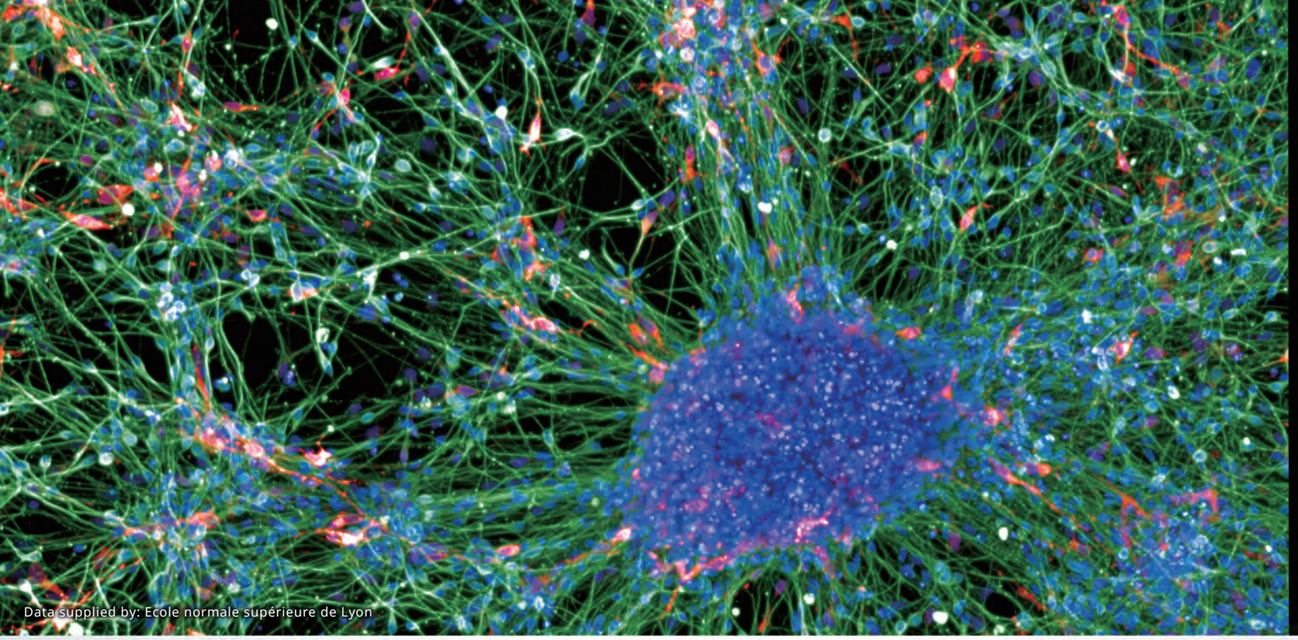
YOKOGAWA

Co-innovating tomorrow™

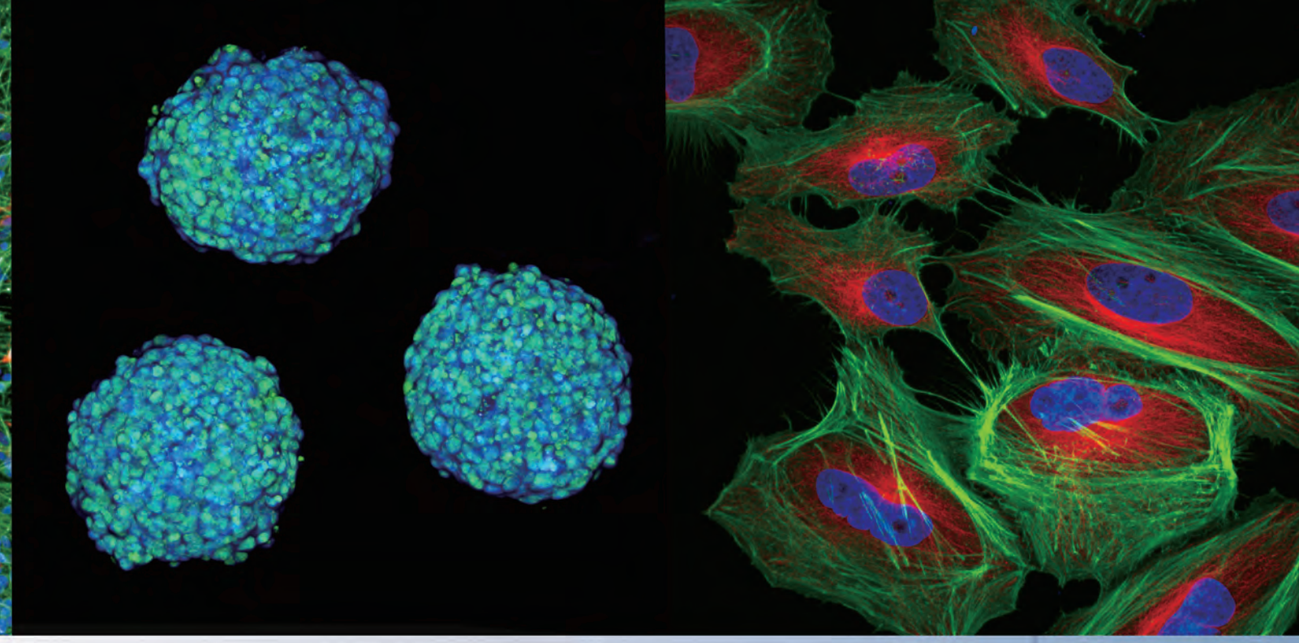
High Content Analysis Software

CellPathfinder™ R3.07

Bulletin 80K01B01-01E



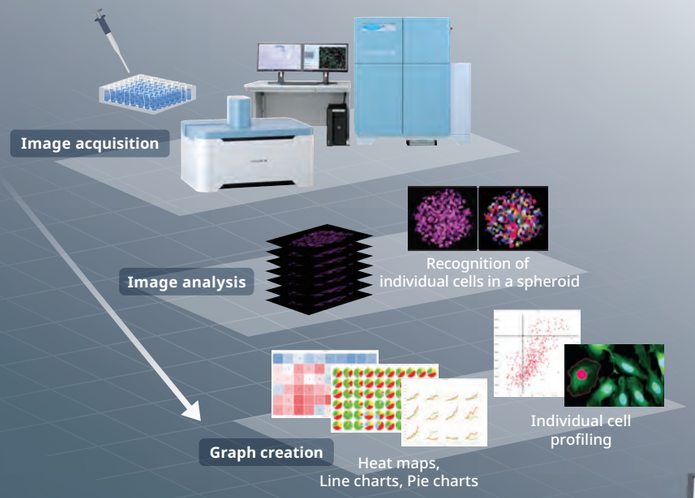
Data supplied by: Ecole normale supérieure de Lyon



summary

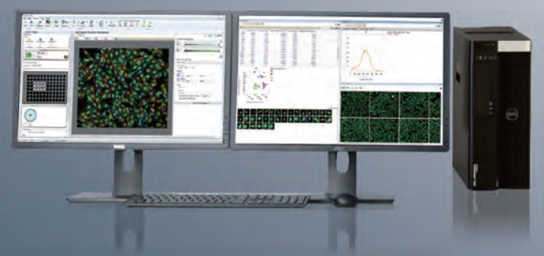
Introduction

Compared with biochemical experiments, high content analysis (HCA), which analyze phenomena occurring in cells based on microscopic images, allows to acquire wide-ranging data in a single experiment, including not only the amount of the target molecules but also the dynamics such as localization and the morphological information of cells as well as intracellular organelles.
In addition, the phenomena can be verified through actual images, and the non-specific phenomena that may result in false positives in traditional high throughput screening (HTS) can also be eliminated.
Moreover, after acquiring images once, HCA allows to analyze them any number of times from various angles, which provides an efficient and multidimensional understanding of cell's physiological phenomena. Owing to this, the necessity for HCA in basic research and drug discovery is increasing.
On the other hand, experimental systems which reproduce the environments similar to that in vivo such as live-cell systems using biomarkers and 3D culture, in order to capture phenomena occurring in the organism, have become complicated. Furthermore, assays without cell labeling, which minimizes the effect on cells, have become popular in recent years especially in regenerative medicine. Thus the demand for the label-free analysis is increasing.



Solution

The CellPathfinder analysis software, with the intuitive and easy-to-use interface, guides the user from analyzing thousands of image data in various angles to visualize the results by generating numerous graph types.
In addition, the Machine Learning and Deep Learning function increase the target recognition capability dramatically. It is also ideal for the analysis with the complexity and high-degree-of-difficulty such as analyzing the data from 3D culture and live-cell imaging. Furthermore, the Machine Learning and the Deep Learning function are also highly usable for analyzing bright field images.
There it is covering a wide range of analysis steps of fluorescence as well as of bright field images.
The CellPathfinder is a powerful tool that broadens the capability of HCA.



Cell Voyager CellPathfinder
High Content Analysis Software

CellPathfinder Resolves Difficulties

For high throughput screening Users

CellPathfinder resolves screening bottlenecks

- A specialized interface for inspecting multiple samples makes image comparison easy, improving efficiency.
- Advanced analysis using the Machine Learning and the Deep Learning function is possible through simple operation, even for beginners.
- Various graph, image and video generation function are available, reducing hassles at the time of reporting.

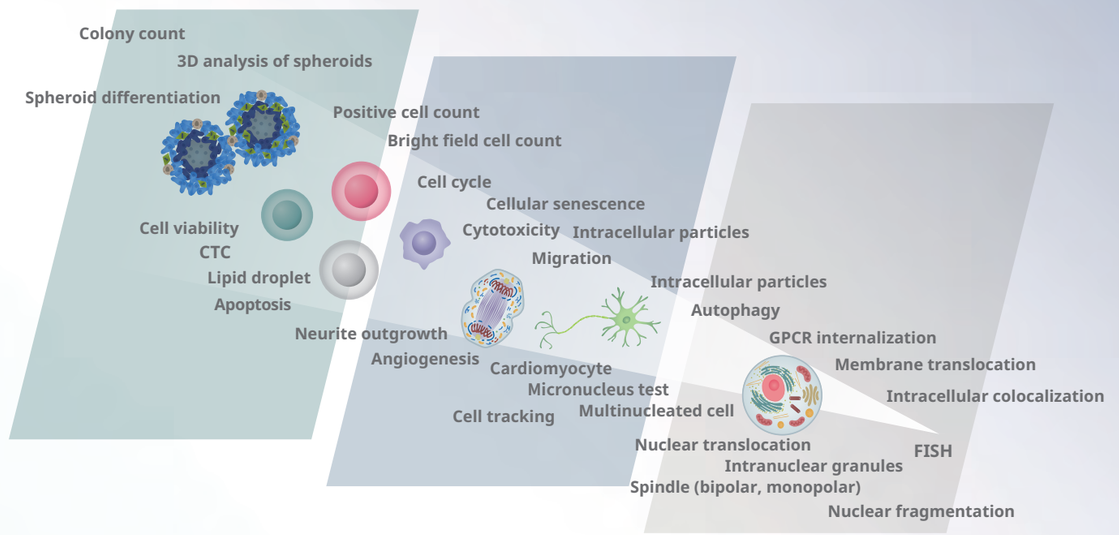
For cancer researchers and regenerative medicine researchers

CellPathfinder provides leading HCA through proprietary analysis technology

- Label-free analysis of sensitive samples is possible using Yokogawa's proprietary image generation technology "CE Bright Field" *1.
- Newly-developed easy-to-use Machine Learning and Deep Learning make previously difficult phenomena detection easy.
- Detection of rare events (CTC, etc.) with high speed and high accuracy.

*1 Refer to P.9 for details on CE Bright Field.

Application example



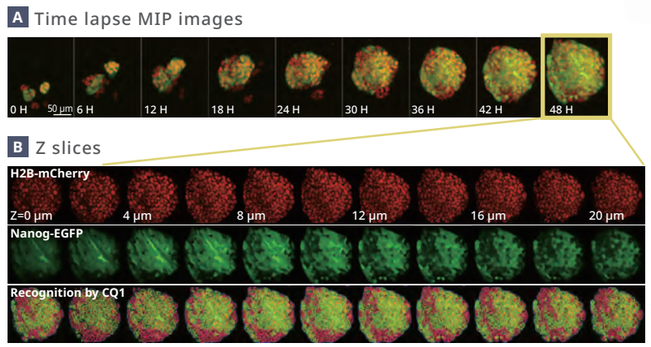
Application example

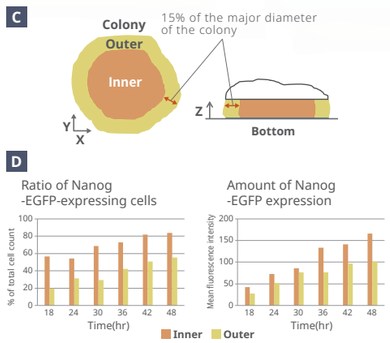
Regenerative Medicine Research

Differentiation of ES Cell Colonies

Time lapse · Quantitative · 3D · Multi-color

Analysis of not only colony size, but also the differentiation states of individual cells in the colony





3D time-lapse analysis of an ES cell colony. Images were acquired for 48 hrs at 30 min intervals. Cells expressing a differentiation marker Nanog-EGFP were analyzed.

A. Time lapse change of a colony B. Z slice images of a colony after 48 hrs
C. The colony was separated into two regions (outer and inner) based on the colony diameter, and 3D analysis was performed for Nanog-expressing cells in each region.
D. Nanog-EGFP expression levels for the inner and outer regions. Both regions show a continuous increase in expression level over time.

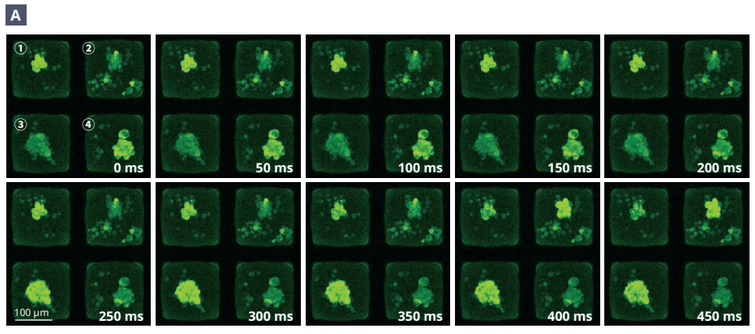
Objective lens: 40x / Ex: 488 nm (Nanog-EGFP), 561 nm (H2B-mCherry) / Time lapse: 48 hrs at 30 min intervals

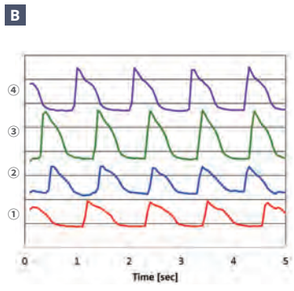
Data supplied by: Prof. Kyoji Horie, Department of Physiology II, Nara Medical University

Imaging of Calcium Signals in iPSC-derived Cardiomyocytes

Quantitative · Time lapse · High speed

High speed time lapse (20 fps) imaging of individual spheroids' calcium flux





iCell Cardiomyocytes (FUJIFILM Cellular Dynamics, Inc) were cultured on Elplasia (Kuraray Co., Ltd.). After spheroids were formed, the culcium oscillation was visualized using a calcium indicator dye. The mean fluorescence intensity for individual spheroid was quantified.

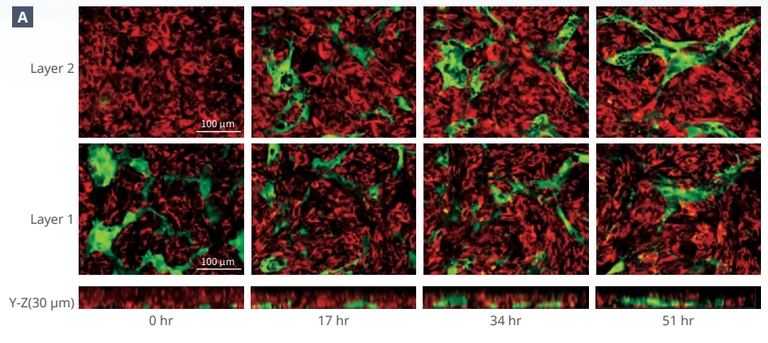
A. High speed time lapse of calcium signals in iPSC-derived Cardiomyocytes
B. Signal changes in individual spheroids 1 - 4

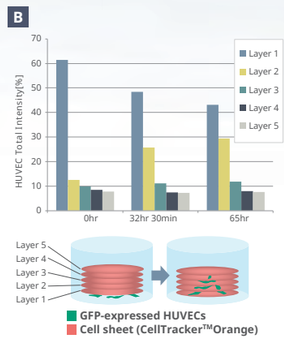
Objective lens: 10x / Ex: 488 nm (Early Tox Cardiotoxicity Kit)/ Time lapse: imaged at 50 millisecond intervals

3D Analysis of HUVEC Migration across Cell Sheets

Quantitative · 3D · Time lapse

3D analysis of HUVECs' upward migration through layered cell sheets





GFP-expressing HUVECs were seeded in the bottom layer of 5 layered cell sheets, and time lapse imaging was conducted over a duration of 67 hrs at 30 min intervals. The total intensity of HUVECs in each layer was calculated.

A. HUVECs at representative time points for Layers 1 and 2, and YZ cross-sections.
B. Distribution of fluorescence representing HUVECs along different layers at 0 hr, 32 hr30 min and 65 hrs. HUVECs decreased over time in Layer 1; however they increased in Layer 2.

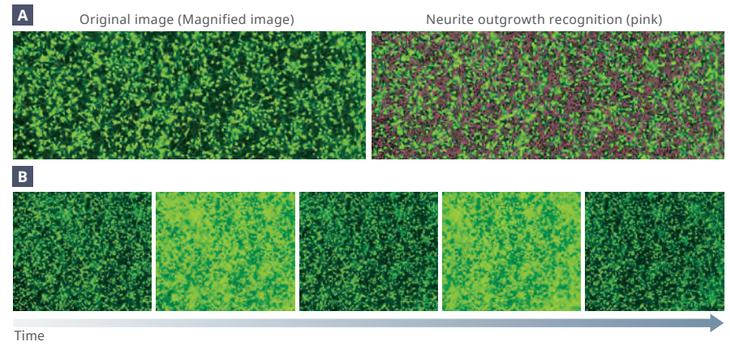
Objective lens: 40x / Ex: 488 nm (HUVEC-GFP), 561 nm (Cell sheet-CellTracker Orange) / Time lapse: 67 hrs at 30 min intervals

Data supplied by: Associate Professor Eiji Nagamori, Department of Biomedical Engineering, Graduate School, Osaka Institute of Engineering of Technology

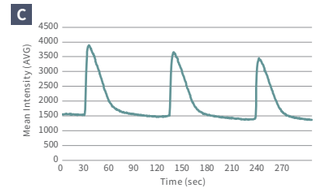
Neurite Outgrowth of iPSC-derived Neurons

Quantitative · Time lapse

Analysis of neurite outgrowth and spontaneous activity of iCells labeled with a calcium indicator



	Outgrowth Total Length (µm)	Outgrowth Total JunctionCount	Outgrowth Total BranchCount
Day20	166978.8	5384	18308



iCell DopaNeurons (FUJIFILM Cellular Dynamics, Inc) were cultured in a mixed culture medium of BrainPhys Neuronal Medium (STEMCELL Technologies. Inc) and Neuron Culture Medium (Wako Pure Chemical Corporation).

A. Analysis of neurite outgrowth after 20 days.
Total length of neurite outgrowth (Outgrowth Total Length), total junction count (Outgrowth Total Junction Count), and total branch count (Outgrowth Total Branch Count) were calculated.
B. Spontaneous activity after 20 days. C. The mean intensity at each time point was calculated.

Cell culturing conditions: cultured in Corning 96-well half-area plate (80,000/well)
Objective lens: 10x / Ex:488(Cal-520AM)/ Time lapse: 299.5 seconds at 0.5 second intervals

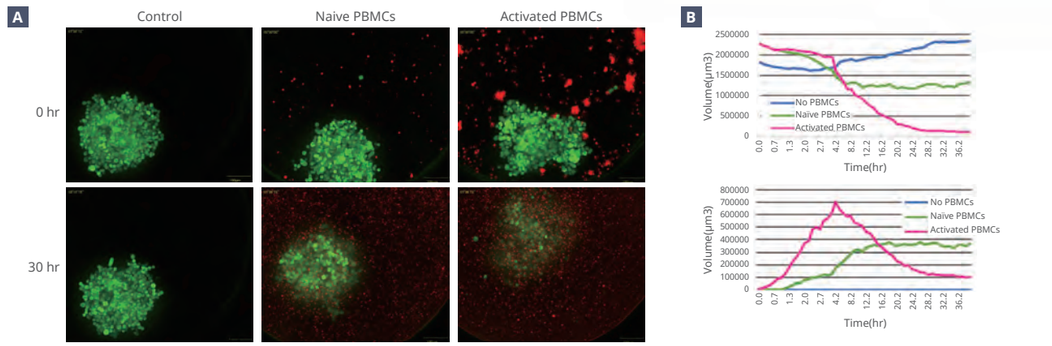
Application example

Cancer Research

Immuno Oncology
– Immune-cell infiltration into Tumor Microtissue –

Quantitative | Time lapse | Multi-color

Temporal and spatial quantification of immune cell infiltration in 3D lung carcinoma model



3D tumor microtissues comprised of A549-GFP (human lung cancer) cells were exposed to either naïve or CD3/CD28-activated immune cells labeled with CellMask™ Deep Red. Time-lapse imaging was performed for 39 hours.

A. Merged images of 488 nm and 640 nm of each condition after 0 and 30 hrs.
A 3D tumor microtissue treated with the activated PBMCs was destructed 30hrs later.
B. Top: The volume of 3D tumor microtissue.
Bottom: The total volume of immune cells touching to the 3D tumor microtissue.

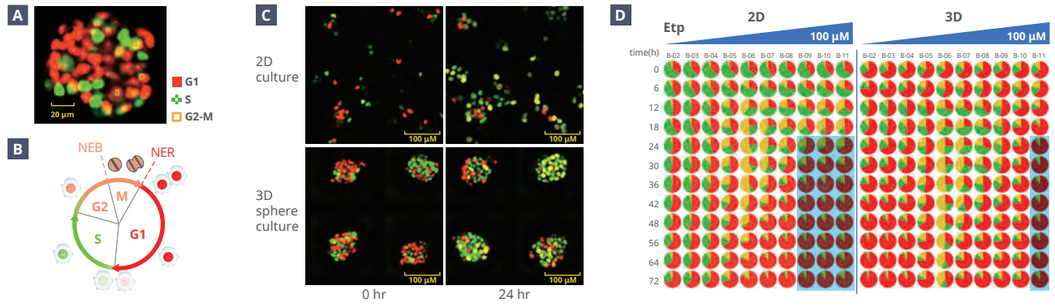
Objective lens: 20x / Ex: 488 nm (A549-GFP), 640 nm (CellMask™)
Time lapse: 39 hrs at 10 min interval (timepoint 1-20) and 60 min interval (timepoint 20-56)

Wardwell-Swanson, J., Suzuki, M., et al., A Framework for Optim izing High Content Imaging of 3D Models for Drug Discovery. SLAS Discovery. 2020, Aug;25(7): 709-722

Cell Cycle

Quantitative | Time lapse | Multi-color

Effects of anticancer drugs on cell cycle progression in 2D versus 3D cultures



Time-lapse imaging of Fucci(CA)5-stably transduced HepG2 cells for 72 hours at 1 hour intervals. This Fucci probe can effectively resolve G1, S, and G2-M phases in time-lapse imaging, allowing for automatic quantification of the number and percentage of cells in each cell cycle phase. h2-3-hGem(1/110) and AzaleaB5-hCdt1(1/100)Cy(-) were excited at 488 and 561 nm, respectively.

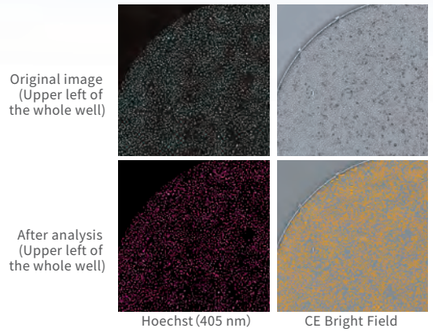
A. A snapshot image of a sphere (3D) culture showing a triple color-distinct separation of G1, S, and G2-M. Z range of 70 μm was imaged with 7.8 μm steps.
B. The cell-cycle phasing capability of Fucci(CA)5. (NEB: nuclear envelope breakdown/NER: nuclear envelope reformation)
C. Cell-cycle alterations in 2D (top) and 3D (bottom) cultures after the addition of 30 nM Etoposide, a topoisomerase II inhibitor, for 24 hours. Cell-cycle arrest at S or G2 was noticed.
D. Temporal profiles of the cell populations in the three cell-cycle phases (G1, S, and G2-M) with various concentrations of Etoposide (Etp) in 2D (left) and 3D (right) cultures. Shaded areas indicate the conditions in which cell death occurred.

Objective lens: 20x / Ex: 488 nm (h2-3-hGeminin(1/110)), 561 nm (AzaleaB5-hCdt1(1/100)Cy(-)) /
Z Range: 70 μm, Z step: 7.8 μm (Slice analysis, 3D) / Time lapse: 72 hrs at 1 hr intervals

Monitoring of Cell Proliferation

Quantitative | Label-free | Machine-learning | Tiling

Counting of all cells in a whole well without staining
Creation of multi-field tiled images and precise recognition of cells near the edge of the 96-well is also possible



Cell Count

	1	2	3
Hoechst (405 nm)	14351.6	10867.6	6944.3
CE Bright Field	14316.3	10847.6	6942.0
Ratio_CE Bright Field/405 (%)	**99.7**	**99.8**	**99.97**

n=3wells

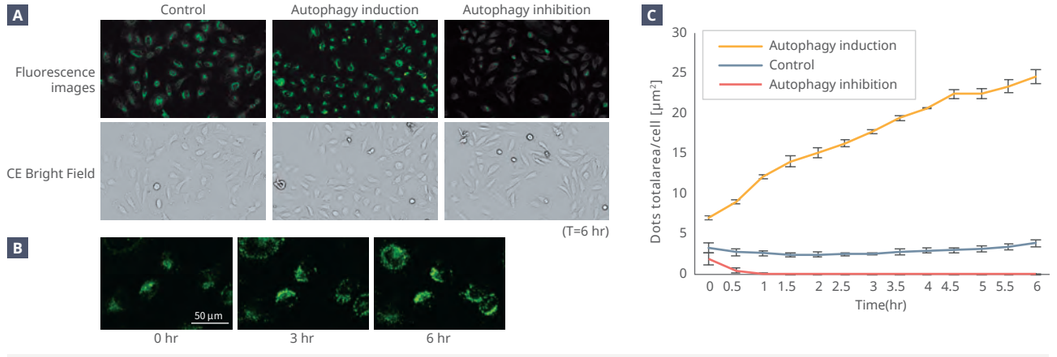
Hela cells were cultured at three different densities. Nuclei were stained with Hoechst33342, and fluorescence images and bright field (CE Bright Field) images were acquired. Cells were counted using each image and the results were compared. Very similar results were acquired for the CE Bright Field and nuclear stained images for all three densities. Using CE Bright Field images cell number is properly counted without labeling even in a small wells of 96-well plates.

Objective lens: 10x / Ex: 405 nm, Bright field (CE Bright Field image created at the time of analysis) /Plate: Greiner 96-well plate

Autophagy

Quantitative | Time lapse | Label-free | Machine-learning

Autolysosome formation analysis without nuclear staining



Hela cells cultured in a 96-well plate were treated with DAL Green (Dojindo Laboratories) and the media were replaced by three different culture media: a normal medium, autophagy inducer medium or an autophagy inhibition medium (Bafilomycin added to an inducer medium). Time lapse imaging was then conducted for 6 hrs and cell count, granule count, total area of granules are calculated.

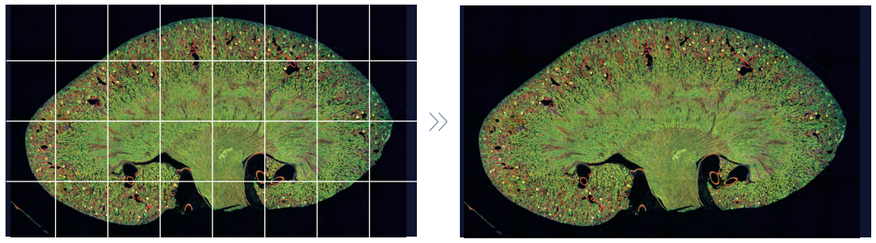
A. Images of cells in each culture medium.
B. Formation of autolysosomes over time in the autophagy induction medium.
C. Change of autolysosome area per cell over time. Autophagy granules were detected using fluorescence images, and cells were counted using CE Bright Field images.

Objective lens: 20x / Ex: 405 nm (DALGreen), Bright field (CE Bright Field image created at the time of analysis) / Time lapse: 6 hrs at 30 min intervals

Functionality Enabling Complex Analysis through Easy Operation

Image Stitching

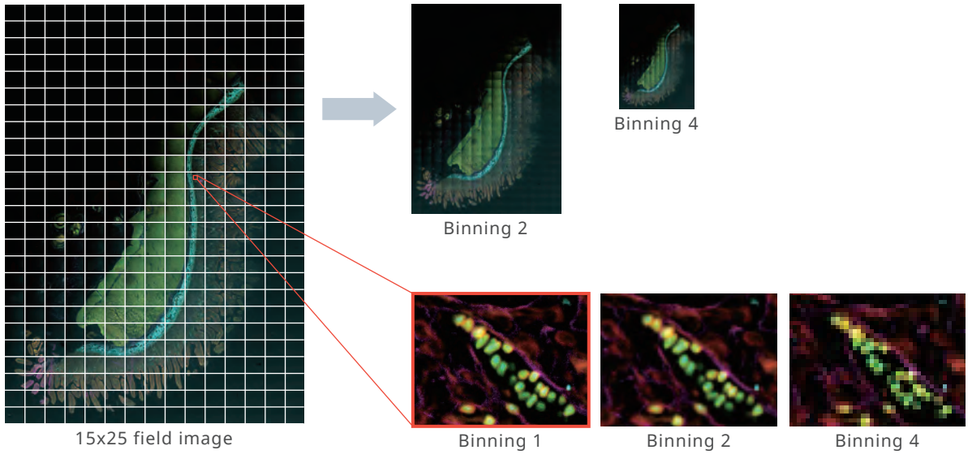
Tiled images are generated through image stitching and analyzed, allowing for accurate quantification.
Ideal for analysis spanning across fields, such as of spheroids, tissue sections and neurites.



8x4 field image　　Tiled image

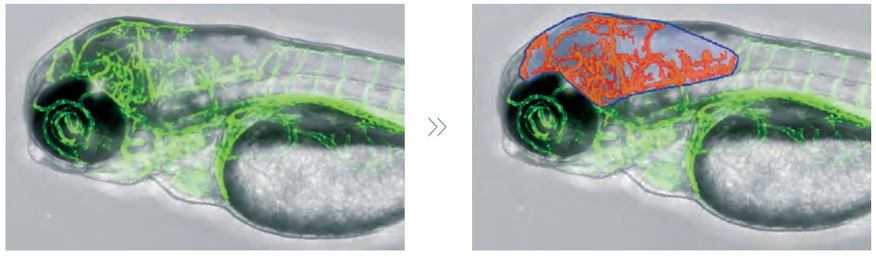
Support for downsampling

When spatial resolution is not required, fast analysis is possible.
It also makes it easier than ever to handle huge tile images.



Manual Region Specification

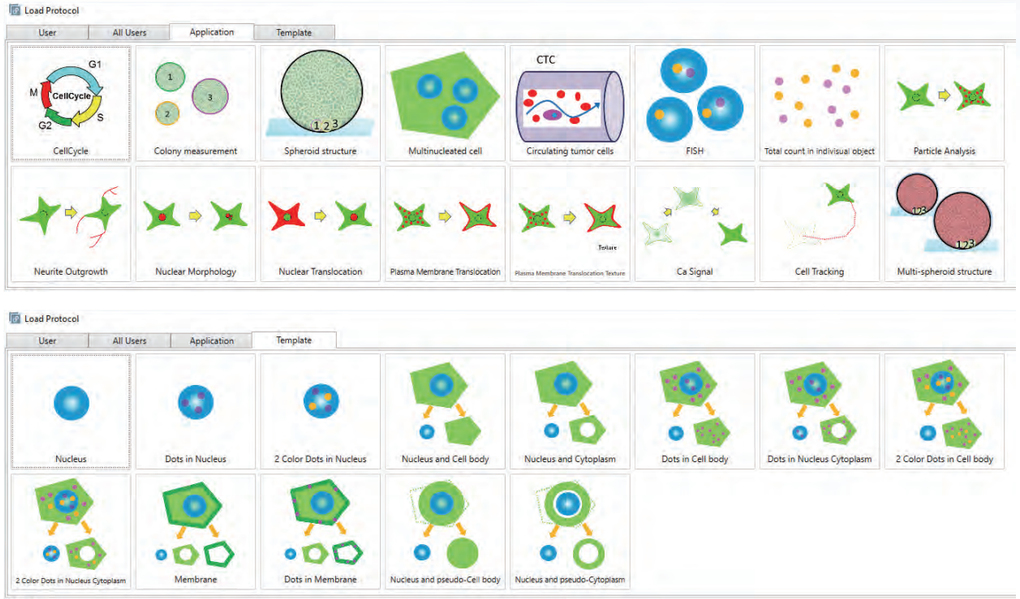
Manual specification of analysis regions is possible for complex samples that are difficult to identify through automated image processing. Facilitate the analysis of only the specified regions such as tissue section.



Data supplied by: Dr. Yasuhito Shimada, Department of Integrative Pharmacology, Graduate School of Medicine, Mie University

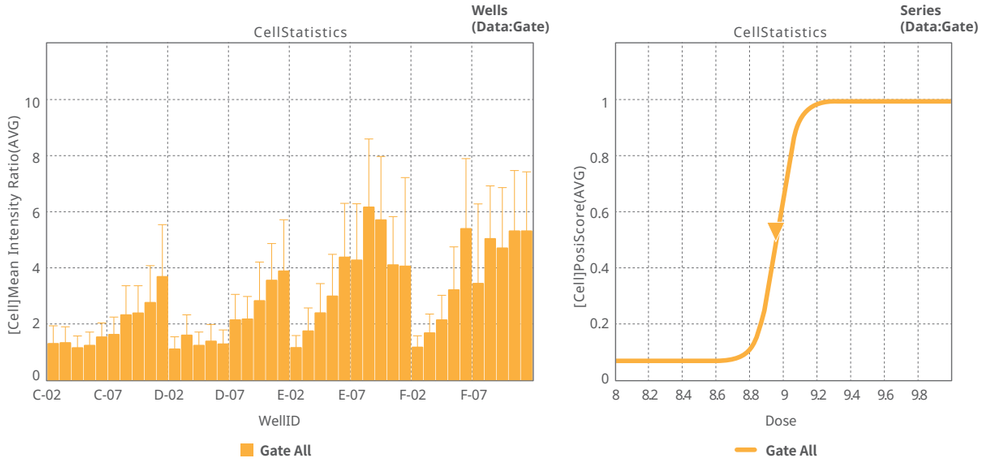
Abundant Pre-installed Analysis Menu

The analysis menu is displayed using easy-to-understand icons. Protocols can be loaded simply by clicking an icon. Beginners can start the image analysis easily.



Convenient Graphing Tools

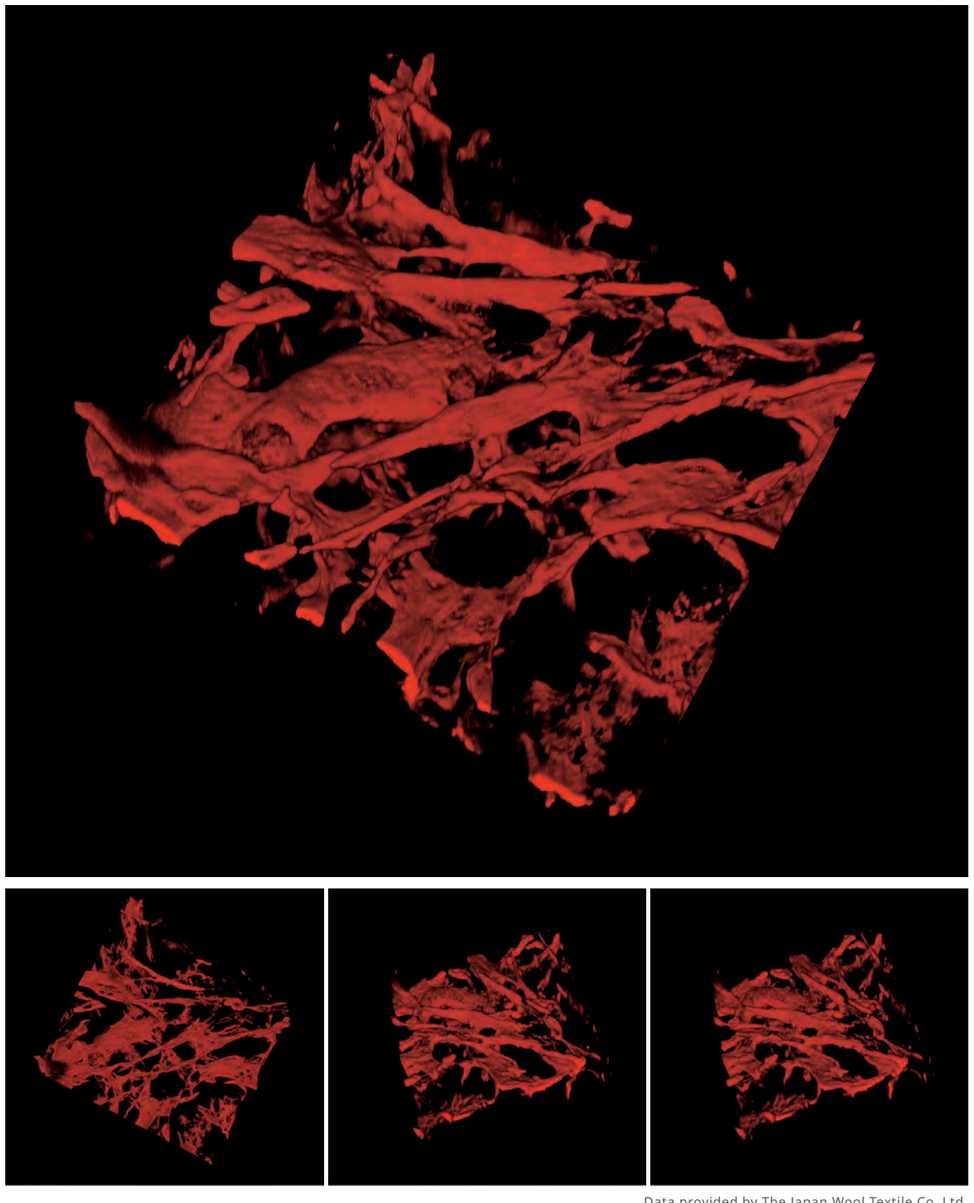
Z'-factor display/ EC50 (IC50) display/
Bar chart / Line chart / Pie chart / Scatter plot / Heatmap / Histogram



Understand the 3D structure as if it were in your hands

Newer 3D Viewer

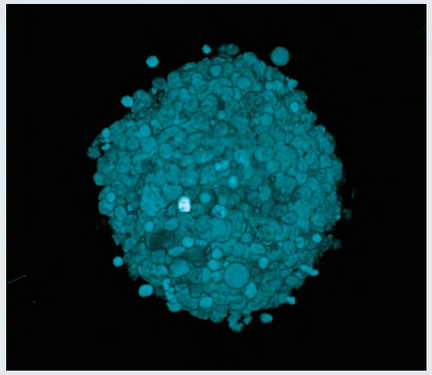
The functionality of the 3D viewer has been greatly enhanced,
allowing you to easily create high-definition 3D images from Z-stack data.



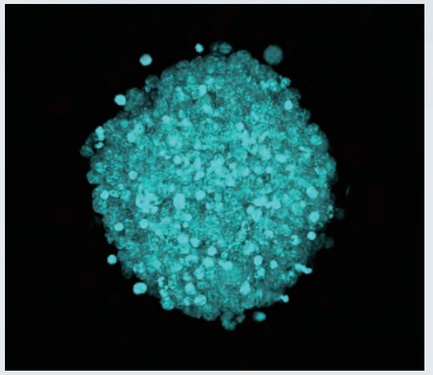
Data provided by The Japan Wool Textile Co. Ltd.
iPSC-derived cardiomyocytes cultured on gelatin fiber substrate Genocel plates for cell culture,
phalloidin-actin staining

Various display methods

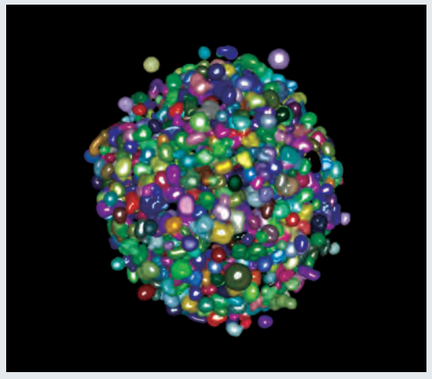
- **Supports Ray casting and MIP 3D image display methods. Object recognition results obtained via image analysis can also be displayed in 3D.**

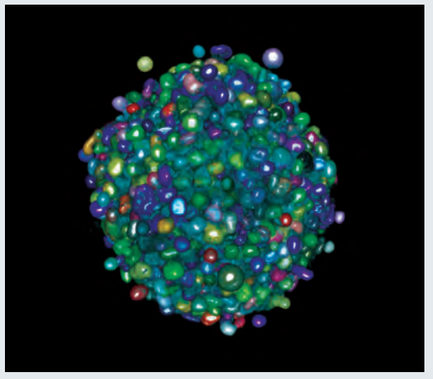


Original 3D image (Ray casting)

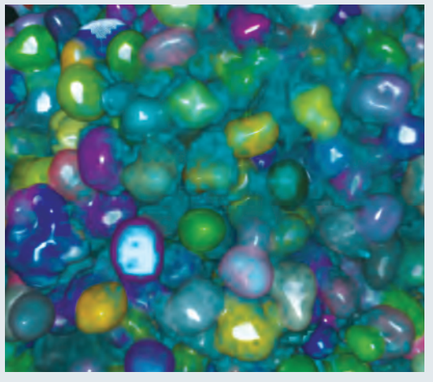


Original 3D image (MIP)





Object recognition results



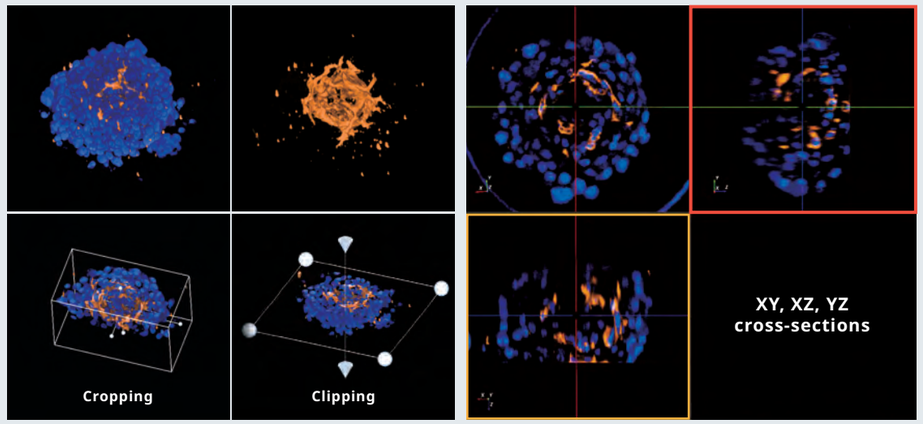
Overlay of original 3D image (Ray casting) and object recognition results

Understand the 3D structure as if it were in your hands

Various display methods

- **Freely visualize the internal structure of objects by displaying XY, XZ, and YZ cross-sections, and by using the clipping and cropping functions.**

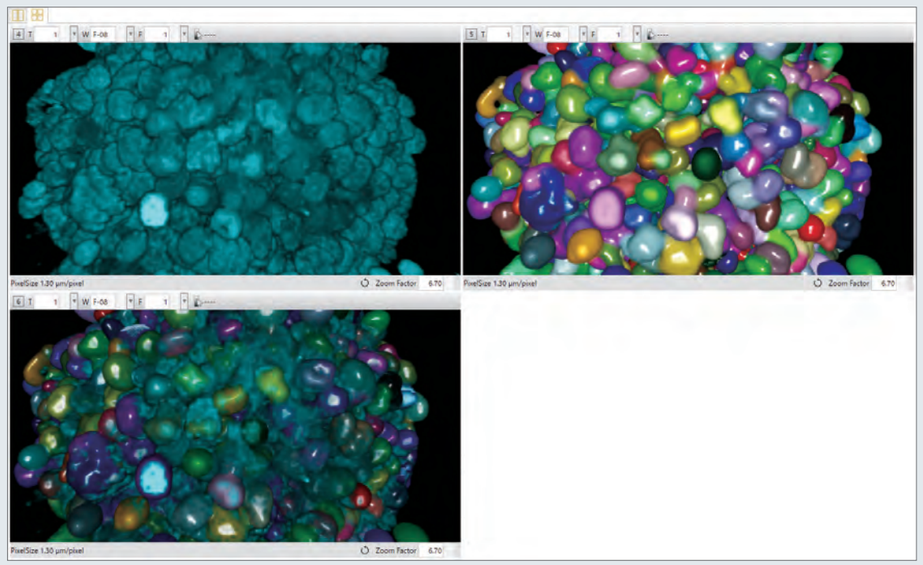
Spheroids of adipose stem cells and vascular endothelial cells (yellow) with cell nuclei in blue, created using the 3D cell culture vessel MicoCell™.



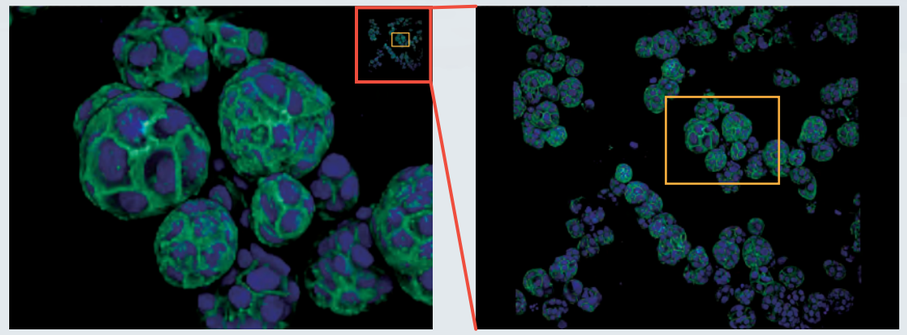
NIPPON SHOKUBAI

Data provided by Nippon Shokubai Co., Ltd.

- **Easy comparison by displaying original 3D images, object recognition results, and their overlays side-by-side.**

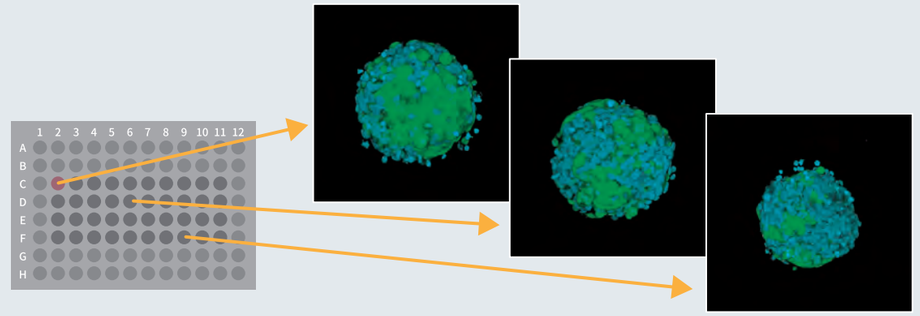


- **"Navigation" display is useful for knowing which part of the entire image is being enlarged.**



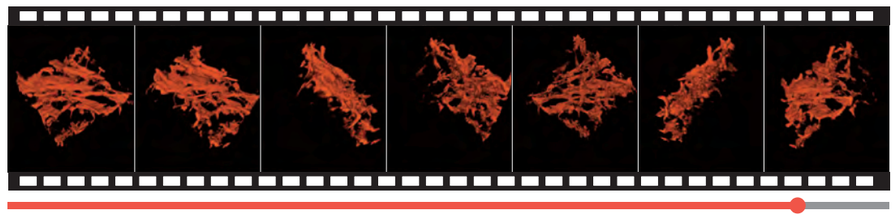
Data provided by the Baylar College of Medicine

- **Easily change wells displayed in 3D with a single click.**



- **Create still images and movies**

・Snapshots
・Rotate images automatically or manually and output them as movies

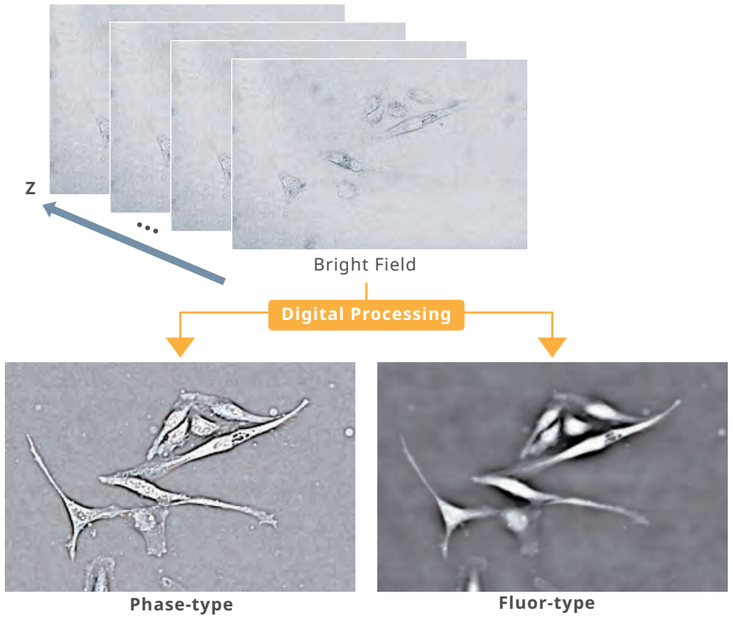


A variety of optional functions enable various analyses

The Basic Pack includes the basic functions necessary to acquire various quantitative data on the morphology and brightness of cells from fluorescence images.
In addition, by adding optional functions, a variety of analyses that are not possible with the basic pack become possible.

Contrast-Enhanced Bright Field

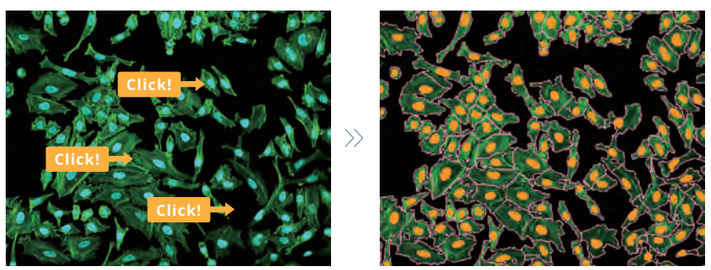
By using Yokogawa's "CE Bright Field" proprietary image creation technology, two types of images can be output from bright field images.
This is a powerful pre-processing function for analysis using the Deep Learning function of Bright Field images.



- **Phase-type: Images such as those taken by phase-contrast microscopy. It is useful for high-precision recognition of cell contours and analysis of cell phenotypes.**
- **Fluor-type: Fluorescence-like images. It is useful for nuclear recognition, etc.**

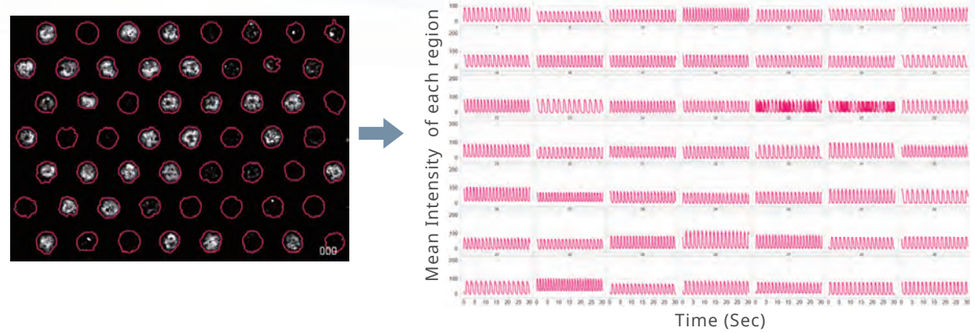
Machine Learning

Machine Learning functionality allows for unbiased digitization in experiments evaluated through appearance. Furthermore, automated shape recognition can be performed by simply clicking on the shape you wish the software to learn.



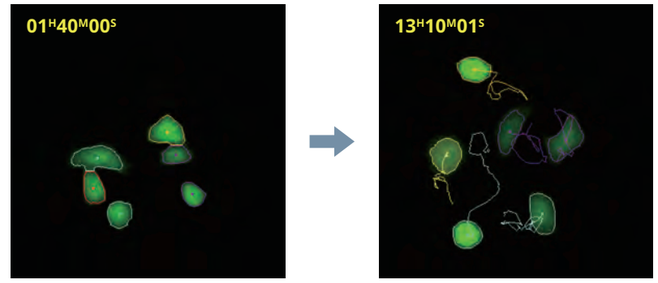
Same Region over time

The fast calcium oscillations of cardiac muscle and neuronal activities can be represented as waveforms by measuring intensities in the same region throughout the time-lapse.



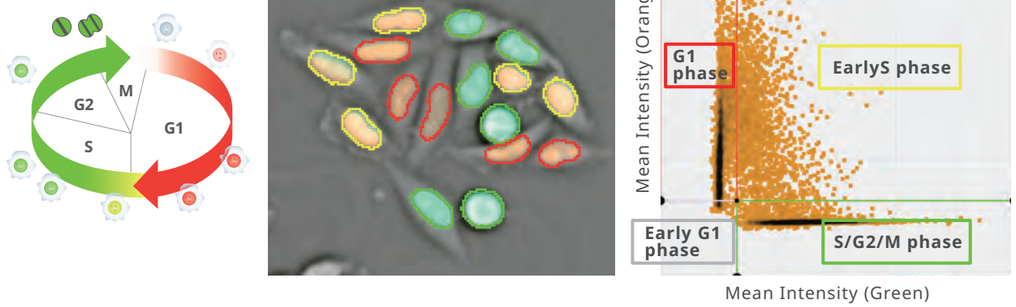
Object Tracking

You can monitor dynamic cell behavior by tracking individual cell.
It can also track daughter cells after cell division, enabling analysis of cell lineage.



Classification (Gate)

Cells can be classified into groups of cells with similar characteristics. This function enables to evaluate the number of cells and the ratio of cells in each cell group, and the feature quantities in each specific cell group.



Option

Deep Learning

Deep learning-based image recognition has gained much attention in recent years. Yokogawa has also been observing this situation and, by recognizing patterns in images to identify what the images show, we succeeded in dramatically improving the recognition accuracy.

Benefits of Adopting Deep Learning

No expertise in image analysis required

Save time for creating analysis protocols

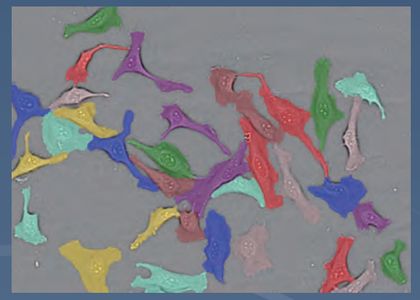
Improve analysis accuracy

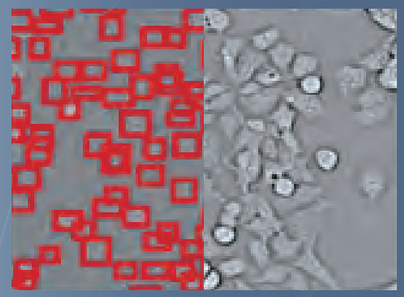
"Something different" relative evaluation of phenotypes

Deep Area Finder

Cell Recognition

You can recognize targeted objects, such as cells and intracellular organelles by painting them using not only fluorescence images but also bright field images.
This function is useful when the analysis accuracy with conventional analysis methods are not enough.





Deep Detection

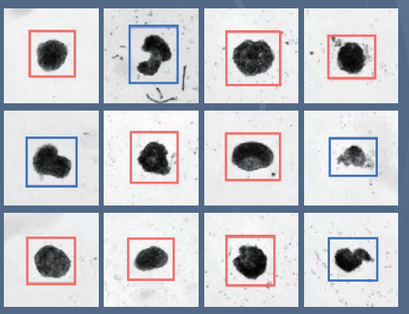
Cell Counts

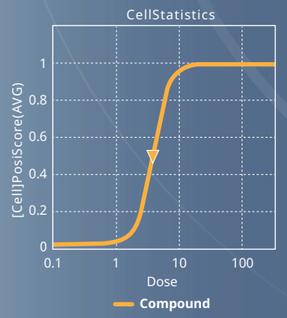
This function detects cells with with simple operation of enclosing cells.
No experties are required.
It is possible to count cells in high-density on bright field images as well as fluorescence images.

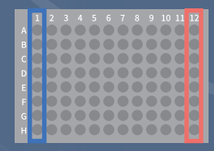
Deep Image Gate

Cell Classification

You can classify phenotypes that are difficult to quantify but appear to be "something different".
Simple operation of selecting the cell groups to be classified.
No need to select effective features or set thresholds.



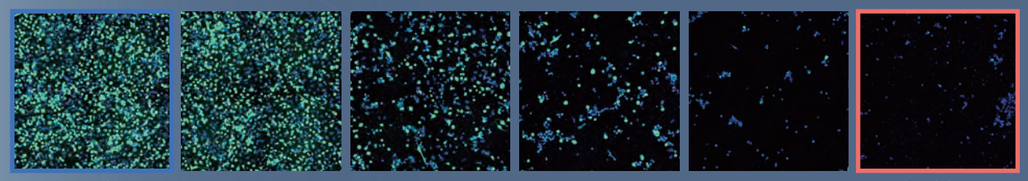




Deep Image Response

EC50/IC50 Calculation

This function enables comprehensive quantification of complex phenotypes using whole images.
Simple operation of selectiong nagative and positive wells and entering compound concentration information.
Any protocol to segment cells is not necessary.



Negative

Positive

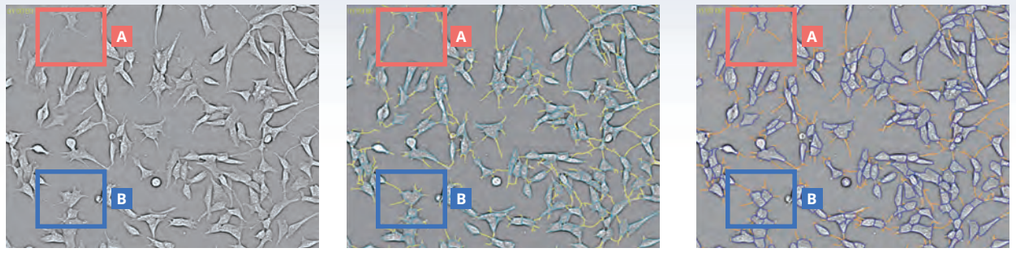
Option Analyses using Deep Learning

Evaluation of Neurite Outgrowth

Label-free Segmentation

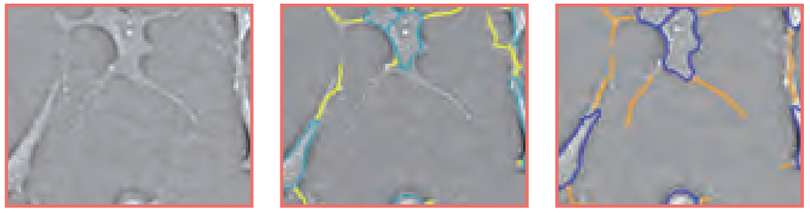
Analysis of neurite outgrowth without staining

- **Using CE Bright Field images**
- **Comparison of Deep Learning and Machine Learning results**



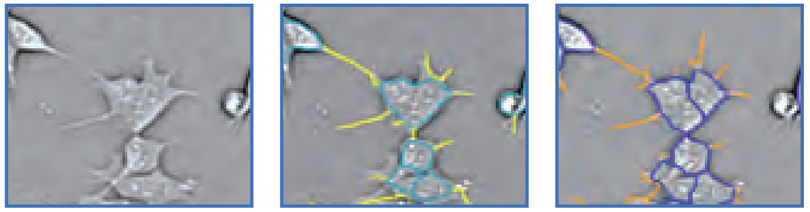
CE Bright Field(CE) | Machine Learning(ML) | Deep Learning(DL)

A



CE | ML | DL

B



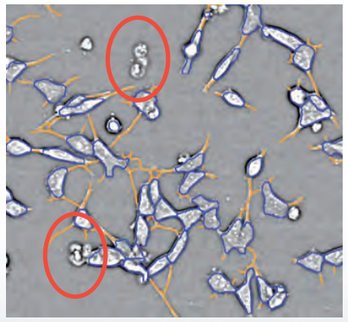
CE | ML | DL

C

	DL	ML
Number of cells	397	354
Average area of cells (μm²)	280	234
Average number of branches per cells	0.76	0.19

Deep Learning analysis boosts the accuracy of cell recognition and enables to obtain highly-accurate results.

- The number of recognized cells in increased
- Average cell area is increased
- Average number of branches in increased



Debris can be excluded from analysis.

A. Deep Learning increases the accuracy of recognition of low-contrast neurite outgrowths and cell morphology.
B. Deep Learning increases accuracy of segmenting densly packed cells.
C. Comparison of Deep Learning and Machine Learning results.

Objective lens: 20x / Ex: Bright field (CE Bright Field images were prepared during analysis)

Data provided by: Biochemistry Research Group, Biological Research Department, DAIICHI SANKYO RD NOVARE Co., Ltd.

Measurement of inhibition of osteoclast differentiation

Label-free Count

Background

Bone is made by osteoblasts and absorbed by osteoclasts. Attempts to prevent bone roughness by inhibiting the differentiation of osteoclasts have been common for many years. In cell tests, TRAP staining, which detects tartrate-resistant acid phosphatase (TRAP), which is considered to be a differentiation marker for osteoclasts, has been used to verify the inhibition of differentiation.
On the other hand, in the quantification by TRAP staining, differences in cell morphology and staining were severe depending on the test system, and even now, cell counting by human visual observation is the mainstream, and it was not suitable for the automatic detection. The analysis using deep learning function enabled us to automatically count TRAP-positive cells with a probability of more than 90%.

Images for training | Recognition result

RANKL was added to RAW 264.7 cells to promote their differentiation into osteoclasts, and differentiated cells were detected by TRAP staining. Using CellVoyager (CQ1, CV 8000), we acquired the stained cells, and after learning the osteoclast images differentiated by the deep learning function, we analyzed them quantitatively. We can search for foods, cosmetics, medicines, etc.

Method

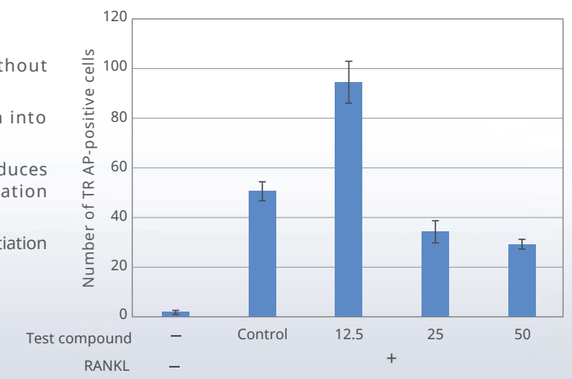
Treatment with RANKL and the test compound on the day following cell seeding

Nuclear and TRAP staining at appropriate times with confirmation of cell fusion

Acquired with CellVoyager CV 8000 and analyzed with CellPathfinder.
After learning TRAP-positive cells using separately prepared wells for Deep Learning, analysis was performed in a batch in multiple wells

Test analysis example

- No osteoclast differentiation occurred without RANKL(RANKL-, Test compound 0)
- Addition of RANKL induces differentiation into osteoclasts(RANKL+, Test compound 0)
- Furthermore, addition of Test compound induces further differentiation in the low concentration zone(RANKL+, Test compound 12.5)
- Concentration of Test compound inhibits differentiation into osteoclasts(RANKL+, Test compound 25, 50)



Assessment of neuronal toxicity

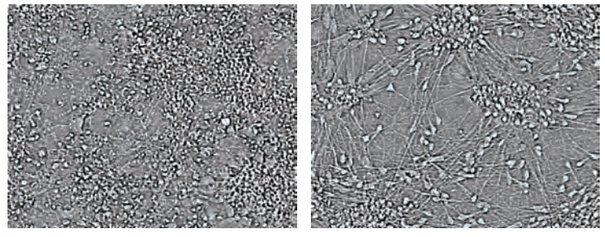
Response Label-free

Toxicity assessment without cell recognition or feature quantities selection in label free

- **Evaluation can be done by simply learning negative and positive wells.**
- **No need for expertise in image analysis**
- **Enables evaluation of viable cells using label free images**

Cells were treated with 1287 compounds and Bright Field images were captured by CellVoyager CV7000S to create CE Bright Field images.
Wells treated with the toxin and without the test substance were trained as negative, and wells without the toxin and without the test substance were trained as positive, and the counteracting effect of cytotoxicity was evaluated by Deep Image Response.
Then, the results were compared with the evaluation by ATP level.

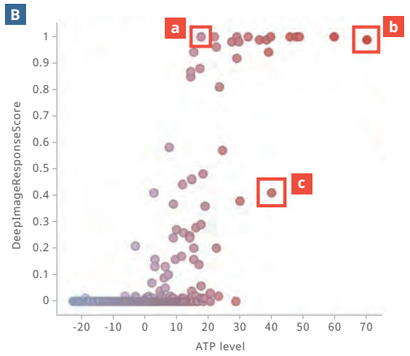
A

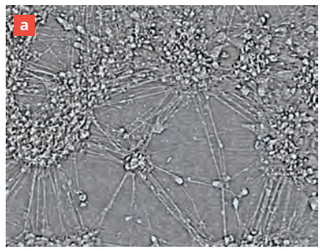


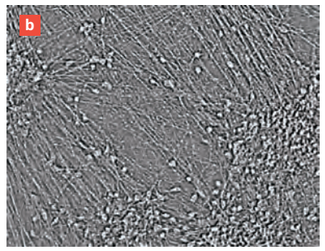
Negative
(with the toxin, without the test substance)

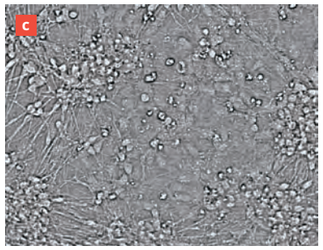
Positive
(without the toxin, without the test substance)

B









A. Negative and positive wells used in the learning
B. Comparison of ATP level and Deep Image Response score
a. ATP level is in the middle, but Deep Image Response score is high.
b. ATP level and Deep Image Response score are both high.
c. ATP level is high, but Deep Image Response score is low.

Confirmed a certain relationship between ATP level and Deep Image Response score.
In addition, as shown in c., there were cases in which the ATP level seemed to be rescued, but the Deep Image Response score was low. The difference between the ATP level and the Deep Image Response score is not apparent when only the ATP level is used as an index.

Objective lens: 20x /Ex: Bright Field/ Plate: 384well plate

Detection and Evaluation of Spheroids in Bright Field Images

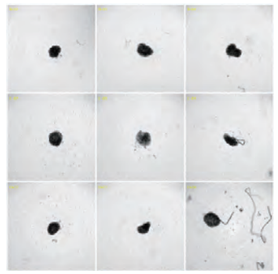
Label-free Count Gate

Automatic recognition and classification of spheroids

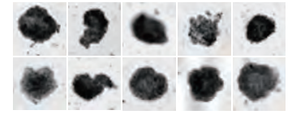
- **Learning and detecting spheroids**
- **Classification of high quality spheroids and others by learning their morphology**
- **Automatic identification of high quality spheroids from a large number of spheroids**

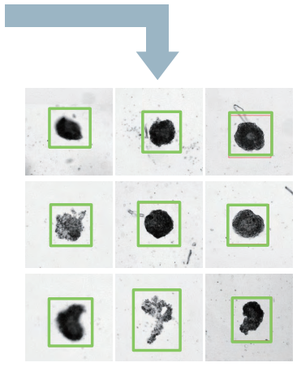
Since all spheroids produced in large quantities are not uniform, high quality spheroids that can be used in the assay must be selected from among them.
All spheroids were acquired in bright field, and recognition of spheroid and sort of high-quality spheroids, were automatically performed by the Deep Learning function.

A



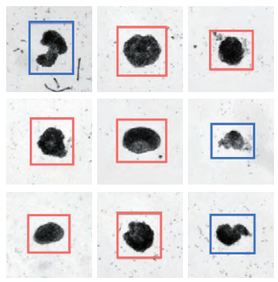
Images for learning



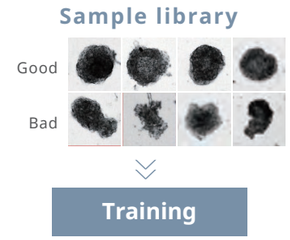


Detection results/Images for learning

B



Classification results



A. Automatic detection by learning the morphology of the spheroid using the Deep Learning function.
B. Learn the morphology of high quality spheroids and others using the Deep Learning function, and automatically identify them.

By combining two types of Deep Learning functions, everything from spheroid detection to identification of the target spheroid can be done automatically. This makes it possible to easily identify a large number of spheroids without any knowledge of image analysis.

Objective lens: 4x /Ex: Bright Field/ Plate: U-bottom 96well plate

Selection of CellPathfinder Features

Have you ever had these worries?

Do I need this function?

- I don't use all the functions regularly.
- I want only what I need.

What can I do about the starting costs?

- I can afford this every year if it's only this much.
- I'll be able to pay somehow if it's just for necessary options.

Solve your problems with CellPathfinder fixed-term licenses

Choose the features you need!

You can select and use only the features that you need.
No need to pay for features that will not see any use.

Basic Pack

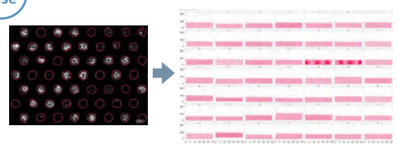
Use case
- Cell count
- Granule analysis
- Colocalization analysis
- Morphological analysis
- Neurite outgrowth analysis

etc.

+ Options

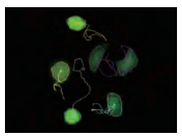
Same Region over time

Use case
- Time-series analysis of calcium signaling



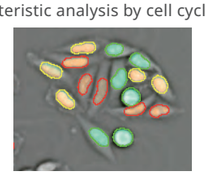
Object Tracking

Use case
- Cell behavior analysis
- Behavioral analysis of daughter cells after division



Classification (Gate)

Use case
- Characteristic analysis by cell cycle classification

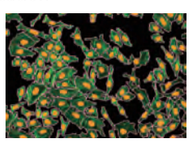


Contrast-Enhanced Bright Field

Use case
- Phenotype analysis and nuclear localization analysis

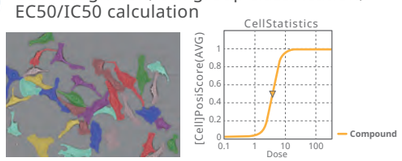
Machine Learning

Use case
- Objective cell recognition and cell group classification



Deep Learning

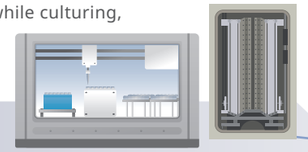
Use case
- Cell recognition, cell group classification, EC50/IC50 calculation

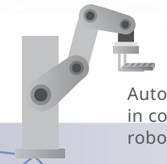


Offering Total Solutions, from Culturing and Storage to Analysis

1 Culturing and Storage

Store multiple plates while culturing, and transfer by robot. Suitable for long-term live cell imaging and handling of large numbers of plates.



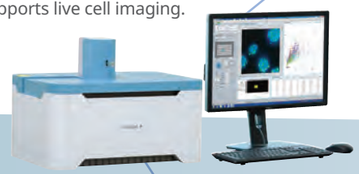


Automated plate transfer in cooperation with a trusted robot vender.

2 Acquisition

CellVoyager CQ1 *Confocal Quantitative Image Cytometer*

Space-saving benchtop design.
A simple confocal imaging system capable of automated imaging of multiple samples.
Also supports live cell imaging.



CellVoyager CV8000 *High-throughput Cytological Discovery System*

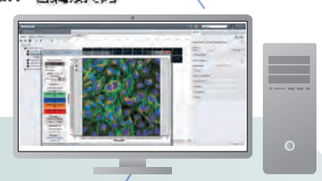
A high-end HCA system enabling high quality and high-speed screening by use of water immersion lenses and multiple cameras.
Can also perform kinetic measurement using a dispenser.

3 Data Storage

Save, access, and directly analyze large amounts of image data via the network. Archive data for safe, long-term storage.

CellVoyager CellLibrarian *High Content Data Management System*

As the core of the CellVoyager high content analysis system, it performs image storage and data management and analysis. The database is accessible via the Internet.



4 Analysis

CellVoyager CellPathfinder *High Content Analysis Software*

Analyze image data from CellVoyager CV8000 and CQ1 to create graphs and output various types of data.
Label-free analysis is also possible through CE Bright Field, Machine Learning, and Deep Learning functions.
Easy even for beginners through a wide variety of preset analysis templates.

Specifications

Application example	Cell count, Cell cycle, Colony measurement, Spheroid structure, Multinucleated cells, Nuclear fragmentation, CTC, FISH, Granule detection/localization, Neurite outgrowth, Membrane translocation, Nuclear translocation, Calcium flux, Cell tracking, etc.
Basic functions	3D analysis, Tile analysis, Texture analysis, Graphing functions (Bar charts, Line charts, Pie charts, Scatter plots, Heat maps, Histograms), 3D Viewer, EC50/IC50, Z'-factor
Option functions	Same Region over time, Object Tracking, Classification (Quadtree gating, Quadtree with hinge gating, Rectangle gating, Polygon gating, Linear gating), CE Bright Field[*1], Machine Learning[*4](Segmentation, Gating), Deep Learning[*4](Segmentation, Cell Count, Classification (Gate), EC50(IC50))
Analysis modes	Single analysis, Batch analysis, Automated analysis
Output data formats	Numeric data: CSV Image data: PNG, JPEG, TIFF Video data: Windows Media Video (WMV), MPEG4
Compatible equipment	CellVoyager CV7000, CV8000, CQ1
Standard Workstation[*6]	Model: Dell Precision[*2] CPU: Intel Xeon Memory: 128GB HDD: System drive (C:)4TB Data drive (D:)4TB OS: Microsoft Windows10 IoT Enterprise[*5] 64bit English GPU: Quadro P620 or NVIDIA T400 Interface: Mini DisplayPort×4 or Mini DisplayPort x3(with Mini DisplayPort to DisplayPor adapter) Power Supply: 100 to 240VAC/ 50 or 60Hz, 950Wmax Chassis: W176.5mm×D518.3mm×H417.9mm Weight: 17kg
Workstaton with high-performance GPU[*7]	Model: Dell Precision[*2] CPU: Intel Xeon Memory: 128GB HDD: System drive (C:)4TB Data drive (D:)4TB OS: Microsoft Windows10 IoT Enterprise[*5] 64bit English GPU: Quadro RTX5000 or NVIDIA RTX A4500 Interface: DisplayPort×4 Power Supply: 100 to 240VAC/ 50 or 60Hz, 950Wmax Chassis: W176.5mm×D518.3mm×H417.9mm Weight: 17kg
Monitor[*2*3]	Two 24" wide-screen monitors with resolution of 1920 × 1200

If you wish to prepare your own workstation, please refer to the following.

Resource	Basic Pack		With Machine Learning Option		With Deep Learning Option
	Minimum specification[*11]	Recommended specification	Minimum specification	Recommended specification	Recommended specification
CPU	Intel Xeon(PassMark score[*9] 7389) or equivalent	Intel Xeon(PassMark score[*9] 8479)or faster equivalent			
GPU	NVIDIA Quadro(PassMark score[*9] 2263) or equivalent	NVIDIA Quadro(PassMark score[*9] 3469) or faster equivalent			Quadro RTX5000 or NVIDIA RTX A4500
RAM	32GB	64GB		128GB[*10]	
Storage	200MB of free disk space (Data area is required separately.)	1st: 2TB 2nd: 4TB			
Monitor	1920×1080	1920×1200×2			
Network	1node	10GbE 1node			
OS	Windows10 22H2[*12] 64bit				

All functionality of CellPathfinder can be experienced free of charge[*8].
Please scan the QR code for more information.

*1 Refer to P. 13 for details on CE Bright Field. *2 Dell Precision and monitors are certified in accordance with each countries' laws and regulations by their manufacturer, Dell Inc. *3 Arranged by local distributors for overseas sales. *4 The Machine Learning option and the Deep Learning option require the Gate option. *5 Windows 10 IoT Enterprise is an OS that can only be shipped by distributors that have signed an OEM agreement with Microsoft Corporation and is not installed on general-purpose workstations. *6 Specification if the high-performance GPU option is not selected. *7 Specification if the high-performance GPU option is selected. *8 Please contact our sales representative or the address shown below if you hope to use the Deep Learning options. *9PassMark score is one of the benchmarks used to evaluate hardware performance. *10 When analyzing tiled images using the Machine Learning option, 128 GB of memory is recommended. *11 This specification is not recommended for automated analysis. *12 This is the recommended version as of November 2023.

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