



臺大醫學院研發分處 第一共同研究室顯微影像核心

IMAGEJ顯微影像分析 與程式設計

零基礎的學生也能掌握基本顯微影像分析能力



2025 3.3-4.28 周一 13:30-14:30 共7堂
影像前處理、AI應用、自動化分析

海報網址

報名網址

課程資訊 及 授課教師

2025/3/3(一) 【生物影像分析概論】
溫榮崑 中央研究院 生化所 生物影像核心設施
研究助教師

2025/3/10(一) 【生物影像流程與小組討論編組】
許紹君 臺灣大學分子影像重點技術平台
助研究專家

2025/3/17(一) 【影像分析自動化】
張仁乾 日本理化學研究所
專門技術員

2025/3/24(一) 【互動式影像分析流程建立】
朱韋臣 中央研究院 細生所 公共儀器室影像組
專案研發學者

2025/3/31(一) 【物件追蹤分析】
黃紀穎 中央研究院 植微所 細胞核心實驗室光學顯微鏡組
專案研究人員

2025/4/7(一) 【AI-機器學習與深度學習工具介紹】
羅安琦 臺灣大學分子影像重點技術平台
副技師

2025/4/28(一) 小組發表
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朱韋臣 中央研究院 細生所 公共儀器室影像組 專案研發學者

主辦單位：臺大醫學院研發分處 第一共同研究室顯微影像核心
協辦單位：中央研究院 生物化學研究所
地點：基醫大樓講堂區 5 樓 未來教室 (原 508 教室)



GloBIAS Bioimage Analysis Conference 2025

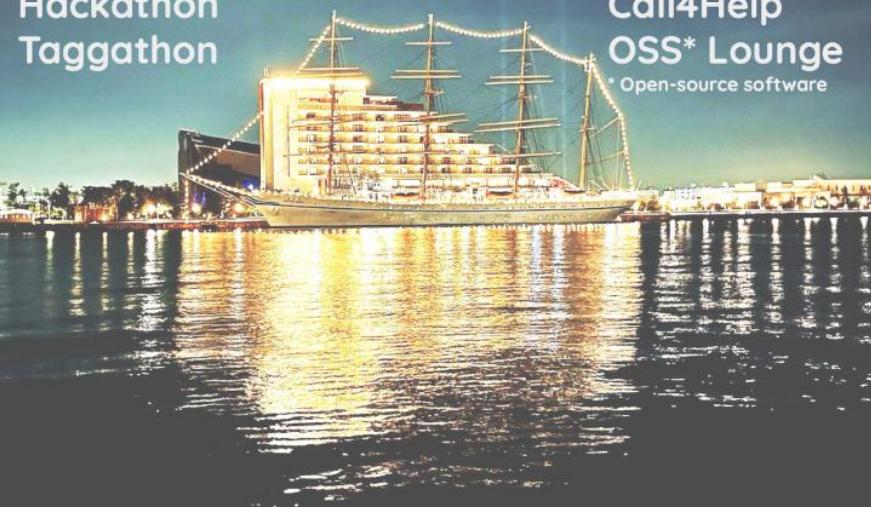
26-31 October 2025

KOBE, Japan @RIKEN BDR

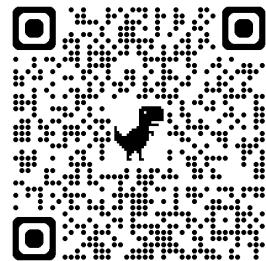


26-29 October
Training Schools
Hackathon
Taggathon

29-31 October
Symposium
Call4Help
OSS* Lounge
* Open-source software



<https://www.globias.org/activities/bioimage-analysis-conference-2025-in-kobe>



線上簽到



課程材料與相關連結

課後意見調查

我們正在準備明年Python的課程，
如果您也想成為我們的講師群，歡迎與
我們聯絡！

peggyschsu@ntu.edu.tw

許紹君

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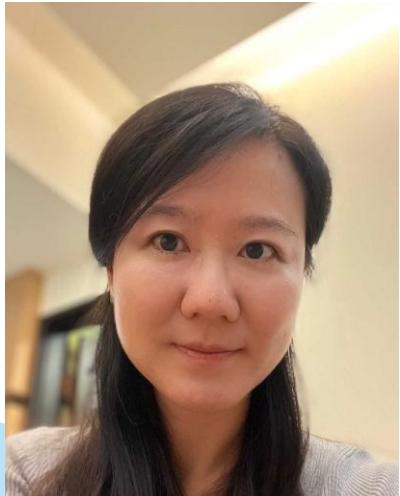


國立臺灣大學
重點技術平台

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IMAGEJ顯微影像分析與程式設計

小組發表與線上資料庫之介紹



許紹君

Shao-Chun Hsu (Peggy)

Assistant Research Specialist

NTUCM Imaging Core/

NTU Consortium of Molecular Imaging Key Technology

2025-4-28

1. 小組發表
2. BiII
3. HerelM
4. Zenodo
5. 授權說明



•Topic

- Group 1: Tracking
- Group 2: AI Segmentation
- Group 3: Colocalization

•Presentation Format

- Demonstrate the group work in **10 minutes** for each group.
- The presentation should cover:
 - 1. Workflow Diagram** – Explain the aim and the pipeline of this analysis script.
 - 2. Work demonstration** – Showcase the workflow of this script.
 - 3. Discussion** – Share insights, challenges, and key takeaways from developing this workflow.



1. 小組發表
2. Biii
3. Herelm
4. Zenodo
5. 授權說明



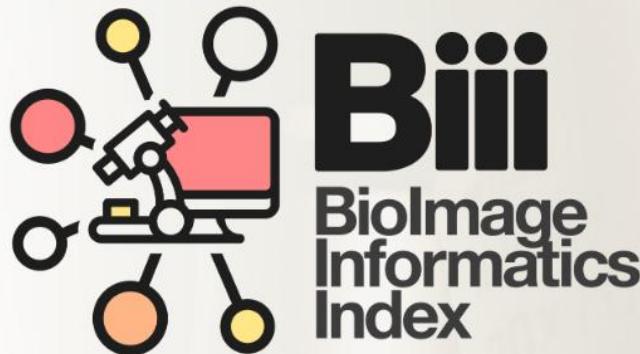


<https://biii.eu/>

BiiI (BiolImage Informatics Index)

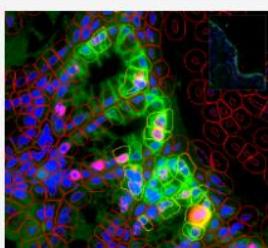
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Oocytor
Component

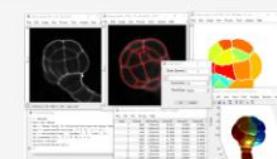
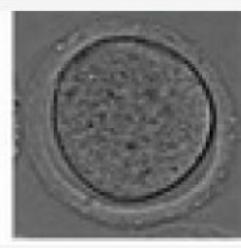


ImageM
Collection



Fast4DReg

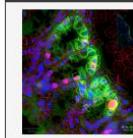


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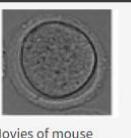
Qupath Multiplex Analysis Workflow



Segmentation of membrane of mouse, sea urchin and human oocytes from transmitted light images



Oocytor Component



Movies of mouse oocyte maturation in transmitted light



ImageM Collection



Fast4DReg Component

Most viewed



CMTK Component



Tensorflow Collection



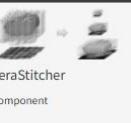
MIPAV Collection



McLuigi Component



Luigi Component



TeraStitcher Component

67202 views

Category

| Type | Pages |
|-------------------|-------|
| Training Material | 96 |
| Dataset | 37 |
| Software | 1,406 |

Type of Software Resource

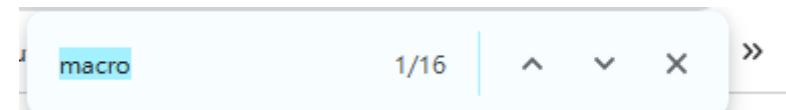
| Type | Pages |
|---------------|-------|
| Component | 923 |
| Collection | 346 |
| Workflow | 190 |
| I do not know | 10 |

Training material

Category

| Type | Pages |
|-------------------|-------|
| Training Material | 96 |
| Dataset | 37 |
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GPU-Accelerating ImageJ
Macro Image Processing
Workflows Using CLIJ

1840

Daniela Vorkel, Robert Haase
Book
Chapter

ImageJ
Macros, Image
processing

Bioimage Data Analysis
Workflows - Advanced
Components and Methods

1839

drosophila, fruit
fly, cell
migration

book

Image analysis,
Machine
learning, Data
handling,
Plotting,
Python,
ImageJ Macros

GPU-Accelerating ImageJ Macro Image Processing Workflows Using CLIJ

This chapter is part of [this book](#). The chapter introduces GPU-accelerated image processing in ImageJ/Fiji. The reader is expected to have some pre-existing knowledge of ImageJ Macro programming. Core concepts such as variables, for-loops, and functions are essential. The chapter provides basic guidelines for improved performance in typical image processing workflows.

40 views

Tool(s) used for training

[ImageJ](#)

URL

[Book chapter](#)

Author(s)

Daniela Vorkel

Robert Haase

Topics covered

[ImageJ Macros](#)

[Image processing](#)

Format

[Book Chapter](#)

Content type

[Workflow](#)

Parent

[Bioimage Data Analysis Workflows - Advanced Components and Methods](#)

Expected duration

2hours



Bioimage Data Analysis Workflows - Advanced Components and Methods

This open access textbook aims at providing detailed explanations on how to design and construct image analysis workflows to successfully conduct bioimage analysis.

Addressing the main challenges in image data analysis, where acquisition by powerful imaging devices results in very large amounts of collected image data, the book discusses techniques relying on batch and GPU programming, as well as on powerful deep learning-based algorithms. In addition, downstream data processing techniques are introduced, such as Python libraries for data organization, plotting, and visualizations. Finally, by studying the way individual unique ideas are implemented in the workflows, readers are carefully guided through how the parameters driving biological systems are revealed by analyzing image data. These studies include segmentation of plant tissue epidermis, analysis of the spatial pattern of the eye development in fruit flies, and the analysis of collective cell migration dynamics.

The presented content extends the *Bioimage Data Analysis Workflows* textbook (Miura, Sladoje, 2020), published in this same series, with new contributions and advanced material, while preserving the well-appreciated pedagogical approach adopted and promoted during the training schools for bioimage analysis organized within NEUBIAS – the Network of European Bioimage Analysts.

This textbook is intended for advanced students in various fields of the life sciences and biomedicine, as well as staff scientists and faculty members who conduct regular quantitative analyses of microscopy images.

59 views

Tool(s) used for training

ImageJ

Python

MATLAB

URI

[Open access to the book](#)

Date

Sat, 12/31/2022 - 12:00

Topics covered

Image analysis

Machine learning

Data handling

Plotting

Python

ImageJ Macros

Format

book

Content type

Workflow

Expected duration

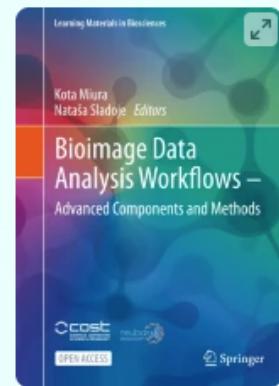
15hours

Additional keywords

drosophila

fruit fly

cell migration

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Bioimage Data Analysis Workflows – Advanced Components and Methods

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Overview

Editors: [Kota Miura, Nataša Sladoje](#)

- This book is open access, which means that you have free and unlimited access
- The book explains computational methods in the context of biological questions
- Provides real examples and hands-on experience
- Gives detailed instructions on how to design and implement bioimage analysis workflow

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Sections

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Kota Miura
Nataša Sladoje *Editors*

Bioimage Data Analysis Workflows – Advanced Components and Methods



OPEN ACCESS

Springer

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Type of Software Resource

| Category | |
|-------------------|-------|
| Type | Pages |
| Training Material | 96 |
| Dataset | 37 |
| Software | 1,406 |

Type of Software Resource

Type

Component

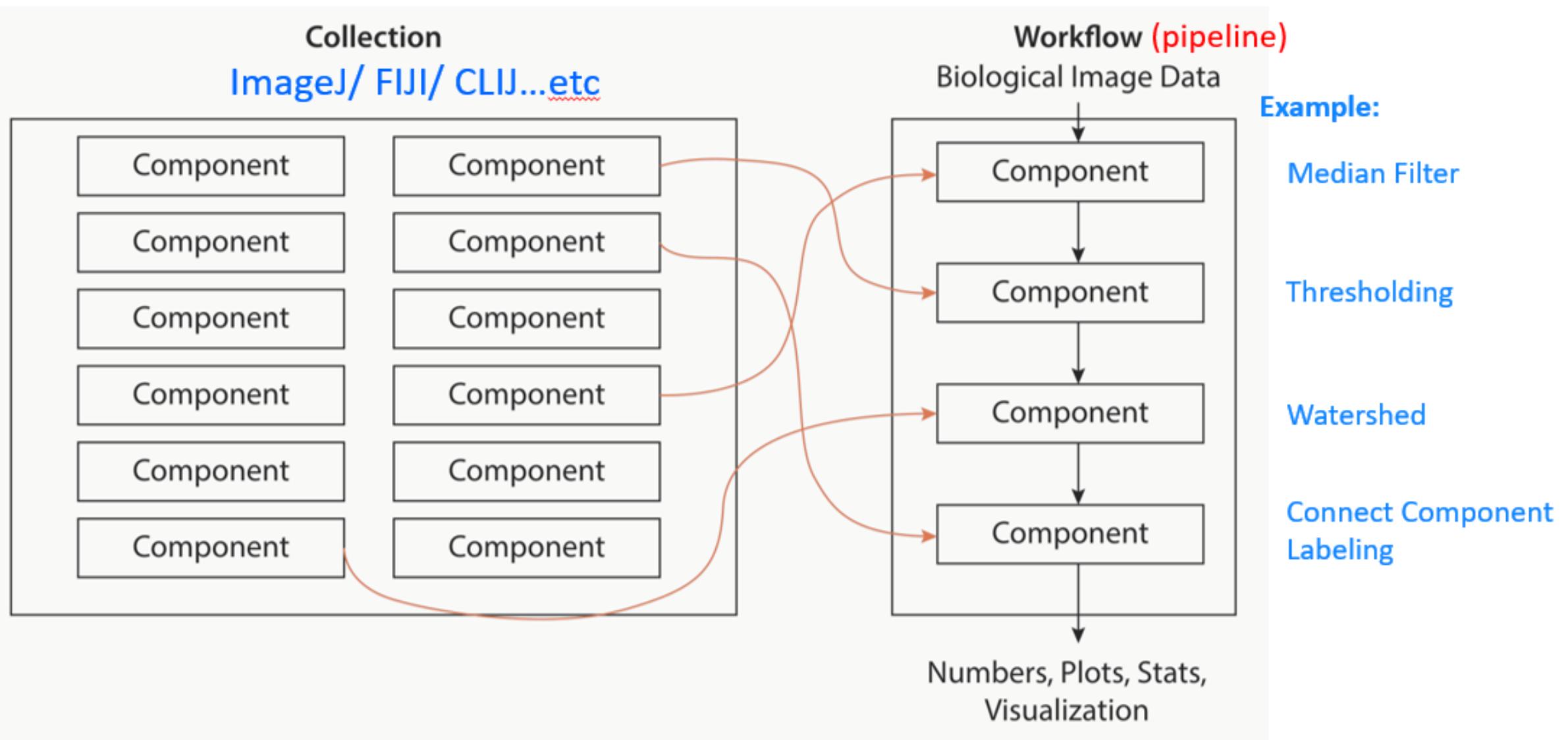
Collection

Workflow

I do not know



Software -> components, collection and workflow



https://biii.eu/taxonomy/term/3568?items_per_page>All

Type of Software Resource

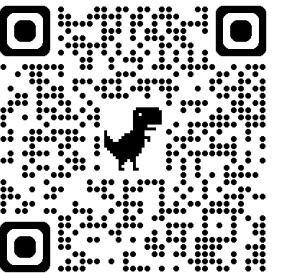
Type

Component

Collection

Workflow

I do not know



Workflow

A workflow is a set of components assembled in some specific order to

1. Measure and estimate some numerical parameters of the biological system or
2. Visualization

for addressing a biological question. Workflows can be a combination of components from the same or different software packages using several scripts and manual steps.

Items per page

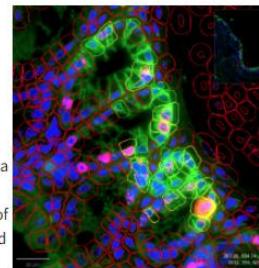
Qupath Multiplex Analysis

Workflow

Description

Scripts that allow to automatize a multiplex analysis in qupath. The input is a multi channel image with one channel containing a staining of cell nuclei and the other channels containing markers for a specific molecule. The goal is to obtain a count of positive cells for the markers in the different channels and for the combinations of positive markers. The workflow also adds the total numbers of positive cells for each marker to the results table (cells positive for multiple markers are not counted positive for the individual markers in the original qupath result).

[Read more](#) [Log in or register](#) to post comments 113 views



Spine Analyzer

Workflow

Description

Spine Analyzer allows to semi-automatically segment dendritic spines in 3D+t images and to measure their volumes and the intensities of the signal within in different channels over time.

has topic

Bioimage informatics

Digital histology

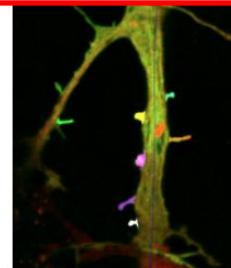
Microscopy

Fluorescence microscopy

has function

Interactive segmentation

[Read more](#) [Log in or register](#) to post comments 45 views



HistoMetriX

Component

Workflow

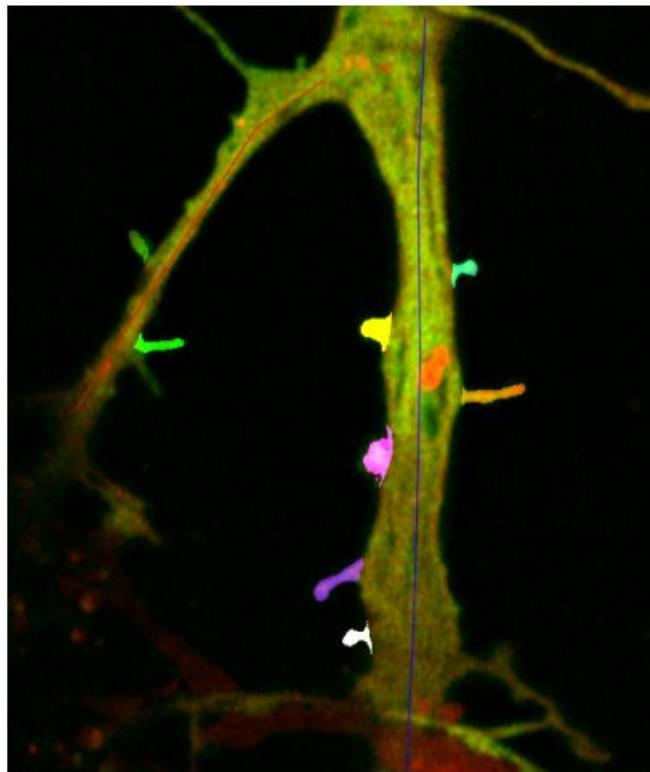
Description

HistoMetrix is an advanced histology analysis software designed to simplify image processing and



Illustration, date, download link and tutorial material must be available.

Spine Analyzer



Type

Workflow

Author

Bäcker Volker orcid.org/0000-0002-9129-6403

License/Openness

Free and open source

Description

Spine Analyzer allows to semi-automatically segment dendritic spines in 3D+t images and to measure their volumes and the intensities of the signal within in different channels over time.

has function

Interactive segmentation

has topic

Bioimage informatics

Digital histology

Microscopy

Fluorescence microscopy

has biological terms

Dendritic Spine

Entry Curator

volker

Post date: 10/25/2024 - 14:56

Last modified: 10/25/2024 - 15:09

Download Page

[Spine-Analyzer](#)

Documentation Link

[Spine-Analyzer Documentation](#)

GitHub, the open repository for your work



The tools allow to semi-automatically segment dendritic spines in 3D+t images and to measure their volumes and the intensities of the signal within in different channels over time.



https://github.com/MontpellierRessourcesImagerie/imagej_macro_s_and_scripts/wiki/Spine-Analyzer

Biii is mainly curated by the activity-- Taggathon



GloBIAS Bioimage Analysis Conference 2025

26-31 October 2025
KOBE, Japan @RIKEN BDR

26-29 October
Training Schools
Hackathon
Taggathon

29-31 October
Symposium
Call4Help
OSS* Lounge
*Open-source software



<https://www.globias.org/activities/bioimage-analysis-conference-2025-in-kobe>



GloBIAS Bioimage Analysis Conference 2025

Oct 26, 2025 - Oct 31, 2025 | Kobe, Japan

Venue: RIKEN BDR, Kobe, Japan

Registration via Google Forms here:

<https://tinyurl.com/3dtajhh6>

Please follow the links for more info [Taggathon](#)

[Training School 2025](#)

Date: Oct 27 am to Oct 28 pm, Kobe, Japan

[Hackathon 2025](#)

Organisers

Kota Miura (Bioimage Analysis & Research, Japan & Germany)

[Taggathon 2025](#)

Aim

The aim is to organize bioimage analysis tools and curate the [Bio Image Information Index \(BIII\)](#).

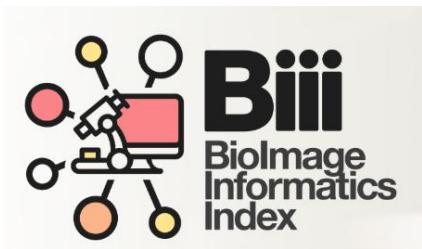
[Symposium 2025; including poster session, OSSL and Call4Help](#)



Taggathon

Since the number of available *components* and *workflows* publicly offered is increasing on a daily basis, the content of the *webtool* needs to be updated constantly. At the same time, the *webtool* itself needs a considerable amount of effort for its infrastructure development. A **Taggathon** is a strategic event where *bioimage analysts and developers* meet physically and work together to feed and tag information of *components* and *workflows* into the *Webtool* manually, and also develop its functionalities and discuss about future development and interesting content to include. The word **Taggathon** was invented in 2013 by NEUBIAS members, the first one of which was held in October 2013 and led to a pilot platform available at <http://biii.info>. For more details, read [Taggathon](#) page.

1. 小組發表
2. Biii
3. Herelm
4. DOI--Zenodo
5. 授權說明





HereIm

Why is HereIm?

High Efficiency,
Reproducibility, Executability Imaging
database.



Life scientists



Imaging scientists

- ✓ Offer an open platform for surveying image analysis workflows for life scientists.
- ✓ As a public portfolio for imaging scientists or bioimage analysts.
- ✓ Reduce the repeated effort in creating the tool for similar application.
- ✓ Easier for tool reusability.
- ✓ Seeds: Collect the workflows answering questions to imaging core facilities.
- ✓ Community contribution: Collect the workflows from all bioimage analysts.



<https://hereimntuic.com/>



Home About Tools Imaging Scientists FAQ



Type and hit enter...



TOOLS

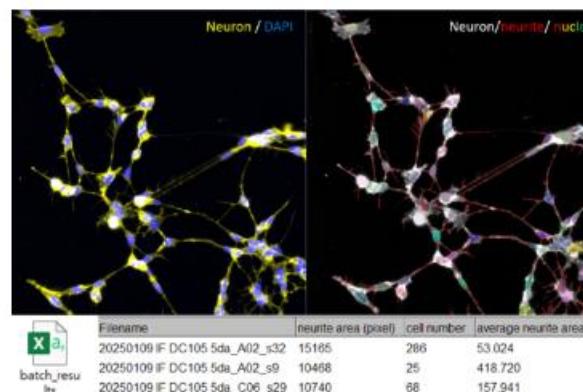
- › Cell colocalization
- › Color Image
- › Complexity
- › Fluorescence
- › Mitocondria



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TOOLS

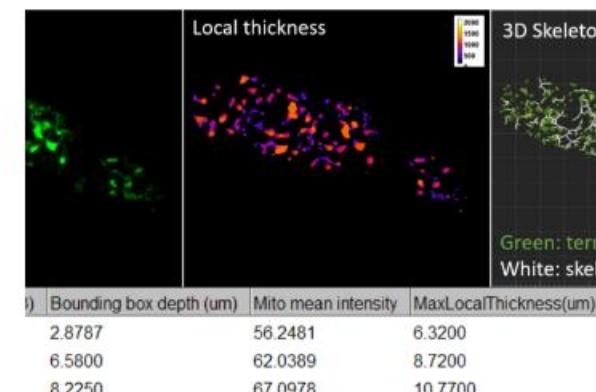


Complexity

Neurite Measurement For The Whole Image

28 3月, 2025

IM-00008 Neurite-M ...

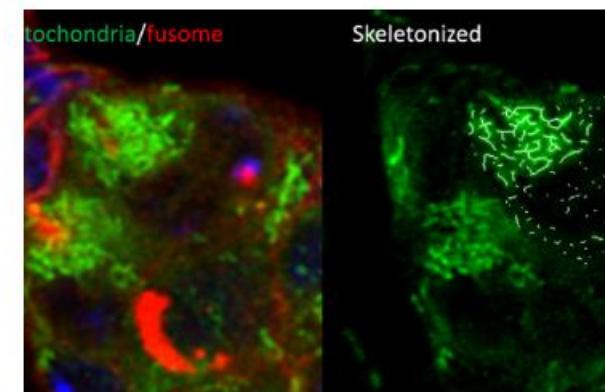


Complexity ▾ Mitocondria

Mitochondrial Branch And Thickness

9 1月, 2025

IM-00007 C. elegan ...



Mitocondria

Fruit Fly Mitochondrial Morphology Assay

29 11月, 2024

IM-00006 Fruit fly ...

Figures for a quick glance

HereIM

Home About Tools Imaging Scientists FAQ

Raw image

Analyzed result

Attribute

Neuron / DAPI

Neuron/neurite/nucleus

| Complexity | Filename | neurite area (pixel) | cell number | average neurite area/cell |
|-------------------------------|----------|----------------------|-------------|---------------------------|
| 20250109 IF DC105 5da_A02_s32 | 15165 | 286 | 53.024 | |
| 20250109 IF DC105 5da_B01_s32 | 10468 | 25 | 418.720 | |
| 20250109 IF DC105 5da_C06_s29 | 10740 | 68 | 157.941 | |

Neurite Measurement for the Whole Image

28 3月, 2025

Taiwan University Technology Platform

Summarize the critical info in a table

| IM-00008 | Neurite-Measurement-for-the-Whole-Image | |
|-------------|---|--|
| Application | Whole-image neurite measurement | Cell or sample types. Please also include the image provider. |
| Demo image | SH-SY5Y cells (courtesy of Dr. Ling-Wei Hsin) | |
| Language | IJM | |
| Author | Szu-Ting Lin | Herelm users can contact the author directly, if the author is willing to share the email. |
| DOI | 10.5281/zenodo.15099139 | Digital object identifier makes this workflow citable. |
| YouTube | https://www.youtube.com/watch?v=P5_T8jfzbk | |
| GitHub | Neurite-Measurement-for-the-Whole-Image | This tutorial material is prepared for publication on the "NTU Imaging Core" YouTube channel. The narration will be delivered in Chinese and later translated by an AI agency to provide versions in both Chinese and English. |
| | Personal GitHub space | |

Introduction part can be the same as the “read me” file from GitHub



Introduction

This Fiji batch macro is designed to process neuron images with extensive clustering, especially those with low-contrast neurites. By utilizing the Local Thickness [1] and Skeletonize [2] plugins, we have developed a workflow for whole-image neurite measurement. The automatically saved Excel file provides the total neurite length and cell count for the entire image.

#Examples

1. The confocal image of SH-SY5Y cells was acquired using high-content imaging. (courtesy of Dr. Ling-Wei Hsin (Department of Pharmacy, National Taiwan University).

#Description

1. This is a batch IJM script.
2. The demo image contains two channels: SH-SY5Y cells (green) and DAPI (blue).
3. The script begins by splitting the channels and renaming them accordingly.
4. Neurite Measurement
5. Then creating neuron mask by using the RenyiEntropy[3] thresholding method.
 1. The neuron mask is duplicated, and local thickness is applied to approximate the soma.
 2. The neuron mask is skeletonized, and the soma mask is subtracted to isolate the neurites.
 3. The total length of the neurites is measured.
6. Cell Count
 1. Otsu[4] thresholding is applied to the DAPI channel, and the result is converted to a binary mask.
 2. The DAPI mask is multiplied with the normalized neuron mask to remove non-neuritic pixels.
 3. The individual nucleus is identified by StarDist[5].
7. The total cell number is counted, and the average neurite area per cell is calculated.

Instruction

1. Place the image in the same directory for batch analysis. Also, create a null file to serve as the output file.
2. Drag the script and the demo image to Fiji.
3. Press “Run” and choose the input and output file respectively.
4. The collection table will be saved as an Excel file.

Acknowledgements

Thank to Dr. Shao-Chun, Peggy, Hsu, and Ms. Anchí Luo for their invaluable teaching and guidance! Demo images are captured by Yu-Hsuan Lin and courtesy from Dr. Ling-Wei Hsin (Department of Pharmacy, National Taiwan University).

This work was supported by National Science and Technology Council NSTC 113-2320-B-002-076 to Shao-Chun Hsu.

Reference

1. R. P. Dougherty and K.-H. Kunzelmann, “Computing Local Thickness of 3D Structures with ImageJ,” in Microscopy & Microanalysis 2007 Meeting, Ft. Lauderdale, FL, USA, Aug. 2007.
2. T. Y. Zhang and C. Y. Suen, “A fast parallel algorithm for thinning digital patterns,” Communications of the ACM, vol. 27, no. 3, pp. 236–239, 1984.
3. P. Sahoo, C. Wilkins, and J. Yeager, “Threshold selection using Renyi’s entropy,” Pattern Recognition, vol. 30, no. 1, pp. 71–84, Jan. 1997.

Personal GitHub space

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Code Issues Pull requests Actions Projects Security Insights

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20250319_Neurite_measurement.ijm Add files via upload last month

README.md Update README.md last month

demo_image.tif Add files via upload 3 weeks ago

Readme Activity 1 star 1 watching 0 forks Report repository

Neurite-Measurement-for-the-Whole-Image

DOI 10.5281/zenodo.15099139

Neuron / DAPI Neuron/neurite/ nucleus

Releases 1

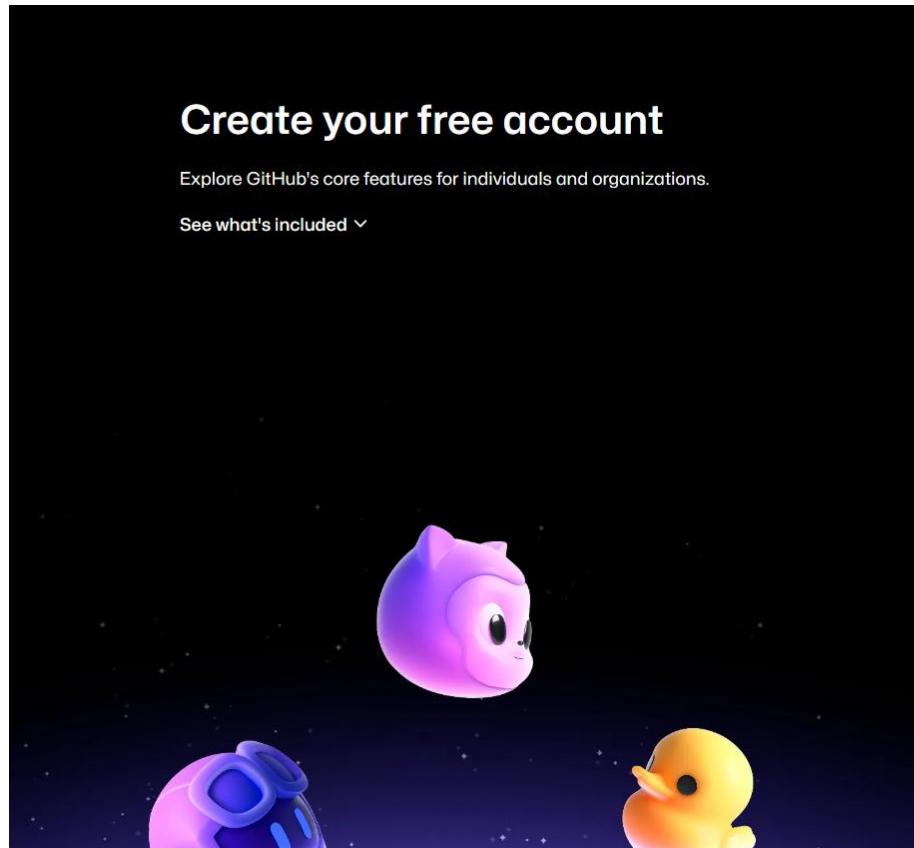
N neurite-Measurement-for-the... Latest on Mar 28

Dockerfiles

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To be a bioimage analyst.....

1. Use what you have learned in this course.
2. Create your own workflow for a specific bioimage analysis question.
3. Create a GitHub account.



Already have an account? [Sign in →](#)

Sign up to GitHub

Email*

Password*

Password should be at least 15 characters OR at least 8 characters including a number and a lowercase letter.

Username*

Username may only contain alphanumeric characters or single hyphens, and cannot begin or end with a hyphen.

Your Country/Region*

For compliance reasons, we're required to collect country information to send you occasional updates and announcements.

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4. Save your workflow in a repository

peggyscshu

Overview Repositories 20 Projects Packages Stars

Type / to search

Customize your pins



Shao-Chun, Peggy, Hsu
peggyscshu

Work on high-end microscope, and image and data analysis with the compiling on IJM, VBA, KNIME, Amira, Imaris, and MetaMorph. Step in Python.

Edit profile

Popular repositories

- Analysis-on-membrane-labeled-cell** Public
Distinguish cells labeled with membrane structure and analyze the volume and intensity in each cell.
ImageJ Macro 2
- Cell-grouping** Public
The red fluorescence labeled cells are distributed in a cluster manner. These tools are used to define the cluster code for each interested nucleus.
VBA 1 1
- Myotome-volume-Nucleus-count-and-Color-analysis** Public
The tools in this repository are designed to analyze the confocal images of zebrafish myotome whose membrane is labeled by the multicolor cell barcode (ref1). Three types of analysis done by five s...
ImageJ Macro 1

- Batch-assay-in-oil-red-stain** Public
This Fiji macro is designed to automatically measure the oil red occupation and intensity in tissues from tif files collected in a folder.
ImageJ Macro 2
- Mitosis-phase-analysis** Public
A cell cycle occurs as a cell divides. The somatic cell leaves interphase, undergoes mitosis and eventually gives out two daughter cells. Mitosis is composed by a series of events including prophas...
ImageJ Macro 1
- Automatic-billing-system** Public
To integrate the charging from the optical microscope, the advanced optical microscope and the electronic microscope, I designed this system to automatically sort bills to each PI and generate mont...

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5. Prepare “README” file and upload the script and demo images.

szutinglin / Neurite-Measurement-for-the-Whole-Image

Type / to search

Code Issues Pull requests Actions Projects Security Insights

Watch 1 Fork 0 Star 1

Neurite-Measurement-for-the-Whole-Image Public

main 1 Branch 2 Tags Go to file Add file Code

szutinglin Add files via upload 6de2f07 · 3 weeks ago 47 Commits

20250319 Neurite measurement.ijm Add files via upload last month

README.md Update README.md last month

demo_image.tif Add files via upload 3 weeks ago

README

Neurite-Measurement-for-the-Whole-Image

DOI 10.5281/zenodo.15099139

Neuron / DAPI Neuron/neurite/ nucleus

About

This Fiji batch macro is designed to process neuron images with extensive clustering, especially those with low-contrast neurites.

Readme Activity 1 star 1 watching 0 forks Report repository

Releases 1

Neurite-Measurement-for-the... Latest on Mar 28

Packages

6. Register a DOI for this workflow

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Code Issues Pull requests Actions Projects Security Insights

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20250319 Neurite measurement.ijm Add files via upload last month

README.md Update README.md last month

demo_image.tif Add files via upload 3 weeks ago

README

Neurite-Measurement-for-the-Whole-Image

DOI 10.5281/zenodo.15099139

Neuron / DAPI Neuron/neurite/ nucleus

About

This Fiji batch macro is designed to process neuron images with extensive clustering, especially those with low-contrast neurites.

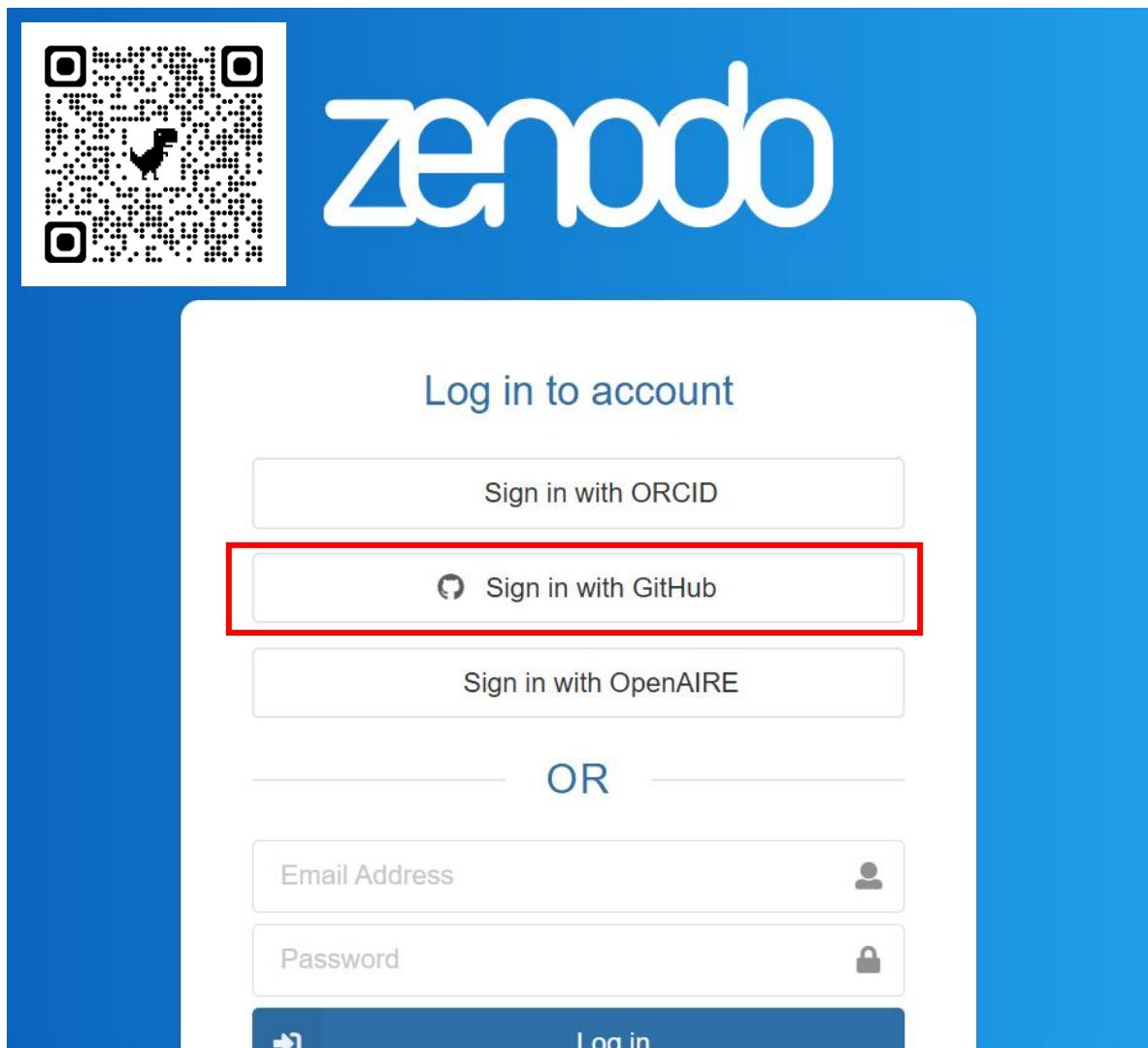
Readme Activity 1 star 1 watching 0 forks Report repository

Releases 1

Neurite-Measurement-for-the... Latest on Mar 28

Packages

6-1 Login Zenodo with your GitHub account



<https://zenodo.org/login/?next=/>

6-2 Link to the repositories in your GitHub

zenodo

Search records... 

Communities My dashboard  

peggysch... 

Profile Change password Notifications Security Linked accounts Applications GitHub Log out

Planned intervention: On Monday, April 28th between 04:00-04:30 (UTC), Zenodo will be unavailable for 5 minutes because of a scheduled upgrade in our storage system.

Featured communities

 EU Open Research Repository 

Open repository for EU-funded research outputs from Horizon Europe, Euratom, and earlier Framework Programmes

6-3 Flip the switch

Settings

- Profile
- Change password
- Notifications
- Security
- Linked accounts
- Applications
- GitHub**

GitHub Repositories (updated 3 months ago) 

Get started

- 1 Flip the switch**

Select the repository you want to preserve, and toggle the switch below to turn on automatic preservation of your software.

ON  (example)
- 2 Create a release**

Go to GitHub and [create a release](#). Zenodo will automatically download a .zip-ball of each new release and register a DOI.
- 3 Get the badge**

After your first release, a DOI badge that you can include in GitHub README will appear next to your repository below.

DOI [10.5281/zenodo.8475](#) (example)

Enabled Repositories

| Repository | DOI | Switch |
|--|--|---|
| peggyscshu/Analysis-on-membrane-labeled-cell | 10.5281/zenodo.4292333 |  |
| peggyscshu/Batch-assay-in-oil-red-stain | 10.5281/zenodo.4292381 |  |
| peggyscshu/CCP-lifetime | |  |

6-4 Create a release in GitHub

peggyscshu / CCP-lifetime

Type to search

Issues Pull requests Actions Projects Security Insights Settings

CCP-lifetime Public

Pin Unwatch 1 Fork 0 Star 0

main 1 Branch 0 Tags Go to file Add file Code

peggyscshu Add files via upload 89c2f97 · 2 months ago 20 Commits

Elements Rename C_Normalize Ft and St in Colab_20241229.ipynb to ... 2 months ago

One step version Rename One_step_CCP_Lifetime_20250225.ipynb to One ste... 2 months ago

Workflow Add files via upload 2 months ago

Demo data.zip Add files via upload 2 months ago

LICENSE Initial commit 4 months ago

One_step_CCP_Lifetime_20250227.ipynb The latest version 2 months ago

About

No description, website, or topics provided.

MIT license Activity 0 stars 1 watching 0 forks

Releases

No releases published [Create a new release](#)

Packages

No packages published [Publish your first package](#)

Contributors 2

README MIT license

CC-BY-NC-SA

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6-5 Fill in required info



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6-6 Get the badge

Settings

- Profile
- Change password
- Notifications
- Security
- Linked accounts
- Applications
- GitHub**

Github Repositories (updated 3 months ago) [Sync now](#)

Get started

- 1 Flip the switch**
Select the repository you want to preserve, and toggle the switch below to turn on automatic preservation of your software.
ON (example)
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Enabled Repositories

| | | |
|--|--|------------------------------------|
| peggyscshu/Analysis-on-membrane-labeled-cell | DOI 10.5281/zenodo.4292333 | ON <input type="checkbox"/> |
| peggyscshu/Batch-assay-in-oil-red-stain | DOI 10.5281/zenodo.4292381 | ON <input type="checkbox"/> |
| peggyscshu/CCP-lifetime | | ON <input type="checkbox"/> |

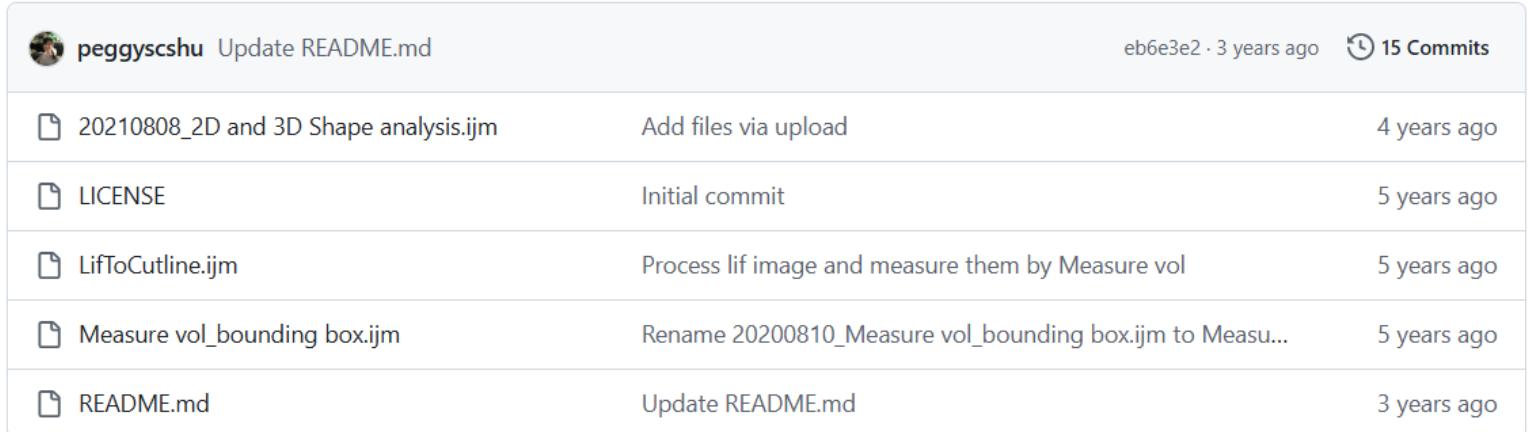
A red arrow points from the text "After your first release, a DOI badge that you can include in GitHub README will appear next to your repository below." to the DOI link of the third repository row.

7. Paste the DOI badge in the “README” in GitHub

 Analysis-on-membrane-labeled-cell Public

Pin Unwatch 1 Fork 0 Star 2

main 1 Branch 1 Tag Go to file Add file Code



| File | Message | Date |
|---------------------------------------|--|-------------|
| 20210808_2D and 3D Shape analysis.ijm | Add files via upload | 4 years ago |
| LICENSE | Initial commit | 5 years ago |
| LifToCutline.ijm | Process lif image and measure them by Measure vol | 5 years ago |
| Measure vol_bounding box.ijm | Rename 20200810_Measure vol_bounding box.ijm to Measu... | 5 years ago |
| README.md | Update README.md | 3 years ago |

Readme Apache-2.0 license

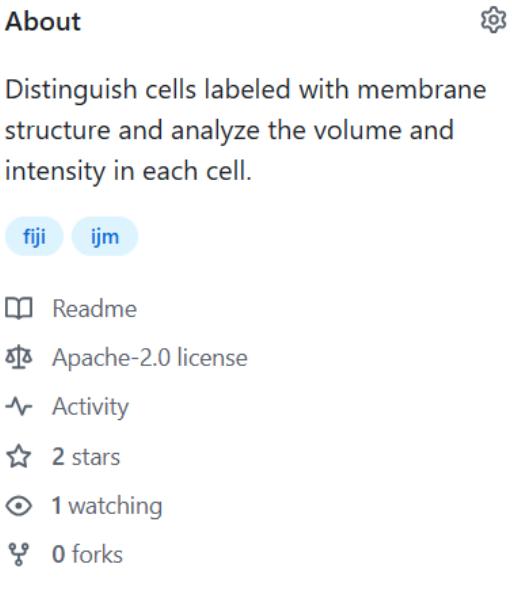
Analysis-on-membrane-labeled-cell

Distinguish cells labeled with membrane structure and analyze the volume and intensity in each cell in a batch mode.

#Examples

1. Membrane-tagged fluorescent cells
2. Cell wall labeled plant cells

DOI 10.5281/zenodo.4292333



Distinguish cells labeled with membrane structure and analyze the volume and intensity in each cell.

fiji ijm

Readme Apache-2.0 license Activity 2 stars 1 watching 0 forks

Releases 1

cell analysis, membrane label, g... Latest on Nov 26, 2020

Packages

No packages published [Publish your first package](#)

Published March 28, 2025 | Version Neurite-Measurement-for-the-Whole-Image

Software Open

szutinglin/Neurite-Measurement-for-the-Whole-Image: Neurite-Measurement-for-the-Whole-Image-ver1

szutinglin¹; Shao-Chun, Peggy, Hsu¹

Show affiliations

This Fiji batch macro is designed to process neuron images with extensive clustering, especially those with low-contrast neurites. **Full Changelog:** <https://github.com/szutinglin/Neurite-Measurement-for-the-Whole-Image/commits/Neurite-tracing>

Files

[szutinglin/Neurite-Measurement-for-the-Whole-Image-Neurite-Measurement-for-the-Whole-Image.zip](#)

 [szutinglin/Neurite-Measurement-for-the-Whole-Image-Neurite-Measurement-for-the-Whole-Image.zip](#) 

 [szutinglin/Neurite-Measurement-for-the-Whole-Image-650ad89](#)

 [20250319 Neuron tracing_batch.ijm](#) 4.1 kB

 [README.md](#) 3.4 kB

17

Views

0

Downloads

[Show more details](#)

Versions

Version Neurite-Measurement-for-the-Whole-Image

Mar 28, 2025

10.5281/zenodo.15099139

Cite all versions? You can cite all versions by using the DOI [10.5281/zenodo.15099138](https://doi.org/10.5281/zenodo.15099138). This DOI represents all versions, and will always resolve to the latest one. [Read more](#).

External resources

Archived in

 [Software Heritage](#)

swh:1:dir:720864381fd6eeecbab00468dacd10fb1e61b0d4



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8. Submit your workflow to HerelM

HereIM

Home About Tools Imaging Scientists FAQ

Neuron / DAPI

Neuron/neurite/nucleus

| Complexity | Filename | neurite area (pixel) | cell number | average neurite area/cell |
|---|-------------------------------|----------------------|-------------|---------------------------|
| 20250109 IF DC105 5da_A02_s32 | 15165 | 286 | 53.024 | |
| Neurite Measurement for the Whole Image | 20250109 IF DC105 5da_C06_s29 | 10740 | 25 | 418.720 |
| 26 3月 2025 | 10740 | 68 | 157.941 | |

IM-00008 | Neurite-Measurement-for-the-Whole-Image

Application Whole-image neurite measurement

Demo image SH-SY5Y cells (courtesy of Dr. Ling-Wei Hsin)

Language IJM

Author Szu-Ting Lin

DOI [10.5281/zenodo.15099139](https://doi.org/10.5281/zenodo.15099139)



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How to contribute?



Home About Tools Imaging Scientists [FAQ](#)

CONTRIBUTE TO HEREIM

How to |

Types of Submissions

All tools related to biological microscopy image analysis are welcome for submission.

Submission Guidelines

Please refer to the [Submission Guidelines](#) pages.

Review Process

All submissions will undergo a preliminary editorial review. Authors will be notified of the decision within 2-3 weeks of submission.

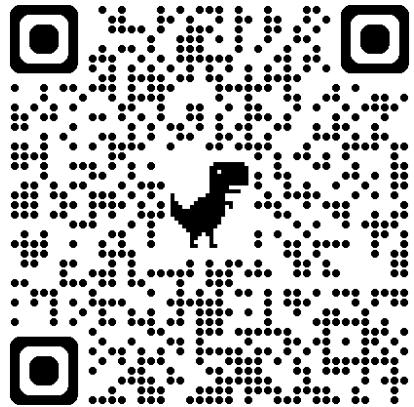
How to Submit

Please submit your manuscript to [HereIM Tool Submission Form](#).

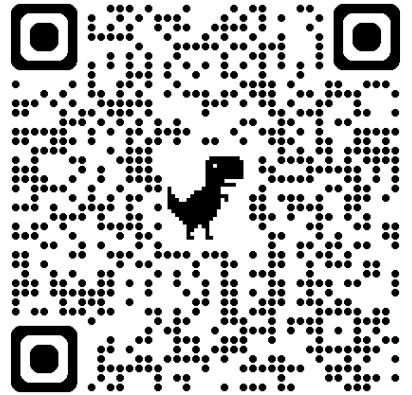
Contact

For inquiries regarding the submission process, please contact us at [peggyschsu@ntu.edu.tw].





線上簽到



課後意見調查

我們正在準備明年Python的課程，如果您也想成為我們的講師群，歡迎與我們聯絡！

peggyschsu@ntu.edu.tw

許紹君

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 IBC



<https://www.globias.org/activities/bioimage-analysis-conference-2025-in-kobe>

 German BioImaging
Gesellschaft für Mikroskopie und Bildanalyse



GloBIAS Bioimage Analysis Conference 2025

26-31 October 2025

KOBE, Japan @RIKEN BDR

26-29 October
Training Schools
Hackathon
Taggathon



 GloBIAS
Global BioImage Analysts' Society

29-31 October
Symposium
Call4Help
OSS* Lounge
* Open-source software

