CSR Biotech
Transforming Tools Changing Lives

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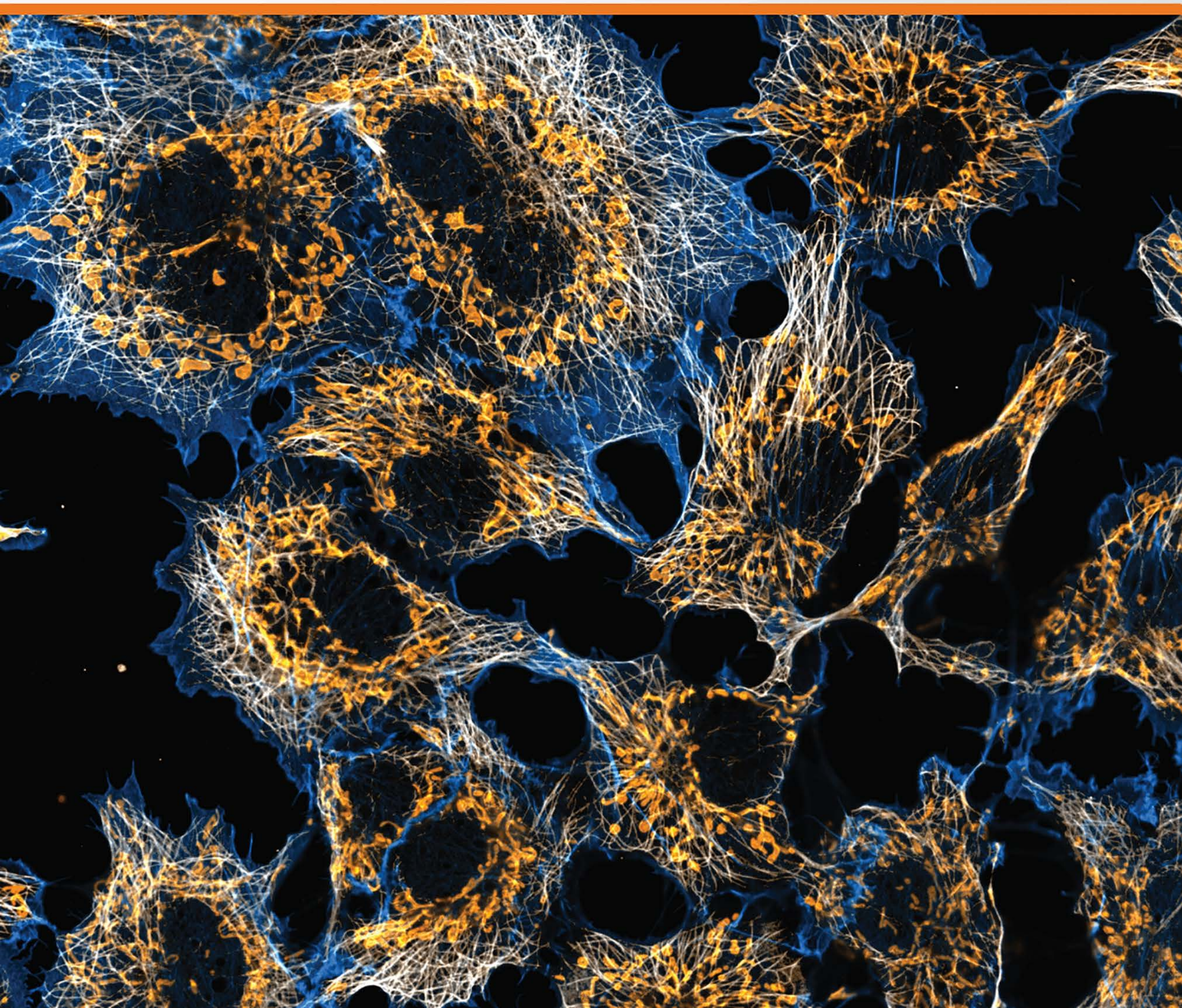
MicroscopeX FINER

Universal Image Analysis Software

All-in-one processing· End-to-end analysis



What is MicroscopeX FINER?

MicroscopeX FINER: An all-purpose imaging analysis platform

MicroscopeX FINER is a general-purpose microscopy image analysis software for multi-modal fluorescence imaging. It uses a proprietary deconvolution algorithm to deliver high-fidelity reconstruction and enhance images under low SNR, low contrast, and out-of-focus interference. It features adaptive, one-click enhancement with automatic scene recognition and intelligent parameter optimization, along with advanced tools for devignetting, bleaching correction, image registration, deep learning–based denoising and segmentation, and high-dimensional analysis.

A universal platform for fluorescence image processing

- Breaks modality barriers to support diverse imaging modalities across full workflow, from import to visualization.
- Intelligent engine auto-detects modalities and optimizes parameters.
- One-click, high-precision enhancement and analysis.

SIM Widefield FRET Airyscan STED
Lightsheet STORM Confocal PALM
FRAP SMLM Spinning Disk Confocal

One platform for all image formats

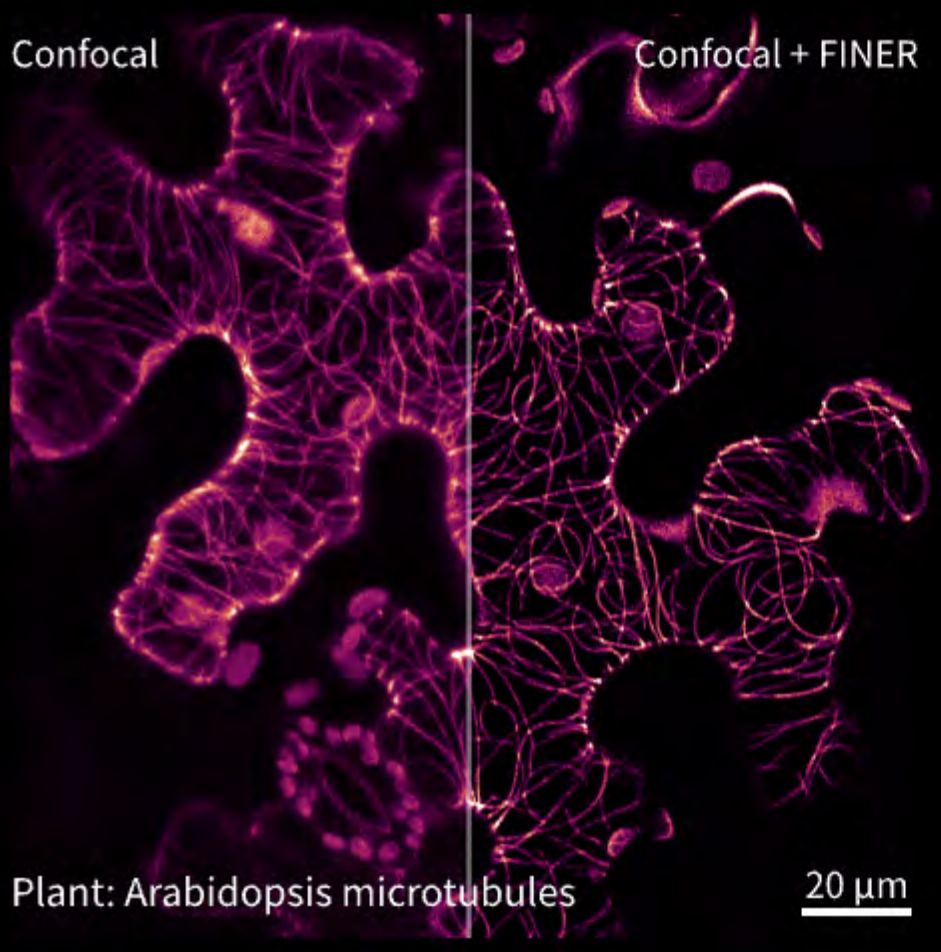
FINER directly imports large-scale fluorescence datasets from major microscope manufacturers, with optimized readout for widefield, point-scanning confocal, spinning disk, multiphoton, light-sheet, and super-resolution imaging. No format conversion is required for immediate analysis.

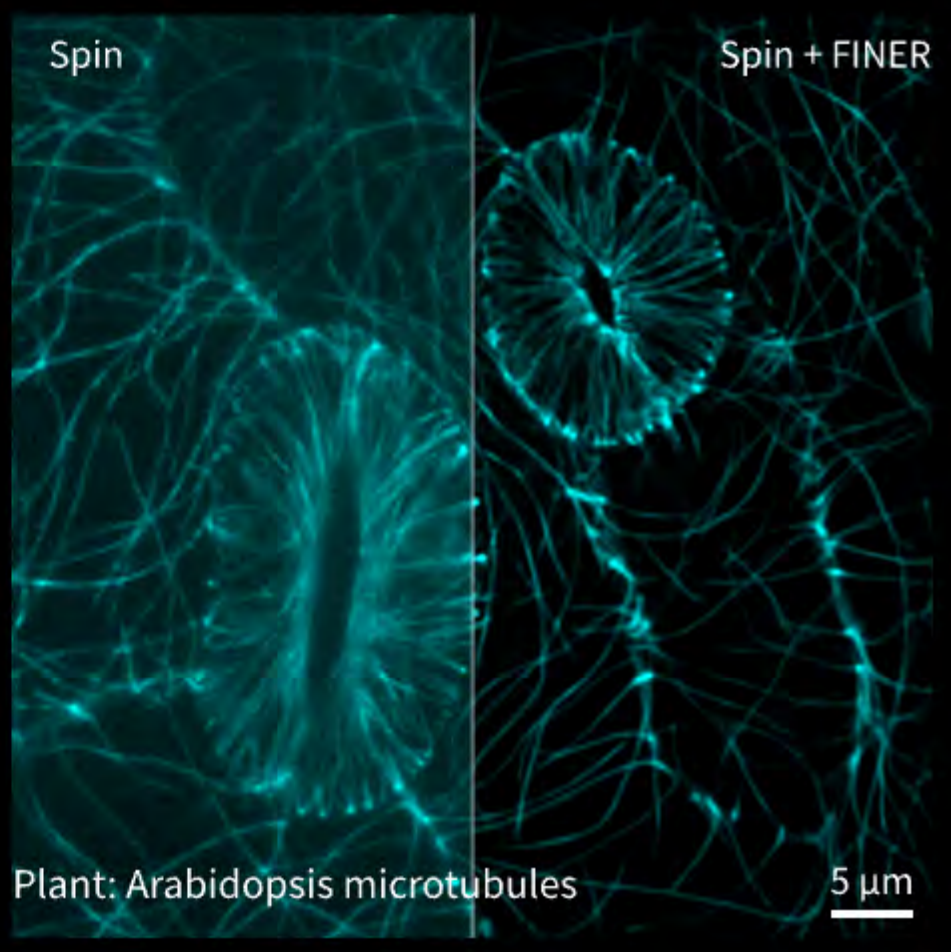
CSR	Evident	Nikon	Leica	Zeiss	Abberior	General
TIF	VSI OIR	ND2	LIF	CZI	OBF MSR	OME-TIF
✓	✓	✓	✓	✓	✓	✓

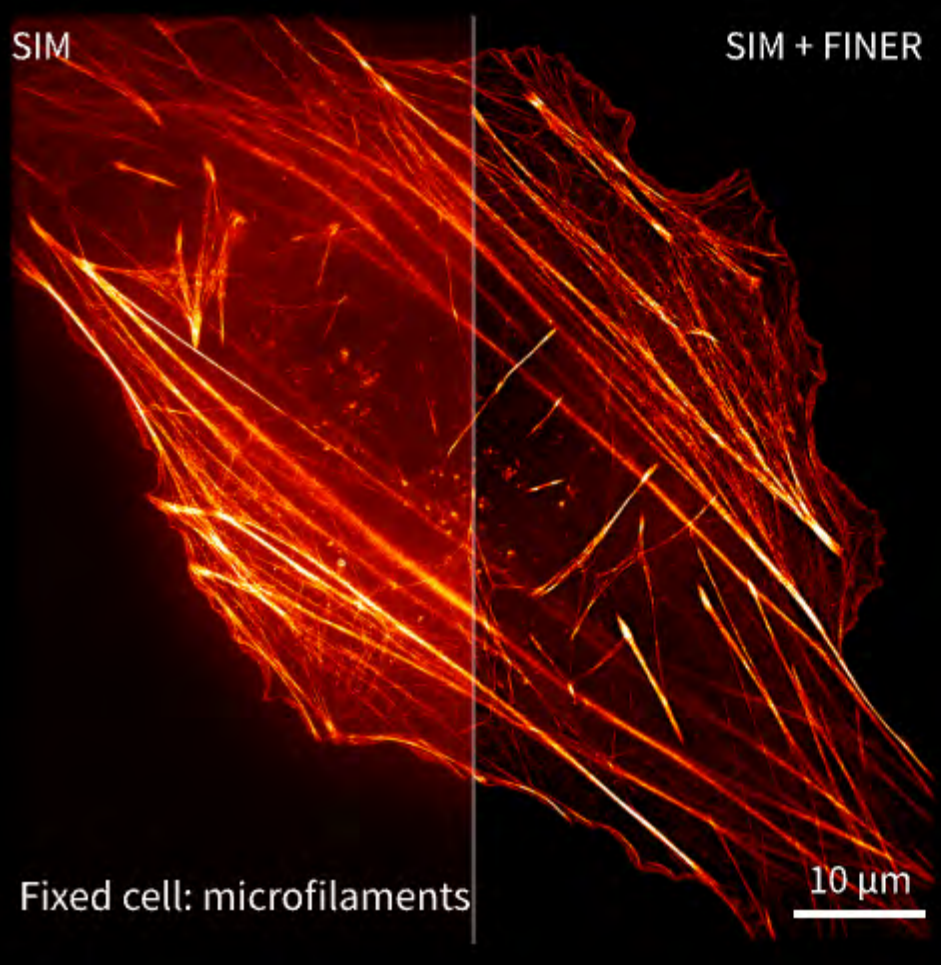
One-click optimization for end-to-end image processing

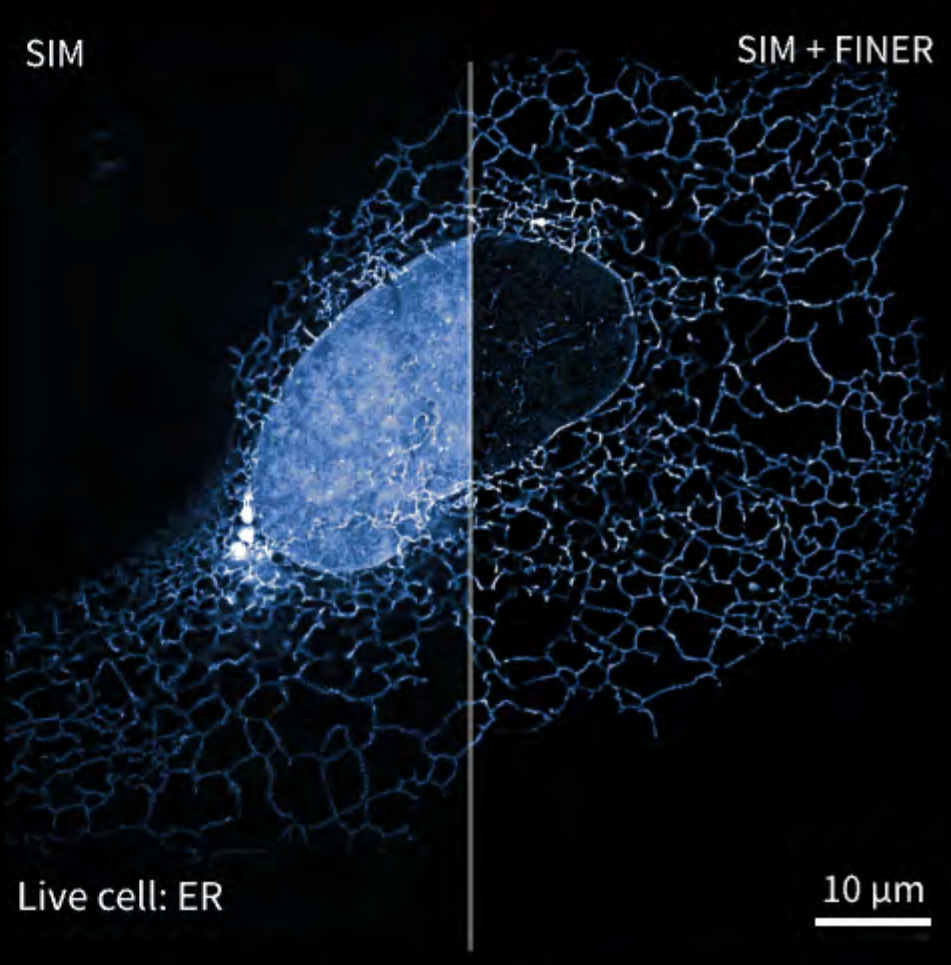
FINER integrates model-based deconvolution algorithms, AI deep learning-based denoising, spatiotemporal image registration, and devignetting algorithm to enhance resolution and contrast across diverse fluorescence microscopy images while effectively removing noise and out-of-focus background.

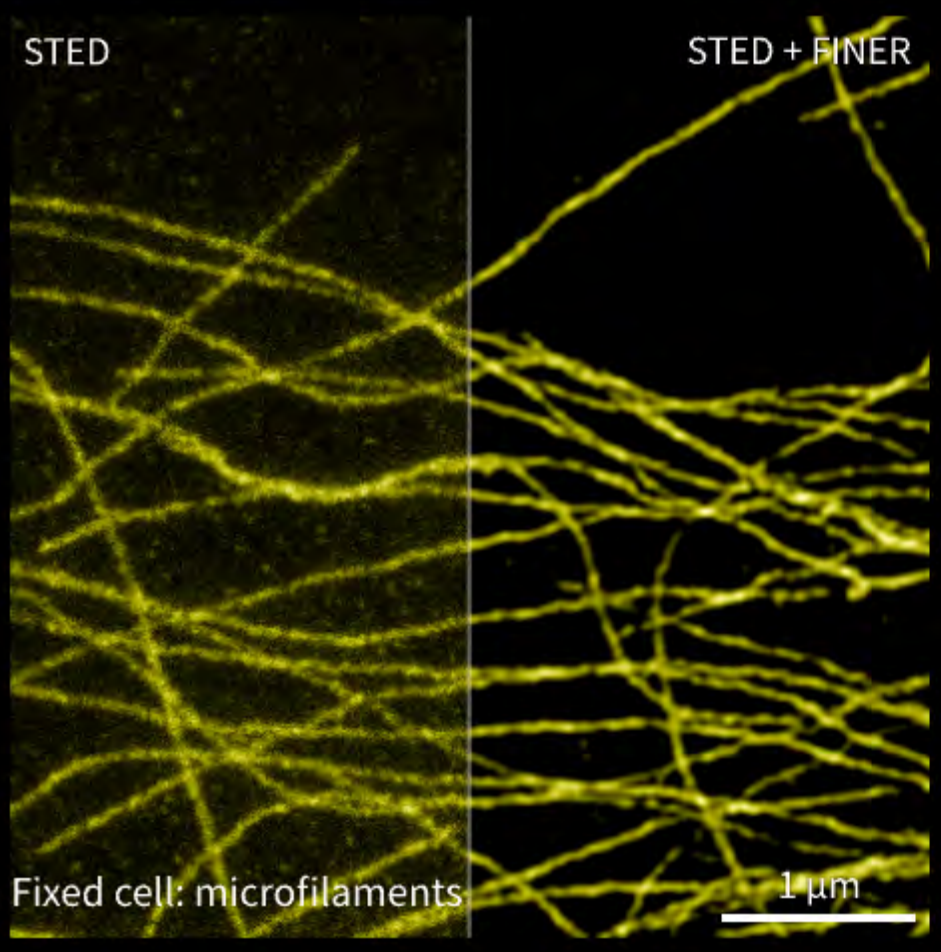
What is MicroscopeX FINER?











FINER: A one-stop image processing solution

Image import → Deconvolution → Post-processing → Quantification → Visualization → Export

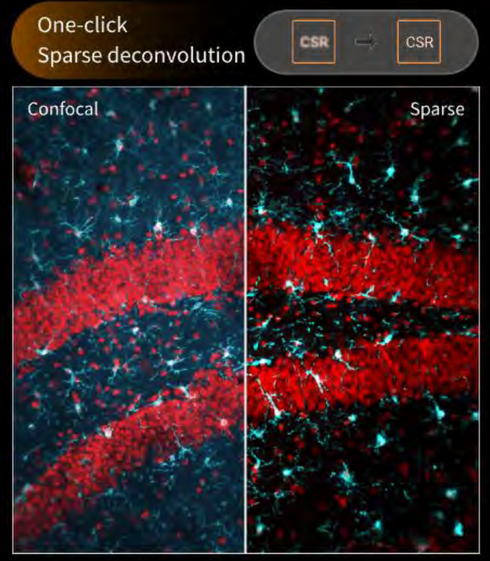
MicroscopeX FINER delivers a complete pipeline

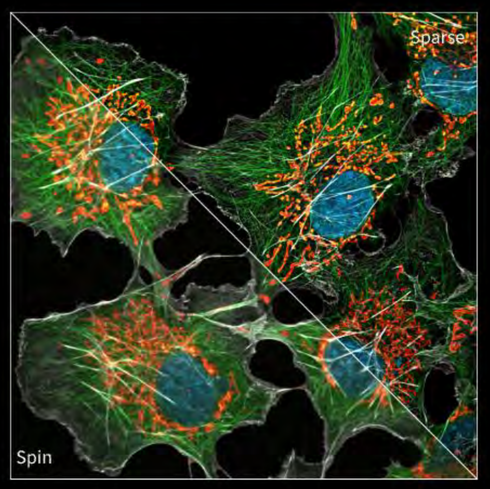
- Advanced image enhancement: sparse 2D/3D deconvolution, AI denoising, time-shift correction, and devignetting for improved visualization and quantitative analysis
- Versatile analysis tools: AI segmentation of organelles, tracking, colocalization, profile analysis, and histogram statistics for comprehensive insights
- Multi-dimensional visualization: volume/surface rendering, projections, and orthogonal views for 3D, time-series, and large-FOV data
- Broad compatibility: supports images from major microscope manufacturers across import, enhancement, analysis, visualization, and export, with intelligent one-click optimization

Mathematical algorithm | Mathematical algorithm & deep learning | Mathematical algorithm & deep learning & statistics | Mathematical algorithm & graphics

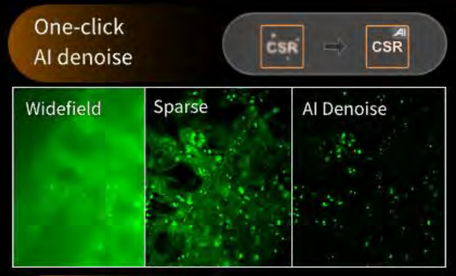
Image import → **Deconvolution** → **Post-processing** → **Quantification & statistics** → **Visualization** → **Export**

One-click Sparse deconvolution

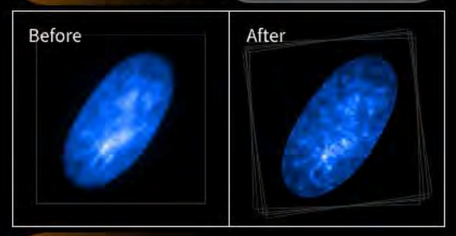




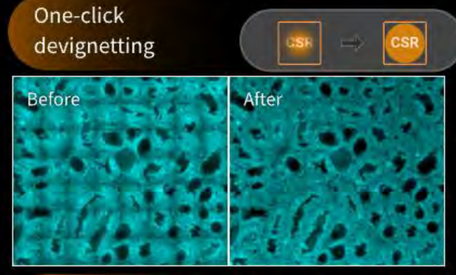
One-click AI denoise



One-click spatial registration

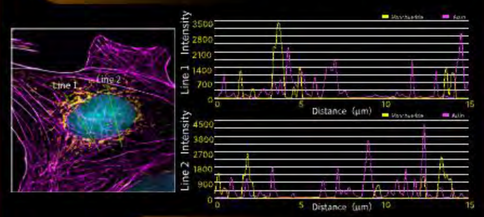


One-click devignetting

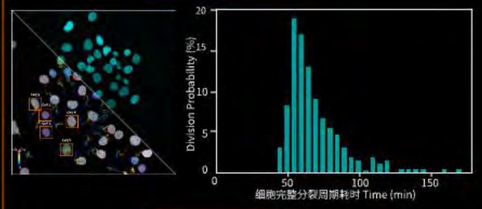


One-click bleach correction

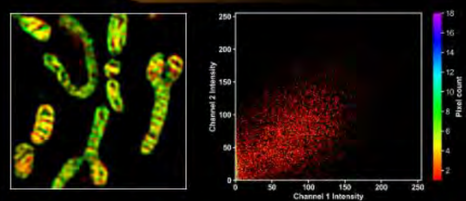
Fluorescence intensity quantification



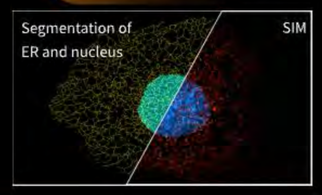
Target tracking



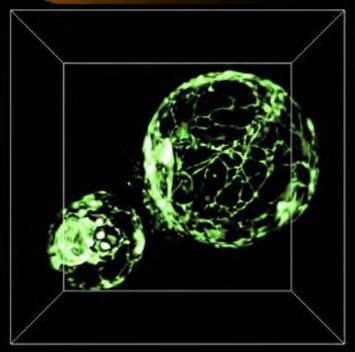
Co-localization analysis



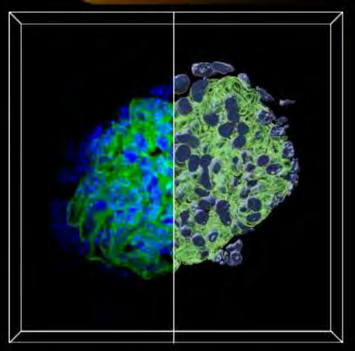
AI segmentation



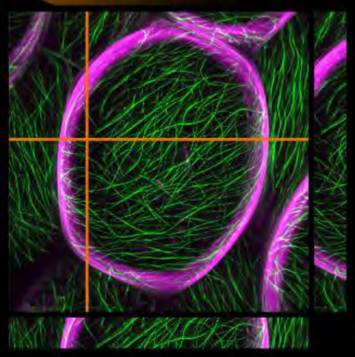
3D volume rendering



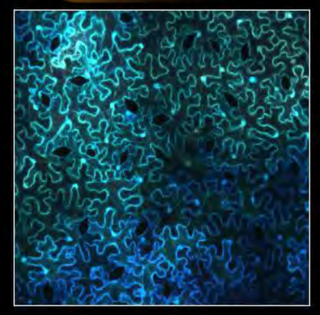
3D surface rendering



Orthogonal view



Max projection



FINER: Rich collection of advanced image processing tools

Proprietory technology: Sparse-SIM, a novel and robust deconvolution algorithm

In November 2021, the founding scientific team of CSR published our original work on the sparse-SIM super-resolution deconvolution algorithm in *Nature Biotechnology*[1], advancing model-based, data-fidelity-driven super-resolution reconstruction to a new level. It was the first peer-reviewed method to achieve 60 nm resolution in live-cell imaging, demonstrating broad applicability across fluorescence microscopy platforms. As FINER's core algorithm, sparse-SIM enables high-performance, universally compatible image processing.

Full upgrade: FINER, a universal image enhancement software

In April 2021, CSR initiated a comprehensive upgrade of sparse-SIM, including expanded imaging modalities and applications, computational optimization, cross-platform enhancement, accelerated parallel processing, and UI integration. In December 2022, the company launched MicroscopeX FINER, a versatile and user-friendly fluorescence image enhancement software.

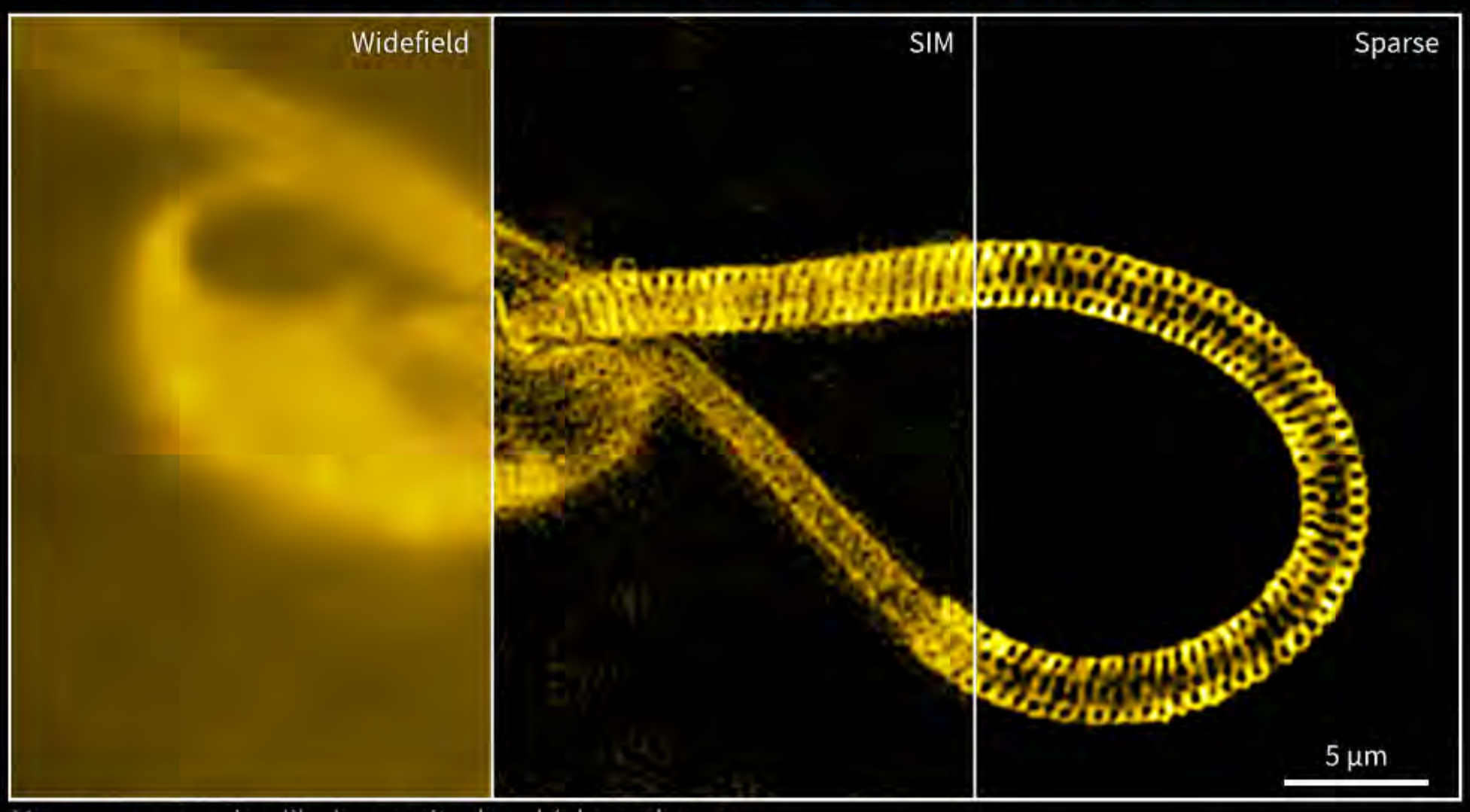
Intelligent adaptation: Auto-recognition of diverse fluorescence image types

Continuously updated and upgraded by CSR, FINER now adapts to diverse fluorescence imaging data across modalities, formats, types, and dimensions, enabling automatic recognition and intelligent processing of 13 imaging modalities and 9 file formats.

Easy to use: One-click auto enhancement

FINER supports diverse biological samples and intelligently recommends reconstruction workflows based on imaging modality and file format. It further optimizes parameters according to sample type, data characteristics, image structure, and raw image quality, eliminating manual tuning and enabling one-click processing for a seamless user experience.

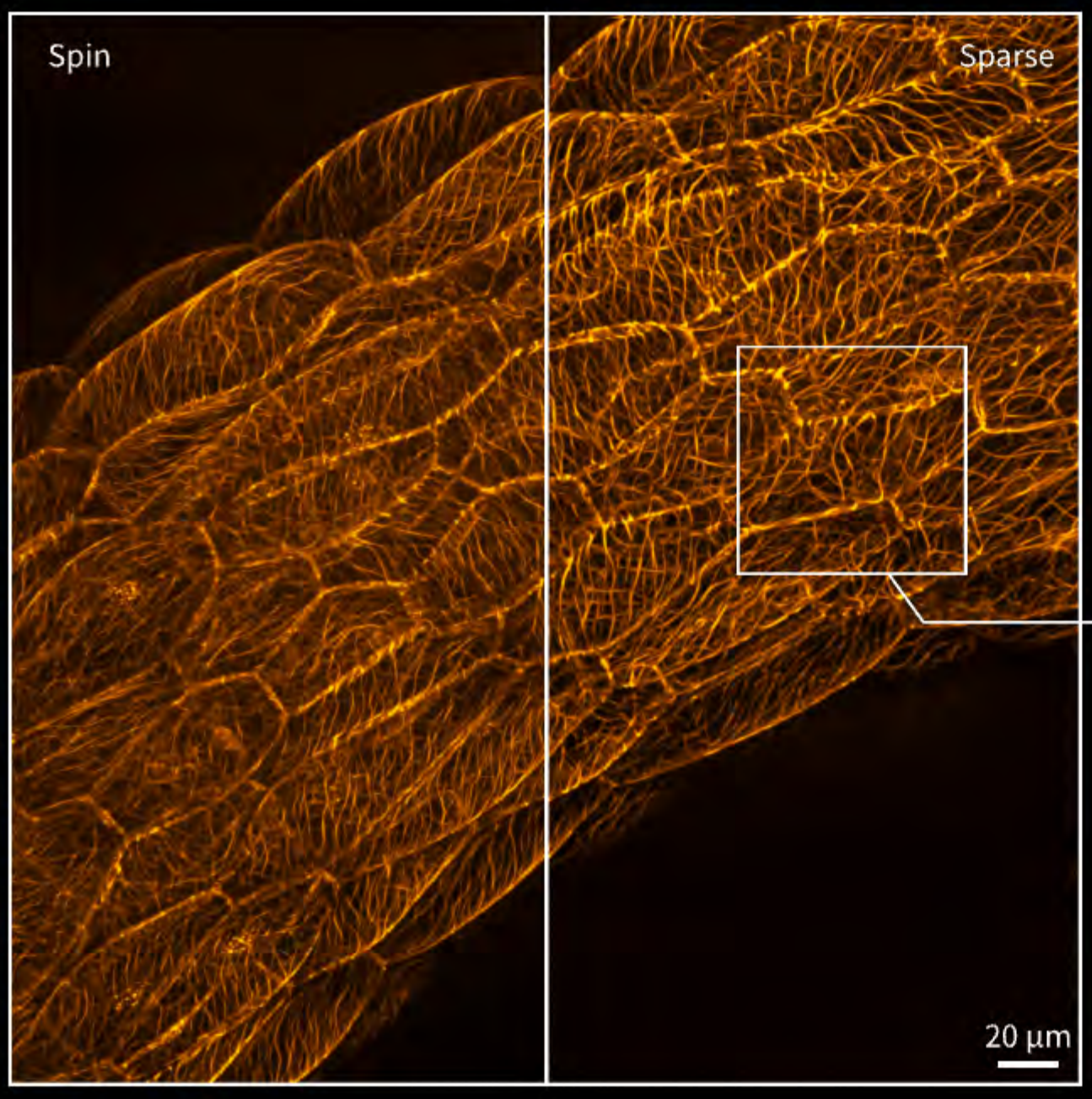
Deconvolution resolves the ultrastructure of inner mitochondrial membrane



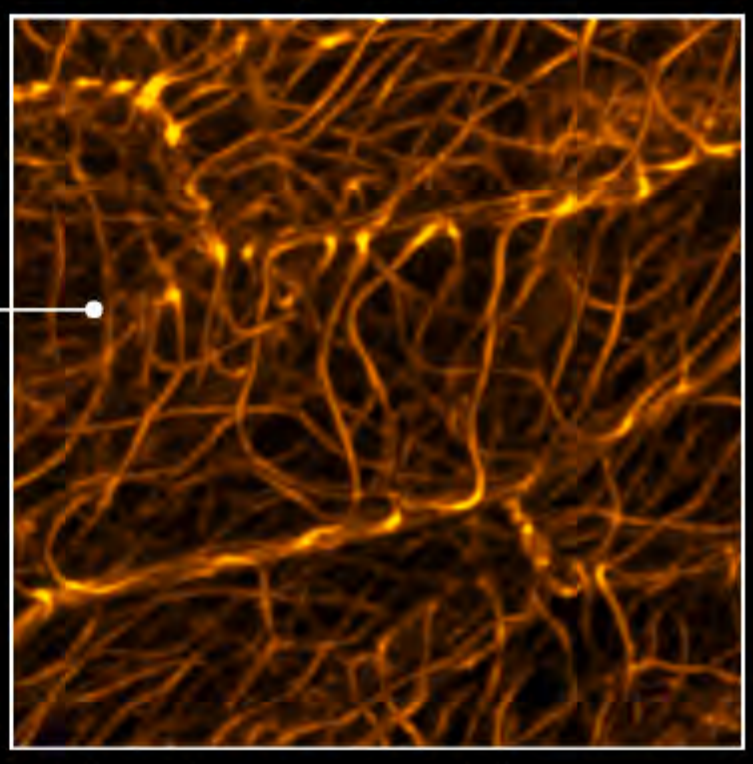
Mouse sperm: spring-like inner mitochondrial membrane
Data source: Prof. Zhang, Shenzhen Institutes of Advanced Technology

[1] Proprietary techonology: Weisong Zhao et al, *Nature Biotechnology* , 2021. Patented.

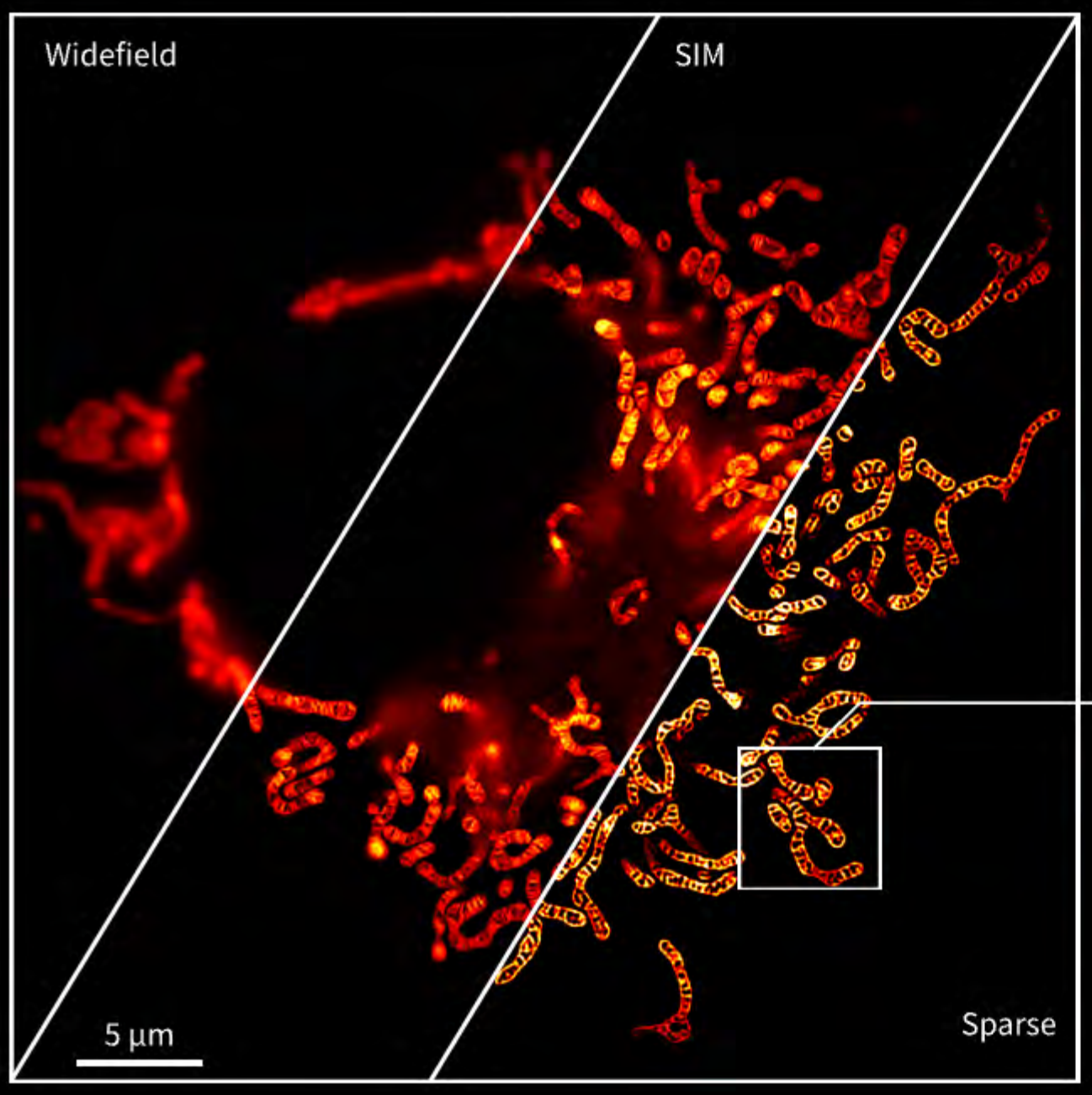
FINER: Rich collection of advanced image processing tools



Sparse deconvolution reveals fine microtubule structures in the Arabidopsis hypocoty



Arabidopsis hypocoty microtubule
Data source: CSR Biotech



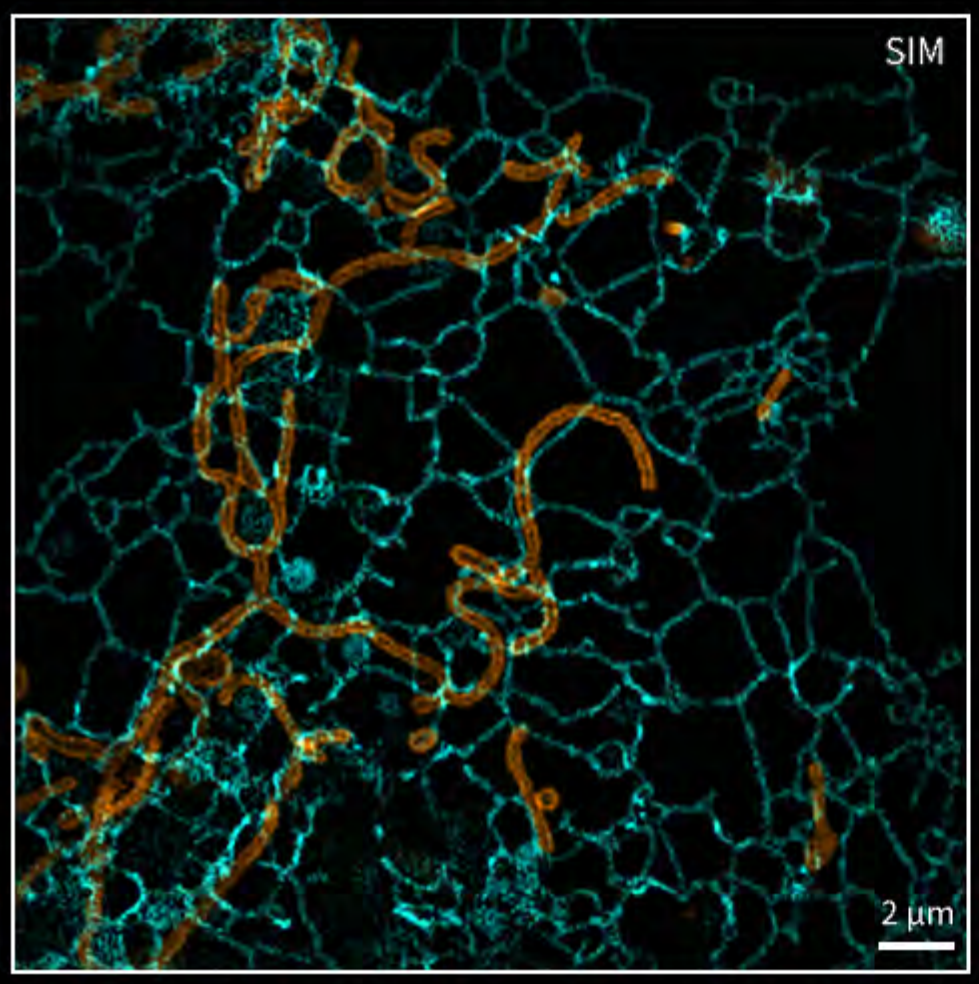
Sparse deconvolution reveals fine inner mitochondrial membrane structures in live cells

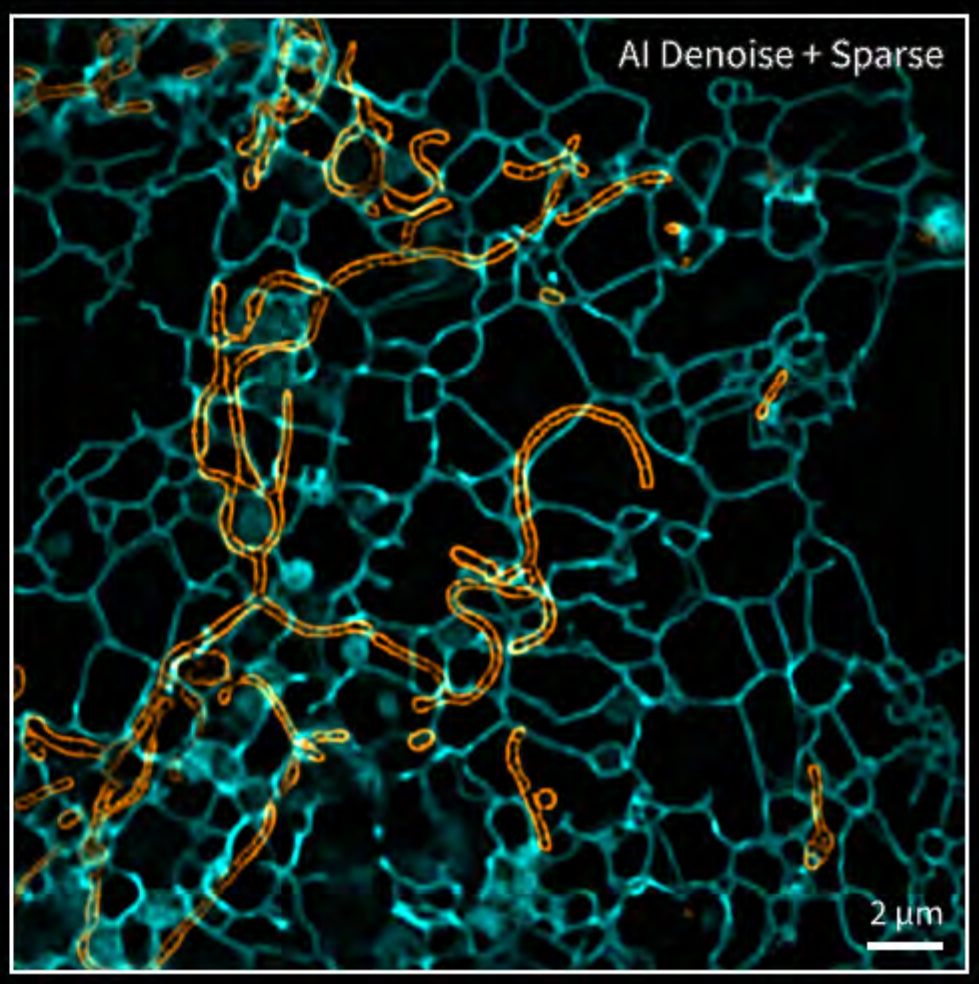
COS7 inner mitochondrial membrane (live cell)
Data source: CSR Biotech

FINER: Rich collection of advanced image processing tools

AI denoise significantly reduces image noise

FINER features a universal deep learning denoising model trained on large-scale, multi-dimensional datasets spanning diverse microscopes, imaging modalities, biological structures, resolutions, and noise levels. As a powerful post-processing tool after deconvolution, it further suppresses noise and enhances signal detail.

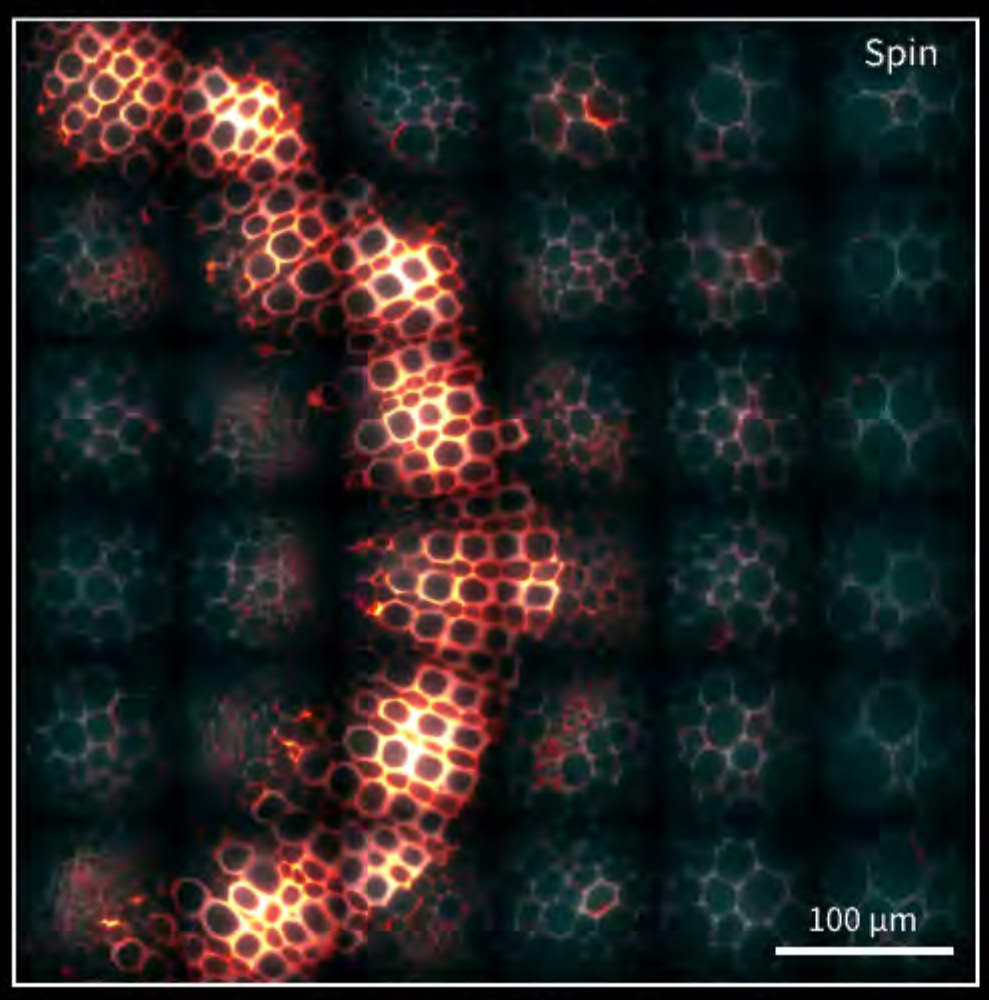


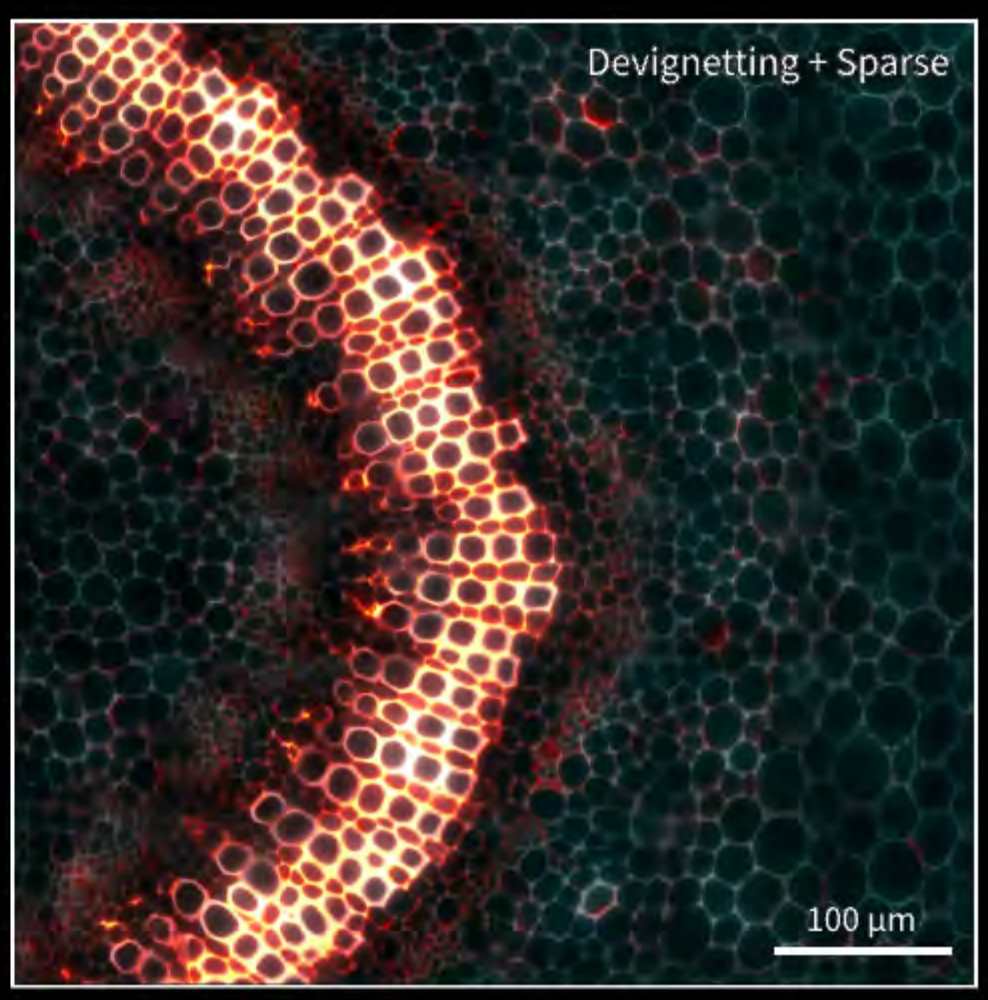


Outer mitochondrial membrane (yellow); endoplasmic reticulum (cyan)
Data source: Prof. Chen, Peking University School of Life Sciences

Devignetting restores uniform signal distribution

- Estimates illumination falloff using a physics model on vignetting and applies intensity correction to effectively remove uneven shading.
- Automatic adaptation for single-field and stitched images and optimization of correction strategies across varying systems and conditions.





Oleander leaf section: stomata (red); cell wall (cyan)
Data source: CSR Biotech

FINER: Rich collection of advanced image processing tools

Multi-parameter batch image processing workflow

FINER chains complex algorithms into an automated image processing pipeline, enabling one-click execution for both single-image refinement and large-scale, multi-dimensional batch processing. It eliminates repetitive operations while ensuring consistency and traceability across datasets, freeing researchers from repetitive tasks. In the example below, live cells were labeled for mitochondria, actin cytoskeleton (microfilaments), and nuclei, followed by long time-lapse imaging. Using FINER's multi-parameter batch workflow, channel-specific processing parameters were applied and optimized in a single run for efficient multi-channel image enhancement.

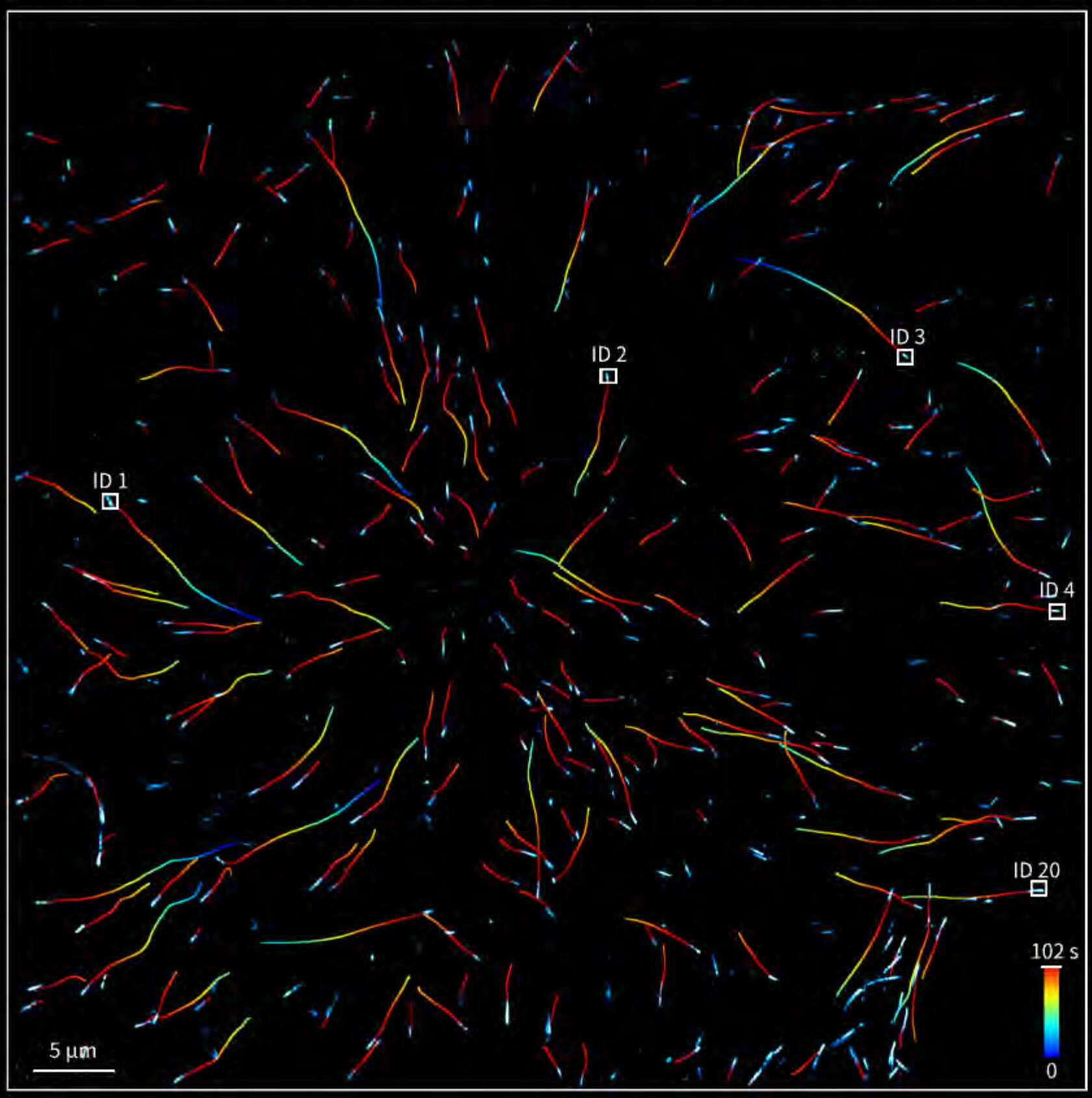
U2OS cells: nucleus (blue); microfilament (purple); mitochondria (yellow)
Data source: CSR Biotech

FINER: Quantitative measurement and statistical analysis

Deep learning-based target tracking

FINER features a deep learning tracking module for automatic single- and multi-target tracking across multi-modal, multi-channel, long-term image sequences at up to 20 Hz. It outputs fluorescence intensity, morphology, motion, and interaction dynamics in one click, enabling efficient analysis of complex biological processes.

In this example, EB3 trajectories were tracked over 102 s, with metrics including average speed, instantaneous velocity, and travel distance, enabling quantitative analysis of microtubule growth and dynamic cellular responses.



EB3 protein

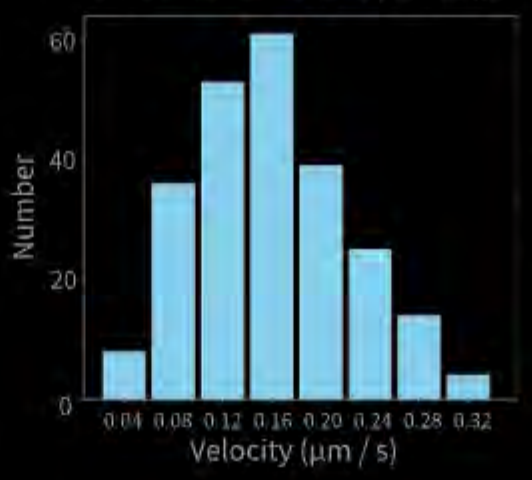
Data source: CSR Biotech

- Quantifies statistical metrics for each target and supports one-click export.

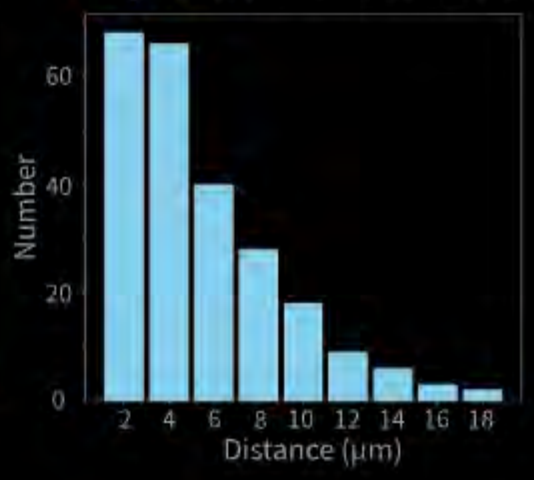
Target ID	Average intensity	Average velocity (μm / s)	Total distance (μm)
1	213	0.163	16.575
2	163	0.160	9.260
3	171	0.166	16.413
4	239	0.158	8.255
. . .	. . .	. . .	. . .
20	255	0.167	11.960
. . .	. . .	. . .	. . .

- Quantifies real-time velocity and travel distance distributions of EB3 protein.

EB3 instantaneous velocity



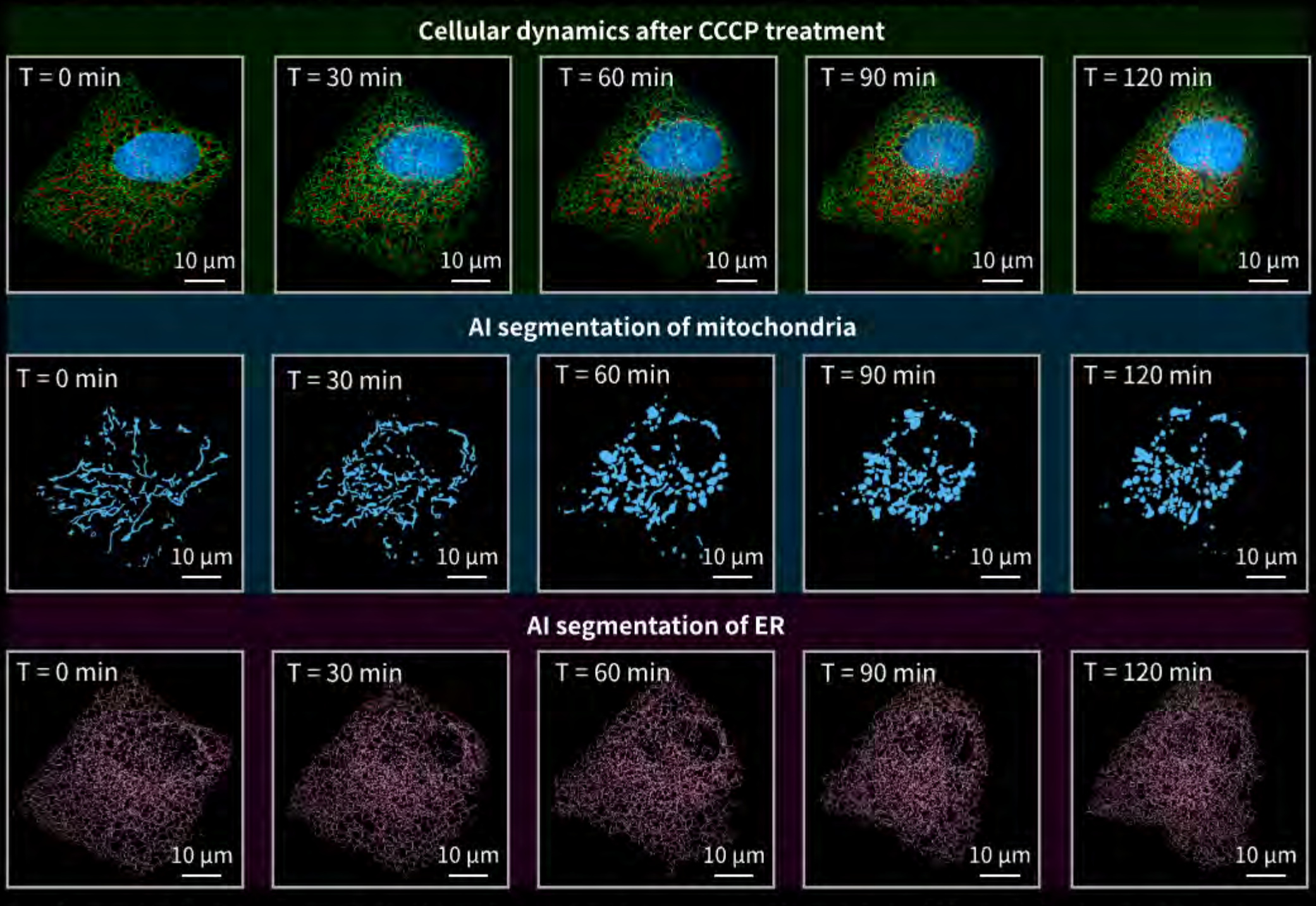
EB3 protein total distance travelled



FINER: Quantitative measurement and statistical analysis

Deep learning image segmentation

FINER features a next-generation deep learning segmentation engine trained on large-scale multi-modal fluorescence datasets, operating at up to 30 Hz. It enables pixel-level organelle segmentation (mitochondria, ER, lysosomes, nuclei) with one-click output of key quantitative metrics including cell count, area, intensity distribution, morphology, and colocalization, streamlining complex workflows into automated, high-throughput analysis.
In this example, CCCP-treated U2OS live cells were used to model mitochondrial stress. Frame-by-frame segmentation of organelles in time-lapse data was performed using FINER, generating quantitative metrics for mitochondrial morphology (area, perimeter, aspect ratio, number) and ER area for dynamic stress analysis.

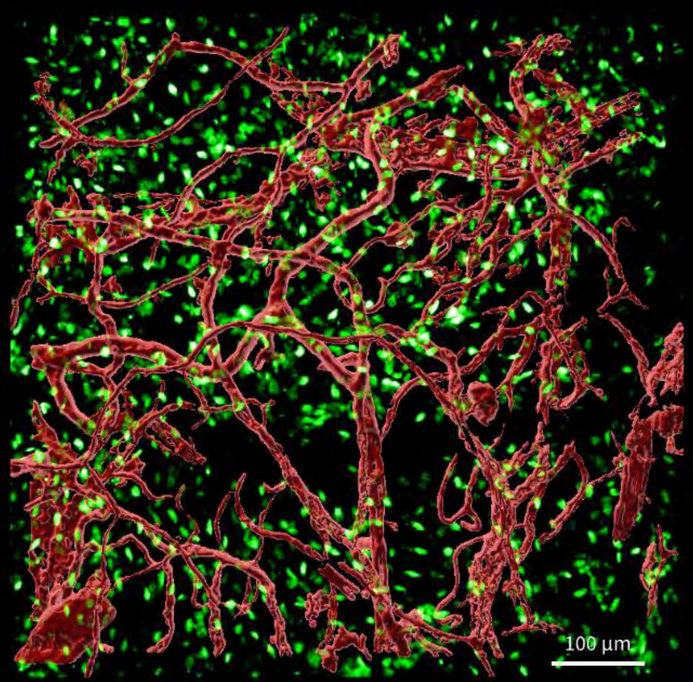


FINER segmentation shows that with increasing CCCP treatment, mitochondrial aspect ratio decreases, indicating a shift from tubular to fragmented morphology and mitochondrial damage. ER area also declines, consistent with cellular shrinkage.

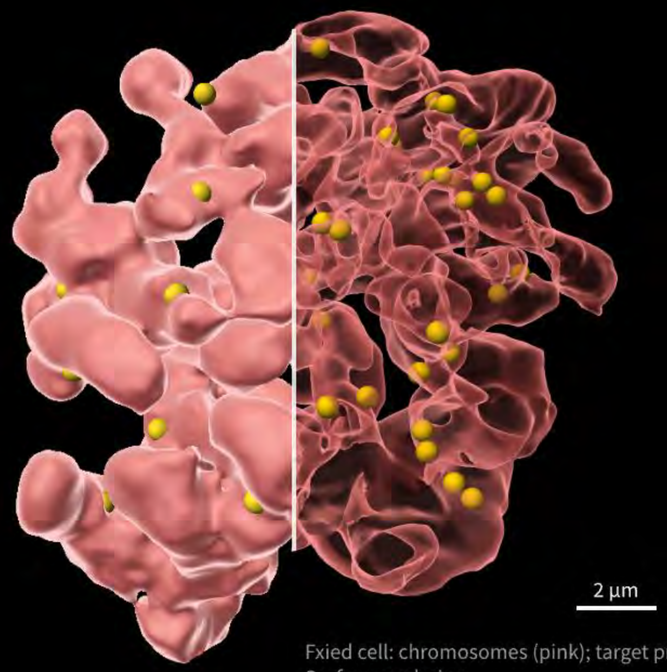
U2OS cells: nucleus (blue); mitochondria (red); ER (green); mitochondria segmentation (blue); ER segmentation (pink)
Data source: CSR Biotech

FINER: 3D rendering visualization

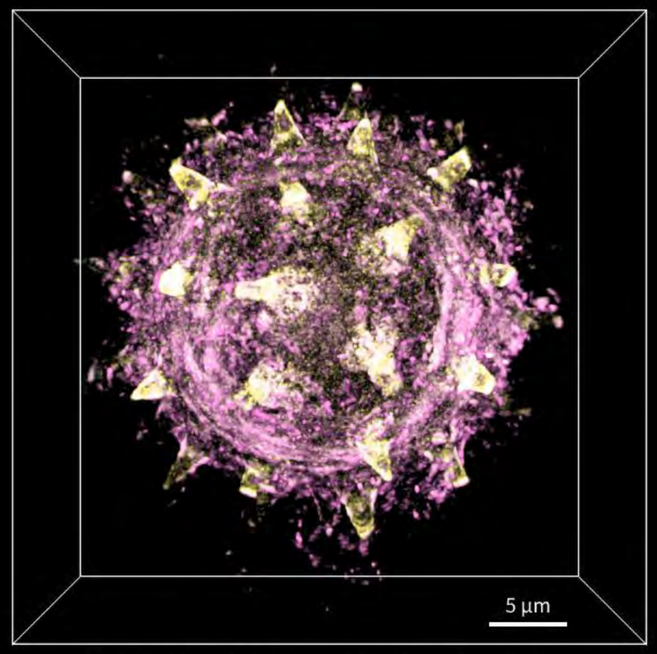
FINER provides diverse visualization tools including volume rendering, surface rendering, projections, and orthogonal views. Users can fine-tune lighting, color, material, transparency, smoothing, and connectivity with real-time feedback, along with scale bars, bounding boxes, view switching, and cross-comparison of processed data. It also supports lossless video animationexport for comprehensive, multi-dimensional visualization and biological interpretation.



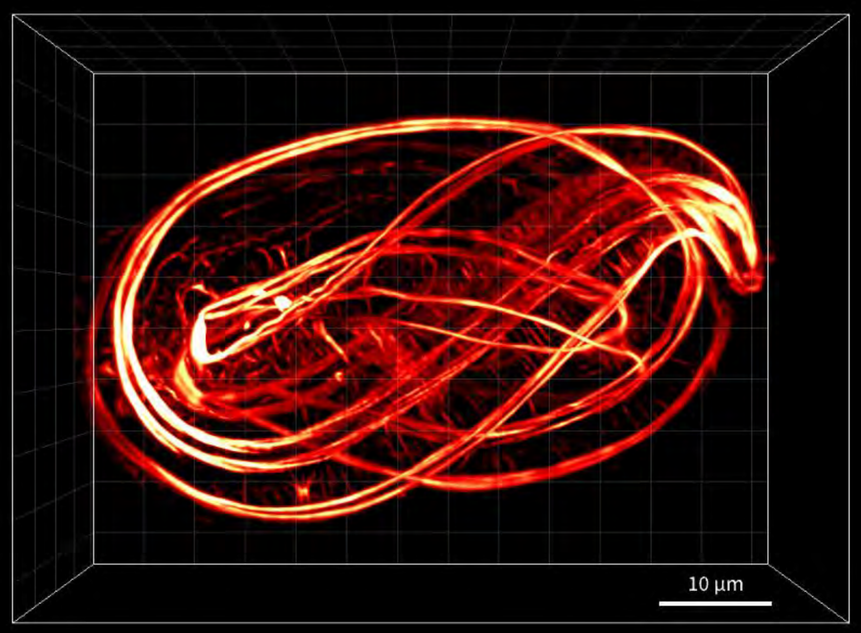
Mouse skull: vasculature (red); osteocytes (green)
Vascaluture: surface rendering; osteocyte: volume rendering (MIP)
Data source: CSR Biotech



Fxied cell: chromosomes (pink); target protein (yellow)
Surface rendering
Data source: Prof. Zhang, National Center for Protein Sciences

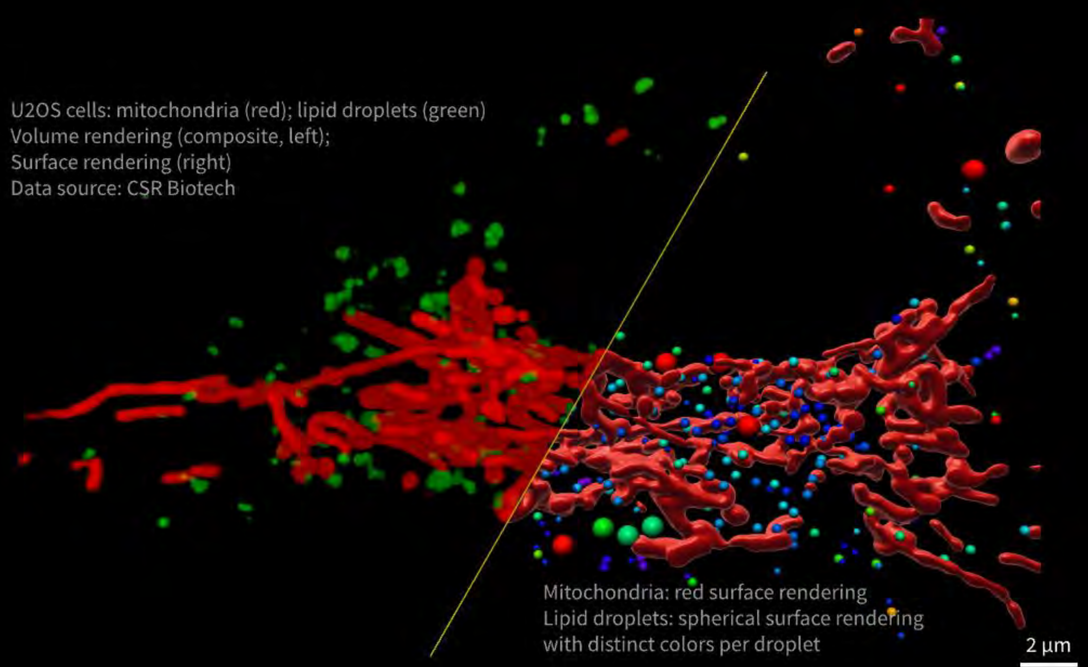


Plant pollen: punctate protein (purple); DAPI (yellow)
Volume rendering (MIP)
Data source: Prof. Xu, Shanghai Jiao Tong University



C.elegans: actin filaments
Volume rendering (MIP)
Data source: CSR Biotech

U2OS cells: mitochondria (red); lipid droplets (green)
Volume rendering (composite, left);
Surface rendering (right)
Data source: CSR Biotech



Mitochondria: red surface rendering
Lipid droplets: spherical surface rendering
with distinct colors per droplet

FINER: High-throughput quantitative analysis of dose-dependent Erastin-induced ferroptosis

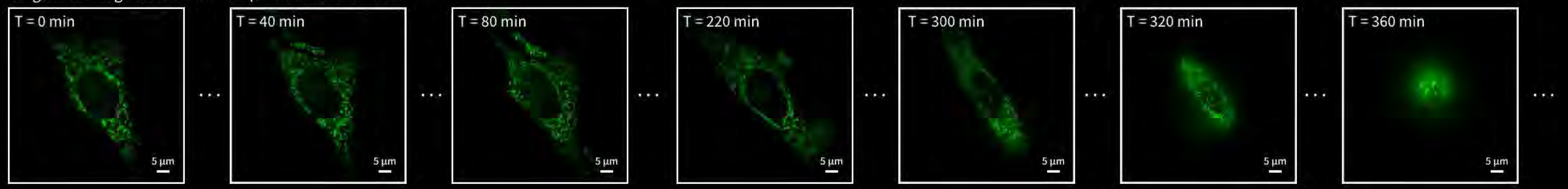
Ferroptosis is a distinct form of regulated cell death with important pathological relevance, and a key feature distinguishing itfrom apoptosis and pyroptosis is mitochondria-specific morphological alteration. FINER enables end-to-end quantitative analysis of ferroptosis by enhancing high-throughput imaging data, segmenting mitochondria, and extracting morphologicaldynamics over time.

In this example, 8 experimental groups (including control) were imaged across 150 fields per group over 15 hours. AI-basedsegmentation was used to track changes in mitochondrial morphology at each site.

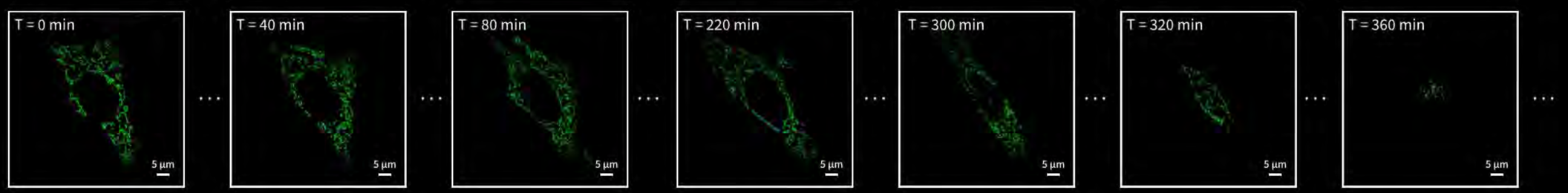
These changes were then used to quantify cell death timing and survival rates across large populations, enabling systematicevaluation of the effects of different Erastin concentrations on ferroptosis.

Single-cell image series under 0.5 μM Erastin treatment

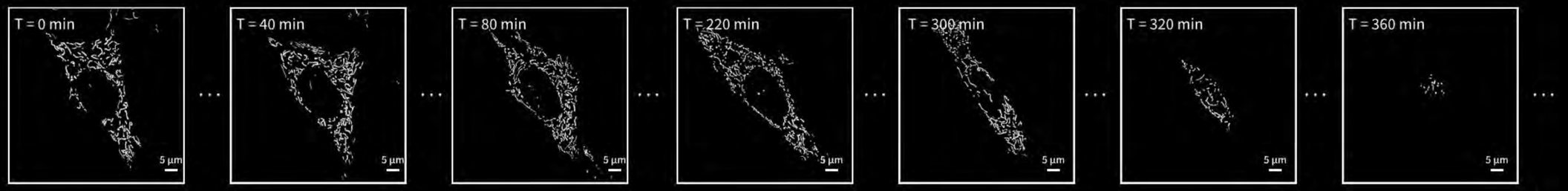
Deconvolution yields super-resolution mitochondrial images



AI denoise



AI segmentation



Morphological analysis based on segmented mitochondria

Mitochondrial segmentation and morphological statistics at one time point

ID [1]	Length (μm)	Width (μm)	Area (μm²)	Shape
1	0.457	0.228	0.192	Sphere
2	0.563	0.163	0.271	Sphere
3	2.149	0.163	0.895	Rod
4	0.419	0.228	0.395	Sphere
5	0.235	0.293	0.252	Sphere
. . .	. . .	. . .	. . .	. . .

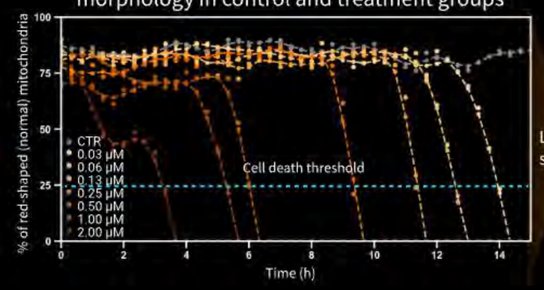
Time course

0.5 μM treatment: overall mitochondrial state in cells over time

Time (min)	Total area of spherical mitochondria (μm)	Total area of rod-shaped mitochondria (μm)	% of rod-shaped mitochondria
0	17.973	104.872	85.369
40	22.311	109.823	83.115
. . .	. . .	. . .	. . .
300	7.608	20.212	72.652
320	10.083	11.319	52.887
360	3.438	0.966	24.272

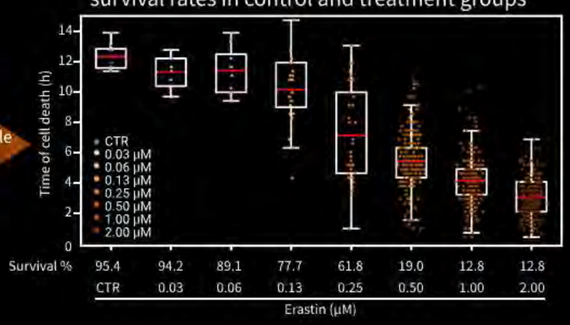
Time course curve of one recplicate

Time-course curves of mitochondrial morphology in control and treatment groups



Large-scale statistics

Large-scale statistics of cell death timing and survival rates in control and treatment groups



[1] Each connected segmented region was counted as one mitochondrion.

Software Specifications

Sparse Deconvolution	Sparse deconvolution is supported across multiple imaging modalities. Standard: widefield and confocal images Optional: SIM and STED super-resolution images, single-molecule super-resolution images, multiphoton and light-sheet images
Conventional Deconvolution	A general-purpose deconvolution method based on mathematical and physics models, enables diverse fluorescence image enhancement in batch, improving resolution and contrast, suppressing noise, and removing defocused background.
Time-shift Correction	Includes long time-lapse shift correction, with multiple correction and target recognition algorithms for precise post-processing alignment across multimodal images.
AI Denoise	One-click removal of noise and background using an AI-powered model.
AI Segmentation	Deep learning–based segmentation supports intelligent identification of target structures in both fluorescence and label-free images, enabling one-click segmentation and extraction of metrics such as area, perimeter, and intensity.
AI Tracking	Deep learning–based tracking automatically identifies and tracks targets in real-time, outputting long-term morphology, intensity, and velocity metrics.
Quantification & Analysis	Includes diverse measurement and statistical tools for feature identification, profiling, colocalization, histogram analysis, and motion quantification.
Multi-dimensional Visualization	Provides multiple visualization modes, including 3D volume rendering, surface rendering, projections, and orthogonal views.

System Requirements

	Minimum	Recommended
System Version	Windows 10 or above	Windows 10
System Memory	⩾ 8 GB	128 GB
Monitor Resolution	⩾ 2560 × 1600	3840 × 2160
GPU	NVIDIA discrete CPU，memory ⩾ 6 GB	NVIDIA discrete CPU，memory 24 GB

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FINER _brochure_ENG_VUNV.02.06_CN released on May.27, 2026

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