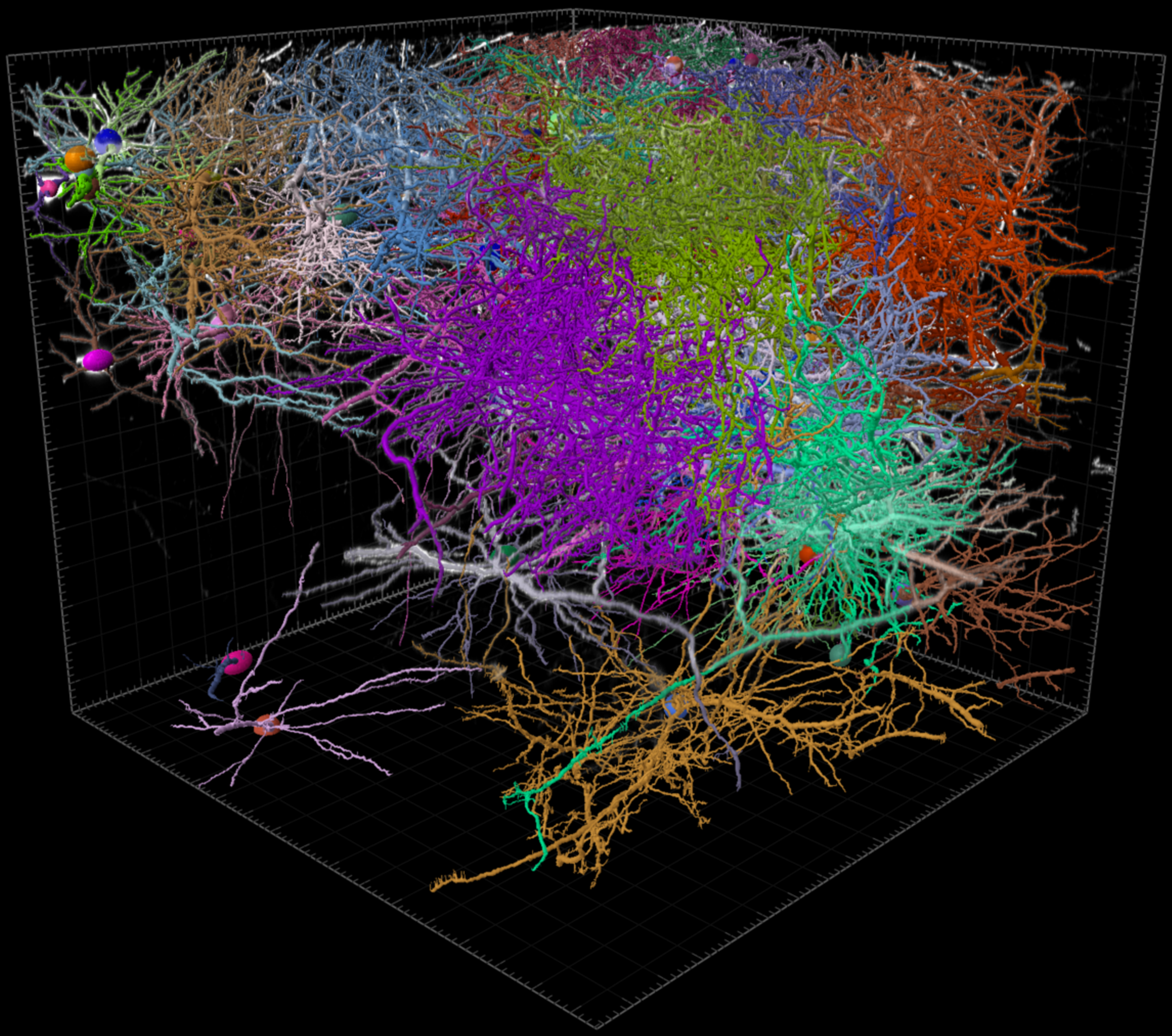

ZEISS arivis: Publication Highlights

How Life Sciences researchers around the world use arivis to
advance science and industry

Generated April 2026 | 2021–2026

ZEISS arivis Pro is formerly known as Vision4D. ZEISS arivis Pro VR is formerly known as VisionVR. ZEISS arivis Hub is formerly known as VisionHub. ZEISS arivis Cloud is formerly known as APEER.

2026

Siglec-E deletion alters AT macrophages phenotypes, induces an inflammatory response, and adipogenesis during diet-induced obesity

A Rakib et al.

AI · Image Analysis · Cell Biology · Immunology · Liver Research

HOW ARIVIS HELPED

ZEISS arivis Cloud (previously APEER) and ZEISS arivis Pro (previously Vision4D) enabled AI-based quantification of hepatic lipid accumulation in a study on Siglec-E's role in adipose tissue inflammation and adipogenesis during obesity

See how arivis Cloud was used to train an AI segmentation model on H&E-stained liver sections, and arivis Pro was used to apply the trained model offline to quantify lipid area and size across liver samples from high-fat diet-fed mice.

This helped this research by providing automated, reproducible quantification of hepatic lipid accumulation, supporting the broader finding that Siglec-E deletion promotes inflammatory macrophage infiltration, adipogenesis, and metabolic dysfunction in obese conditions.

Read the paper

Sixteen isotropic 3D fluorescence live imaging datasets of Tribolium castaneum gastrulation

F Kraemer et al.

Image Analysis · 3D Visualization · Cell Biology · Developmental Biology · Light Sheet Microscopy · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled manual 3D nuclei segmentation and volumetric visualization in a live imaging dataset collection documenting Tribolium castaneum gastrulation

See how arivis Pro was used to manually segment blastodermal and serosa nuclei using the Magic Wand tool in 2D viewer mode, review segmentations in both 2D and 3D viewer modes for quality control by a second researcher, and generate transparency-based volume renderings overlaying voxel data with segmented nuclei centroids displayed as a ventral-dorsal heatmap.

This helped this research by providing accurate, reproducible 3D nuclei segmentation across sixteen live imaging datasets of entire embryos, establishing benchmark segmentation data to support future quantitative analyses of gastrulation dynamics and image processing algorithm development in Tribolium.

Read the paper

U-Net Optimization for Hyperreflective Foci Segmentation in Retinal OCT

P Kodiyalbail Chakrapani et al.

AI · Image Analysis · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Cloud (previously APEER) enabled consensus-based annotation of hyperreflective foci in retinal OCT images for training U-Net segmentation models

See how the APEER Annotate cloud-based platform was used by two ophthalmologists to jointly annotate hyperreflective foci in OCT B-scans, resolving disagreements through discussion to produce consensus ground-truth masks exported in OME-TIFF format for model training and evaluation.

This helped this research by providing reliable, bias-free annotations that served as the reference standard for training and assessing U-Net architectures, with the best-performing model achieving a dice score of 0.5207 and a 19.4% improvement in recall for hyperreflective foci detection compared to the attention U-Net baseline.

Read the paper

Autophagy regulates PVALB (parvalbumin) interneuron excitability and memory

T Chalatsi et al.

AI · Image Analysis · 3D Visualization · Neuroscience · Cell Biology · Light Sheet Microscopy · Tissue Clearing

HOW ARIVIS HELPED

ZEISS arivis Vision4D enabled whole-brain 3D reconstruction and machine learning cell segmentation in a study linking autophagy to parvalbumin interneuron function and memory

See how arivis Vision4D was used to stitch and reconstruct light sheet images of CLARITY-cleared mouse brains, and to run random forest machine learning segmentation for counting TdT-positive PVALB neurons across eight brain regions using Allen Brain Atlas-derived binary masks.

This helped this research by enabling unbiased, brain-wide quantification of interneuron numbers across genotypes, demonstrating that PVALB interneurons survive independently of autophagy across the brain, which was foundational to the study's conclusion that autophagy deficiency impairs inhibitory neurotransmission and hippocampus-dependent memory without causing interneuron loss.

Read the paper

Early glymphatic failure inAppNL-Fknock-in mice is linked to parenchymal border macrophages loss

N Liu et al.

Image Analysis · 3D Visualization · Neuroscience · Alzheimer's Research · Tissue Clearing · Light Sheet Microscopy

HOW ARIVIS HELPED

ZEISS arivis Vision4D enabled 3D reconstruction and quantitative analysis of glymphatic function in a study linking parenchymal border macrophage loss to early Alzheimer's disease progression

See how arivis Vision4D was used to import and reconstruct iDISCO+-cleared whole-brain light sheet image stacks, and to quantify glymphatic clearance using the built-in Analysis Pipeline to calculate sum intensity and sum volume of voxels above a constant threshold.

This helped this research by enabling brain-wide quantification of CSF tracer influx and clearance, revealing that glymphatic dysfunction in AppNL-F mice emerges at 6 months before substantial plaque deposition and correlates with parenchymal border macrophage loss rather than parenchymal amyloid burden.

Read the paper

Cyclase-associated protein 2 gene delivery: A potential multi-target approach for preventing synaptic failure in Alzheimer's disease

R Stringhi et al.

Image Analysis · 3D Visualization · Neuroscience · Cell Biology · Alzheimer's Research · Drug Discovery

HOW ARIVIS HELPED

ZEISS arivis Vision4D enabled 3D colocalization analysis of cofilin-actin rods and CAP2 in a study exploring gene therapy for Alzheimer's disease synaptic failure

See how arivis Vision4D was used to reconstruct 3D Airyscan confocal images of hippocampal neurons, segment cofilin-actin rods using an intensity threshold segmenter, detect CAP2 dots with the blob finder segmenter, and perform compartment operation analysis to identify CAP2 voxels located inside rods.

This helped this research by enabling precise quantification of CAP2-positive versus CAP2-negative actin rods and characterization of their morphological differences, revealing that CAP2 preferentially accumulates in larger, more elongated rods specific to amyloid-beta oligomer exposure, supporting CAP2 as a component and potential therapeutic target in Alzheimer's cytoskeletal pathology.

Read the paper

Mesenchymal stem cell-extracellular vesicles deliver microRNAs that prevent nerve growth factor-induced sensory neuron sensitization

L Qiu et al.

AI · Image Analysis · 3D Visualization · Neuroscience · Cell Biology · Drug Discovery

HOW ARIVIS HELPED

ZEISS arivis Pro enabled super-resolution 3D reconstruction and machine learning segmentation of extracellular vesicle uptake into sensory neurons in a study on MSC-EV-mediated pain relief

See how arivis Pro was used to calculate Nyquist-optimal z-stack acquisition parameters, generate maximum intensity projections and 3D reconstructions of PKH26-labelled EVs in DRG neurons, and train a machine learning-based segmentation model to classify EVs, background, and peripheral gap regions across 3D image stacks from Airyscan super-resolution data.

This helped this research by enabling precise quantification of EV internalization into sensory neurons, demonstrating that protease-mediated surface shaving inhibited EV uptake and abolished the ability of MSC-EVs to prevent NGF-induced sensitization, thereby establishing cellular internalization as a mechanistic requirement for EV therapeutic activity.

Read the paper

Simultaneous Immunofluorescence-Based In Situ mRNA Expression and Protein Detection in Bone Marrow Biopsy Samples

AL Sierras et al.

Image Analysis · Cell Biology · Cancer Research · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled spatial RNA and protein quantification in bone marrow biopsy samples in a study developing a combined RNA-FISH and immunofluorescence protocol for acute lymphoblastic leukemia

See how arivis Pro was used to segment TGFB1 and PDGFA1 RNA signal objects and nuclei via intensity threshold segmentation, export surface size measurements for normalized expression calculations, and measure sum intensities of transcript signals in manually identified single cells across CD45+, CD271+, and megakaryocyte populations.

This helped this research by enabling spatially resolved, single-cell quantification of transcript expression within the bone marrow microenvironment, supporting the characterization of differential TGFB1 and PDGFA1 expression across hematopoietic and non-hematopoietic cell populations in ALL patients.

Read the paper

Near-equiprobable binary branching decisions underlie filament patterning in the moss Physcomitrium patens

J Abitbol

Image Analysis · 3D Visualization · AI · Cell Biology · Developmental Biology · Light Sheet Microscopy · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Vision4D enabled whole-sporeling 3D cell segmentation and chloroplast quantification in a study uncovering probabilistic rules of branching morphogenesis in moss filaments

See how arivis Vision4D was used to segment individual cells from light sheet image stacks using a membrane detection and segmentation pipeline based on tensor voting, curate segmentation results interactively, and detect chloroplasts using the Blob Finder algorithm to estimate chloroplast density per cell.

This helped this research by enabling single-cell resolution reconstruction of 33 complete sporelings into mathematical tree structures, providing the quantitative foundation for revealing that moss filament branching follows a near-equiprobable binary decision model that may have broader relevance across branching morphogenesis in the plant kingdom and beyond.

Read the paper

Quantitative 3D cytoarchitecture of human brain organoids using light-sheet microscopy

OS Vinchure et al.

AI · Image Analysis · 3D Visualization · Cell Biology · Neuroscience · Organoid Research · Developmental Biology · Light Sheet Microscopy · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled machine learning segmentation and 3D quantification of human brain organoid cytoarchitecture in a study validating the LUCID-org light-sheet imaging pipeline

See how arivis Pro was used to run Cellpose and Blob Finder segmentation algorithms, train machine learning models for cell type classification and lumen detection, build custom quantification pipelines for feature extraction, and generate volumetric 3D reconstructions of intact cleared organoids.

This helped this research by enabling unbiased, whole-organoid quantification of progenitor density, ventricular zone lumen volume, and neuronal distribution, revealing measurable cytoarchitectural defects in CENPJ-mutated microcephaly organoids compared with healthy controls.

Read the paper

Optimizing the transport properties of sulfide-based composite cathode for sodium solid state batteries: Effects of composition and ball-milling parameters

R Ücüncüoglu et al.

AI · Image Analysis · Materials Science · Quality Control · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Cloud (previously APEER) enabled deep learning-based particle segmentation for quantitative microstructure analysis in sodium solid-state battery cathode research

See how arivis Cloud was used to train a deep learning segmentation model on manually annotated SEM images, which was then imported into ZEISS ZEN core to automatically segment individual particles and extract size metrics including equivalent circular diameter and particle area across composite cathode samples milled at different times.

This helped this research by enabling quantitative, reproducible particle size analysis across a range of length scales, revealing that milling time significantly influences electronic conductivity in composite cathodes and that optimal sodium solid-state battery transport properties are achieved at 50 wt% NaCrO2 active material.

Read the paper

Protocol for analyzing the microstructure of nuclear fiber layers by using structured illumination microscopy coupled with Arivis 4D

M Guan et al.

Image Analysis · Cell Biology · Neuroscience · Super-Resolution Microscopy · Disease Diagnostics · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled quantitative 3D microstructure analysis of nuclear fiber layers from super-resolution microscopy

See how arivis Pro (previously Vision4D) was used as the core analysis platform for processing, 3D reconstruction, and quantitative characterization of nuclear lamin A fiber network structures imaged with the ZEISS Elyra 7 SIM² super-resolution system at 60 nm resolution. This helped this research by providing a complete image processing pipeline, from SIS file conversion, background noise removal using Draw Object masking tools, signal enhancement, through to a novel custom Python script-based algorithm for filamentary structure extraction — that enabled precise quantification of nuclear skeleton microparameters including nuclear surface area, nuclear volume, branching points, number of lines, number of meshes, line distance, mesh surface area, and mesh volume. The software's 2D/3D viewer capabilities allowed systematic inspection across Z-axis levels for quality control, while the analysis pipeline framework enabled researchers to build a reproducible, batch-capable workflow combining preprocessing, segmentation, and custom quantification steps. This protocol establishes a foundation for diagnosing laminopathy-related diseases, including muscular, metabolic, neurological disorders, and accelerated aging syndromes, by providing visual evidence and precise morphological measurements of nuclear skeleton abnormalities that were previously difficult to quantify, addressing an unmet medical need in clinical diagnostics.

Read the paper

Advanced Mounting Technique for Improved Imaging and Analysis of Embedded Spheroids and Migrating Cells in Light Sheet Fluorescence Microscopy

M Mohamadian Namaqi, F Moll…

Image Analysis · Cell Biology · Cancer Research · Drug Discovery · Organoid Research · 3D Cell Culture · Light Sheet Microscopy

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled quantitative 3D analysis of cancer cell migration and chemotherapy response in collagen-embedded spheroids

See how arivis Pro (previously Vision4D) was used for 3D segmentation, cell detection, and migration analysis of ES-2 ovarian cancer spheroids embedded in collagen gels, imaged on a ZEISS Lightsheet 7 microscope with a novel sample holder enabling dual-sided illumination. This helped this research by providing a complete analysis pipeline - including particle enhancement filtering, Blob Finder-based cell segmentation with optimized thresholds, volume filtering, and Distance Operator measurements - that enabled quantitative extraction of cell number, spheroid volume, cell density, and individual cell migration distances directly from 3D light sheet image stacks. The software's volumetric visualization capabilities were critical for optimizing segmentation thresholds across different timepoints, ensuring accurate cell detection without over- or under-segmentation in complex 3D collagen matrix environments. This workflow revealed that ES-2 spheroids undergo early migration without proliferation by day 1, followed by parallel proliferation and outward migration by day 3, with cells detected beyond 180 μm from the spheroid center. When treated with the chemotherapy agent SN-38, the arivis-powered analysis quantitatively demonstrated that cell number and migration distance were significantly arrested compared to untreated controls, findings that support the model's applicability for 3D drug screening in physiologically relevant extracellular matrix environments.

Read the paper

Targeted gene transfer into developmentally defined cell populations of the primate brain

ARR Gomes et al.

3D Visualization · Neuroscience · Developmental Biology · Cell Biology · Light Sheet Microscopy · Tissue Clearing

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled 3D visualization of whole-fetus peripheral nervous system labeling in a study introducing ultrasound-guided fetal intracerebroventricular viral injections for targeted gene transfer in the primate brain

See how arivis Pro (previously Vision4D) was used to import cleared and background-subtracted whole-fetus light sheet image stacks for 3D visualization by adjusting orientation and lookup tables to reveal AAV9-mediated tdTomato labeling of peripheral somatosensory pathways.

This helped this research by providing whole-organism volumetric visualization of transgene distribution across the intact fetal peripheral nervous system, supporting the demonstration that FIVI enables broad and cell-type-selective transgene expression with potential for prenatal gene editing applications across species.

Read the paper

A characterization of axolotl digit regeneration: conserved mechanisms, divergent patterning, and a critical role for hedgehog signaling

JR Griffiths et al.

Image Analysis · 3D Visualization · AI · Cell Biology · Regenerative Medicine · Developmental Biology · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled 3D segmentation and volumetric analysis of regenerating axolotl digit blastemas

See how arivis Vision4D was used for 3D rendering and nuclear segmentation of two-photon and confocal image stacks from FUCCI transgenic axolotls, with manual ROI definition to isolate mesenchymal compartments and neurite volume quantification using the Arivis Threshold Based Reconstructor.

This helped this research by enabling longitudinal quantification of cell cycle dynamics in innervated versus denervated blastemas, revealing G1-phase arrest following denervation, and confirming that interdigital differences in joint regenerative fidelity — ranging from 100% in digit DII to 8% in digit DIII — could not be explained by differences in innervation or proliferation, pointing investigators toward Hedgehog signaling as essential for interphalangeal joint regeneration.

Read the paper

Ribosome biogenesis is increased in hepatocellular carcinoma and represents a potential therapeutic target

SB Geisler et al.

AI · Image Analysis · Cell Biology · Cancer Research · Liver Research · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled high-throughput automated nucleolar segmentation and quantification across pan-cancer tissue microarrays in a study identifying ribosome biogenesis as a therapeutic target in hepatocellular carcinoma

See how arivis Pro was used to segment nuclei via Cellpose-based deep learning, detect nucleoli and transcription foci with the Blob Finder module, define nucleoplasmic compartments through object math operations, and extract per-nucleus nucleolar intensity and foci count features from TMA images acquired on the ZEISS Axioscan 7.

This helped this research by enabling unbiased, high-throughput quantification of nucleolar Treacle, Fibrillarin, and Pol II signals across thousands of cells from multiple cancer types, revealing progressive upregulation of nucleolar activity in advanced HCC stages and supporting nucleolar targeting as a viable therapeutic strategy with a broader window than Sorafenib.

Read the paper

2025

New Approaches Based on Serial-Block Face Electron Microscopy to Investigate the Peripheral Nervous System

V Borisovs et al.

AI · Image Analysis · 3D Visualization · Neuroscience · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled deep learning-based segmentation and 3D rendering of peripheral nerve ultrastructure from SBF-SEM data across multiple sample preparation methods

See how arivis Pro (previously Vision4D) was used to train separate deep learning segmentation models for myelin sheaths, Schwann cells, mitochondria, axons, and nuclei using manual brush annotations of approximately 50 structures per tissue compartment, combining segmenters with feature filters to remove erroneous objects prior to 3D reconstruction.

This helped this research by enabling fully automated, cross-method 3D reconstruction of peripheral nerve and dorsal root ganglia ultrastructure, demonstrating that automated uranyl-free staining can achieve segmentation quality comparable to the gold standard high molecular weight protocol, particularly for peripheral nerve specimens.

Read the paper

RatDISCO, a tissue clearing and immunolabelling protocol for large rat brains

KJ Craigie et al.

Image Analysis · 3D Visualization · Neuroscience · Tissue Clearing · Light Sheet Microscopy · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled custom 3D rat amygdala atlas creation and automated cell quantification in a study introducing RatDISCO as an optimized tissue-clearing protocol for adult rat brains

See how arivis Pro (previously Vision4D) was used to manually draw volumetric 3D atlas objects for amygdala subregions based on anatomical landmarks, register the atlas to light sheet image datasets, and run Blob Finder-based analysis pipelines to automatically detect and quantify FoxP2 and cFos immunolabeled nuclei within defined compartments across cleared rat brain hemispheres.

This helped this research by enabling spatially resolved, atlas-registered cell density quantification across amygdala subregions, revealing that RatDISCO achieves dramatically higher FoxP2-positive cell densities than iDISCO+ in all four major basolateral amygdala complexes, demonstrating superior antibody penetration in adult rat tissue.

Read the paper

Functional thalamocortical innervation of VIP-and SST-expressing GABAergic interneurons in mouse barrel cortex

M Feyerabend et al.

Image Analysis · Neuroscience · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled confocal image tile stitching for morphological evaluation of thalamocortical circuits in mouse barrel cortex

See how arivis Pro (previously Vision4D) was used to manually stitch confocal image stack tiles of the barrel field for evaluation of cellular morphology and thalamocortical injection patterns, with individual cells subsequently selected for manual reconstruction in Neurolucida.

This helped this research by providing complete, accurately assembled views of neuronal arborizations across the barrel cortex, enabling selection and reconstruction of VIP and SST interneurons sufficient for characterizing the laminar extent and incidence of VPM and POm thalamic inputs.

Read the paper

In situ quantification of ribosome number by electron tomography

M El Hankouri et al.

Image Analysis · 3D Visualization · Cell Biology · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled automated ribosome segmentation from electron tomography data and 3D cell volume quantification from confocal fluorescence images in a study developing a microscopy-based method for whole-cell ribosome counting

See how arivis Pro (previously Vision4D) was used to segment ribosomes from inverted, denoised electron tomography subvolumes using the Blob Finder with a 30 nm diameter parameter, apply touching edge and feature filters to remove artefacts, and separately segment cell membrane and nuclear volumes from confocal Z-stacks using the magic wand tool and bilateral denoising for cytoplasmic volume determination.

This helped this research by enabling direct quantification of ribosome concentrations averaging 7,282 per cubic micrometre at the 50-voxel threshold, and whole-cell cytoplasmic volume measurements that together produced total ribosome counts in the same order of magnitude as established biochemical RNA electrophoresis methods.

Read the paper

Self-renewal of neuronal mitochondria through asymmetric division

TP Waingankar et al.

Image Analysis · Cell Biology · Neuroscience

HOW ARIVIS HELPED

ZEISS arivis Pro enabled automated quantification of mitochondria, mtDNA, and metabolic labeling foci in a study discovering asymmetric mitochondrial division as a self-renewal mechanism in sensory neurons

See how arivis Pro (previously Vision4D) was used to segment and count mitochondria, TFAM puncta, EdU and EU metabolic labeling foci, and ATP reporter intensities within manually defined neuronal ROIs, with cell bodies and non-neuronal cells masked prior to pipeline execution to restrict quantification to axonal compartments.

This helped this research by enabling systematic, field-of-view-level quantification of mtDNA replication and transcription activity across neurite and branch-point mitochondrial populations, revealing that branch-point mitochondria are preferentially enriched in mtDNA, engaged in active replication, and undergo asymmetric division that sheds mtDNA-free daughters into neurites.

Read the paper

Long Term cultures of Xenopus and Drosophila neurons and glial cells

F Noémie et al.

AI · Image Analysis · Cell Biology · Neuroscience · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled automated nucleus segmentation and multi-channel marker quantification in long-term Xenopus and Drosophila CNS cell cultures

See how arivis Pro was used to segment DAPI-labeled nuclei using the Blob Finder tool with Gaussian smoothing, Laplacian enhancement, and watershed segmentation, and to quantify cell-type marker positivity by measuring mean fluorescence intensity across all channels within each segmented nucleus using species-specific size and intensity thresholds.

This helped this research by enabling consistent, high-throughput quantification of neuronal and glial cell populations across 14-day cultures from two non-rodent model organisms, supporting the demonstration that both Xenopus and Drosophila cultures maintain representative CNS cell populations including oligodendrocytes, astrocytes, and microglia comparable to more established culture systems.

Read the paper

EnteropathogenicEscherichia colimanipulates the host exocyst complex to enhance pedestal formation

TUB Herath et al.

AI · Image Analysis · 3D Visualization · Cell Biology · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled AI-assisted segmentation, 3D reconstruction, and volumetric quantification of bacterial pedestals and exocytosis in a study revealing how EPEC co-opts host exocytosis for pedestal formation

See how arivis Pro was used to process Airyscan super-resolution Z-stacks, perform AI-assisted segmentation of F-actin pedestals and VAMP3-EGFP exocytosis signals, generate 3D reconstructions and movies from optical sections, and quantify pedestal and exocytosis volumes across hundreds of individual structures.

This helped this research by enabling precise volumetric comparison of pedestals between wild-type and mutant EPEC strains, revealing that EspH and exocyst components Sec3 and Stx4 each contribute 23 to 30% of pedestal volume, and that exocytosis and actin polymerization make additive, independent contributions to pedestal formation.

Read the paper

Remodelled cholesteryl ester enriched lipid droplets fuel flavivirus morphogenesis

A Banducci

Life Sciences · Cell Biology

HOW ARIVIS HELPED

ZEISS arivis Pro enabled automated lipid droplet segmentation, per-cell counting, and cell tracking in a study identifying cholesteryl ester-enriched lipid droplets as essential host components for flavivirus morphogenesis

See how arivis Pro was used to segment nuclei using the integrated Cellpose Cyto2 algorithm, detect lipid droplets with the Blob Finder tool, apply size filtering to exclude artifacts below 15 μm^3, assign droplets to individual cells via the compartments operation, and track cells over time using Brownian motion-based tracking from segmented nuclei centroids.

This helped this research by enabling quantitative, per-cell lipid droplet analysis across time-lapse experiments, supporting the discovery that SOAT1/2 activity drives cholesteryl ester-enriched lipid droplet formation during flavivirus infection and that disruption of this process results in a ~100-fold reduction in viral production.

Read the paper

Registration-based 3d light sheet fluorescence microscopy and 2d histology image fusion tool for pathological specimen

M Brettmacher et al.

3D Visualization · Cancer Research · Protocol/Methods · Light Sheet Microscopy

HOW ARIVIS HELPED

ZEISS arivis Pro enabled analysis of light sheet fluorescence microscopy data in a study introducing LitSHi, an automated registration tool for multimodal fusion of 3D LSFM and 2D histology images of pathological specimens

See how arivis Pro was used to analyze LSFM image data from cleared testicular tumor specimens acquired on the UltraMicroscope Blaze, providing the 3D volumetric foundation for the multimodal registration workflow developed in LitSHi.

This helped this research by enabling high-resolution 3D visualization of intact tissue specimens that, when fused with 2D histological sections via the LitSHi registration pipeline, demonstrated improved structural correspondence between modalities and significantly reduced the manual intervention required compared to traditional registration approaches.

Read the paper

Superovulation-induced changes in murine ovarian perifollicular angiogenesis

G Mappa et al.

Image Analysis · 3D Visualization · Reproductive Biology · Light Sheet Microscopy · Tissue Clearing · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled 3D vessel segmentation and quantitative vascular analysis of perifollicular capillary beds in the first comprehensive 3D study of superovulation-induced angiogenic changes in murine ovaries

See how arivis Pro (previously Vision4D) was used alongside Fiji to perform 3D volume rendering, vessel segmentation, and quantification of metrics including vessel volume, length, branching, density, and spatial arrangement from light sheet fluorescence microscopy images of optically cleared ovarian samples.

This helped this research by enabling the first comprehensive quantitative 3D profiling of thecal vasculature in murine antral follicles, revealing dose-dependent and time-dependent perifollicular angiogenic responses to PMSG superovulation, including premature neoangiogenesis at 7.5 IU and reduced vessel density at 2.5 IU compared to naturally cycling controls.

Read the paper

Oleuropein Aglycone, an Olive Polyphenol, Influences Alpha-Synuclein Aggregation and Exerts Neuroprotective Effects in Different Parkinson's Disease Models

MJ Basellini, JM Granadino

Image Analysis · 3D Visualization · Cell Biology · Neuroscience · Parkinson's Disease Research · Drug Discovery

HOW ARIVIS HELPED

ZEISS arivis Pro enabled 3D reconstruction and volumetric quantification of alpha-synuclein aggregates in a study evaluating the neuroprotective effects of oleuropein aglycone in Parkinson's disease models

See how arivis Pro (previously Vision4D) was used to reconstruct cell bodies and nuclei via intensity threshold segmentation, detect alpha-synuclein preformed fibrils using the Blob Finder pipeline, and quantify the volumetric relationship between aggregates and cells to distinguish internalized from membrane-associated PFFs.

This helped this research by revealing that larger aggregates remain hooked to the cell membrane while smaller ones are internalized, and enabling quantification of a 69% reduction in internalized PFF volume upon oleuropein aglycone treatment, supporting its neuroprotective potential against alpha-synuclein pathology.

Read the paper

Tracking of single virus: Dual fluorescent labeling of pseudorabies virus for observing entry and replication in the N2a cells

M Li et al.

Image Analysis · 3D Visualization · Cell Biology

HOW ARIVIS HELPED

ZEISS arivis Pro enabled 3D reconstruction and live-cell visualization of single pseudorabies virus particles during entry and replication in neuronal cells

See how arivis Pro (previously Vision4D) was used to analyze time-lapse Z-stack images, perform 3D reconstruction of viral genome and envelope protein signals, and assemble color-rendered 3D videos capturing PRV infection dynamics including nuclear membrane disruption by progeny viral particles.

This helped this research by providing 3D visualization evidence that PRV replication produces numerous progeny viral particles within the nucleus causing nuclear membrane breakdown, and supporting single-virus tracking experiments that revealed dual invasion pathways of endocytosis and plasma membrane fusion in Neuro-2a cells.

Read the paper

Microbiota modulate immune cell populations and drive dynamic structural changes in gut-associated lymphoid tissue

J Pačes et al.

Image Analysis · 3D Visualization · Immunology · Cell Biology · Light Sheet Microscopy

HOW ARIVIS HELPED

ZEISS arivis Pro enabled intestinal surface area measurement, image stitching, villi segmentation, and light sheet data analysis in a study revealing how microbiota drive structural and cellular changes in gut-associated lymphoid tissue

See how arivis Pro (previously Vision4D) was used to stitch and analyze fluorescent stereomicroscopy images for intestinal surface area quantification, manually segment individual villi, stitch whole-intestine images for SILT follicle mapping, and analyze LSFM datasets of cleared intestinal segments for cell quantification in individual villi and cornea.

This helped this research by enabling quantitative comparison of intestinal surface area, villus density, SILT follicle number and volume, and APC distribution across germ-free, conventional, and gnotobiotic mouse models, revealing that microbiota directly regulate both the functional and structural configuration of gut-associated lymphoid tissue.

Read the paper

Spatiotemporal analysis ofde novoKSHV infection using Crispr/Cas9-based 3D live cell imaging at single episome resolution

T Günther et al.

Image Analysis · 3D Visualization · Cell Biology

HOW ARIVIS HELPED

ZEISS arivis Pro enabled detection and quantification of individual KSHV episomes across multiple cell divisions in a live cell imaging study of viral genome dynamics during de novo infection

See how arivis Pro was used to detect and quantify individual SunTag/SunSeT fluorescent signals representing single KSHV episomes in 3D Z-stack time-lapse images, tracking episome counts along cell division trajectories over five days across four cell generations.

This helped this research by enabling single-episome resolution quantification of viral genome distribution through successive cell divisions, providing direct evidence of how KSHV episomes are spatially redistributed and inherited during latency establishment in the context of host chromatin dynamics.

Read the paper

Combined Multicolor Immunofluorescence Staining and Spatial In Situ messenger RNA Expression Analysis Identifies Potential Fibrosis Drivers in Acute …

S Bräunig et al.

AI · Image Analysis · Cell Biology · Cancer Research · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled multicolor image registration, volumetric cell segmentation, and spatial RNA expression quantification in a study identifying fibrosis drivers in pediatric acute lymphoblastic leukemia bone marrow

See how arivis Pro was used to overlay sequential immunofluorescence scans based on nuclear landmarks, segment mesenchymal stromal cells and nuclei using Blob Finder with intensity and morphology filtering, and quantify TGFB1 and PDGFA1 RNA signal surface areas via intensity threshold segmentation for normalized single-cell expression analysis.

This helped this research by enabling spatially resolved, single-cell quantification of cytokine transcript expression across distinct bone marrow cell populations, revealing that megakaryocyte TGFB1 and PDGFA1 expression correlates with fibrosis grade in ALL and identifying these cells as likely drivers of bone marrow fibrosis in pediatric patients.

Read the paper

Optical tissue clearing and 3D imaging of intact primate testicular tissue: a novel technology development

PW Kibui et al.

Image Analysis · Cell Biology · Reproductive Biology · Tissue Clearing · Light Sheet Microscopy · 3D Visualization

HOW ARIVIS HELPED

ZEISS arivis Pro enabled large-volume 3D visualization and tile stitching of optically cleared primate testicular tissue

See how arivis Pro (Version 4.1.1) was used for tile stitching, large-volume 3D visualization, volume rendering, and movie export of light sheet fluorescence microscopy datasets from optically cleared intact testicular tissues across three primate species — human (transgender model), common marmoset, and macaque. The arivis Pro TileSorter enabled pre-alignment and stitching of mosaic tiled image stacks with 20% overlap, while the Arivis SIS Converter processed raw LSFM data into arivis-compatible files for handling these large 3D volumes. This helped this research by providing the 4D viewer's volume rendering and X/Y/Z clipping capabilities that were essential for deep tissue visualization of dense primate testicular architectures, revealing intricate details such as spermatogonial clones organized as singlets, pairs, quartets, and groups of eight, cellular bridges between germ cells, and the spatial relationship between spermatogonia and vasculature — details that classical 2D histology sections would struggle to capture. The software's storyboard and movie export features enabled the creation of 3D videos demonstrating that what appeared as multiple separate tubules in 2D microtome sections was actually a single convoluting seminiferous tubule, a significant finding that overcomes long-standing limitations of classical histology. Critically, this arivis-powered 3D analysis identified testicular pathology in the transgender model, including tubules with depleted germ cells alongside tubules with persisting spermatogonial clones following hormonal suppression — establishing a foundation for spatial evaluation of spermatogenesis kinetics in health and disease.

Read the paper

In situ cryo-ET visualization of mitochondrial depolarization and mitophagic engulfment

K Rose et al.

AI · Image Analysis · 3D Visualization · Cell Biology · Neuroscience · Parkinson's Disease Research

HOW ARIVIS HELPED

ZEISS arivis Pro enabled machine learning segmentation and compartment-based quantification of mitochondrial subdomains in a live Airyscan cryo-ET study of mitochondrial depolarization and mitophagy

See how arivis Pro (previously Vision4D) was used to segment ATP synthase signal via normalized watershed thresholding, train a machine learning segmenter on mitochondrial outer membrane and enclosed region classes, and quantify ATP synthase distribution between cristae and inner boundary membrane domains using object math intersection analysis.

This helped this research by enabling quantitative mapping of ATP synthase relocalization from cristae to the inner boundary membrane following depolarization treatment, providing live-cell fluorescence evidence complementing cryo-ET observations of the structural consequences of mitochondrial depolarization in the context of Parkinson's disease-related mitophagy.

Read the paper

Aberrant inheritance of extrachromosomal DNA amplifications promotes cancer evolution

S Marom et al.

AI · Image Analysis · Cell Biology · Cancer Research

HOW ARIVIS HELPED

ZEISS arivis Pro enabled machine learning segmentation of micronuclei and 3D colocalization analysis of ecDNA signals in a study uncovering how extrachromosomal DNA inheritance drives cancer genome evolution

See how arivis Pro was used to segment micronuclei via pixel classification with subsequent exclusion of nuclear objects, quantify micronuclear areas and intensities, and perform 3D colocalization analysis of FISH signals using machine learning segmentation and blob finder detection with distance-based and overlap-based colocalization criteria.

This helped this research by enabling precise quantification of micronuclear and nanonuclear ecDNA content and structural colocalization, supporting the discovery that nanonuclear ecDNA undergoes autophagic degradation and ongoing structural rearrangement that facilitates cancer cell adaptation under selective pressure.

Read the paper

Spatial analysis of mitochondrial gene expression reveals dynamic translationhubsand remodeling in stress

A Begeman et al.

AI · Image Analysis · 3D Visualization · Cell Biology · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled machine learning segmentation of the mitochondrial network and compartment-based colocalization analysis of RNA and ribosomal components in a study revealing dynamic translation hubs and stress-induced mitochondrial RNA sequestration in human cells

See how arivis Pro (previously Vision4D) was used to train machine learning models for mitochondrial network segmentation, apply Blob Finder and intensity threshold segmenters for punctate and continuous signals respectively, filter objects by proximity to the mitochondrial network using the compartmentalization function, and export object intersection data for Monte Carlo-based statistical comparison against random colocalization.

This helped this research by enabling systematic spatial analysis of mitochondrial RNA and ribosomal distribution within the mitochondrial matrix, revealing that processed mitochondrial RNAs consolidate into discrete translation hubs distal from transcription sites and are sequestered into stress bodies upon proteotoxic stress downstream of dsRNA accumulation.

Read the paper

HGS+ enlarged vesicular compartment serves as site for coronavirus assembly at later infection stage

X Long et al.

AI · Image Analysis · 3D Visualization · Cell Biology

HOW ARIVIS HELPED

ZEISS arivis Pro enabled machine learning-assisted segmentation of intracellular organelles from FIB-SEM volumes in a study identifying HGS+ enlarged vesicular compartments as coronavirus assembly sites

See how arivis Pro was used to train a machine learning segmentation model on manually annotated FIB-SEM datasets, generating accurate ground truth for automated segmentation of double-membrane vesicles, multivesicular bodies, autophagolysosomes, mitochondria, and nuclei from whole-cell volume EM data at 5×5×10 nm voxel resolution.

This helped this research by enabling precise 3D delineation of intracellular compartments within infected cells, supporting the demonstration that HGS deficiency abolishes the enlarged vesicular compartments and markedly reduces assembled virions, establishing these structures as essential platforms for coronavirus assembly.

Read the paper

Macrophage invasion into theDrosophilabrain requires JAK/STAT-dependent MMP activation in the blood–brain barrier

B Winkler et al.

AI · Image Analysis · 3D Visualization · Neuroscience · Immunology · Cell Biology

HOW ARIVIS HELPED

ZEISS arivis Pro enabled machine learning-based macrophage counting and neural lamella surface visualization in a study identifying JAK/STAT-dependent MMP activation as the mechanism driving immune cell invasion across the Drosophila blood-brain barrier

See how arivis Pro (previously Vision4D) was used to define CNS boundaries from HRP signal, segment mCherry-labeled macrophage nuclei with the Blob Finder, classify infiltrated versus non-infiltrated macrophages using a machine learning object classifier trained on spatial and morphological parameters, and generate isosurface reconstructions of the neural lamella to visualize extracellular matrix remodeling across developmental timepoints.

This helped this research by enabling systematic, quantitative counting of brain-infiltrating macrophages across multiple genetic backgrounds, revealing that MMP1, MMP2, and STAT92E knockdown each significantly reduce macrophage invasion, and providing 3D visualization evidence that JAK/STAT-driven MMP activity remodels the neural lamella to permit immune cell entry.

Read the paper

HIV-1 nuclear import is selective and depends on both capsid elasticity and nuclear pore adaptability

Z Hou et al.

Image Analysis · 3D Visualization · Cell Biology · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro enabled 3D nuclear segmentation and spatial classification of HIV-1 core puncta in a cryo-correlative study dissecting the mechanics of HIV-1 nuclear import

See how arivis Pro (previously Vision4D) was used to segment nuclei from confocal Z-stacks using the integrated Cellpose algorithm, detect mNeonGreen-labeled HIV-1 core puncta with the Blob Finder tool, and classify each punctum as imported or decorating based on spatial colocalization with 3D nuclear boundaries.

This helped this research by enabling systematic, quantitative categorization of HIV-1 cores at distinct nuclear import stages, supporting the discovery that the nuclear pore complex acts as a selective filter favoring smaller, elastic cores and that CPSF6 binding is required for complete nuclear translocation.

Read the paper

SVEP1 enables efficient binding of Angiopoietin-2 to the TIE1 receptor, allowing receptor phosphorylation and downstream signaling

K Uphoff et al.

Image Analysis · Cell Biology · Vascular Research

HOW ARIVIS HELPED

ZEISS arivis Pro enabled nuclear and cytoplasmic pixel intensity quantification for FOXO1 localization analysis in a study defining the molecular mechanism by which SVEP1 enables ANG2-TIE1 receptor signaling in lymphatic endothelial cells

See how arivis Pro was used to measure pixel intensities within nuclear and cytoplasmic compartments of individual cells identified by ZO-1 staining, enabling calculation of the nuclear-to-cytoplasmic ratio of FOXO1 signal across treatment conditions in superresolution Apotome images.

This helped this research by providing quantitative evidence that combined SVEP1 and ANG2 stimulation promotes nuclear exclusion of FOXO1 more effectively than either factor alone, supporting the proposed model of TIE1 receptor multimerization and downstream AKT signaling amplification in lymphangiogenesis.

Read the paper

Increased RhoA pathway activation downstream of αIIbβ3/SRC contributes to heterozygous Bernard Soulier syndrome

L Lordier et al.

Image Analysis · Cell Biology · Regenerative Medicine · Drug Discovery

HOW ARIVIS HELPED

ZEISS arivis Pro enabled platelet diameter measurement in a study identifying RhoA pathway overactivation as a driver of macrothrombocytopenia in heterozygous Bernard Soulier syndrome

See how arivis Pro (previously Vision4D) was used to measure diameters of ex vivo-released platelets adhered on polylysine-coated slides across multiple patient-derived iPSC megakaryocyte conditions, including treatment with the ROCK1/2 inhibitor Y27632, across cohorts of up to 136 platelets per condition.

This helped this research by providing precise, quantitative platelet size measurements confirming macrothrombocytopenia in GPIbα mutant lines and demonstrating that Y27632 treatment significantly restores platelet size in heterozygous BSS patients carrying GP1BA mutations, supporting RhoA inhibition as a potential therapeutic strategy.

Read the paper

Stability of Locus Coeruleus cell counts despite volume loss in cognitively impaired aged rhesus macaques

KE McDermott, CA Barnes

AI · Neuroscience · Image Analysis · Aging Research

HOW ARIVIS HELPED

ZEISS arivis Pro enabled precise cell analysis in locus coeruleus aging research

See how arivis Pro was used for automated segmentation and surface area analysis of tyrosine hydroxylase-positive neurons in the locus coeruleus of aged rhesus macaques. This helped this research by incorporating Cellpose model operations for accurate cell segmentation and automated measurement of neuronal surface areas across an average of 264 neurons per animal, enabling researchers to determine that age-related volume loss in the locus coeruleus medial compartment was not due to changes in cell size or number. The automated analysis capabilities of arivis Pro allowed for standardized, objective measurements across multiple animals and brain regions, providing crucial quantitative data that supported the finding that locus coeruleus neurons remain remarkably stable during normative aging despite volumetric changes.

Read the paper

Pharmacologically increasing O-GlcNAcylation increases complexity of astrocytes in the dentate gyrus of TgF344-AD rats

ML Garcia et al.

AI · Image Analysis · 3D Visualization · Neuroscience · Alzheimer's Research · Drug Discovery

HOW ARIVIS HELPED

ZEISS arivis Pro enabled semi-automated 3D morphological reconstruction of astrocytes, microglia, and axons in a study assessing the effects of increased O-GlcNAcylation on Alzheimer's disease pathology in TgF344-AD rats

See how arivis Pro (previously Vision4D) was used to reconstruct GFAP-labeled astrocytes and Iba-1-labeled microglia in 3D using the probabilistic NeuronTracer algorithm, quantify amyloid plaque voxel counts via intensity thresholding, reconstruct TH-positive axons with automated thresholding, and measure distances between glial cells and nearest amyloid plaques across nearly 5,000 astrocytes and 1,700 microglia.

This helped this research by enabling spatially resolved, morphology-based quantification revealing that O-GlcNAcylation selectively increases astrocyte process length and branching in TgF344-AD rats specifically near amyloid plaques, suggesting a dual beneficial effect on astrocyte reactivity without altering microglial morphology or plaque burden.

Read the paper

Impairment of lysosomal quality control in Huntington disease

P Rusmini et al.

Image Analysis · Cell Biology · Neuroscience

HOW ARIVIS HELPED

ZEISS arivis Pro enabled volumetric quantification of lysosomal structures in a study linking mutant Huntingtin aggregation to impaired lysosomal quality control

See how arivis Pro was used to quantify the volume of LAMP-1-positive endolysosomal vesicles from double immunofluorescence image stacks, enabling comparison of lysosomal size across cells expressing wild-type and mutant Huntingtin with varying polyglutamine tract lengths.

This helped this research by providing quantitative evidence that mutant Huntingtin increases lysosomal volume in a polyQ length-dependent manner, supporting the broader finding that TFEB and TFE3 sequestration in aggregates impairs lysosomal quality control and increases neuronal vulnerability to lysosomal membrane permeabilization in Huntington disease.

Read the paper

Whole-Tissue Distribution Analysis for Visualization of Nanoplastics in the Mouse Brain

Y Mi et al.

Image Analysis · 3D Visualization · Neuroscience · Light Sheet Microscopy · Tissue Clearing

HOW ARIVIS HELPED

ZEISS arivis Pro enabled whole-brain 3D reconstruction and regional fluorescence quantification of nanoplastic biodistribution in neonatal mouse brains

See how arivis Pro (previously Vision4D) was used to stitch, visualize, and render whole-brain light sheet image stacks into 3D reconstructions, and to perform segmentation and volumetric quantification using built-in analysis tools with regional ROI-based mean fluorescence intensity measurements across cerebellum, cortex, hindbrain, and thalamus.

This helped this research by enabling the first whole-brain 3D mapping of nanoplastic accumulation without sectioning, revealing that 50 nm polystyrene nanoplastics distribute throughout the neonatal brain with the highest accumulation in the thalamus and brainstem, demonstrating size-dependent brain uptake 24 hours after oral exposure.

Read the paper

Parental origin of transgene modulates amyloid-β plaque burden in the 5xFAD mouse model of Alzheimer's disease

AO Sasmita et al.

AI · Image Analysis · 3D Visualization · Alzheimer's Research · Light Sheet Microscopy · Tissue Clearing

HOW ARIVIS HELPED

ZEISS arivis Pro enabled whole-brain plaque segmentation and 3D quantification in a light-sheet study revealing that parental origin of the 5xFAD transgene doubles amyloid plaque burden

See how arivis Pro (previously Vision4D) was used to stitch light sheet image stacks, segment amyloid plaques using the Blob Finder algorithm in 5xFAD hemibrains and a machine learning segmenter trained on multiple datasets for APPNLGF hemibrains, define anatomical ROIs for isocortex, hippocampus, and alveus, and render plaques as centroids or surface models for quantitative comparison.

This helped this research by enabling unbiased, whole-hemibrain plaque quantification across multiple cohorts, revealing a consistent 2-fold higher plaque burden with paternal versus maternal transgene inheritance and identifying parental origin as an underreported but significant confound in 5xFAD-based Alzheimer's disease research.

Read the paper

PARylation in Parkinson's disease: a bridge between Lewy body formation and neuronal cell death

C Novello et al.

Image Analysis · 3D Visualization · Neuroscience · Parkinson's Disease Research · Cell Biology

HOW ARIVIS HELPED

ZEISS arivis Pro enabled 3D reconstruction and colocalization analysis of PAR, alpha-synuclein, and mitochondrial markers in post-mortem human Parkinson's disease brain tissue

See how arivis Pro (previously Vision4D) was used to reconstruct confocal Z-stacks through intensity threshold segmentation of continuous markers and Blob Finder detection of punctate PAR and VDAC1 signals, with gamma correction and denoising applied prior to pipeline execution on 100x deconvolved acquisitions.

This helped this research by enabling high-resolution 3D visualization of PAR accumulation within Lewy bodies at different aggregation stages, revealing that PARylation precedes alpha-synuclein oligomer formation and that PAR colocalizes with mitochondria in substantia nigra neurons of PD patients, positioning PARylation as a potential therapeutic target in Parkinson's disease.

Read the paper

Transcriptional and epigenetic rewiring by the NUP98:: KDM5A fusion oncoprotein directly activates CDK12

S Troester et al.

Image Analysis · Cell Biology · Cancer Research

HOW ARIVIS HELPED

ZEISS arivis Pro enabled automated nuclear segmentation and gamma-H2AX intensity quantification in a study identifying CDK12 as a druggable vulnerability in NUP98::KDM5A-driven pediatric acute myeloid leukemia

See how arivis Pro (previously Vision4D) was used to import Airyscan confocal images and run a manually designed automated segmentation pipeline to identify individual nuclei, followed by manual proofreading and mean pixel intensity calculation for the gamma-H2AX DNA damage signal in each nucleus.

This helped this research by enabling quantitative, per-nucleus measurement of DNA damage levels across drug treatment conditions, supporting the demonstration that CDK12 inactivation causes increased DNA damage and AML cell death downstream of NUP98::KDM5A target gene regulation.

Read the paper

Modular in vivo assembly of Arabidopsis FCA oligomers into condensates competent for RNA 3’ processing

GJ Jang, A Payne

Image Analysis · 3D Visualization · Cell Biology · Developmental Biology

HOW ARIVIS HELPED

ZEISS arivis Pro enabled 3D condensate segmentation and colocalization quantification of RNA-binding protein foci in plant nuclei in a study revealing the modular assembly mechanism of FCA biomolecular condensates

See how arivis Pro (previously Vision4D) was used to apply the Blob Finder algorithm to segment FCA-mScarlet-I, FCA-mTurquoise, and FLL2-eYFP foci in Airyscan super-resolution Z-stacks, calculate intersections between dual-channel segmentations to identify colocalized condensates, and extract volume, mean intensity, and sphericity metrics for each object class across 18 nuclei.

This helped this research by enabling size-resolved quantification of FCA and FLL2 condensates and their colocalization, revealing that FLL2 predominantly associates with larger FCA condensates and that the FCA RRM domain mutation reduces both particle and condensate size without disrupting the core oligomer.

Read the paper

On-the-go assessment of the grapevine trunk's diameter: a comparison of different convolutional neural networks

A Zanchin et al.

AI · Image Analysis · Food Science · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Cloud enabled semantic segmentation model training for automated grapevine trunk detection in a study comparing deep learning approaches for on-the-go vineyard diameter estimation

See how arivis Cloud was used to train semantic segmentation models on RGB images of grapevine trunks, leveraging the EfficientNet CNN encoder to generate binary masks distinguishing trunk pixels and measurement tape markers from background across a dataset acquired under varying field conditions and camera angles.

This helped this research by enabling pixel-level trunk localization that outperformed regression-based convolutional neural network approaches, achieving a higher R-squared value of 0.842 and a lower normalized root mean square error of 0.071 compared to the Xception regression model, supporting automated large-scale vineyard variability mapping.

Read the paper

3D in vitro glioma-neuron-astrocyte biomimetic composites recapitulate key molecular mechanisms linked to glioblastoma multiforme pathophysiology

MSA Mier et al.

AI · Image Analysis · 3D Visualization · Cell Biology · Cancer Research · Neuroscience · Drug Discovery

HOW ARIVIS HELPED

ZEISS arivis Pro enabled 3D cell segmentation and motion tracking in a biomimetic glioblastoma model recapitulating tumor microenvironment interactions with neurons and astrocytes

See how arivis Pro was used to preprocess time-lapse image stacks with denoising, adaptive normalization, and membrane detection filters, segment individual cells using the membrane-based segmenter, and track cellular movements using Brownian motion-based tracking with mean squared displacement analysis exported for quantitative comparison.

This helped this research by enabling quantitative 3D visualization and tracking of glioblastoma cell dynamics within the hydrogel tumor microenvironment, supporting characterization of tumor-neuron-astrocyte interactions and the hijacking of neuronal signaling pathways that drive glioblastoma proliferation in the 3D in vitro model.

Read the paper

Integrin CD103 reveals a distinct developmental pathway of autoreactive thymocytes in TCR transgenic mice

N Liman et al.

Cell Biology · Image Analysis · Immunology

HOW ARIVIS HELPED

See how arivis Cloud was used for automated image segmentation to quantify syneresis (fluid diffusion) in Golden Delicious apple purée subjected to varying thermal treatment conditions. This helped this research by providing an objective, automated method to segment fluid diffusion spots from RGB images, replacing subjective visual assessment or conventional centrifugation-based methods with a measurement approach that more closely reflects real consumer-facing product behavior after packaging. The cloud-based segmentation returned precise masks from which syneresis was calculated as the fractional area of fluid diffusion on standardized paper substrates, enabling the researchers to determine that short-duration heating at higher temperatures (>100°C, <12 min) achieved desirable rheological properties but intensified browning, while batch-to-batch fruit variability remained the dominant factor affecting biochemical characteristics — insights critical for optimizing industrial apple purée processing and quality control.

Read the paper

Tight Spaces, Tighter Signals: Spatial Constraints as Drivers of Peripheral Myelination

L Bartesaghi et al.

AI · Neuroscience · Cell Biology · Image Analysis

HOW ARIVIS HELPED

ZEISS arivis automated peripheral nerve myelination analysis

See how both ZEISS arivis Pro and arivis Cloud were used to automatically detect and quantify myelin internodes, cell nuclei, and mitotic cells in peripheral nerve co-cultures using deep learning segmentation models. This helped this research by enabling high-throughput analysis of myelination patterns across microfluidic compartments and different culture conditions - replacing manual counting that would have been impractical for thousands of microscopy images. The integrated workflow allowed researchers to train neural networks on representative datasets in arivis Cloud, then seamlessly deploy these automated segmentation models in arivis Pro to consistently measure how spatial constraints and cellular density influence Schwann cell differentiation and myelin formation, revealing that mechanical forces alone can trigger myelination without chemical stimulation.

Read the paper

Siglec-E augments adipose tissue inflammation by modulating TRAF3 signaling and monocytic myeloid-derived suppressor cells during obesity

A Rakib et al.

AI · Image Analysis · Cell Biology · Immunology

HOW ARIVIS HELPED

ZEISS arivis Cloud (previously APEER) and ZEISS arivis Pro enabled AI-based segmentation and quantification of adipocytes and nuclei in H&E-stained adipose tissue sections in a study investigating Siglec-E's role in obesity-driven inflammation

See how arivis Cloud (previously APEER) was used to annotate adipocytes, nuclei, and background across 12 representative images to train an AI segmentation model, and arivis Pro (previously Vision4D) was used to apply the trained model offline to quantify object size and count per field across adipose tissue sections from high-fat diet and normal diet fed mice.

This helped this research by enabling reproducible, automated histological quantification of adipocyte and nuclear morphology, supporting the broader finding that Siglec-E deficiency promotes adipogenesis and inflammatory macrophage infiltration in adipose tissue during obesity.

Read the paper

A novel AAV capsid-mediated RS1 gene therapy restored retinal function to wild-type levels in Rs1R213W mouse model

X Wei et al.

AI · Image Analysis · Drug Discovery · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Cloud (previously APEER) enabled expert consensus annotation of retinal cysts in OCT images as ground truth data for an automated segmentation platform in an XLRS gene therapy study

See how the APEER platform was used by two experienced ophthalmologists to manually annotate cyst cavities in 2,500 OCT B-scans from Rs1R213W mice, with a cross-review and discussion protocol to produce a single consolidated annotation set for training the Deep-OCT-MCCSEG automated computing platform.

This helped this research by providing reliable, bias-minimized ground truth labels enabling automated quantification of retinoschisis progression and treatment response, supporting the demonstration that AAV.IVT18-mediated RS1 gene therapy restored ERG b-wave amplitudes to wild-type levels by 16 weeks post-injection.

Read the paper

A Machine Learning Approach to Quantitative Analysis of Enamel Microstructure from Scanning Electron Microscopy Images

C Marsico et al.

AI · Image Analysis · Materials Science · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Cloud (previously APEER) enabled manual pixel-level annotation of enamel rod microstructure in SEM images as ground truth training data for a machine learning segmentation pipeline

See how APEER was used by researchers to manually paint individual pixels labeling visible enamel rods in three SEM training images and one validation image, producing binary segmentation masks of 300 to 600 rods each that served as the training dataset for a VGG16-expanded random forest classifier.

This helped this research by providing high-quality annotated ground truth data that enabled training of a generalizable segmentation model with as few as three images, ultimately supporting quantitative microstructural analysis of decussated enamel rods across multiple mammalian species from SEM data.

Read the paper

Generation of a High-Precision Whole Liver Panorama and Cross-Scale 3D Pathological Analysis for Hepatic Fibrosis

X Zhang et al.

AI · Image Analysis · Drug Discovery · Liver Research

HOW ARIVIS HELPED

ZEISS arivis Cloud and arivis Pro enabled automated liver pathology analysis in fibrosis research

See how arivis Cloud was used to train deep learning models for automatic segmentation of steatotic hepatocytes in liver fibrosis, followed by arivis Pro (previously Vision 4D) for local deployment and analysis. This helped this research by enabling comprehensive 3D analysis of liver pathology across an entire mouse liver, with the cloud-based training achieving over 99% accuracy and 90% IoU after 3,500 iterations, then allowing automated segmentation of injured hepatocytes throughout the whole dataset. The seamless integration between arivis Cloud for model training and arivis Pro for local processing enabled researchers to quantify that 30.76% of liver volume consisted of steatotic regions, revealing region-specific pathological changes and the relationship between steatosis severity and proximity to central veins - insights that would have been impossible to obtain through manual analysis of such large-scale 3D datasets.

Read the paper

The inner core enables transient touch detection in the Pacinian corpuscle

LH Ziolkowski et al.

AI · Neuroscience · Cell Biology · Image Analysis

HOW ARIVIS HELPED

ZEISS arivis Cloud and arivis Pro enabled comprehensive 3D reconstruction of cellular ultrastructure in touch sensation research

See how arivis Cloud was used to train deep learning models for automated segmentation of organelles, cells, and subcellular structures from electron microscopy images, followed by arivis Pro for 3D reconstruction and quantitative analysis. This helped this research by enabling detailed volumetric analysis of Pacinian corpuscles at 8nm resolution, revealing the precise 3D architecture including 12 lamellar Schwann cells with interleaving lamellae around a 48μm afferent terminal with 29 spike-like protrusions. The AI-driven segmentation using customized U-Net architecture and subsequent 3D modeling capabilities allowed researchers to challenge the prevailing understanding of touch detection, demonstrating that the inner core rather than the outer core is responsible for the corpuscle's sensory tuning properties.

Read the paper

Recombinant ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1) decreases vascular calcification and prevents osteomalacia in a rat model of chronic …

K O'Brien et al.

AI · Image Analysis · Drug Discovery · Vascular Research

HOW ARIVIS HELPED

ZEISS arivis Cloud enabled AI-based artery segmentation for quantification of vascular calcification in a rat model of chronic kidney disease treated with recombinant ENPP1

See how arivis Cloud was used to annotate and train a segmentation model distinguishing artery tissue from background, which was then deployed within ZEISS ZEN software to automatically segment aortic and iliac artery regions, with calcification subclasses quantified by global intensity thresholding across two to three tissue levels per animal.

This helped this research by enabling reproducible, automated quantification of percent calcified area across vascular cross-sections, demonstrating that INZ-701 treatment significantly reduces vascular and soft tissue calcification in adenine-induced CKD rats and supporting its potential as a therapeutic strategy for CKD-mineral bone disorder.

Read the paper

Neurons ensheathed by perineuronal nets are prone to hyperphosphorylation of tau protein in the hibernating Syrian hamster brain

V Berrouschot et al.

AI · Neuroscience · Image Analysis · Alzheimer's Research

HOW ARIVIS HELPED

ZEISS arivis Cloud enabled automated deep learning segmentation for neurobiology research

See how arivis Cloud was used to train deep learning models for automated detection of perineuronal nets, neurons, hyperphosphorylated tau protein, and parvalbumin in brain tissue sections. This helped this research by providing reliable, high-throughput quantitative analysis of thousands of brain images with consistent accuracy. The AI-powered segmentation capabilities in arivis Cloud enabled researchers to discover unexpected relationships between perineuronal nets and tau protein during hibernation, challenging existing assumptions about neuroprotective mechanisms in the brain.

Read the paper

Protocol: An absolute egg-to-adult viability assay in Drosophila melanogaster

C Schneider et al.

AI · Image Analysis · Developmental Biology

HOW ARIVIS HELPED

ZEISS arivis Cloud enabled automated egg counting in Drosophila fitness studies

See how arivis Cloud was used to train an AI model to automatically detect and count Drosophila eggs from digital images of food surfaces. This helped this research by providing an automated alternative to manual microscope counting for measuring egg-to-adult viability, a critical fitness component in genetic studies. The AI-powered segmentation allowed researchers to process large numbers of vials efficiently while maintaining high correlation with manual counts, enabling scalable measurement of absolute fitness metrics that are essential for detecting survivorship biases in Drosophila genetic experiments.

Read the paper

Geometrical constraints dictate assembly and phenotype of human iPSC-derived motoneuronal spheroids

E Mello et al.

AI · Neuroscience · Organoid Research · Cell Biology · Image Analysis

HOW ARIVIS HELPED

ZEISS arivis Cloud enabled automated spheroid analysis in motor neuron research

See how arivis Cloud was used to segment spheroids in brightfield images and extract quantitative metrics from them. This helped this research by enabling high-throughput analysis of thousands of motor neuron spheroids with consistent, objective measurements of size, shape, and morphological parameters. The automated segmentation and measurement capabilities allowed researchers to systematically compare how different microwell geometries affected spheroid development and gene expression, providing crucial data that would have been impractical to obtain through manual analysis alone.

Read the paper

Deep learning methods for phase segmentation in backscattered electron images of cement paste and SCM-blended systems

Y Yu, G Geng

AI · Image Analysis · Materials Science · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Cloud enabled manual pixel-level annotation of cement paste phases in backscattered electron images as ground truth training data for deep learning segmentation models

See how arivis Cloud (previously APEER) was used to manually annotate anhydrous cement and supplementary cementitious material particles in BSE images, producing labeled masks paired with raw images to create training datasets of up to 27,000 augmented image pairs for U-Net model training.

This helped this research by providing high-quality annotated ground truth that enabled deep learning models to achieve phase segmentation precision comparable to QXRD measurements for cement, limestone, quartz, and slag systems, demonstrating the viability of CNN-based microstructure quantification for complex cementitious materials.

Read the paper

Effervescence description of No-Low alcohol wines at different temperatures and ethanol concentrations through image analysis

A Zanchin et al.

AI · Image Analysis · Food Science · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Cloud enabled semantic and instance segmentation model training for automated bubble detection and foam characterization in sparkling no-low alcohol wine research

See how arivis Cloud was used to train a semantic segmentation model distinguishing foam from free wine surface and an instance segmentation model detecting individual bubbles, with approximately 77 manually labelled images from a 1,100-image dataset containing over 8,000 annotated bubble instances, achieving an experimental accuracy of 0.977 and mean intersection over union of 0.729.

This helped this research by enabling automated, continuous quantification of bubble count, diameter, and foam persistence across temperature and ethanol concentration conditions, revealing that alcohol reduction promotes smaller, more stable bubbles and enhanced visual foam appeal in sparkling NoLo wines.

Read the paper

Establishment of an AI-supported scoring system for neuroglial cells

A Bitsch et al.

AI · Image Analysis · Neuroscience · Cell Biology · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Cloud enabled machine learning-based nucleus segmentation and microglial process counting in a study establishing an AI-supported scoring system for neuroglial cell morphology in hippocampal tissue cultures

See how arivis Cloud (previously APEER) was used to develop segmentation models for microglial cell nucleus identification based on Iba1-marked borders and DAPI signal, and to count microglial projections within a defined zone of influence around each nucleus, complementing ZEN Intellesis-based cell area segmentation.

This helped this research by enabling automated, unbiased quantification of microglial nucleus area, process number, and activation state across large hippocampal image datasets, revealing that TNF overexpression reduces microglial projection counts and supporting the linking of neuroglial morphology to functional activity status.

Read the paper

Recombinant ENPP1 decreases vascular calcification and prevents osteomalacia in a rat model of CKD

K O'Brien et al.

AI · Cell Biology · Drug Discovery · Image Analysis · Kidney Research · Vascular Research

HOW ARIVIS HELPED

ZEISS arivis Cloud provided AI-powered vascular calcification analysis in kidney disease research

See how ZEISS arivis Cloud was used for automated segmentation and analysis of arterial calcification in a chronic kidney disease study. This helped this research by enabling objective, AI-based quantification of calcification patterns in aorta and iliac artery images, allowing researchers to demonstrate that INZ-701 treatment significantly reduced vascular calcification and changed the calcification pattern from circumferential to punctate distributions. The automated analysis capabilities of arivis Cloud were essential for processing multiple tissue levels per animal and calculating mean percent area calcified, providing the quantitative evidence needed to evaluate this potential therapeutic intervention for cardiovascular complications in kidney disease patients.

Read the paper

A high-throughput ImmunoHistoFluorescence (IHF) method for sub-nuclear protein analysis in tissue

KC Oxe et al.

AI · Image Analysis · Cancer Research · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled fully automated sub-nuclear segmentation and high-throughput quantification of nucleolar protein distribution in FFPE tissue samples as part of a new ImmunoHistoFluorescence pipeline

See how arivis Pro was used to apply Richardson-Lucy deconvolution, segment nuclei via Cellpose-based deep learning, detect nucleoli as dark holes in RNA Pol II staining using the Blob Finder module, identify Treacle foci within nucleolar compartments, and export per-nucleus intensity and foci count data from TMA and FFPE cell block images acquired on the ZEISS Axioscan 7.

This helped this research by enabling reproducible, scalable automated quantification of sub-nuclear protein redistribution with 82.62% accuracy versus manual scoring, supporting the transfer of in vitro nucleolar stress findings into clinically relevant FFPE tissue contexts for biomarker discovery and translational research.

Read the paper

The Syk inhibitor BI 1002494 impairs thrombus infill in a murine femoral artery occlusion without affecting hemostasis

MO Faruque et al.

AI · Image Analysis · Cell Biology · Thrombosis Research · Drug Discovery

HOW ARIVIS HELPED

ZEISS arivis Pro and ZEISS arivis Cloud enabled deep learning-based mapping of clot cellular components and structural analysis of thrombus architecture at single-cell resolution in a study evaluating the Syk inhibitor BI 1002494 in murine femoral artery occlusion

See how arivis Cloud was used to train deep learning segmentation models for four clot components including tightly packed platelets, elongated platelets, red blood cells, and white blood cells using convolutional neural networks, while arivis Pro was used to stitch wide-area TEM montage frames, measure inter-platelet spacing, and apply the trained models to whole blended images via a deep learning pipeline.

This helped this research by enabling quantitative mapping of clot microarchitecture across perpendicular and parallel sections, revealing that Syk inhibitor treatment produces a highly porous, infill-impaired thrombus rich in dispersed discoid platelets while leaving hemostatic clot structure at femoral puncture wounds unaffected.

Read the paper

Tight spaces, tighter signals: Spatial constraints as drivers of peripheral myelination

L Bartesaghi et al.

AI · Image Analysis · Cell Biology · Neuroscience · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro and ZEISS arivis Cloud enabled automated segmentation of nuclei, mitotic cells, and internodes in a study investigating how spatial constraints regulate peripheral myelination in Schwann cell-DRG co-cultures

See how arivis Pro was used to detect nuclei and mitotic cells using the Blob Finder Particles operation with size and threshold parameters, and how arivis Cloud was used to train an instance segmentation deep learning model on 20 representative images for internode identification, with the resulting model imported into arivis Pro for batch processing across the full dataset.

This helped this research by enabling reproducible, automated quantification of myelination parameters across microfluidic and hydrogel co-culture conditions, with validation against manual counts confirming reliability, and supporting the findings that cellular density thresholds and spatial confinement are key regulators of Schwann cell differentiation and myelin formation.

Read the paper

The Syk inhibitor Bi 100249f impairs thrombus infill in a murine femoral artery occlusion without affecting hemostasis

MO Faruque et al.

AI · Cell Biology · Drug Discovery · Image Analysis · Thrombosis Research

HOW ARIVIS HELPED

ZEISS arivis Pro and arivis Cloud enabled comprehensive analysis of blood clot structure

See how both ZEISS arivis Pro and arivis Cloud were used to analyze platelet organization within blood clots from wide-area transmission electron microscopy images. This helped this research by enabling automated identification and quantification of four distinct clot components - tightly packed platelets, elongated platelets, red blood cells, and white blood cells - using AI-powered deep learning algorithms. The integrated approach allowed researchers to stitch together massive montaged images in arivis Pro while leveraging cloud-based machine learning to train neural networks that could precisely map cellular distributions throughout entire clots, revealing how Syk inhibitor treatment selectively impaired clot formation by preventing proper platelet aggregation without affecting initial hemostasis.

Read the paper

Volume Electron Microscopy of Cortical Organoids: Methods for Region Identification, Connectome Reconstruction, and Organelle Segmentation

S Dallere et al.

Image Analysis · AI · Organoid Research · Neuroscience · Connectomics · Cell Biology

HOW ARIVIS HELPED

ZEISS arivis Cloud supported automated organoid growth monitoring in a cortical organoid connectomics study

See how arivis Cloud was used to train a deep learning model for automated area measurement of human cortical organoids as part of an image analysis pipeline integrated with ZEISS ZEN software, supporting long-term growth monitoring over 180 days of organoid differentiation. This helped this research by providing automated, consistent quantification of organoid growth across the extended culture period, as part of a broader workflow that established the first micro-connectomic reconstruction in human cortical organoids using volume electron microscopy. The organoids monitored with this arivis-powered pipeline were subsequently processed for FIB-SEM imaging, enabling 3D reconstruction of synapses, neurites, and intracellular organelles at nanometer resolution, demonstrating the feasibility of applying connectomic approaches to organoid-based models of human brain development and disease.

Read the paper

A neuronal architecture underlying autonomic dysreflexia

JE Soriano et al.

Image Analysis · 3D Visualization · Neuroscience · Protocol/Methods · Tissue Clearing · Light Sheet Microscopy

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled whole-spinal-cord image stitching and automated Fos-positive neuron quantification in a study mapping the neuronal architecture underlying autonomic dysreflexia

See how arivis Pro (previously Vision4D) was used to stitch large-volume light sheet image stacks from mesoSPIM and COLM acquisitions, and to run a custom segmentation pipeline applying morphology, denoising, and normalization filters followed by threshold-based 3D segmentation of Fos signal within grey matter regions of interest.

This helped this research by enabling segment-by-segment quantification of neuronal activity across the entire spinal cord using spatial coordinates of Fos-positive cells, providing the anatomical resolution needed to map circuits driving autonomic dysreflexia following spinal cord injury.

Read the paper

ISTFA 2024 ARTIFICIAL INTELLIGENCE (AI) IN FAILURE ANALYSIS USER GROUP.

P Hoffrogge et al.

AI · Image Analysis · Neuroscience · Cell Biology · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled multi-level machine learning segmentation of Mauthner axons in a high-content zebrafish screen identifying novel regulators of CNS axon diameter

See how arivis Pro (previously Vision4D) was used to train two sequential random forest pixel classifiers covering the full range of image variability, applying a low-resolution model to isolate candidate axonal regions while excluding skin autofluorescence and ectopic muscle expression, followed by a high-resolution model for precise axon boundary segmentation and diameter measurement across 880 screened compounds.

This helped this research by enabling fully automated, objective batch quantification of Mauthner axon diameter across hundreds of live zebrafish images, identifying 33 compounds that alter axon diameter including beta-2 adrenoceptor and dopamine signaling modulators, representing the first discovery screen for axon diameter regulators.

Read the paper

Comprehensive analysis of human dendritic spine morphology and density

KD Schünemann, RM Hattingh…

AI · Neuroscience · Image Analysis

HOW ARIVIS HELPED

ZEISS arivis Pro accelerated human dendritic spine analysis with deep learning integration

See how arivis Pro was used for three-dimensional reconstruction and morphological classification of human dendritic spines from brain tissue samples. This helped this research by enabling comprehensive analysis of nearly 4,000 dendritic spines across 27 patients, with arivis Pro serving as the platform for training and implementing a deep learning model that automated spine segmentation and reduced processing time by over 50%. The integration of deep learning capabilities within arivis Pro made large-scale analysis of human brain tissue feasible, revealing critical insights into sex-specific differences, tissue condition effects, and synaptic plasticity changes over time in culture.

Read the paper

Poly-γ-glutamic acid alleviates cytotoxicity and inflammation induced by pre-formed fibrils of α-synuclein in murine primary astrocytes

C Novello et al.

Neuroscience · Cell Biology · Drug Discovery · Image Analysis · Parkinson's Disease Research

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled 3D reconstruction revealing γ-PGA colocalization with α-synuclein fibrils in Parkinson's disease astrocyte model

See how arivis Pro (previously Vision4D, version 3.6.0) was used for 3D reconstruction and visualization of confocal microscopy data from murine primary astrocytes treated with poly-γ-glutamic acid (γ-PGA) and α-synuclein pre-formed fibrils (PFFs), a cellular model of Parkinson's disease pathology. The software's intensity threshold segmentation pipeline reconstructed continuous staining of α-synuclein PFFs, the astrocyte marker S100β, and nuclei, while the blob finder pipeline was used to reconstruct the punctate distribution pattern of γ-PGA. This helped this research by providing top, side, and lateral 3D views, along with supplementary 3D movies, that were critical for demonstrating that γ-PGA colocalizes with α-synuclein PFFs in the extracellular environment and positions itself between the fibrils and astrocyte cell surfaces. These spatial relationships, which could not be definitively established from 2D confocal images alone, were key to supporting the paper's central finding that γ-PGA reduces α-synuclein PFF uptake by astrocytes and decreases their inflammatory response, establishing γ-PGA as a promising therapeutic candidate for Parkinson's disease by modulating the interplay between pathological protein aggregates and glial cells.

Read the paper

Correlative in situ cryo-ET reveals cellular and viral remodeling associated with selective HIV-1 core nuclear import

Z Hou et al.

Image Analysis · 3D Visualization · Cell Biology · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled 3D nuclear segmentation and HIV-1 core puncta classification in a cryo-correlative study of selective HIV-1 nuclear import

See how arivis Pro (previously Vision4D) was used to segment nuclei from confocal Z-stacks using the integrated Cellpose algorithm, detect mNeonGreen-labeled HIV-1 core puncta with the Blob Finder tool, and spatially classify puncta as imported or decorating based on their colocalization with 3D nuclear boundaries.

This helped this research by enabling quantitative, unbiased classification of thousands of HIV-1 cores at distinct stages of nuclear import, supporting the discovery that nuclear pore complexes selectively favor import of smaller, tube-shaped capsids and that CPSF6 binding is required for successful nuclear translocation.

Read the paper

HIV-1 Reprograms CD4 T Cell Responses by Impairing Antigen-specific Communication with Dendritic Cells

K Morath et al.

3D Visualization · Immunology · Cell Biology

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) and ZEISS arivis VisionVR enabled 4D reconstruction and tracking of T cell-dendritic cell interactions in intravital two-photon microscopy in a study defining how HIV-1 Nef impairs CD4 T cell immune communication

See how arivis Pro (previously Vision4D) was used to reconstruct timelapse two-photon image volumes into 4D movies, and arivis VisionVR was used to manually track and quantify antigen-specific T cell and dendritic cell interactions within popliteal lymph nodes of live mice.

This helped this research by enabling direct visualization and quantification of CD4 T cell-DC contact dynamics in vivo, supporting the discovery that HIV-1 Nef reduces CD4 surface levels to impair antigen-specific T cell activation and disrupt downstream Th1 helper cytokine communication to dendritic cells.

Read the paper

Cell size reduction scales spindle elongation but not chromosome segregation inC. elegans

CW Okafornta et al.

AI · Image Analysis · 3D Visualization · Cell Biology · Developmental Biology · Protocol/Methods

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) and ZEISS arivis Cloud (previously APEER) supported 6D embryo cropping and AI-based chromatid segmentation in a study investigating how cell size reduction scales spindle elongation in C. elegans

See how arivis Pro (previously Vision4D) was used for 6D cropping of embryonic cells across recorded embryos from anaphase onset through cytokinesis, and arivis Cloud (previously APEER) was used as an AI-based segmentation tool to automatically segment chromatids from electron tomography datasets.

This helped this research by enabling precise spatiotemporal isolation of individual embryonic cells for mitotic analysis and automated segmentation of chromatid structures from high-resolution electron tomograms, supporting quantitative investigation of how spindle architecture scales with cell size during early C. elegans development.

Read the paper

Automated 3D Analysis of Transplanted Retinal Ganglion Cell Engraftment Using Deep Learning and Advanced Imaging

H Hadady et al.

AI · Neuroscience · Cell Biology · Image Analysis · Regenerative Medicine

HOW ARIVIS HELPED

ZEISS arivis Pro (previously arivis Vision4D) enabled automated 3D analysis of retinal ganglion cell transplantation

See how arivis Pro (previously arivis Vision4D) was used with deep learning-based segmentation to analyze transplanted retinal ganglion cells in 3D, automatically tracing dendrites and quantifying their integration into specific retinal layers. This helped this research by eliminating manual segmentation biases and providing precise quantitative measurements of neurite outgrowth patterns and layer-specific integration ratios. The automated pipeline in arivis Pro enabled high-throughput analysis of transplanted cell engraftment that would have been impractical to achieve manually, providing a scalable framework for evaluating regenerative therapies in vision restoration research.

Read the paper

2024

REMODELLING OF VASCULATURE AND NERVES IN MURINE JOINTS FOLLOWING SURGICAL JOINT DESTABILISATION

V Batchelor, J Miotla

Neuroscience · Cell Biology · Image Analysis · Bone Research

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled quantitative 3D analysis of joint remodeling in osteoarthritis research

See how arivis Pro (previously Vision4D) was used for segmentation analysis and quantification of vasculature and innervation in 100µm thick joint sections from a murine osteoarthritis model. This helped this research by providing precise volumetric measurements of blood vessels (endomucin, CD31, alpha-smooth muscle actin) and nerves (beta-III tubulin) across different joint compartments including the epiphysis, osteophyte, synovium, and periosteum. The software's 3D visualization and quantitative capabilities revealed that osteoarthritic joints showed decreased vascularization in the epiphysis but increased vessel and nerve volume in the synovium and periosteum, providing objective evidence of the vascular and neural remodeling that may contribute to osteoarthritis pain mechanisms.

Read the paper

Virtual reality-empowered deep-learning analysis of brain cells

D Kaltenecker, R Al

AI · Neuroscience · Image Analysis · Cancer Research

HOW ARIVIS HELPED

ZEISS arivis VisionVR revolutionized training data generation for deep learning brain analysis

See how arivis VisionVR was used for virtual reality-based annotation of c-Fos+ cells in whole-brain light-sheet microscopy datasets, enabling researchers to train deep learning models for automated cell detection. This helped this research by dramatically accelerating the annotation process compared to traditional 2D slice-by-slice methods, while simultaneously improving annotation quality (F1 score increased from 0.74 to 0.80). The immersive 3D VR environment allowed annotators to efficiently generate the substantial amounts of high-quality training data needed for the DELiVR pipeline, which ultimately outperformed existing cell segmentation approaches and enabled comprehensive analysis of neuronal activity patterns across entire mouse brains in cancer research.

Read the paper

Linking acetylated α-Tubulin redistribution to α-Synuclein pathology in brain of Parkinson's disease patients

S Mazzetti et al.

Neuroscience · Image Analysis · Parkinson's Disease Research

HOW ARIVIS HELPED

ZEISS arivis Vision4D enabled precise 3D analysis of Lewy body formation in Parkinson's disease

See how arivis Vision4D was used for 3D reconstruction and quantitative morphometric analysis of high-resolution confocal microscopy images to study the relationship between acetylated α-Tubulin and α-Synuclein oligomers in human brain tissue. This helped this research by providing precise visualization of complex cellular structures and their spatial relationships during Lewy body formation, enabling researchers to identify six distinct stages of aggregate development and quantify the progressive changes in α-Synuclein oligomer distribution. The software's advanced segmentation pipelines and compartmentalization analysis allowed objective measurement of protein volumes and correlations, supporting the hypothesis that acetylated α-Tubulin redistribution is directly linked to α-Synuclein aggregation in Parkinson's disease pathogenesis.

Read the paper

Intravital microscopy with an airy beam light sheet microscope improves temporal resolution and reduces surgical trauma

RI Stegmeyer et al.

Cell Biology · Image Analysis · Immunology

HOW ARIVIS HELPED

ZEISS arivis Vision4D and VisionVR enhanced visualization of leukocyte dynamics in intravital microscopy

See how arivis Vision4D and VisionVR were used for image visualization and analysis of 3D time-lapse intravital microscopy data from murine cremaster muscle microcirculation. This helped this research by providing advanced visualization capabilities for the complex 4D datasets generated by the Airy Beam Light Sheet microscope, enabling researchers to observe leukocyte emigration and vascular interactions with improved temporal resolution. The software's 3D rendering and VR visualization features allowed detailed analysis of neutrophil extravasation and blood flow patterns, supporting the validation that their improved light sheet microscopy approach reduced surgical trauma while maintaining high-quality imaging of inflammatory processes in living tissue.

Read the paper

Enhancing maturation and translatability of human pluripotent stem cell-derived cardiomyocytes through a novel medium containing acetyl-CoA carboxylase 2 …

C Correia et al.

Cell Biology · Drug Discovery · Image Analysis · Cardiac Research · Stem Cell Research

HOW ARIVIS HELPED

ZEISS arivis Pro facilitated precise ultrastructural quantification in cardiac maturation research

See how arivis Pro was used for manual tracing and quantification of mitochondrial morphology and sarcomere content in transmission electron microscopy images of human pluripotent stem cell-derived cardiomyocytes. This helped this research by enabling accurate measurement of mitochondrial surface area and Z-band area as key indicators of cardiomyocyte maturation, providing quantitative evidence that the novel ACC2 inhibitor-containing medium significantly enhanced mitochondrial content and sarcomere organization. The precise morphometric analysis capabilities of arivis Pro allowed researchers to objectively demonstrate the structural improvements achieved by their maturation protocol, supporting the broader functional and metabolic maturation data that validated this approach for improving cardiac disease modeling and drug discovery applications.

Read the paper

Volume microscopic analysis of membrane contact sites in mouse kidney renal proximal tubule epithelial cells

R Pandya et al.

AI · Cell Biology · Image Analysis · Kidney Research

HOW ARIVIS HELPED

ZEISS arivis Pro enabled deep learning segmentation and 3D quantification of membrane contact sites in mouse kidney ultrastructure

See how arivis Pro was used for deep learning segmentation of a massive FIB-SEM dataset with 2,000 consecutive images at 4 nm isotropic voxel resolution covering a 5,793 μm^3 volume, to reconstruct and quantify the ultrastructure of mouse kidney proximal tubule epithelial cells. This helped this research by enabling the segmentation of 10 distinct cells with clear boundaries, along with their intracellular organelles including mitochondria and endoplasmic reticulum (ER), from which a post-deep-learning processing algorithm identified 11,109 3D membrane contact sites (MCS) between mitochondria and ER across the cell population. The arivis Pro-powered segmentation and 3D reconstruction revealed that mitochondria comprise 31.62% and ER comprises 8.91% of representative proximal tubule cell volume, with a single dominant ER object accounting for 93.5% of total ER volume per cell, quantitative insights into organelle architecture and inter-organelle communication that would be impossible to obtain from conventional 2D electron microscopy. This work established a comprehensive, high-resolution 3D volume microscopic atlas of renal proximal tubule cells, providing a foundation for understanding the biochemical identities and physiological functions of these membrane contact sites.

Read the paper

High Resolution Reconstruction of the Proximal Tubule Apical Endocytic Pathway

E Lackner et al.

Cell Biology · Image Analysis · Kidney Research

HOW ARIVIS HELPED

ZEISS arivis Pro enabled 3D reconstruction of kidney endocytic pathways at nanoscale resolution

See how arivis Pro was used for annotation and 3D reconstruction of apical membrane invaginations and endocytic compartments in focused ion-beam scanning electron microscopy volumes of mouse kidney proximal tubule cells at 4nm isotropic voxel resolution. This helped this research by revealing that dense apical tubules (DATs) form a large, highly interconnected network in the subapical region, challenging the previous understanding of these structures as simple budding vesicles. The precise 3D reconstruction capabilities allowed researchers to visualize connections between DAT networks and endosomal compartments as well as apical membrane invaginations, suggesting that DATs function as stable compartments that interact transiently with the apical membrane for receptor recycling rather than as transient budding structures.

Read the paper

Quantitative Analysis of CGRP-IR Afferent Axons in the Mouse Stomach Using ZeissArivis Vision4Dfor Automated Tracing

D Nguyen et al.

AI · Neuroscience · Image Analysis

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) revolutionized automated gastric nerve fiber analysis

See how arivis Pro (previously Vision4D) was used for machine learning-guided automated tracing of CGRP-immunoreactive axons in whole mouse stomach preparations and thick tissue sections. This helped this research by handling massive datasets (hundreds of gigabytes across 300+ image frames per stomach) while providing highly accurate 3D fiber tracing that would have been prohibitively time-consuming with manual methods. The software's advanced capabilities enabled comprehensive quantitative analysis across different gastric regions and tissue layers, revealing that CGRP-IR axon density was highest in blood vessels and showing regional variations with dense innervation in the fundus and antrum-pylorus regions, ultimately creating the first automatically traced map of gastric nociceptive innervation for integration into 3D stomach scaffolds.

Read the paper

Advancing colorectal polyp detection: An automated segmentation approach with colrectseg-unet

J Selvaraj et al.

AI · Cancer Research · Image Analysis

HOW ARIVIS HELPED

See how arivis Pro (previously Vision4D) was used for 3D segmentation, cell detection, and migration analysis of ES-2 ovarian cancer spheroids embedded in collagen gels, imaged on a ZEISS Lightsheet 7 microscope with a novel sample holder enabling dual-sided illumination. This helped this research by providing a complete analysis pipeline — including particle enhancement filtering, Blob Finder-based cell segmentation with optimized thresholds, volume filtering, and Distance Operator measurements — that enabled quantitative extraction of cell number, spheroid volume, cell density, and individual cell migration distances directly from 3D light sheet image stacks. The software's volumetric visualization capabilities were critical for optimizing segmentation thresholds across different timepoints, ensuring accurate cell detection without over- or under-segmentation in complex 3D collagen matrix environments. This workflow revealed that ES-2 spheroids undergo early migration without proliferation by day 1, followed by parallel proliferation and outward migration by day 3, with cells detected beyond 180 μm from the spheroid center. When treated with the chemotherapy agent SN-38, the arivis-powered analysis quantitatively demonstrated that cell number and migration distance were significantly arrested compared to untreated controls — findings that support the model's applicability for 3D drug screening in physiologically relevant extracellular matrix environments.

Read the paper

Distribution and morphology of CGRP-IR axons in flat-mounts of whole male and female mouse atria

K Bendowski et al.

Neuroscience · Image Analysis · Cardiac Research

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled comprehensive mapping of cardiac nociceptive innervation

See how arivis Pro (previously Vision4D) was used for digital tracing and mapping of CGRP-immunoreactive axons in flat-mount preparations of whole mouse atria. This helped this research by providing machine learning-enhanced detection capabilities that accurately traced nerve fibers while avoiding background artifacts and autofluorescence, enabling the first comprehensive comparison of nociceptive innervation patterns between male and female mice. The software's Volume Fusion tool allowed researchers to stitch together hundreds of image frames into complete atrial montages, facilitating precise quantitative analysis that revealed comparable axon densities, varicosity morphology, and distribution patterns between sexes across sinoatrial and atrioventricular node regions.

Read the paper

Transplantation of Neural Progenitor Cells Derived from Stem Cells from Apical Papilla Through Small-Molecule Induction in a Rat Model of Sciatic Nerve Injury

J Koh et al.

AI · Neuroscience · Cell Biology · Image Analysis · Regenerative Medicine · Stem Cell Research

HOW ARIVIS HELPED

ZEISS arivis Cloud enabled automated quantification of nerve regeneration in transplantation therapy

See how arivis Cloud was used to train deep learning models for automated segmentation and counting of myelinated nerve fibers in transverse sections of sciatic nerve conduits. This helped this research by providing objective, accurate quantification of nerve regeneration across different regions (mid-section, joint, and connecting areas) of the transplanted conduits, eliminating manual counting bias and enabling precise comparison between treatment groups. The AI-driven segmentation specifically trained to recognize myelinated fibers allowed researchers to demonstrate that small-molecule cocktail-induced neural progenitor cells from dental stem cells promoted better host myelinated fiber retention compared to control groups, providing quantitative evidence for the therapeutic potential of this regenerative approach.

Read the paper

Artificial intelligence driven image analysis identifies phenobarbital induced hepatocyte hypertrophy in liver microtissues across species

M Elcombe et al.

AI · Drug Discovery · Cell Biology · Image Analysis · Toxicology

HOW ARIVIS HELPED

ZEISS arivis Cloud enabled AI-driven hepatocyte analysis in liver toxicity research

See how arivis Cloud was used to train instance segmentation algorithms for identifying and measuring hepatocyte cytoplasmic areas in H&E stained liver microtissue sections. This helped this research by enabling automated quantification of phenobarbital-induced hepatocyte hypertrophy across human and rat samples, with the AI algorithm achieving high sensitivity, specificity, and precision when validated against manual annotations. The cloud-based training platform allowed researchers to develop a robust assay for measuring this key toxicological endpoint, facilitating cross-species comparison of drug-induced liver changes and supporting human-relevant risk assessment without requiring advanced coding skills or extensive manual measurement.

Read the paper

Dipeptidyl peptidase 4 deficiency improves survival after focal cerebral ischemia in mice and ameliorates microglia activation and specific inflammatory …

C Höfling et al.

AI · Neuroscience · Drug Discovery · Image Analysis

HOW ARIVIS HELPED

ZEISS arivis Cloud and ZEN Intellesis streamlined neuroinflammation analysis in stroke research

See how arivis Cloud and ZEN Module Intellesis were used for automated segmentation and quantification of immunofluorescent stainings in mouse brain tissue following experimental stroke. This helped this research by enabling machine learning-based analysis that avoided user bias and manual measurement errors when quantifying microglial activation states, astrocyte responses, and inflammatory markers like CCL2 across different time points. The automated segmentation capabilities allowed researchers to objectively demonstrate that DPP4 knockout mice had significantly reduced microglial activation and lower inflammatory chemokine levels after cerebral ischemia, providing robust quantitative evidence for the protective effects of DPP4 deficiency in stroke outcomes.

Read the paper

Identification of isoAsp7-Aβ as a major Aβ variant in Alzheimer's disease, dementia with Lewy bodies and vascular dementia

S Schrempel et al.

AI · Neuroscience · Image Analysis · Alzheimer's Research

HOW ARIVIS HELPED

ZEISS arivis Cloud and ZEN Intellesis automated quantification of amyloid pathology across dementia types

See how arivis Cloud was used for machine learning-based training to detect immunohistochemically stained amyloid plaques, followed by ZEN Intellesis for automated batch analysis across 60 cases spanning multiple dementia types. This helped this research by enabling objective, standardized quantification of eight distinct Aβ post-translational modifications across different clinical conditions, revealing that isoAsp7-Aβ is the most abundant variant in all dementia types studied. The iterative training capabilities of arivis Cloud allowed researchers to refine algorithms for each specific Aβ variant staining, while the automated batch processing eliminated manual measurement bias and enabled comprehensive comparative analysis that identified consistent Aβ modification patterns across Alzheimer's disease, dementia with Lewy bodies, and vascular dementia.

Read the paper

Structural and functional dissection of the Pacinian corpuscle reveals an active role of the inner core in touch detection

LH Ziolkowski et al.

AI · Neuroscience · Cell Biology · Image Analysis

HOW ARIVIS HELPED

ZEISS arivis Cloud and Pro enabled comprehensive 3D reconstruction of mechanoreceptor ultrastructure

See how arivis Cloud was used to train deep learning models for automated segmentation of organelles and cellular structures from electron microscopy images, followed by arivis Pro for 3D reconstruction and quantitative analysis of Pacinian corpuscles. This helped this research by enabling precise volumetric analysis at 8nm resolution that revealed the detailed architecture of lamellar Schwann cells and their gap junction connections within the inner core. The AI-driven segmentation and subsequent 3D modeling capabilities allowed researchers to challenge the prevailing understanding of mechanotransduction, demonstrating that the inner core rather than the outer core is responsible for the corpuscle's rapid adaptation and frequency tuning properties, fundamentally advancing our understanding of touch sensation mechanisms.

Read the paper

Comparing the Sensitivity of HER2 Epitope Detection of HercepTest mAb pharmDx (Dako Omnis, GE001) and Ventana PATHWAY Anti-HER-2/neu (4B5) …

F Aidt et al.

AI · Cancer Research · Drug Discovery · Image Analysis

HOW ARIVIS HELPED

ZEISS arivis Cloud (previously APEER) and ZEN software enabled automated quantification of HER2 epitope detection sensitivity

See how arivis Cloud (previously APEER) was used to train a semantic segmentation network for automated classification of epitope-coated microbeads, control beads, and background in HER2 immunohistochemistry assays, followed by ZEN software for intensity measurements. This helped this research by providing objective, quantitative comparison of two widely used HER2 assays (HercepTest and PATHWAY), revealing that HercepTest demonstrates detectability at lower HER2 expression levels (~380,000 vs. 110,000 HER2 molecules per cell). The automated analysis eliminated subjective interpretation bias in measuring stain intensity ratios between test and control beads, providing crucial data for optimizing HER2-low patient identification for targeted therapies like antibody-drug conjugates where accurate detection at lower expression levels is clinically critical.

Read the paper

2023

Islet cells in human type 1 diabetes: from recent advances to novel therapies–a symposium-based roadmap for future research

J Cantley et al.

Cell Biology · Image Analysis · Diabetes Research · Immunology

HOW ARIVIS HELPED

ZEISS arivis Vision4D provided 3D visualization of immune cell infiltration in type 1 diabetes research

See how arivis Vision4D was used for 3D reconstruction of pancreatic islet tissue from a young type 1 diabetes donor, visualizing the spatial relationship between glucagon-positive endocrine cells and infiltrating CD3-positive T cells. This helped this research by enabling clear demonstration of insulitis in three dimensions, showing immune cells interspersed among endocrine cells within the islet of Langerhans. The 3D reconstruction capabilities allowed researchers to visualize the complex cellular interactions that characterize the autoimmune process in type 1 diabetes, providing compelling visual evidence of the immune-endocrine dialogue that drives disease pathogenesis and supporting the development of novel combination therapies targeting both immune system re-education and beta cell protection.

Read the paper

LEVERAGING THE POWER OF 3D BRAIN-WIDE IMAGING AND MAPPING TOOLS FOR BRAIN INJURY RESEARCH IN MURINE MODELS

M Anwer et al.

Neuroscience · Image Analysis · Brain Injury Research

HOW ARIVIS HELPED

ZEISS arivis Vision4D enabled comprehensive 3D brain analysis in traumatic brain injury research

See how arivis Vision4D was used for stitching, 3D rendering, and region-based analysis of whole-brain light sheet microscopy datasets to quantify c-Fos+ neuronal activity after traumatic brain injury. This helped this research by handling massive 300GB image files and providing user-friendly visualization tools for brain-wide analysis, enabling researchers to identify TBI-induced reductions in neuronal activity across the entire brain. The software's blob finder and ROI drawing capabilities allowed validation of automated cell counting methods and facilitated anatomical landmark-based analysis, demonstrating that arivis Vision4D serves as a powerful complement to open-source analysis pipelines for comprehensive brain injury studies requiring both 3D visualization and quantitative regional assessment.

Read the paper

Screening for Key Structural Differences in Thrombosis Versus Hemostasis through Single Platelet Analysis

MO Faruque et al.

AI · Cell Biology · Image Analysis · Thrombosis Research

HOW ARIVIS HELPED

ZEISS arivis Pro and arivis Cloud (previously APEER) enabled comprehensive single platelet analysis in thrombosis research

See how arivis Pro was used for automated single platelet analysis to segment and map tens of thousands of platelets and red blood cells in occlusive clots, while arivis Cloud (previously APEER) models were used to score alpha-granule release states. This helped this research by providing objective quantification of platelet activation states across entire thrombus cross-sections at 3.185 nm resolution, revealing that discoid platelets in clot interiors can partially secrete alpha-granule contents - a previously unknown finding. The automated analysis capabilities enabled researchers to distinguish between thrombotic and hemostatic processes, demonstrating that ~7% of clot area consisted of trapped red blood cells and that discoid platelets with decondensed alpha-granules are present in both hemostatic and thrombotic contexts, potentially identifying new therapeutic targets for selectively affecting thrombotic clots.

Read the paper

RNA methyltransferase NSun2 deficiency promotes neurodegeneration through epitranscriptomic regulation of tau phosphorylation

YA Kim et al.

AI · Neuroscience · Image Analysis · Alzheimer's Research

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled automated quantification of neurodegeneration biomarkers in Alzheimer's disease research

See how arivis Pro (previously Vision4D) was used for automated quantification of NSun2 and phosphorylated tau expression in human brain tissue from control and Alzheimer's disease patients. This helped this research by providing machine learning-based analysis pipelines that objectively measured protein expression levels in over 8,000 individual cells across 409 images, eliminating manual counting bias through blinded automated analysis. The software's AI training capabilities enabled researchers to demonstrate that NSun2 protein expression decreases while the pTau/NSun2 ratio increases in Alzheimer's disease brains, supporting the hypothesis that NSun2 deficiency contributes to tau hyperphosphorylation and neurodegeneration through epitranscriptomic mechanisms.

Read the paper

Sedentary Behavior Impacts on the Epigenome and Transcriptome: Lessons from Muscle Inactivation inDrosophilaLarvae

A Brener et al.

Cell Biology · Image Analysis · Epigenetics

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled automated analysis of muscle inactivity effects on nuclear morphology and epigenetic modifications

See how arivis Pro (previously Vision4D) was used for automated segmentation and quantitative analysis of muscle nuclei in three dimensions, measuring nuclear volumes and fluorescent intensities of epigenetic marks in Drosophila larvae. This helped this research by providing objective quantification of chromatin modifications following muscle inactivation, revealing significant changes in the epigenetic balance between active and inactive marks within a short timeframe. The software's automated pipeline eliminated manual counting bias while analyzing multiple nuclei per image stack, enabling researchers to demonstrate that sedentary behavior (mimicked through temperature-induced muscle paralysis) triggers widespread transcriptional and epigenetic changes affecting genes involved in longevity, DNA repair, and metabolic function - findings with potential implications for understanding human sedentary lifestyle-related diseases.

Read the paper

Deep learning models to map osteocyte networks can successfully distinguish between young and aged bone

SD Vetter et al.

AI · Cell Biology · Image Analysis · Bone Research

HOW ARIVIS HELPED

ZEISS arivis Cloud enabled efficient training data generation for deep learning analysis of osteocyte networks

See how arivis Cloud was used to facilitate manual labeling of osteocyte and dendritic process images and to automatically generate additional training labels for deep learning models analyzing bone microstructure. This helped this research by providing the foundation for training computer vision models that could distinguish between young and aged bone tissue, with the final Attention U-Net model achieving 81.8% accuracy for osteocyte segmentation and 42.1% for dendritic processes compared to manual annotation. The cloud-based annotation tools enabled researchers to create the initial Dataset 1 with manual labels and automatically generate Dataset 2 with 696 training images, demonstrating that deep learning approaches can successfully automate the traditionally time-consuming analysis of osteocyte connectivity patterns that are critical for understanding bone aging and mechanosensitivity.

Read the paper

Identification of cell division cycle protein 20 in various forms of acute and chronic kidney injury in mice

M Swanson et al.

AI · Cell Biology · Drug Discovery · Image Analysis · Kidney Research

HOW ARIVIS HELPED

ZEISS arivis Cloud and arivis Pro enabled AI-driven quantification of kidney fibrosis

See how arivis Cloud (previously APEER) was used to train a convolutional neural network for automated detection of picrosirius red staining, followed by arivis Pro for offline analysis and quantification of fibrotic tissue. This helped this research by providing objective, reproducible measurement of kidney fibrosis in unilateral ureteral obstruction models, eliminating manual annotation bias through pixel-level AI segmentation that differentiated fibrotic regions from background tissue. The AI model's ability to accurately quantify sirius red-positive areas across multiple conditions enabled researchers to demonstrate that CDC20 inhibition with Apcin significantly reduced tissue fibrosis, providing quantitative evidence for the therapeutic potential of targeting cell cycle checkpoints in chronic kidney injury

Read the paper

Pressure induced changes in endothelial cell morphology and Ca2+ signaling in ex vivo pressurized resistance arteries revealed using 4D diSPIM myography and AI …

D Collier

AI · Cell Biology · Image Analysis · Vascular Research

HOW ARIVIS HELPED

See how arivis Pro (Version 4.1.1) was used for tile stitching, large-volume 3D visualization, volume rendering, and movie export of light sheet fluorescence microscopy datasets from optically cleared intact testicular tissues across three primate species — human (transgender model), common marmoset, and macaque. The arivis Pro TileSorter enabled pre-alignment and stitching of mosaic tiled image stacks with 20% overlap, while the Arivis SIS Converter processed raw LSFM data into arivis-compatible files for handling these large 3D volumes. This helped this research by providing the 4D viewer's volume rendering and X/Y/Z clipping capabilities that were essential for deep tissue visualization of dense primate testicular architectures, revealing intricate details such as spermatogonial clones organized as singlets, pairs, quartets, and groups of eight, cellular bridges between germ cells, and the spatial relationship between spermatogonia and vasculature — details that classical 2D histology sections would struggle to capture. The software's storyboard and movie export features enabled the creation of 3D videos demonstrating that what appeared as multiple separate tubules in 2D microtome sections was actually a single convoluting seminiferous tubule, a significant finding that overcomes long-standing limitations of classical histology. Critically, this arivis-powered 3D analysis identified testicular pathology in the transgender model, including tubules with depleted germ cells alongside tubules with persisting spermatogonial clones following hormonal suppression — establishing a foundation for spatial evaluation of spermatogenesis kinetics in health and disease.

Read the paper

Virtual reality empowered deep learning analysis of brain activity

D Kaltenecker, R Al

Image Analysis · AI · Neuroscience · Cancer Research · Tissue Clearing · Light Sheet Microscopy · Virtual Reality

HOW ARIVIS HELPED

arivis VisionVR accelerated ground truth generation for deep learning-based whole-brain activity mapping

See how arivis VisionVR was used for 3D virtual reality annotation of c-Fos-positive neurons in tissue-cleared mouse brains imaged with light sheet fluorescence microscopy, enabling the generation of high-quality training data for the DELiVR deep learning pipeline. This helped this research by providing an immersive VR environment where annotators could place selection cubes on individual cells, adjust them to cell size, and apply adaptive thresholding , achieving annotation speeds 7.1 times faster than conventional 2D slice-by-slice methods and improving annotation quality by 6.5% (instance Dice of 80.3%). The VR-generated ground truth data was used to train a 3D U-Net that dramatically outperformed existing threshold-based methods like ClearMap, capturing 73 times more true positive cells with much higher precision. Using this VR-empowered pipeline, the researchers discovered a novel brain activation pattern distinguishing weight-stable cancer from cancer-associated cachexia in tumor-bearing mice, identifying 73 significantly hyperactivated brain regions, including sensory processing and foraging-related cortical areas and the lateral hypothalamic area, that point to a previously unknown neurophysiological phenotype in cancer-related weight control.

Read the paper

2022

Aging activates the immune system and alters the regenerative capacity in the zebrafish heart

H Reuter et al.

Cell Biology · Image Analysis · Regenerative Medicine

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled comprehensive cardiac regeneration analysis in aging zebrafish

See how arivis Pro (previously Vision4D) was used for 3D reconstruction, animation, and macrophage tracking in zebrafish heart regeneration studies, combined with ZEN Intellesis for machine learning-based tissue segmentation. This helped this research by providing automated tracking of macrophage behavior and morphology changes in aging hearts, revealing that immune cells become more spherical and motile with age. The software's tracking capabilities enabled quantification of cell sphericity, speed, and displacement over time, while the 3D visualization features allowed researchers to demonstrate that old zebrafish hearts show impaired regenerative capacity with increased collagen accumulation and variable wound healing responses, supporting the concept of "inflammaging" in the zebrafish cardiovascular system.

Read the paper

MHC II–EGFP knock-in mouse model is a suitable tool for systems and quantitative immunology

J Pačes et al.

Cell Biology · Image Analysis · Immunology

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled comprehensive quantitative immunology analysis across multiple organs

See how arivis Pro (previously Vision4D) was used for manual segmentation and quantification of immune cell populations across intestinal tissue, lymphoid structures, and corneal tissue in MHC II-EGFP knock-in mice. This helped this research by providing precise 3D visualization and counting capabilities that enabled researchers to quantify 36.7 × 10^6 MHC II+ cells in lamina propria, approximately 1 × 10^6 total villi in the small intestine, and 450 scattered lymphoid tissue follicles. The software's polygon measurement tools and manual segmentation features allowed detailed analysis of tissue architecture and cell distribution patterns, supporting the validation of this transgenic mouse model as a powerful tool for systems immunology and demonstrating how quantitative imaging approaches can overcome methodological discrepancies in immune system analysis.

Read the paper

PROM1+ Biliary Progenitor Cells Reside in Peribiliary Glands and Proliferate into Cholangiocytes in Response to Cholestatic Injury in Murine Biliary Atresia Models

A Zhong et al.

Cell Biology · Image Analysis · Liver Research · Stem Cell Research

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled precise quantification of biliary progenitor cell dynamics in liver injury models

See how arivis Pro (previously Vision4D) was used alongside ImageJ for confocal imaging analysis to quantify peribiliary gland areas and organoid volumes in biliary atresia research. This helped this research by providing accurate measurements that revealed Prom1 knockout mice had significantly larger peribiliary glands compared to wildtype mice (1484.4±1156 vs. 126.1±86.3μm²) and larger organoids in vitro (0.30±0.87 vs. 0.09±0.20 mm³). The software's 3D analysis capabilities enabled researchers to demonstrate that PROM1+ hepatic progenitor cells in peribiliary glands differentiate into cholangiocytes following cholestatic injury, with PROM1 deficiency leading to a cholangiocyte differentiation defect that manifests as enlarged structures both in vivo and in vitro culture systems.

Read the paper

A Method for Assessing Mitotic Spindle Orientation in Cerebral Organoids

S Shute

Organoid Research · Neuroscience · Cell Biology · Image Analysis

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) and VisionVR revolutionized 3D mitotic spindle analysis in cerebral organoids

See how arivis Pro (previously Vision4D) and VisionVR were used for 3D rendering and virtual reality annotation of mitotic spindle orientation in cerebral organoids, enabling accurate measurement of spindle angles relative to ventricular surfaces. This helped this research by providing a faster, more accurate alternative to traditional 2D analysis methods that suffered from systematic biases, allowing researchers to capture cells with spindle orientations perpendicular to viewing planes that would otherwise be missed. The VR annotation capabilities enabled efficient placement of coordinate markers on centrosomes and reference surfaces in 3D space, ultimately revealing that KANSL1 haploinsufficiency in Koolen de Vries Syndrome organoids causes decreased planar divisions at early developmental timepoints - findings that would not have been possible with conventional 2D approaches.

Read the paper

2021

Multiscale photonic imaging of the native and implanted cochlea

D Keppeler, CA Kampshoff…

Neuroscience · Image Analysis · Auditory Research

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled automated cellular quantification in cochlear research across multiple species

See how arivis Pro (previously Vision4D) was used for automated segmentation of spiral ganglion neurons in mouse and marmoset cochleae using blob-finder algorithms that detect round objects within predefined diameter ranges and fluorescence thresholds. This helped this research by providing accurate cell counting capabilities that revealed an average of 9,106 ± 724 spiral ganglion neurons in mouse cochleae, closely matching previously reported values. The software's automated segmentation worked effectively with both light-sheet fluorescence microscopy and X-ray phase-contrast tomography data, enabling quantitative morphological analysis including nuclear sphericity and volume measurements that are crucial for developing optical cochlear implants and assessing cochlear morphology across different animal models used in auditory research.

Read the paper

Visualizing Ocular Morphogenesis by Lightsheet Microscopy Using rx3: GFP Transgenic Zebrafish

RA Petersen, AC Morris

Cell Biology · Image Analysis · Developmental Biology

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled comprehensive time-lapse analysis of zebrafish eye development

See how arivis Pro (previously Vision4D) was used for importing, rendering, and analyzing time-lapse lightsheet microscopy data of rx3:GFP transgenic zebrafish during ocular morphogenesis from 1 somite stage through 24 hours post-fertilization. This helped this research by providing automated volume analysis pipelines that quantified eye field development over 14 hours with 5-minute intervals, enabling precise measurement of volume changes as the single eye field separated into two optic vesicles. The software's 4D visualization capabilities and batch analysis features allowed researchers to track morphogenetic processes in real-time, automatically distinguishing between developing optic vesicles and the smaller rx3:GFP-positive hypothalamic region, providing quantitative data on volume, surface area, and fluorescence intensity throughout the developmental timeline.

Read the paper

Multi-modal characterization of collagen fibril orientation in human cortical bone by a combination of quantitative polarized Raman spectroscopy, nanoscale X-ray …

T Kormilina et al.

AI · Cell Biology · Image Analysis · Bone Research

HOW ARIVIS HELPED

ZEISS arivis Pro (previously Vision4D) enabled machine learning-based analysis of bone microstructure across multiple scales

See how arivis Pro (previously Vision4D) was used for machine learning segmentation of mineralized collagen fibrils in human cortical bone samples analyzed by nanoscale X-ray computed tomography. This helped this research by providing automated fibril orientation analysis in 3D volumes at 50nm resolution, revealing preferred fibril orientations and parallel lamella structures that would be impossible to quantify manually. The software's segmentation capabilities enabled correlation of structural data across multiple imaging modalities (Raman spectroscopy, nano-CT, and electron tomography), supporting the development of new biomarkers for bone quality assessment and potentially improving fracture risk prediction in clinical applications through comprehensive multi-scale characterization of bone architecture.

Read the paper

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