

Build your own BioImage Analysis Workflow with BiaPy

Daniel Franco-Barranco ^{1,2}

¹ University of the Basque Country (UPV/EHU)

² Donostia International Physics Center (DIPC)

eman ta zabal zazu



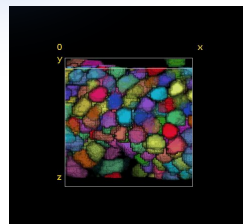
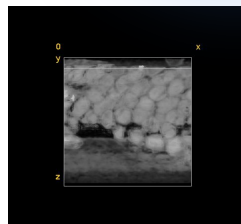
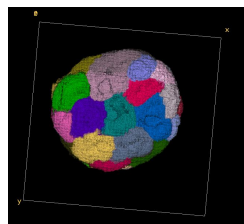
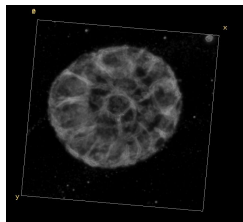
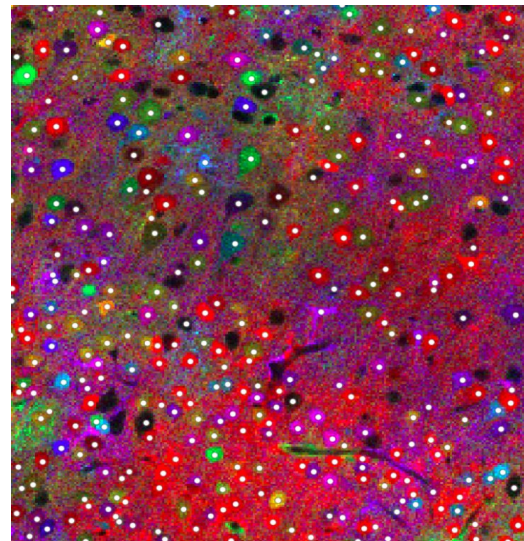
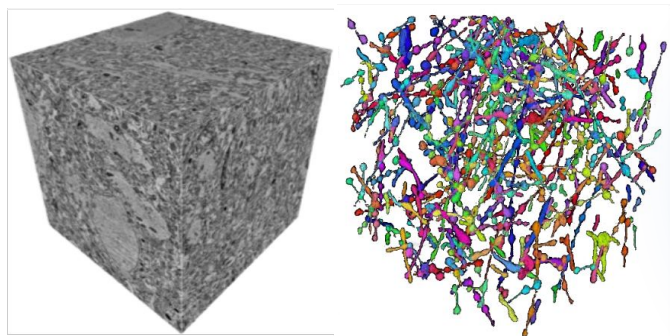
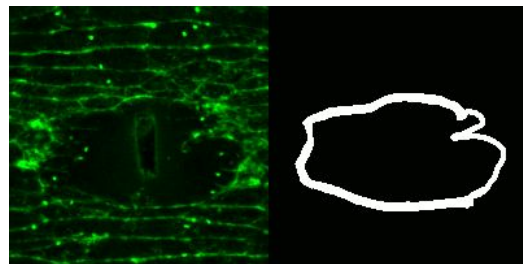
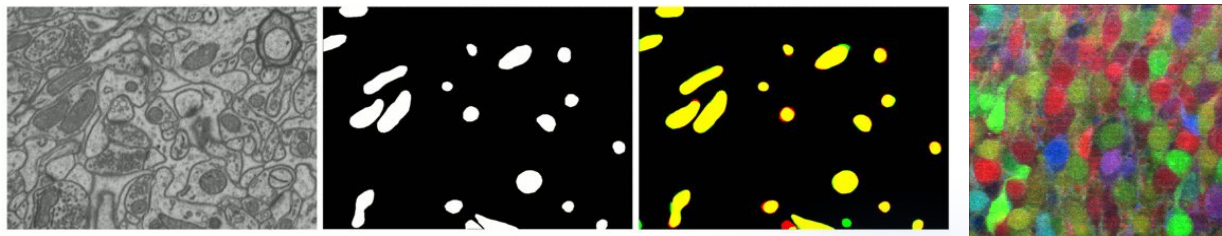
Universidad
del País Vasco

Euskal Herriko
Unibertsitatea

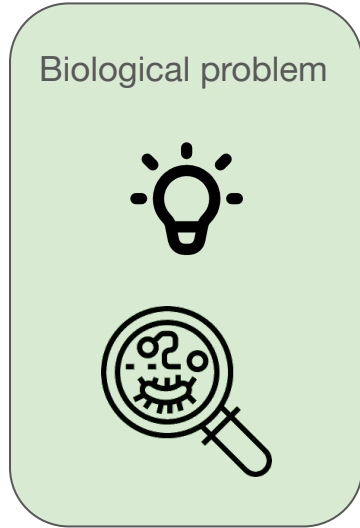


Donostia
International
Physics Center

Deep learning possibilities

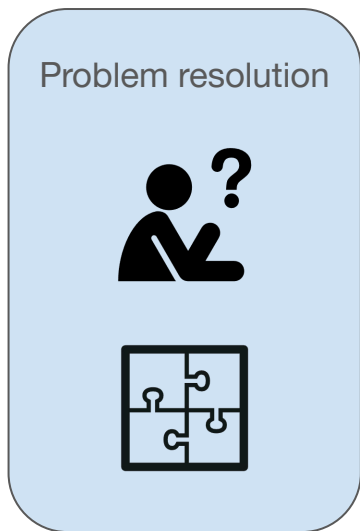


Biological problem resolution



What's a workflow

Sequence of image processing algorithms with a specified parameter set is what we call a “workflow”
(Miura, Kota et. al., 2020)



BiaPy: library for building bioimage analysis workflows



B i a P y

Library that gathers most of the common workflows in the bioimage field.

For every workflow we provide:

- 2D / 3D templates.
- Full documentation.
- Notebooks runnable in Google Colab (with real data).

For some, we provide full **tutorials** to reproduce our publications.

Quick recap: deep learning

Cats and dogs



Cat



Dog

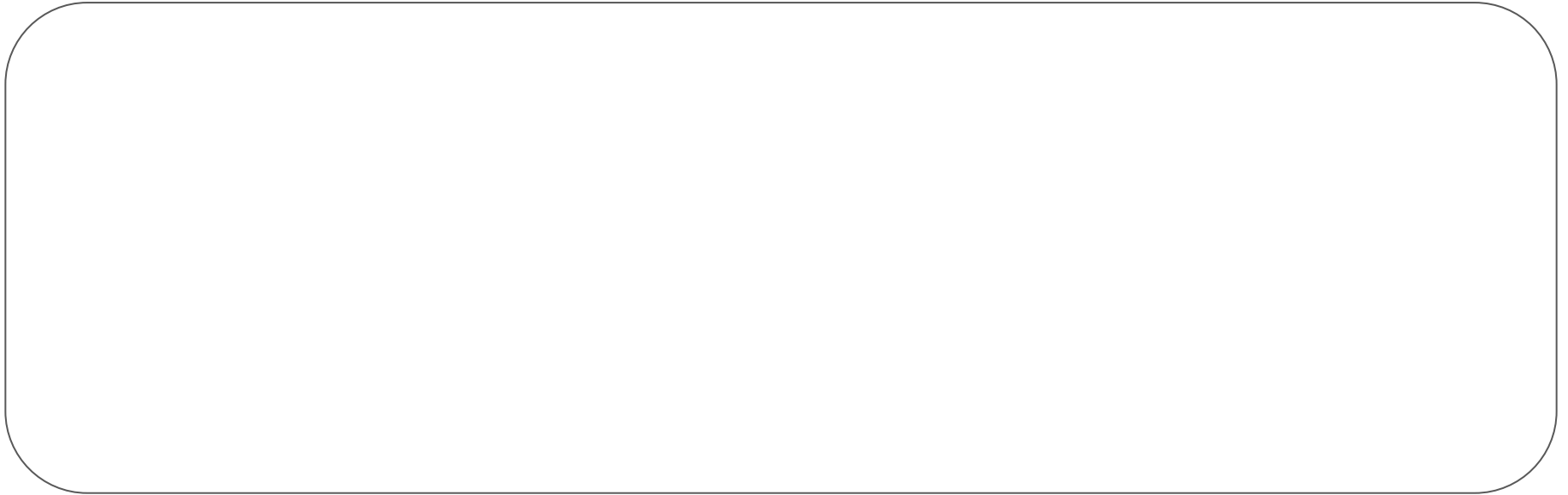
Training phase

Deep learning

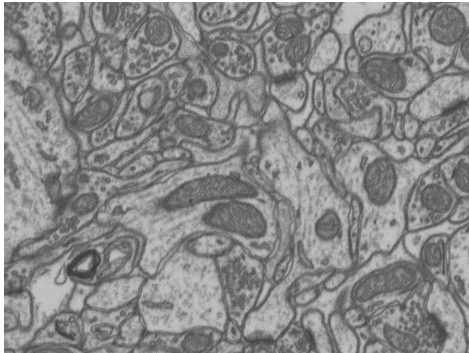
Test phase

Deep learning

Generic deep learning structure



Semantic segmentation



Image



Deep learning model



Semantic mask



Documentation



Templates



2D Jupyter Notebook



3D Jupyter Notebook

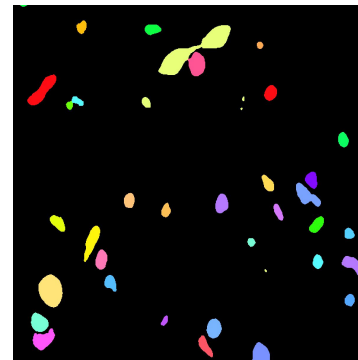
Instance segmentation



Image



Deep learning model



Instance mask



Documentation



Templates



2D Jupyter Notebook



3D Jupyter Notebook

Demo time: 2D instance segmentation

 Open in Colab

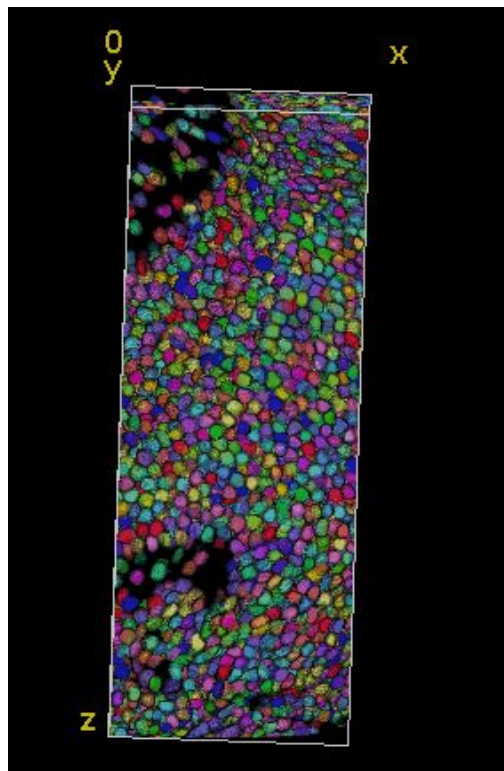
Notebook



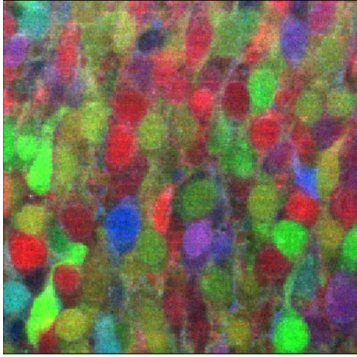
Documentation



Dataset



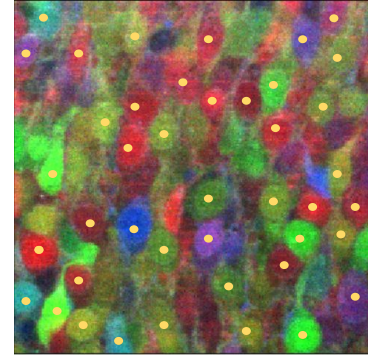
Detection



Image



Deep learning model



Center coordinates
(detection mask)



Documentation



Templates



2D Jupyter Notebook



3D Jupyter Notebook

Denoising

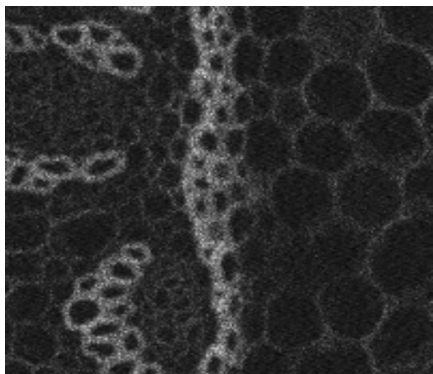
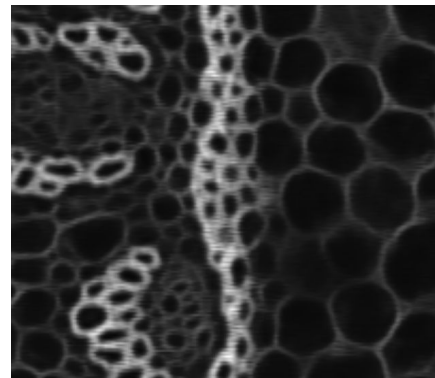


Image with noise



Deep learning model



Clean image



Documentation



Templates

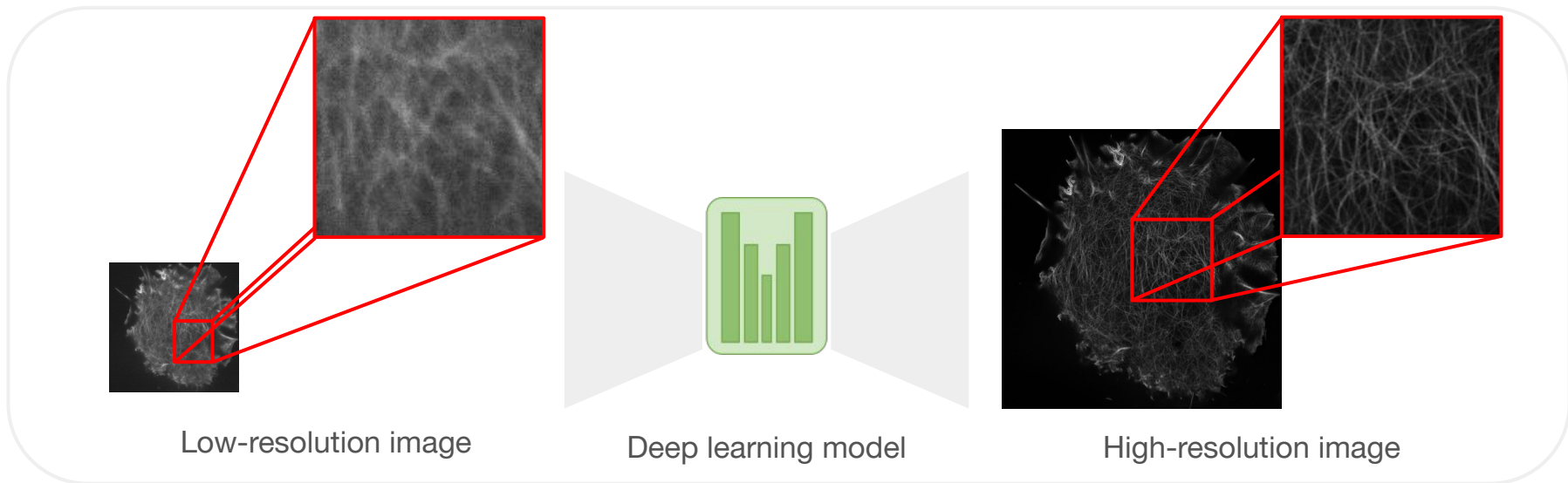
 Open in Colab

2D Jupyter Notebook

 Open in Colab

3D Jupyter Notebook

Super-resolution



Documentation

Templates

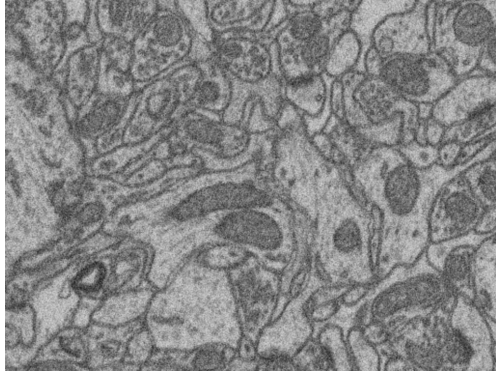
Open in Colab

2D Jupyter Notebook

Open in Colab

3D Jupyter Notebook

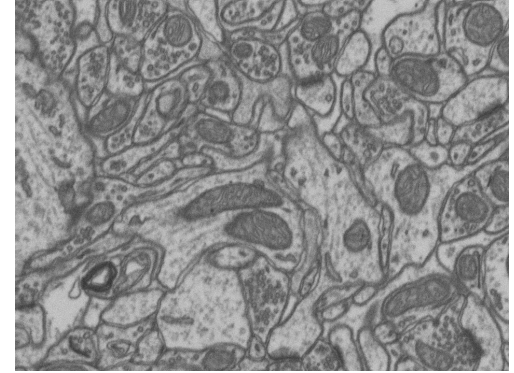
Self-supervised learning



Image



Deep learning model



Reconstructed image



Documentation



Templates



Open in Colab

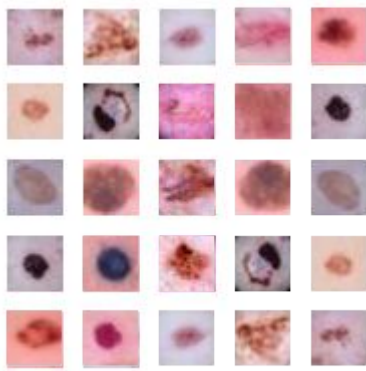
2D Jupyter Notebook



Open in Colab

3D Jupyter Notebook

Classification



Image



Deep learning model

| | | | | |
|---------|---------|---------|---------|---------|
| Class 6 | Class 1 | Class 3 | Class 0 | Class 1 |
| Class 3 | Class 5 | Class 1 | Class 1 | Class 3 |
| Class 1 | Class 2 | Class 0 | Class 0 | Class 6 |
| Class 3 | Class 1 | Class 1 | Class 2 | Class 1 |
| Class 2 | Class 3 | Class 6 | Class 5 | Class 4 |

Classification



Documentation



Templates

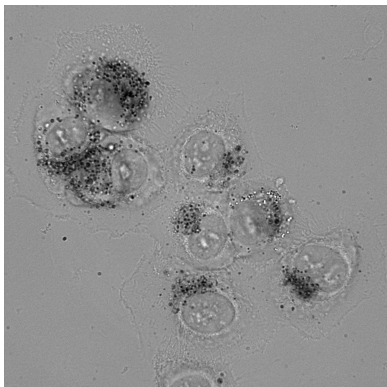


2D Jupyter Notebook



3D Jupyter Notebook

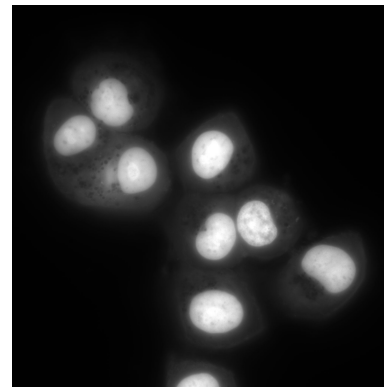
Image to image



Brightfield image



Deep learning model



Nucleus



Documentation



Templates



2D Jupyter Notebook



3D Jupyter Notebook

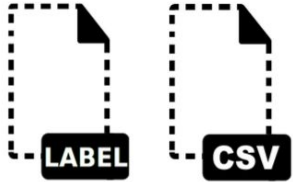
Library overview



B i a P y

Structure

Input



BiaPy workflow

Output

How to configure a workflow

BiaPy YAML file

```
1  PROBLEM:  
2    TYPE: SEMANTIC SEG  
3    NDIM: 2D  
4  DATA:  
5    PATCH_SIZE: (256, 256, 1)  
6    TRAIN:  
7      PATH: /TRAIN_PATH  
8      MASK_PATH: /TRAIN_MASK_PATH  
9    VAL:  
10   SPLIT_TRAIN: 0.1  
11  TEST:  
12  PATH: /TEST_PATH
```



Pre-processing

1 task / problem = 1 YAML template

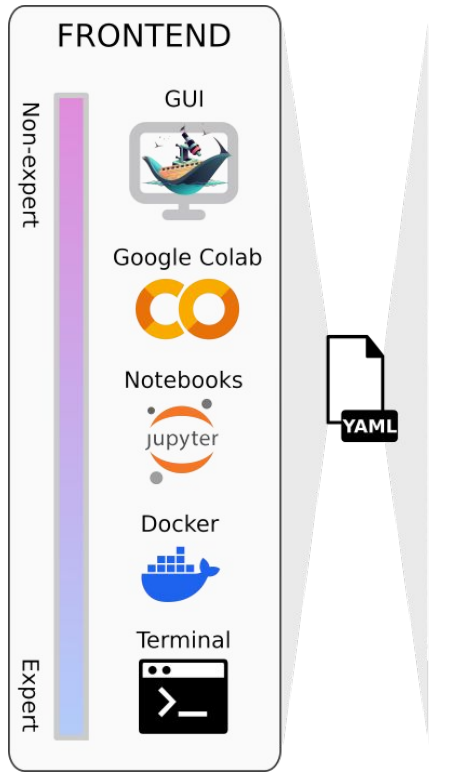
Advantages

- Easy prototyping.
- No need to code, only edit a text file.

Disadvantages

- Long list of keywords...
- BUT not need to know them!

Under the hood



Franco-Barranco et al., "BiaPy: A unified framework for versatile bioimage analysis with deep learning," bioRxiv, 2024.

BiaPy ecosystem

Landing page

Documentation

BiaPy
latest

Search docs

GET STARTED

- Quick start
- Installation
- How it works
- Configuration
- Select workflow
- FAQ & Troubleshooting
- How to contribute

WORKFLOW DESCRIPTION

- Semantic segmentation
- Instance segmentation
- Detection
- Denoising
- Super-resolution
- Self-supervision
- Classification

TUTORIALS

- Semantic segmentation
- Instance segmentation
- Detection
- Denoising
- Super-resolution

BiaPy: Bioimage analysis pipelines in Python

BiaPy

BiaPy is an open source ready-to-use all-in-one library that provides a large variety of bioimage analysis tasks, including 2D image segmentation, object detection, image denoising, single cell analysis and image classification.

BiaPy is a versatile platform designed to accommodate users less experienced in programming. It offers diverse workflows.

This repository is actively under development by the Biomedical Computer Vision group at the University of the Basque Country and the Donostia International Physics Center.

Find a comprehensive overview of BiaPy and its functionality in the following videos:

BiaPy Documentation Tutorials Github About

Bioimage analysis pipelines in Python

Latest release notes

NEWS Check out our last [bioRxiv preprint!](#)

GUI COLAB NOTEBOOKS DOCKER COMMAND LINE

Download

Get Additional Installers

🐧 | 🍏

Please install **Docker** to use the GUI following [these instructions](#).

Find a instructions on how to use the GUI in [this video](#).

Workflow information

Semantic Segmentation

Input image: Ground truth:

The goal of this workflow is to assign a class to each pixel of the input image.

- Input:**
 - Image.
- Output:**
 - Class mask where each pixel is labeled with an integer representing a class.

* Image with the probability of being part of each class.

In the figure above an example of this workflow's **Input** is depicted. This image is a wound of a *Drosophila* embryo and the goal is to segment the contour of that wound correctly. There, only two labels are present in the result. Black pixels, with value 0, represent the background and white ones the contour of the wound, labeled with 1.

The output is a map that only two classes are present, as in this example, it'll be an image where each pixel will have the probability of being of class 1.

Graphical user interface

The screenshot displays the B i a P y graphical user interface. On the left is a blue sidebar with navigation options: Home, Workflow, Generic options, Train, Test, and Run Workflow. The main area features a top header with the B i a P y logo and version information (3.2.0 - GUI: 1.0.0). Below this is an 'External links' section with icons for Project page, Forum, Documentation, Templates, Notebooks, and Citation. The central part of the interface shows two dependency check boxes: 'Docker dependency' with the Docker logo and the text 'Docker installation found', and 'GPU dependency' with a GPU icon and the text '2 NVIDIA GPU cards found'. At the bottom, there are three blue buttons: 'Create new workflow', 'Load and modify workflow', and 'Run workflow'.

BioImage Model Zoo

The screenshot shows the BioImage Model Zoo website. At the top left is the logo "BioImage.IO" with a giraffe icon. On the top right are navigation links: "+ Upload", "Documentation", and "About". The main header area has a blue background with the title "BioImage Model Zoo" and the subtitle "Advanced AI models in one-click". Below this, there are four lines of text: "Integrated with Fiji, Ilastik, ImJoy and more", "Try model instantly with BioEngine", "Contribute your models via Github", and "Link models to datasets and applications". A button labeled "Explore the Zoo" with a rocket icon is positioned below the text. To the right of the text is a low-poly illustration of a savanna scene with a giraffe, a bear, a tree, and rocks. Below the main header is a "Community Partners" section featuring a row of logos: #ZeroCostDL4Mic, a red and white pattern, a blue square with a white 'M', a blue smiley face, a hand holding a flag, three grey hexagons, a red and green circular logo, a magnifying glass over a globe, a yellow star with "DL4MIC" text, a boat with people, a globe with "DL4MicEverywhere" text, and a blue plus sign. Below the partners is a navigation bar with tabs for "All", "models", "applications", and "datasets". A search bar contains the text "Type a keyword and press enter". To the right of the search bar are "Tags & Filters" and a grid icon. At the bottom, there are four preview cards showing various biological images and icons.

BioImage.IO

+ Upload Documentation About

BioImage Model Zoo

Advanced AI models in one-click

Integrated with Fiji, Ilastik, ImJoy and more
Try model instantly with BioEngine
Contribute your models via Github
Link models to datasets and applications

Explore the Zoo

Community Partners

#ZeroCostDL4Mic

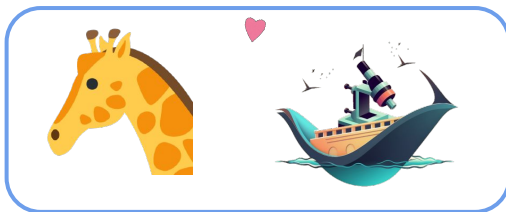
DL4MicEverywhere






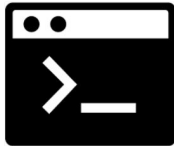

All models applications datasets

Type a keyword and press enter

Tags & Filters

BiImage Model Zoo (2)



| | GRAPHICAL USER INTERFACE  | GOOGLE COLAB  | NOTEBOOKS  | CONTAINERS  Docker  Singularity | TERMINAL  |
|---------------|---|---|---|--|---|
| |  | | | | |
| | NON-EXPERT USER | | | | EXPERT USER |
| Import models | ongoing | ✓ | | ongoing | ✓ |
| Export models | ongoing | ✓ | | ongoing | ✓ |

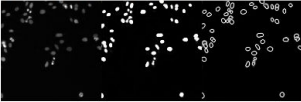
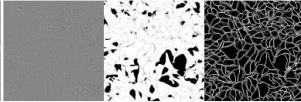
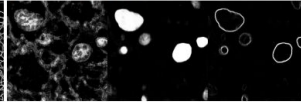
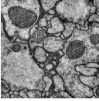

BiImage Model Zoo (3)

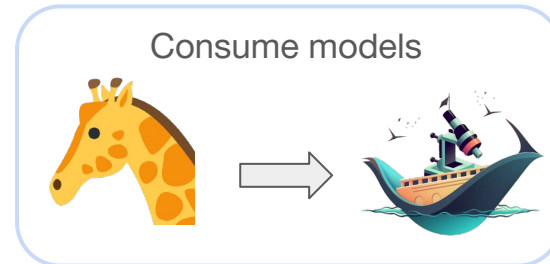
OPTIONAL: Check BiImage Model Zoo (BMZ) models compatible with BiaPy
Use this option if you want to load a pretrained model from BMZ and want to generate a full list of the compatible models with BiaPy.
Important: First you will need to run the next cell and select "BiImage Model Zoo" as the source of the model. Then, paste the DOI into the created field.

BiImage.IO

[Mostrar código](#)

List of models that can be used in BiaPy:

| | | |
|--|--|--|
| NucleiSegmentationBoundaryModel affable-shark (🐋) DOI: 10.5281/zenodo.5764892/6647674 | LiveCellSegmentationBoundaryModel hiding-tiger (🐅) DOI: 10.5281/zenodo.5869899/6647688 | EnhancerMitochondriaEM2D hiding-blowfish (🐡) DOI: 10.5281/zenodo.6406756/6811922 |
|  |  |  |
| MitochondriaEMSegmentation2D shivering-raccoon (🦝) DOI: 10.5281/zenodo.6406803/6406804 | EnhancerBoundaryEM2D amiable-crocodile (🐊) DOI: 10.5281/zenodo.8142283/8171247 | |
|  |  | |



▶ Play to select the source to build the model (BiaPy, Torchvision or BiImage Model Zoo)

[Mostrar código](#)

 Source: BiaPy Torchvision BiImage Model Zoo

DOI:

Biolmage Model Zoo (4)

▼ **Export your model to Biolmage Model Zoo format:**

If you want to export the model into the [Biolmage Model Zoo](#) format, fill the metadata and run the following cell. After the cell is run a `trained_model_name.bmz.zip` file will be downloaded.

🔘 **Construct model's metadata to export it to the Biolmage Model Zoo format. Choose just one option:**

Option 1: Reuse previous Biolmage Model Zoo model configuration

With this option, if you were using a model from Biolmage Model Zoo you can select this option to reuse its configuration instead of provide all fields manually. If that's not the case and you try to use this option an error will be thrown.

`reuse_previous_bmz_model_config:`

Option 2: Manual export fields

With this option you need to introduce manually the metadata of the model.

`trained_model_name:`

`trained_model_authors:`

`trained_model_authors_affiliation:`

`trained_model_description:`

`trained_model_license:`

`trained_model_references:`

`trained_model_references_DOI:`

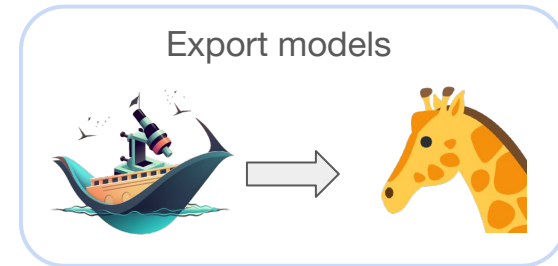
`trained_model_tags:`

`trained_model_documentation:`

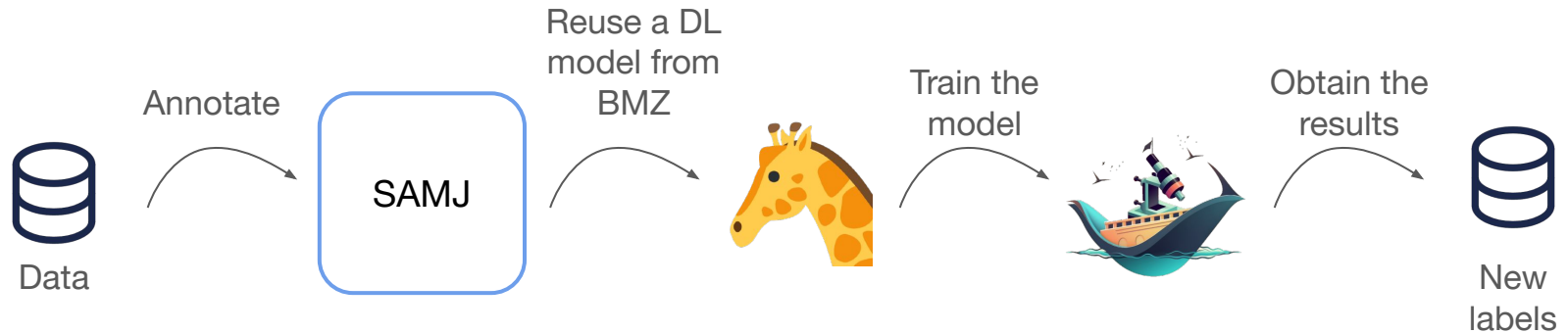
[Mostrar código](#)

🔘 **Play to download a zip file with your [Biolmage Model Zoo](#) exported model**


[Mostrar código](#)















Possible real pipeline



This is us!

 BiaPy [Documentation](#) [Tutorials](#) [Github](#) [About](#)

Meet our team

| | | | | | |
|--|---|---|--|---|--|
|  <p>Ignacio Arganda-Carreras</p> <p>Supervision, Implementation</p> |  <p>Daniel Franco-Barranco</p> <p>Creator, Implementation, Software design</p> |  <p>Pedro Javier Gómez Gálvez</p> <p>Implementation, Supervision</p> |  <p>Jesús Ángel Andrés-San Román</p> <p>Implementation</p> |  <p>Donglai Wei</p> <p>Supervision</p> |  <p>Lenka Backová</p> <p>Implementation</p> |
|  <p>Aitor Gonzalez-Marfil</p> <p>Implementation</p> |  <p>Arrate Muñoz-Barrutia</p> <p>Supervision</p> |  <p>Luis M. Escudero</p> <p>Supervision</p> |  <p>Iván Hidalgo Cenalmor</p> <p>Implementation</p> |  <p>Anatole Chessel</p> <p>Supervision</p> |  <p>Clément Caporal</p> <p>Implementation</p> |

Thank you so much for your attention!