst 34580 (Green) Beta tubulin staining to highlight neurons (Red) Postsynaptic density protein (PSD-95)- synaptic marker. These images were acquired using a CellInsight CX7 LZR High Content Analysis Platform (20x 0.75 NA Olympus, 75 stacks at 3 µM). *Data courtesy of Dr. Stefan Masjosthusmann, IUF – Leibniz Research Institute for Environmental Medicine.*

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.

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

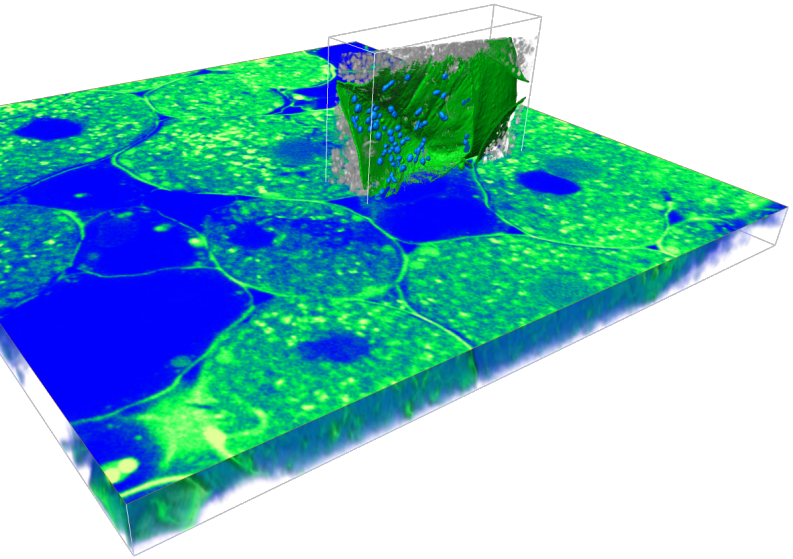
- Advanced video animations
- Charts, spreadsheets, and reports

** Amira Software is not an acquisition software*

A comprehensive set of techniques to serve multiple applications

Correlative imaging

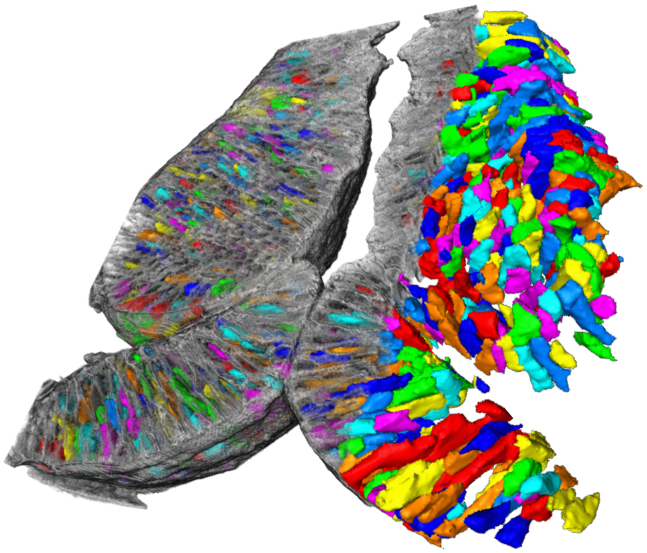
Amira Software supports multi-volume data processing and visualization paired with multiple imaging modalities simultaneously. The automatic registration tools with the Multi-Planar Workroom offer the most commonly used automated registration metrics and allow for adjustable registration parameters to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

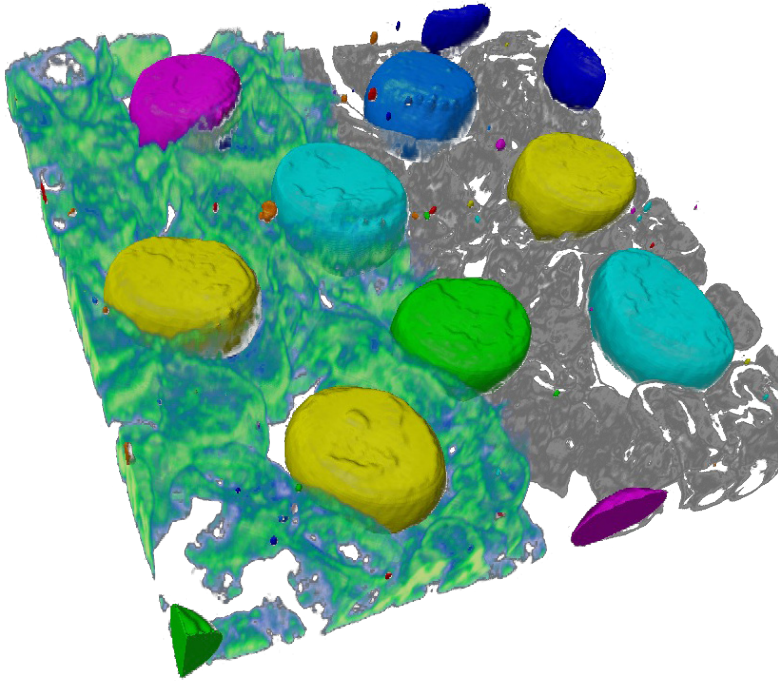
Users can accelerate segmentation with automated detection of cellular features such as membranes and filaments. Amira Software's advanced imaging analysis and combination capabilities allow it to average out noise and sharpen contrast to create a composite model with a higher resolution.



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

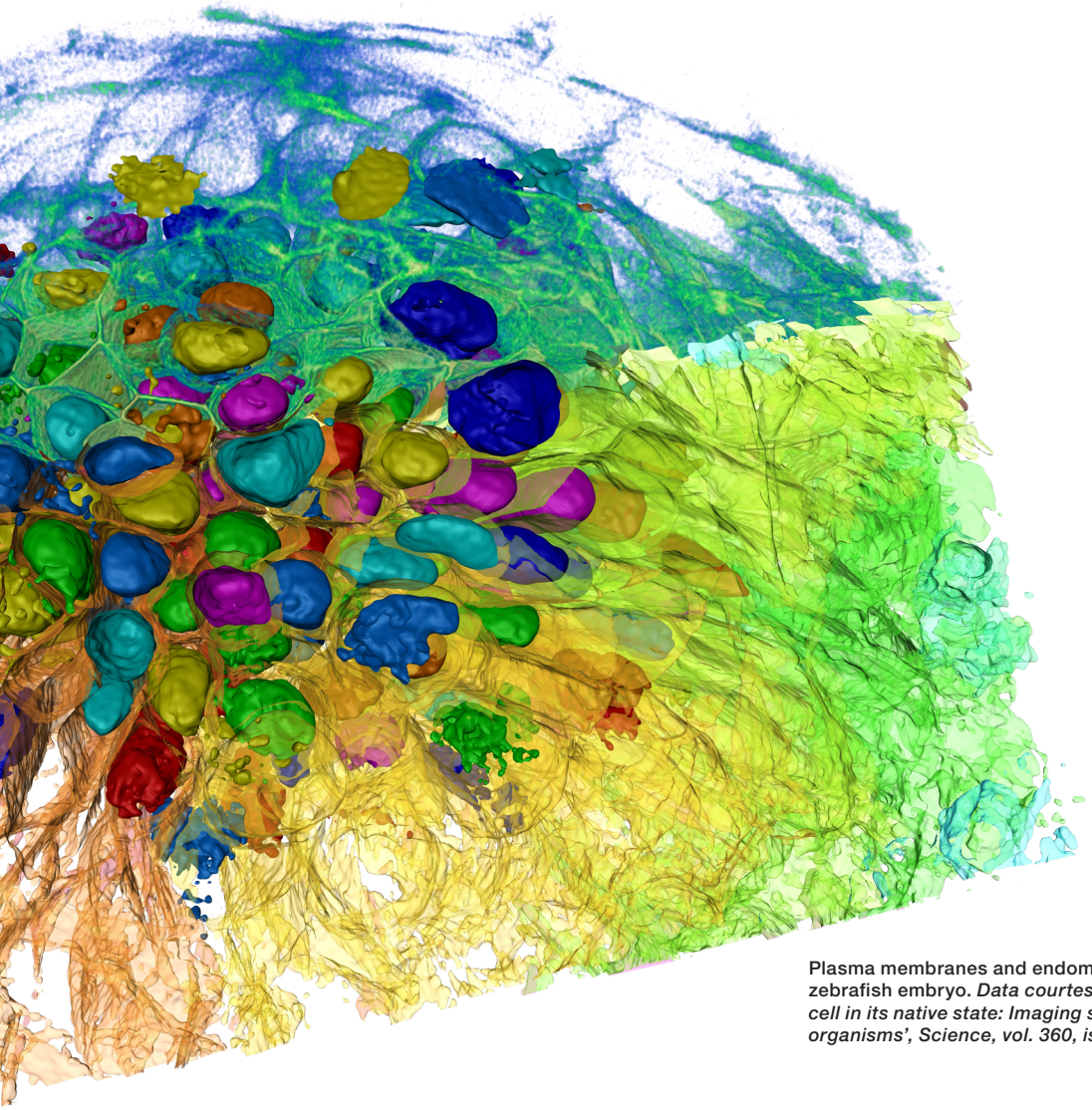
From 3D imaging data on cellular spheroids, Amira Software can automatically identify individual cells and subsequently collect 3D imaging data concerning volumetric, morphometric, and intensity measurements on those individual cells and their nuclei. The potential benefits of analyzing 3D cellular spheroids 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

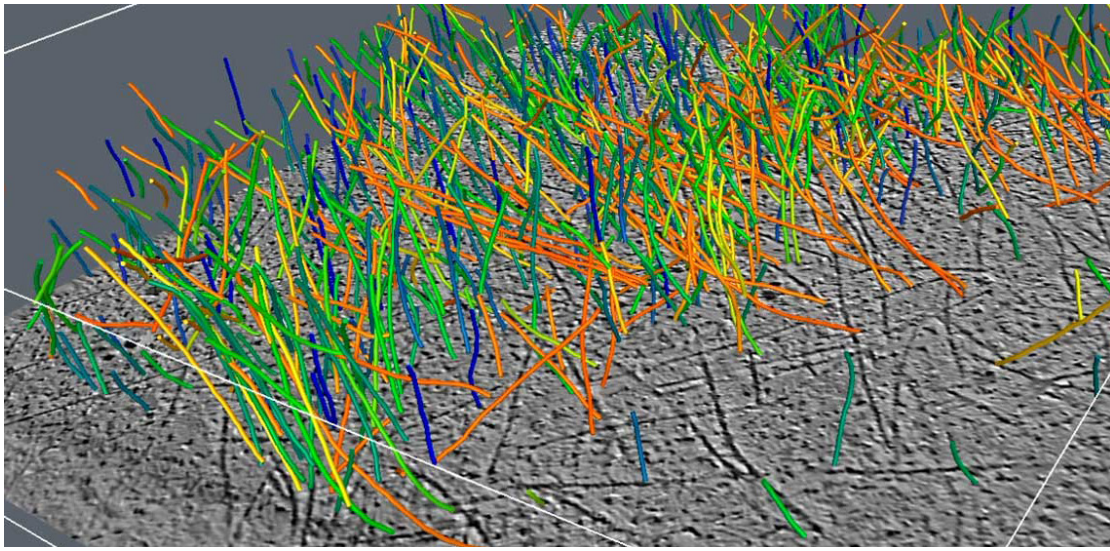
Amira Software allows for easy visualization, correlation, and processing of large multi-channel and time-series data in one platform without worrying about image size or memory limits. With its smart file format, Amira Software can compress all imaging data without losing precious information collected 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.

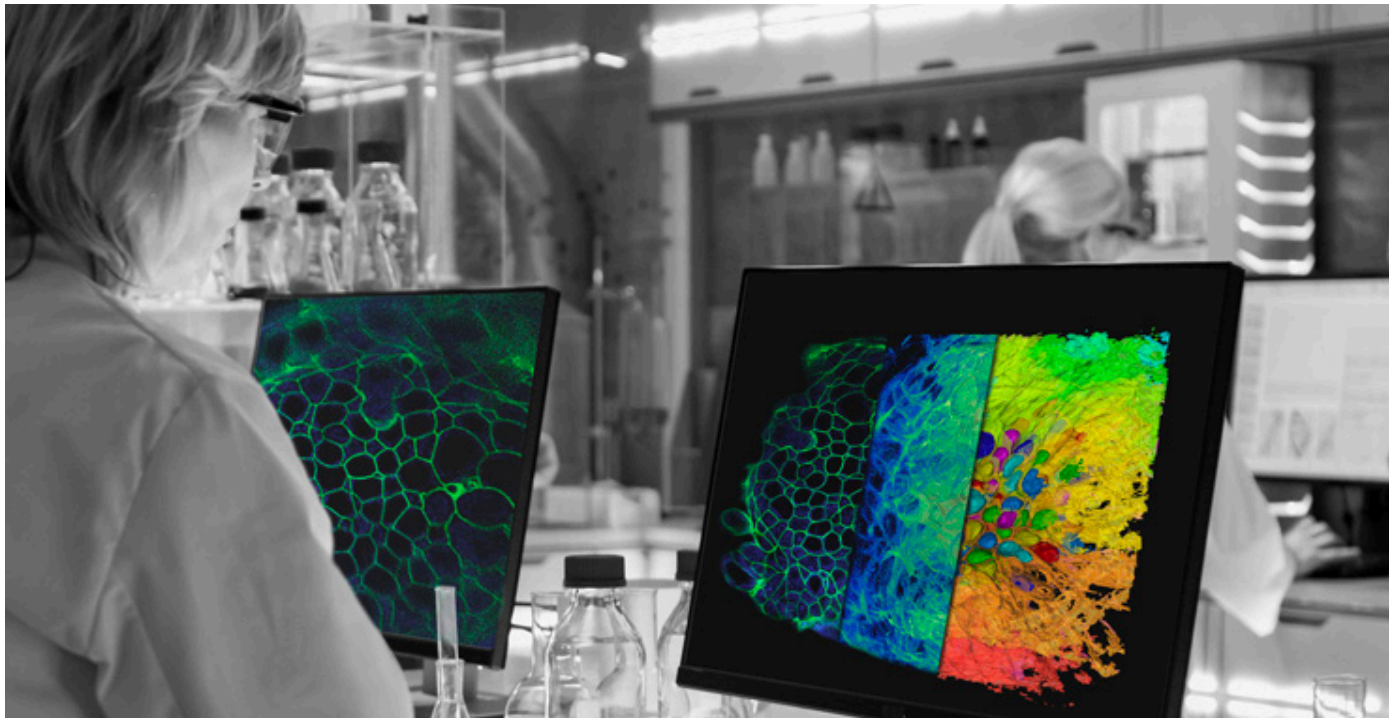
Imaging modalities compatible with Amira Software:

- 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

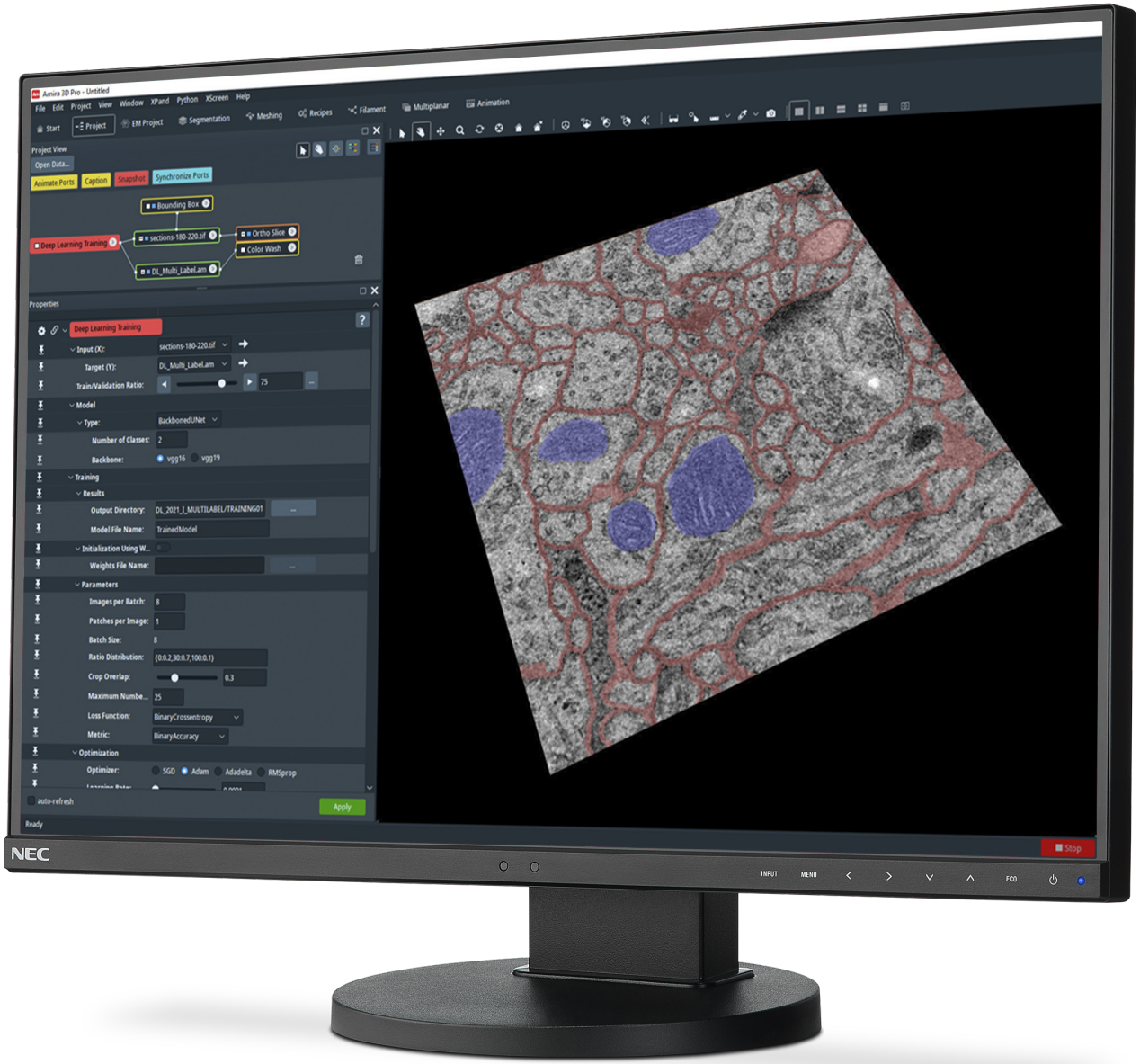
How does deep learning work?

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.



In summary

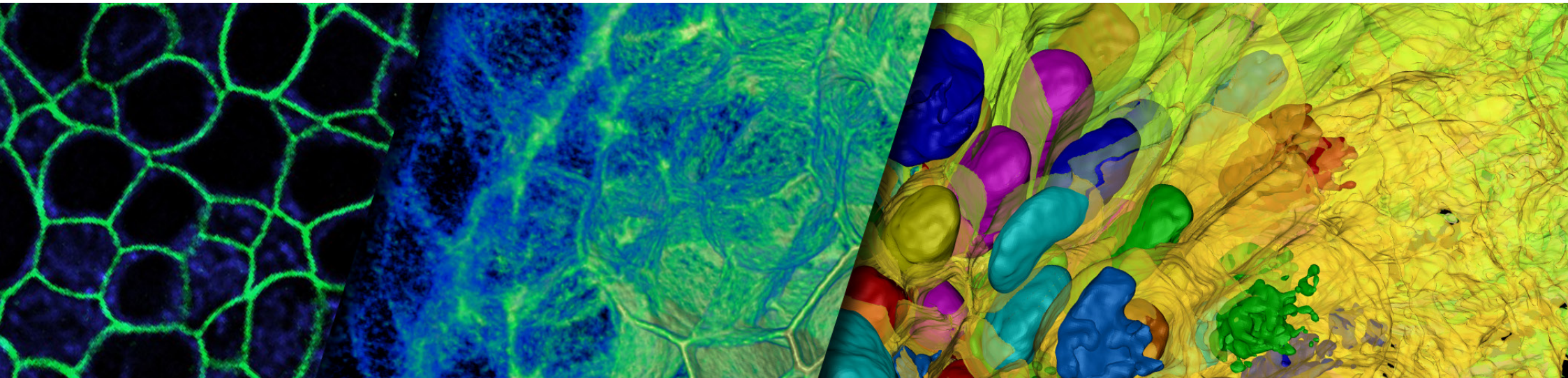
Amira Software is a comprehensive imaging analysis toolbox for pharmaceutical and life science researchers to continue to **push the limits** of their data imaging and analysis. Researchers can accurately observe their quality findings with unparalleled resolution formatting at almost any scale for a breakthrough in drug discovery.

With powerful, trainable **deep learning** neural network models, Amira Software supports research processes by reducing the number of manual, error-prone steps for faster image analysis and **reproducibility.** Additionally, its deep learning capabilities accelerate and improve the segmentation and interpretation of complex data sets, while its intuitive interface reduces the learning curve for even the most novice users.

Amira Software's wide range of applications, its regard within the scientific community, and its continually improving features ensure that it is always designed for **life sciences** researchers. Thermo Fisher Scientific continues to partner with the scientific community to effectively develop technologies that drive pharmaceutical research to interface with *ex* and *in vivo* models, organs, and tissues all the way down to a structural, sub-cellular level.

In pushing these limits, pharmaceutical scientists can better understand how cells function, how cells respond to disease, and what their genetic variations are. Pharmaceutical researchers can also locate and pinpoint physiological responses to drugs, **correlate data** from **multiple modalities** to visualize physiological responses, and then scale their data to meaningfully understand the impact a drug may have on the macro and micro levels. This versatility is essential for pharmaceutical researchers to use their findings to advance research for breakthrough drug discoveries.

Contact us



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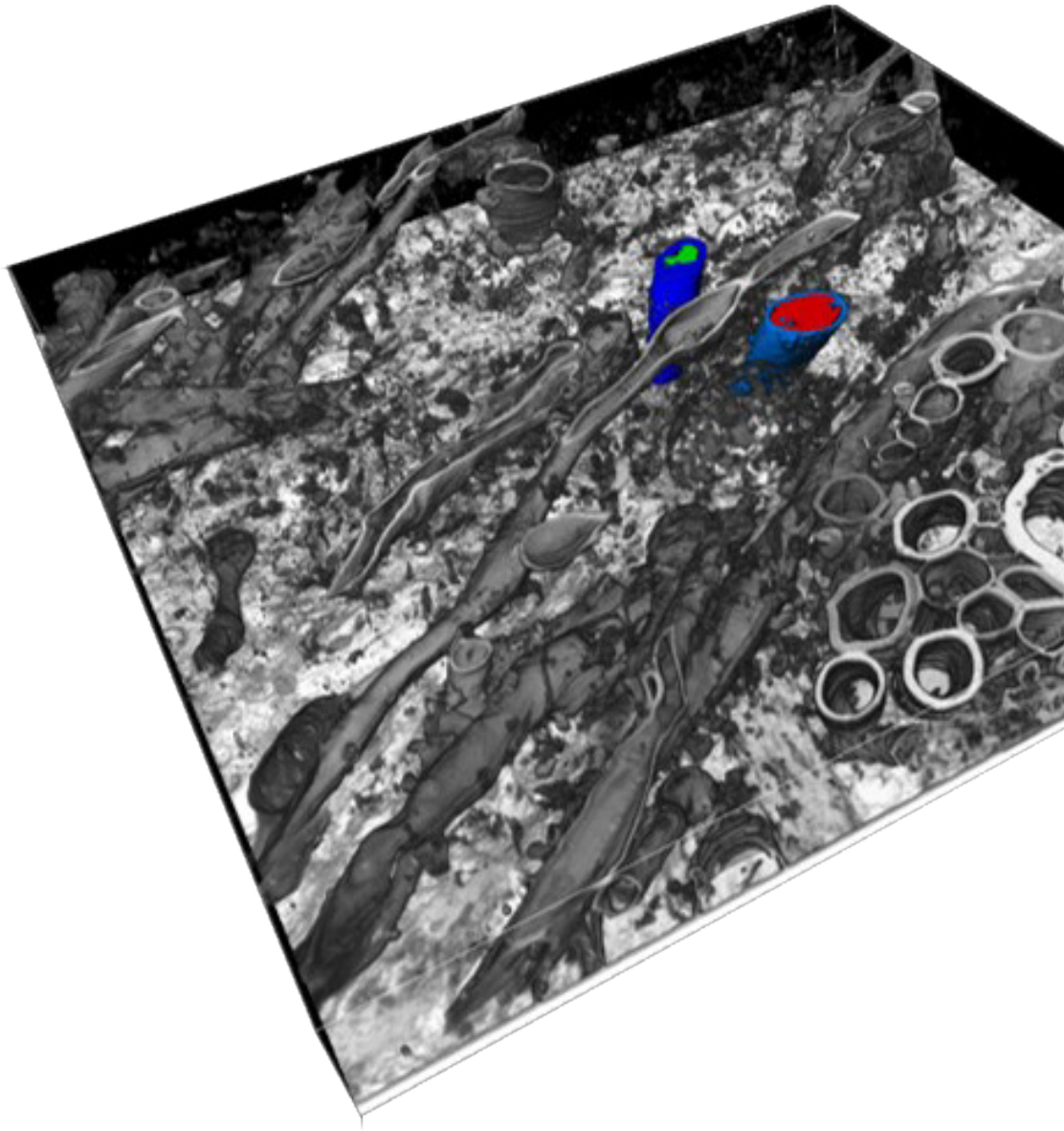
To learn more about Amira Software publications visit our Use Case Gallery.



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

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