

For Cell Pocket™, a Web Application Supporting Cell Observation

Morphology Analysis Plug-in for Mesenchymal Stem Cells

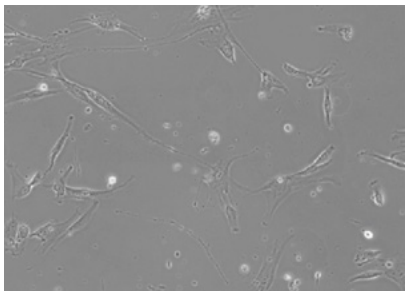
Extracting and Quantifying Cellular Pseudopodia Regions from Microscope Images

This application extracts the filamentous pseudopodia from cellular regions, quantifies the long axis length and its ratio in comparison to the total, and outputs a histogram.

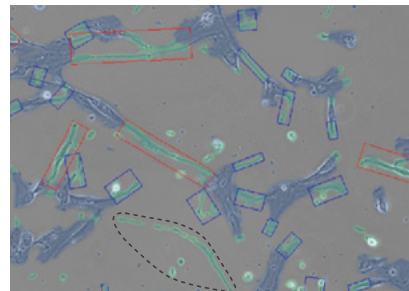
A morphological feature of mesenchyme stem cells is that the filamentous pseudopodia lengthen as passages are repeated. Using this product with Cell Pocket enables quantitative evaluation of the relationship between the number of passages and other cultivation conditions and the length and frequency of filamentous pseudopodia.

Extraction of the Cellular Pseudopodia Regions

[Phase Contrast Microscope Image]



[Analysis Image]



- Counted as long pseudopodia
- Counted as short pseudopodia

For the threshold settings, refer to the parameter adjustments on the back page. Pseudopodia separated from cells (black dashed region) are not counted.

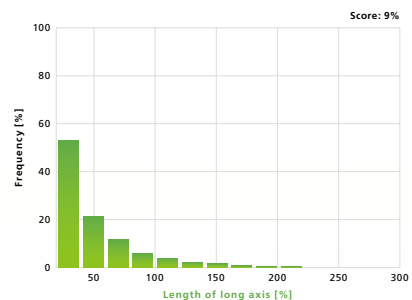
Quantitation

[Analysis Results]

List of Pseudopodia		
x [pixel]	y [pixel]	Length [um]
178	23	30.50
2431	19	42.55
1569	18	23.66
3392	26	35.73
~~~~~		
212	41	52.68

A list of the center of gravity positions and lengths for the pseudopodia counted is output as a .csv file.  
Note: Partial changes were added to the layout.

[ Histogram ]



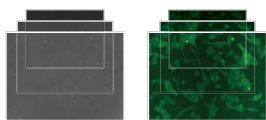
A histogram is created automatically from the analysis results at left. The score indicates the ratio of total pseudopodia that are long pseudopodia.

STEP  
01

## Creating a Trained Model

A trained model to extract the cellular region is created using images from the customer.

### [ Preparing the Data Set ]



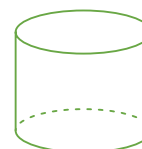
Target image    Labeled image*



### [ Deep Learning ]



### [ Trained Model ]



* Actin-stained images are recommended as labeled images for learning cell outlines.

STEP  
02

## Selecting Analysis Processes (Analysis Scripts)

In the Cell Pocket analysis recipe creation window, select [Trained Model], [combine_images*¹], or [Morphology_analysis_plugin_for_MSC*²].

*1: [Combine_images_01] is preset.

*2: The following script is added when this product is installed in Cell Pocket.  
"Morphology_analysis_plugin_for_mesenchymal_stem_cell"

STEP  
03

## Adjusting the Parameters

The parameters for each analysis script are optimized using a test image.

Some of the default values for the analysis script parameters for this product are as follows.

1	..... sensitivity_detect_pseudopodia		<input type="range" value="4"/>	-	4	+
2	..... define_long_pseudopodia		<input type="range" value="100"/>	-	100	+
3	..... define_short_pseudopodia		<input type="range" value="20"/>	-	20	+
4	..... define_ignore_pseudopodia		<input type="range" value="20"/>	-	20	+

1 : If the short axis is less than the set value, it is extracted as a pseudopodium candidate.

2 : If the long axis of the region extracted is equal to or greater than the set value, it is counted as a long pseudopodium.

3 : If the long axis of the region extracted is equal to or greater than the set value, and less than 2, it is counted as a short pseudopodium.

4 : If the long axis of the region extracted is less than the set value, it is not counted.

* The units are  $\mu\text{m}$ .

Note: Cell Pocket ver. 2 or later is required.

This product is an analysis script developed through collaborative research with Dr. Shin Kawamata at the Research & Development Center for Cell Therapy, Foundation for Biomedical Research and Innovation, in Kobe, Japan.  
The cell images and analysis results were kindly provided from the same facility.

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