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CENTER FOR SCALABLE DATA ANALYTICS AND ARTIFICIAL INTELLIGENCE

Python: File handling & Image Visualization

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SACHSEN

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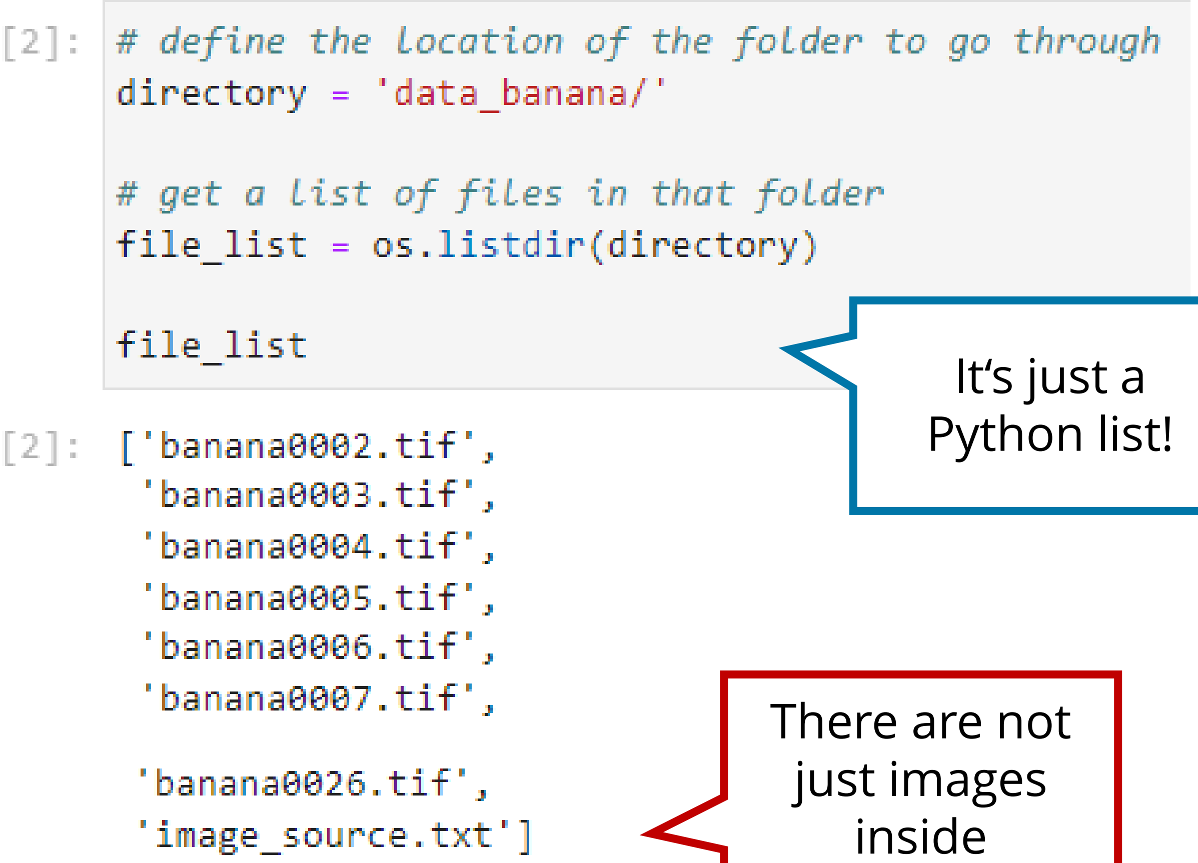
TECHNISCHE UNIVERSITÄT DRESDEN

UNIVERSITÄT LEIPZIG

Working with files in folders

Key-skill when it comes to automating data analysis tasks



```
[2]: # define the location of the folder to go through
     directory = 'data_banana/'

     # get a list of files in that folder
     file_list = os.listdir(directory)

     file_list
```

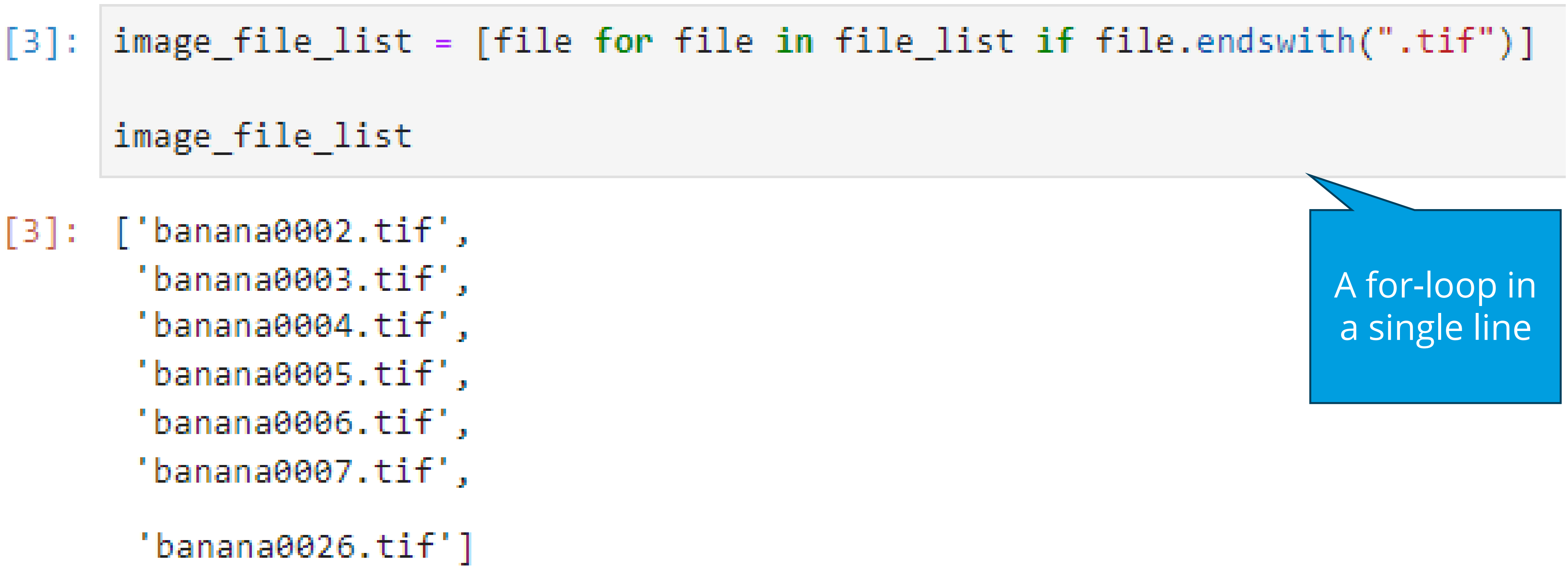
```
[2]: ['banana0002.tif',
      'banana0003.tif',
      'banana0004.tif',
      'banana0005.tif',
      'banana0006.tif',
      'banana0007.tif',

      'banana0026.tif',
      'image_source.txt']
```

It‘s just a Python list!

There are not just images inside

Filtering file lists

To focus on image data, we need to filter the file list



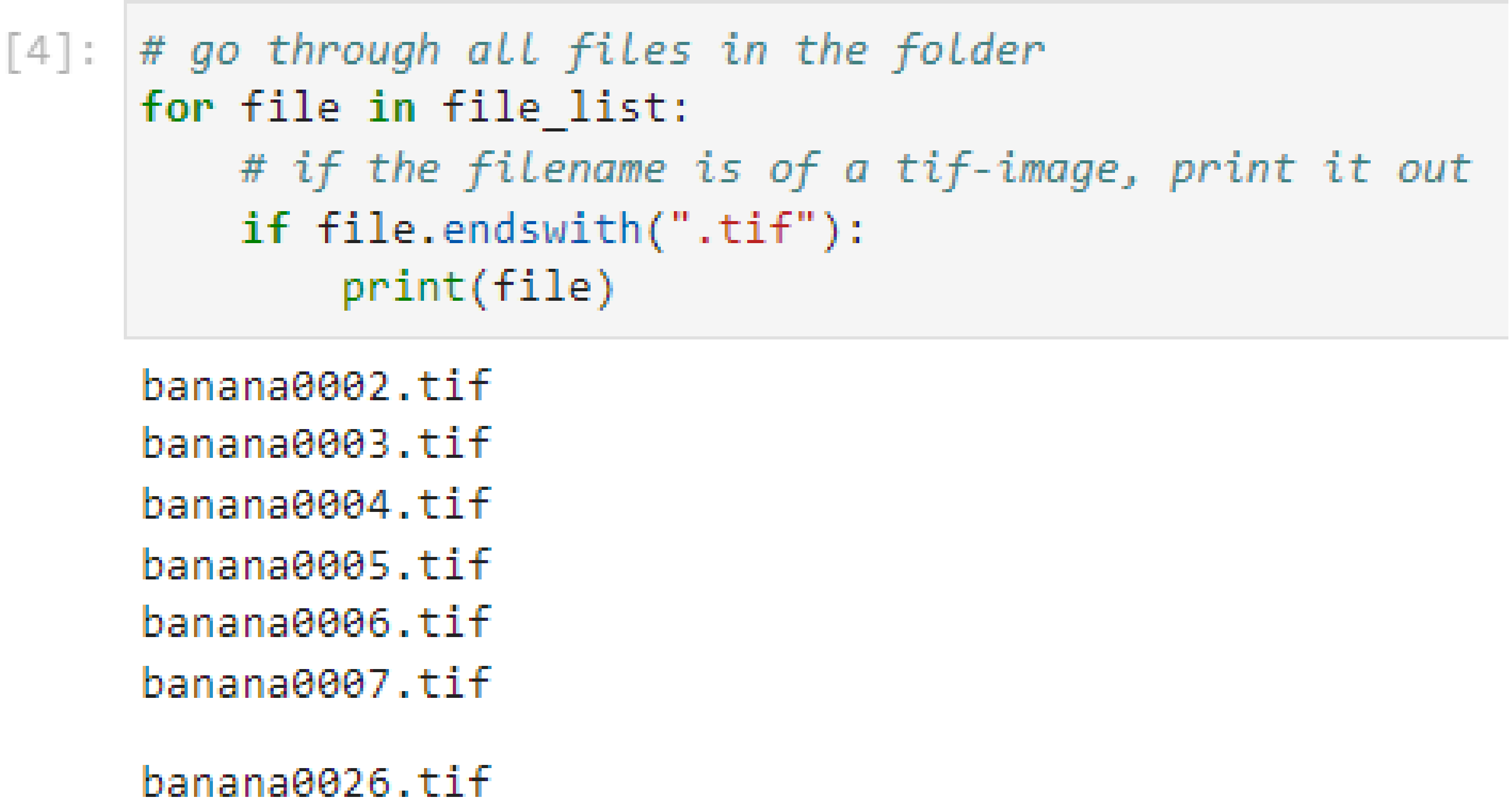
```
[3]: image_file_list = [file for file in file_list if file.endswith(".tif")]

     image_file_list
```

```
[3]: ['banana0002.tif',
      'banana0003.tif',
      'banana0004.tif',
      'banana0005.tif',
      'banana0006.tif',
      'banana0007.tif',

      'banana0026.tif']
```

A for-loop in a single line

Filtering file lists

To focus on image data, we need to filter the file list

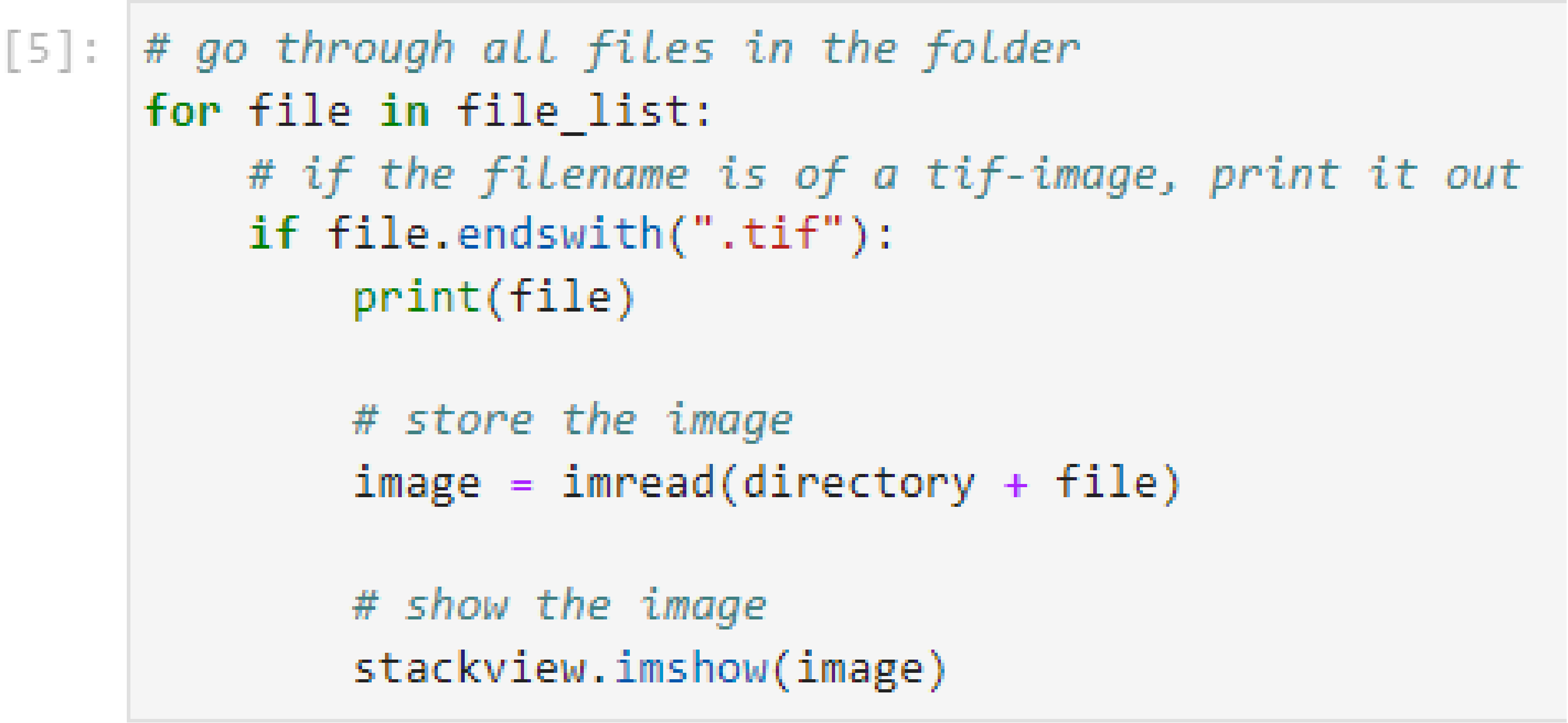


```
[4]: # go through all files in the folder
     for file in file_list:
         # if the filename is of a tif-image, print it out
         if file.endswith(".tif"):
             print(file)
```

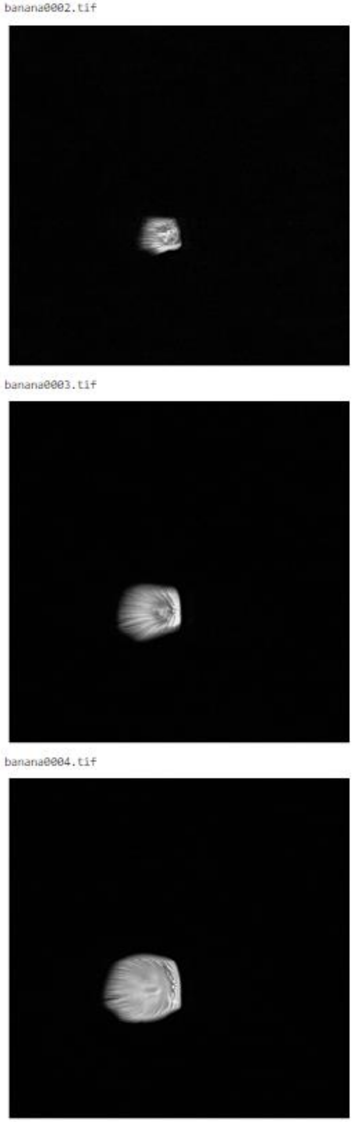
```
banana0002.tif
banana0003.tif
banana0004.tif
banana0005.tif
banana0006.tif
banana0007.tif

banana0026.tif
```

Filtering file lists

To focus on image data, we need to filter the file list



```
[5]: # go through all files in the folder
     for file in file_list:
         # if the filename is of a tif-image, print it out
         if file.endswith(".tif"):
             print(file)

             # store the image
             image = imread(directory + file)

             # show the image
             stackview.imshow(image)
```

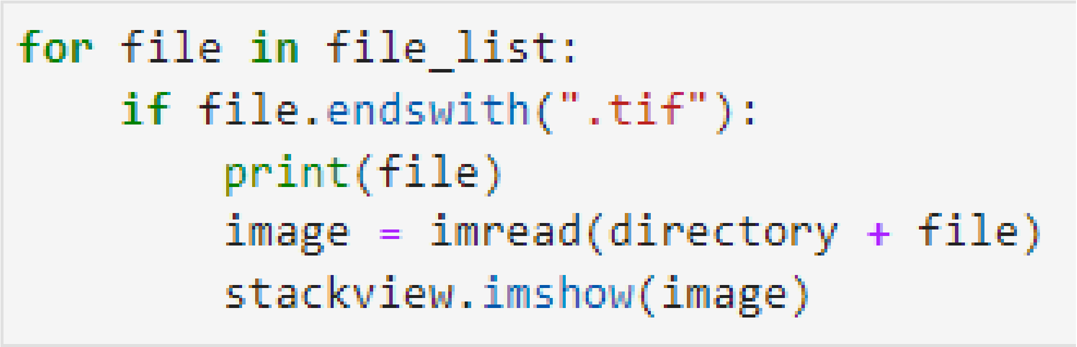


```
banana0002.tif
banana0003.tif
banana0004.tif
```

Side note: comments

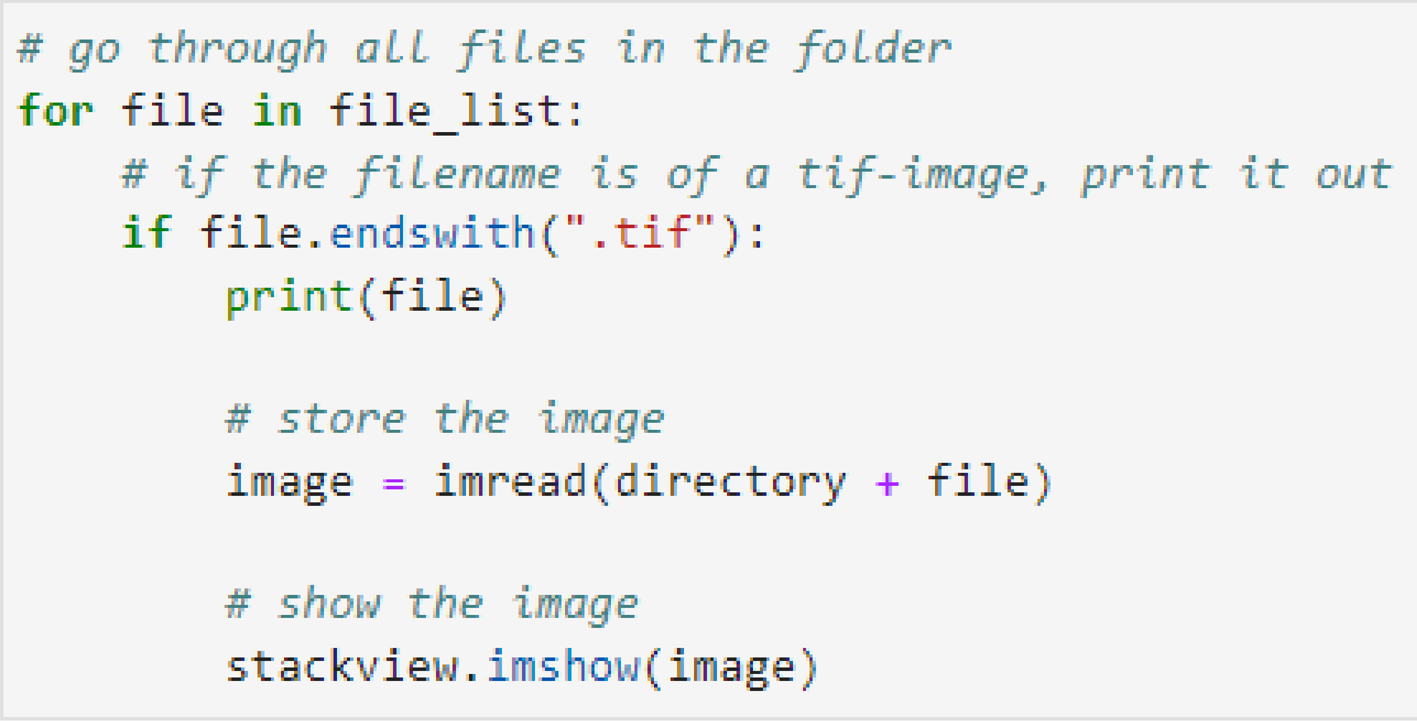
Your code will become longer… Consider structuring it and putting comments and empty lines in between.

✗



```
for file in file_list:
    if file.endswith(".tif"):
        print(file)
        image = imread(directory + file)
        stackview.imshow(image)
```

✓

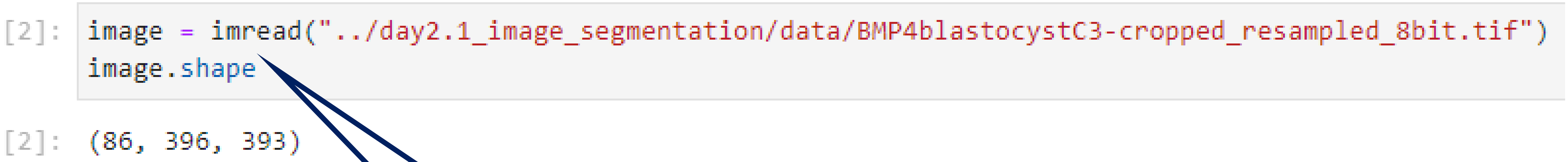


```
# go through all files in the folder
for file in file_list:
    # if the filename is of a tif-image, print it out
    if file.endswith(".tif"):
        print(file)

        # store the image
        image = imread(directory + file)

        # show the image
        stackview.imshow(image)
```

Image visualization

In Python there are many ways to visualize image data.
We focus on Jupyter Notebook compatible ways for now.

Before visualizing image data, get an idea about the dataset.



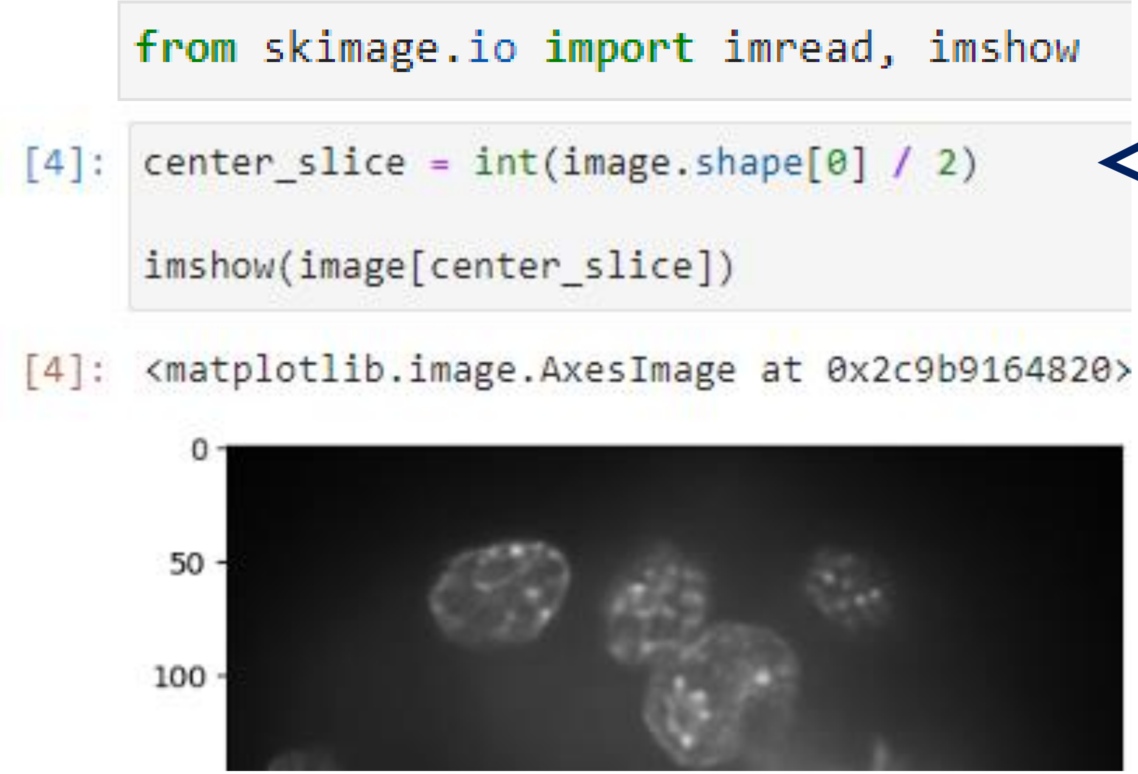
```
[2]: image = imread("../day2.1_image_segmentation/data/BMP4blastocystC3-cropped_resampled_8bit.tif")
     image.shape

[2]: (86, 396, 393)
```

Image.shape tells you the dimensions of an image

Not all image viewers support 3D data

Image visualization

scikit-image‘s `imshow()` (originating from matlab) can only visualize 2 dimensions.



```
from skimage.io import imread, imshow
```

```
[4]: center_slice = int(image.shape[0] / 2)

     imshow(image[center_slice])
```

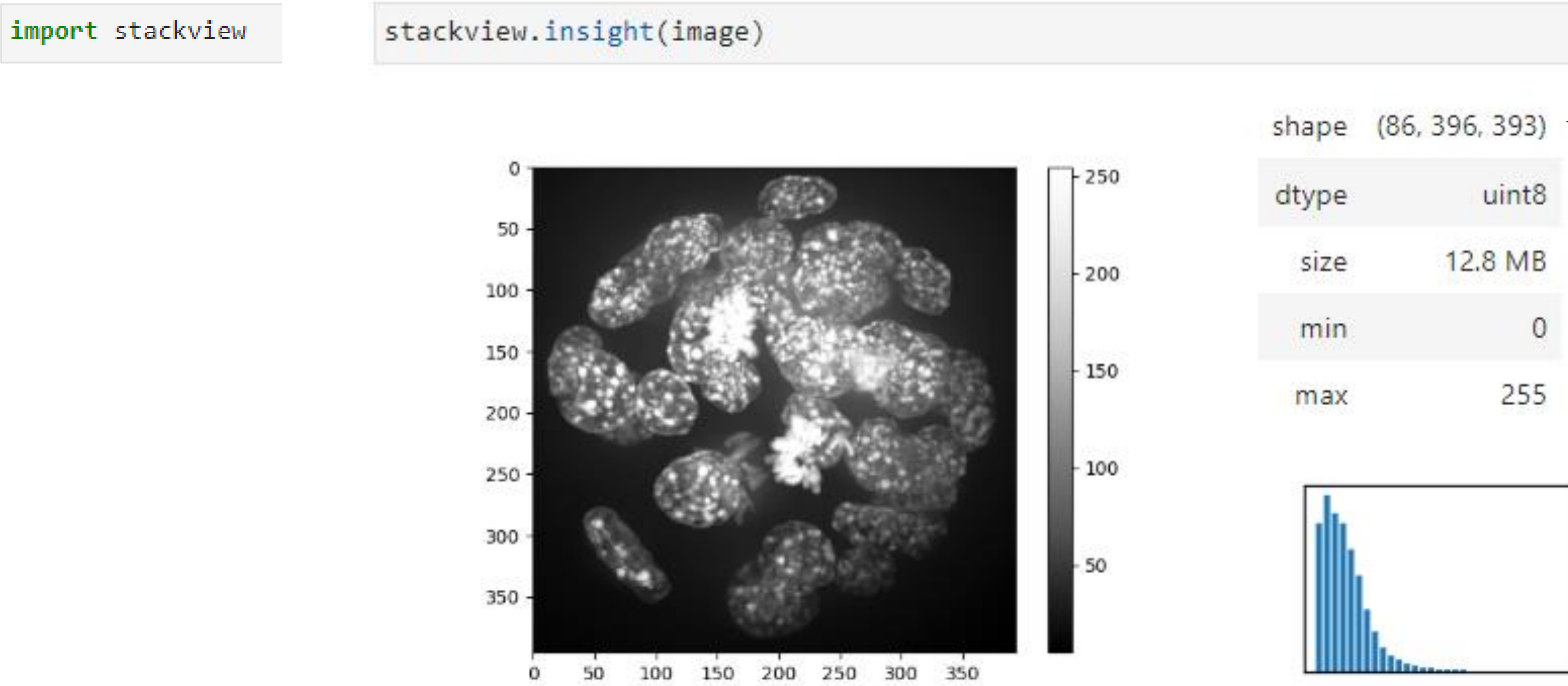
```
[4]: <matplotlib.image.AxesImage at 0x2c9b9164820>
```

The first shape-dimension – 2 is the center plane in Z

Image data in Python is commonly organized in Z-Y-X dimension order.

Image visualization

Stackview can show 3D images (by applying a projection along Z)



```
import stackview
```

```
stackview.insight(image)
```

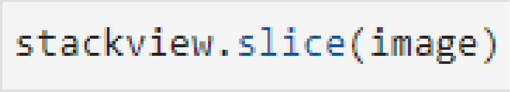
shape	(86, 396, 393)
dtype	uint8
size	12.8 MB
min	0
max	255

dimensions

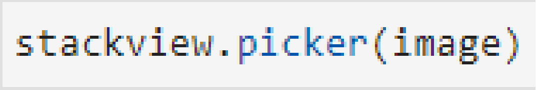
Basic statistics

Image visualization

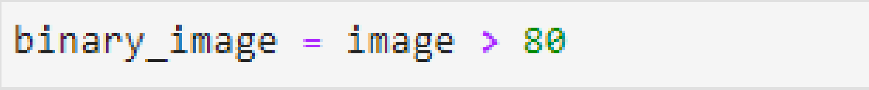
Stackview also has some interactive tools



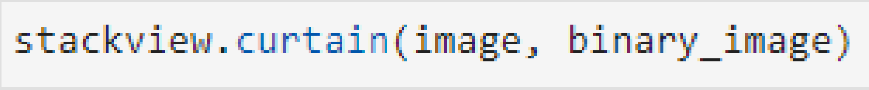
```
stackview.slice(image)
```



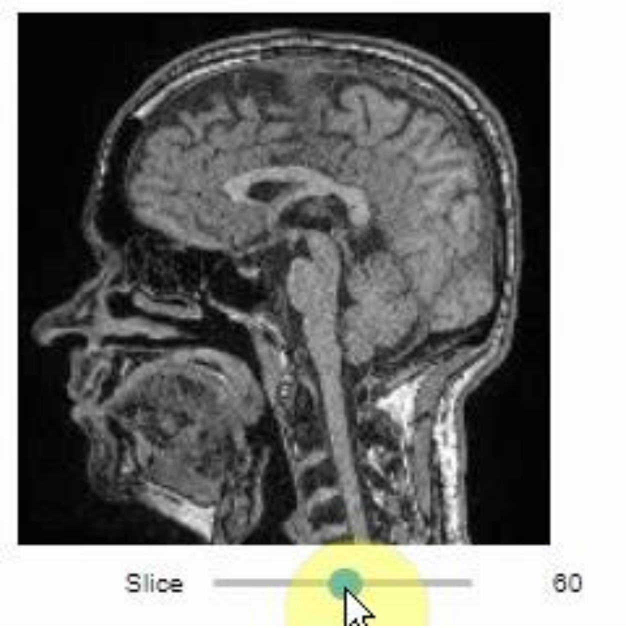
```
stackview.picker(image)
```

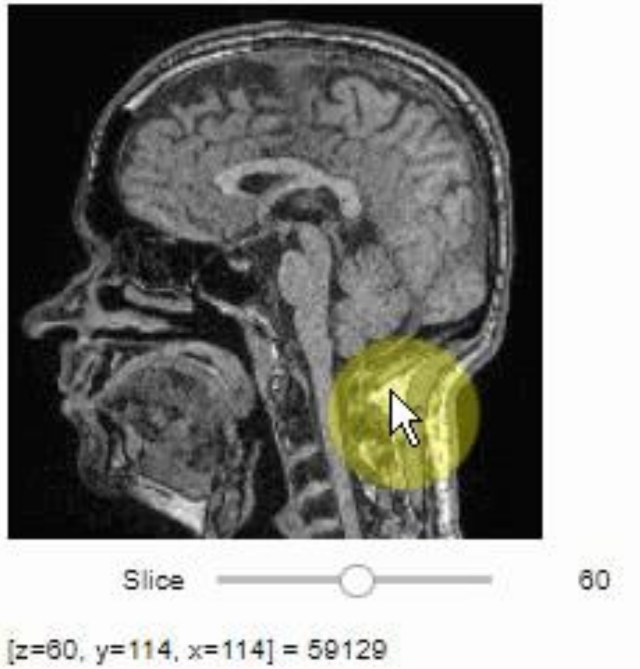


```
binary_image = image > 80
```



```
stackview.curtain(image, binary_image)
```





```
[z=60, y=114, x=114] = 59129
```

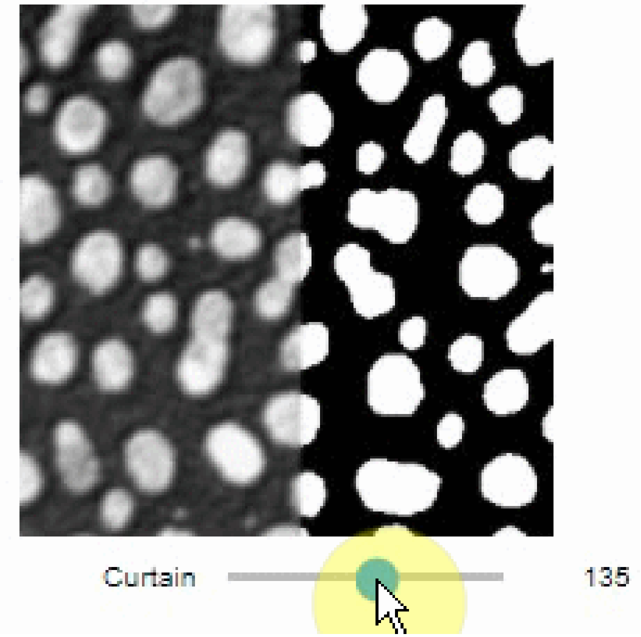
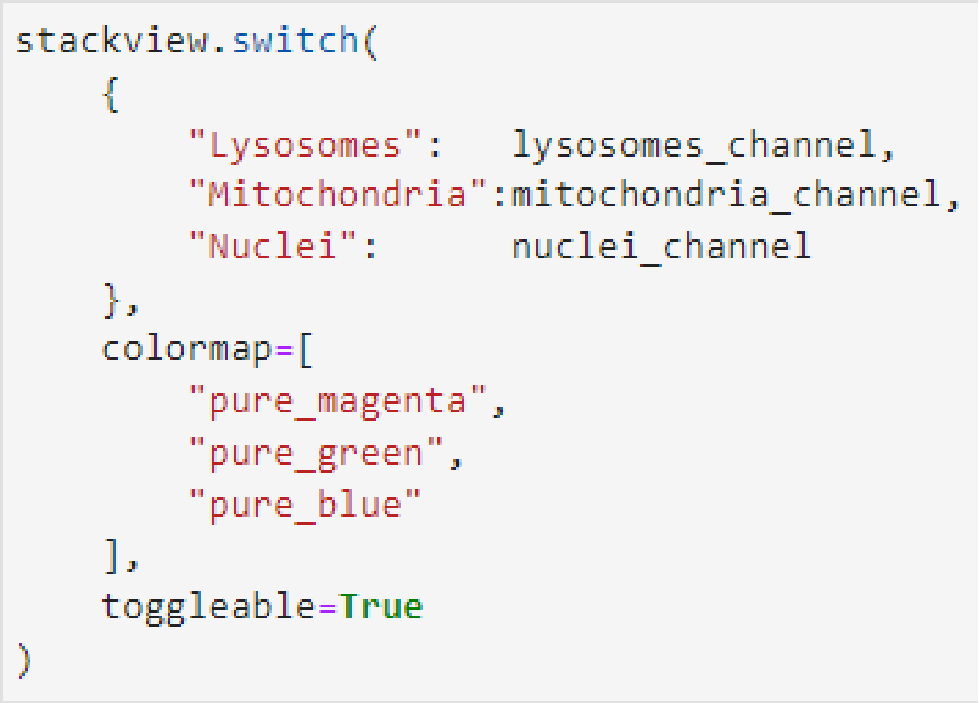
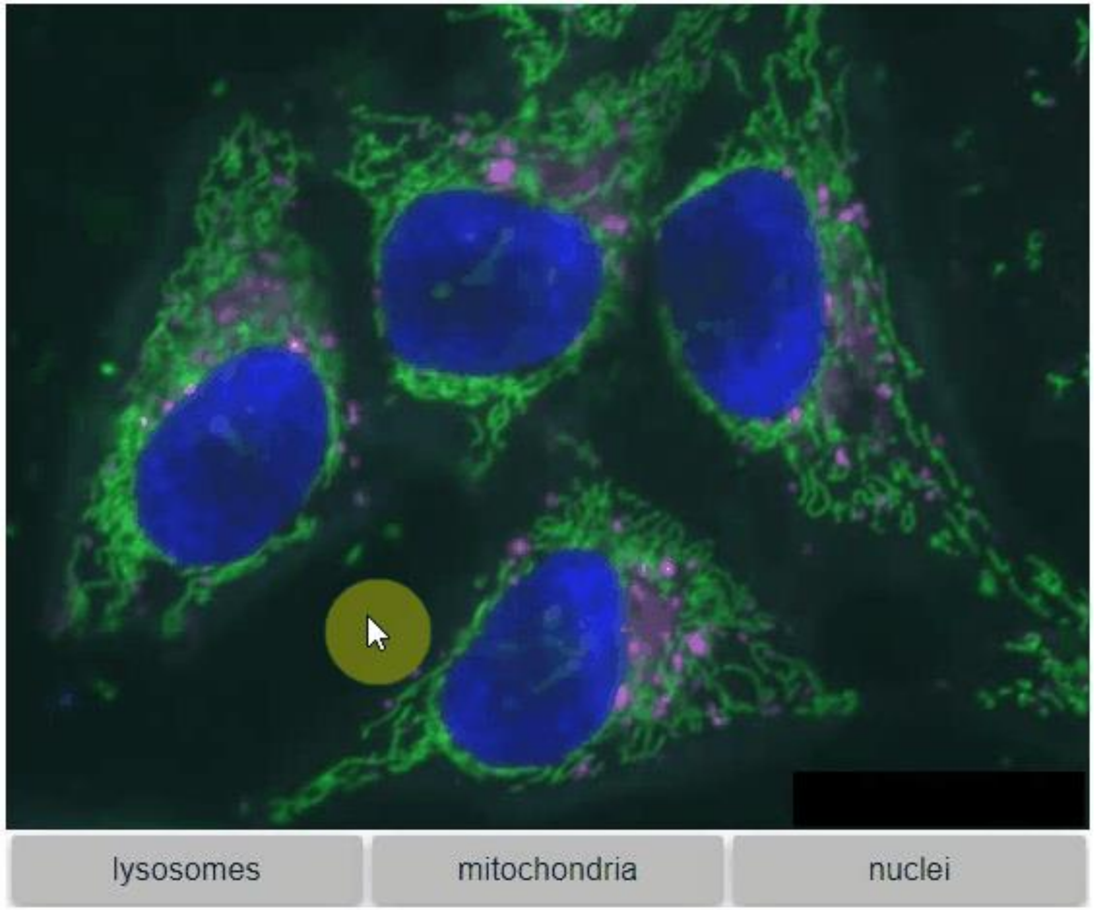


Image visualization

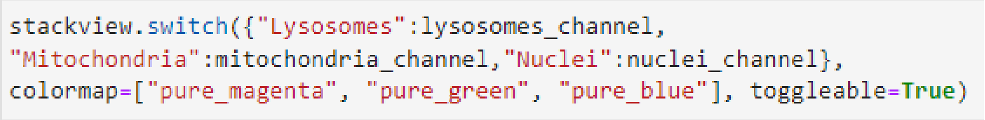
Stackview also has some interactive tools



```
stackview.switch(
    {
        "Lysosomes":   lysosomes_channel,
        "Mitochondria":mitochondria_channel,
        "Nuclei":      nuclei_channel
    },
    colormap=[
        "pure_magenta",
        "pure_green",
        "pure_blue"
    ],
    toggleable=True
)
```



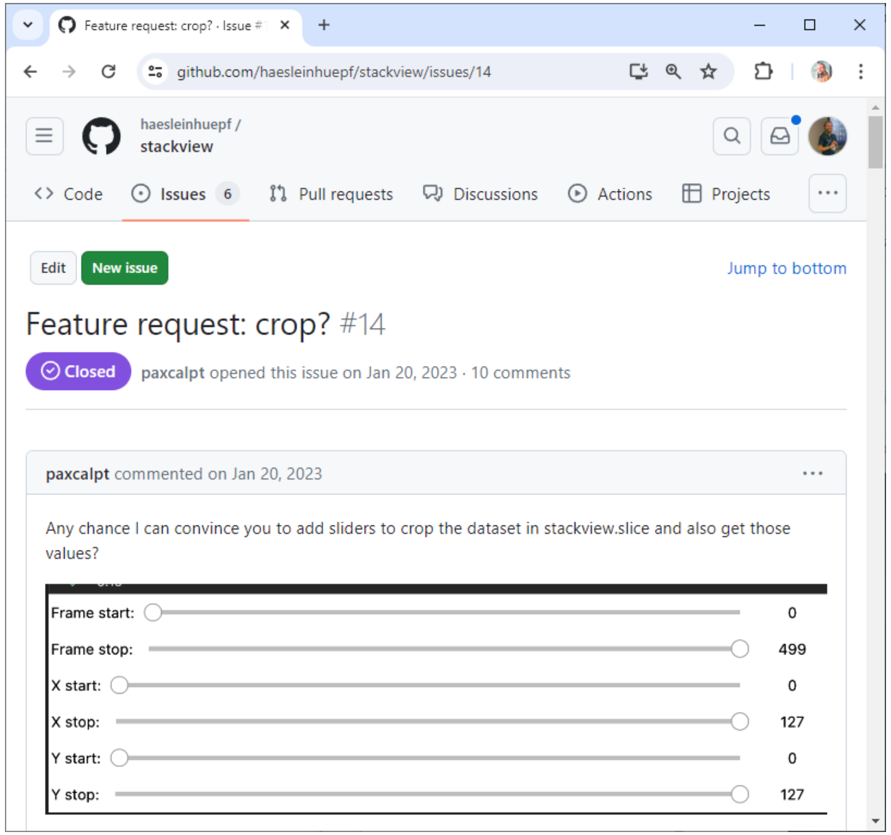
Identical but less readable:



```
stackview.switch({"Lysosomes":lysosomes_channel,
"Mitochondria":mitochondria_channel,"Nuclei":nuclei_channel},
colormap=["pure_magenta", "pure_green", "pure_blue"], toggleable=True)
```

Image Visualization

Stackview is developed for microscopists. If something doesn‘t work as you expect, communicate it :-)



Feature request: crop? #14

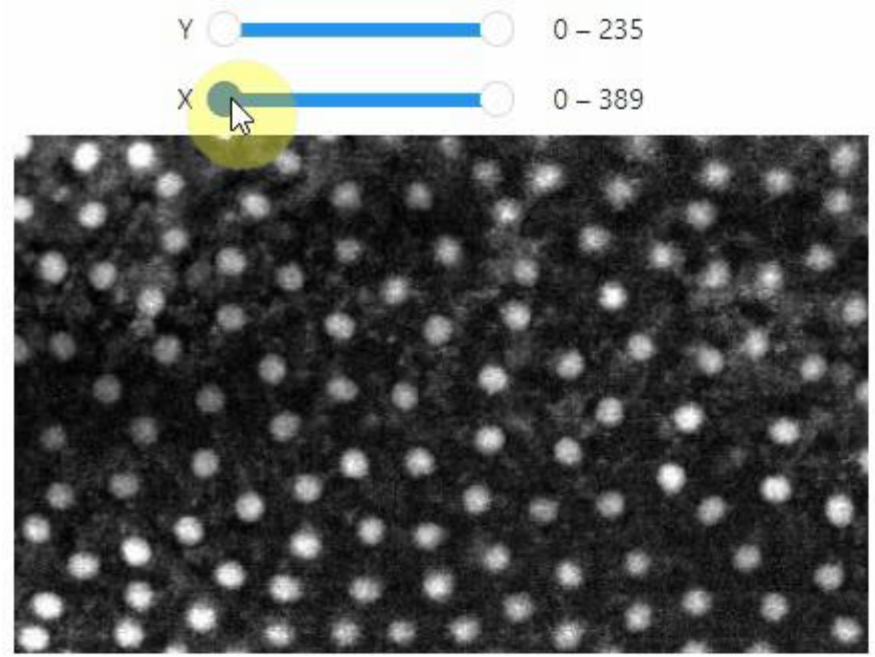
Closed paxcalpt opened this issue on Jan 20, 2023 · 10 comments

paxcalpt commented on Jan 20, 2023

Any chance I can convince you to add sliders to crop the dataset in stackview.slice and also get those values?

Frame start: 0
Frame stop: 499
X start: 0
X stop: 127
Y start: 0
Y stop: 127

```
crop_widget = stackview.crop(image_stack, continuous_update=True)
crop_widget
```

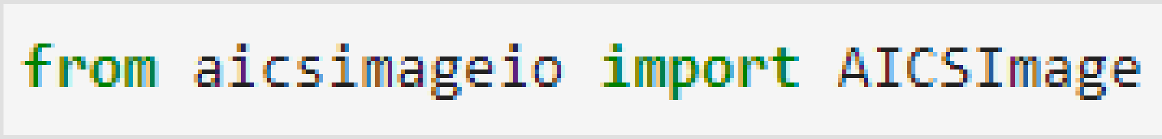


https://github.com/haesleinhuepf/stackview/issues/14

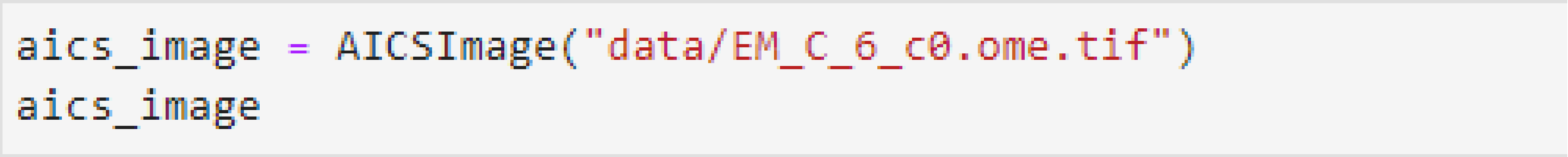
Loading domain-specific file formats

Common Python libraries cannot open file formats such as OME-TIF, CZI, LIF, ND2… Solution: aicsimageio

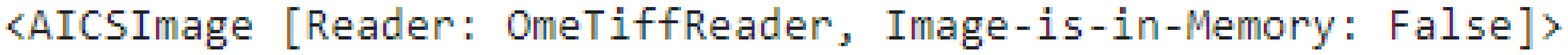
From the Allen Institute for Cell Science



```
from aicsimageio import AICSImage
```



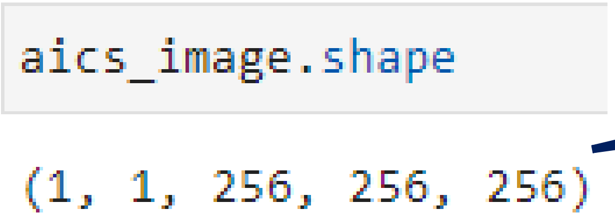
```
aics_image = AICSImage("data/EM_C_6_c0.ome.tif")
aics_image
```



```
<AICSImage [Reader: OmeTiffReader, Image-is-in-Memory: False]>
```

Loading domain-specific file formats

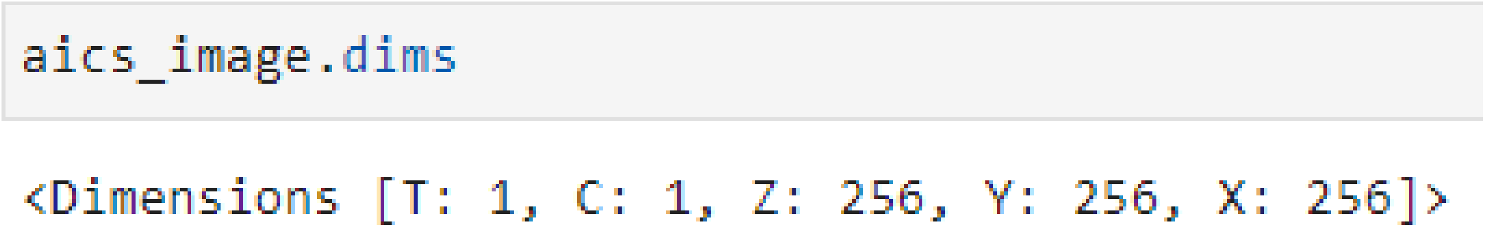
Aicsimageio supports dimension names and physical voxel sizes.



```
aics_image.shape
```

```
(1, 1, 256, 256, 256)
```

What‘s width, height, depth and time?



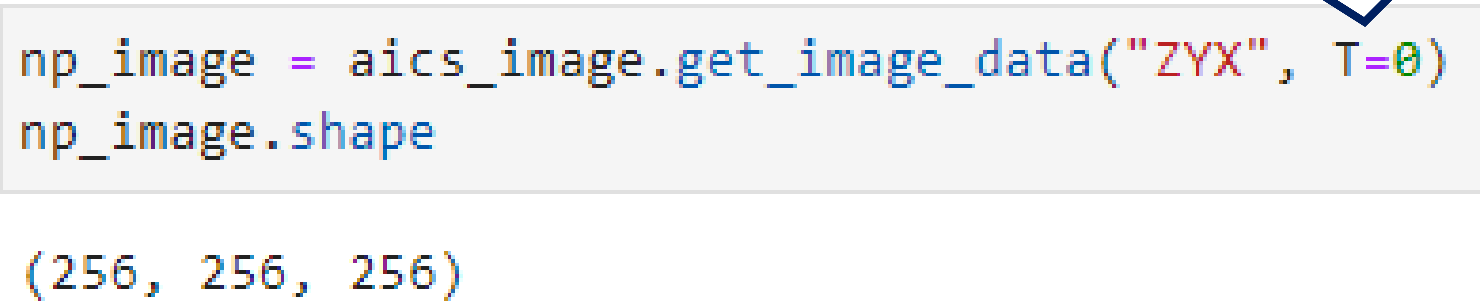
```
aics_image.dims
```

```
<Dimensions [T: 1, C: 1, Z: 256, Y: 256, X: 256]>
```

Key feature when working with big data!

Lazy loading (virtual stacks)

Allows processing files larger than computer memory.

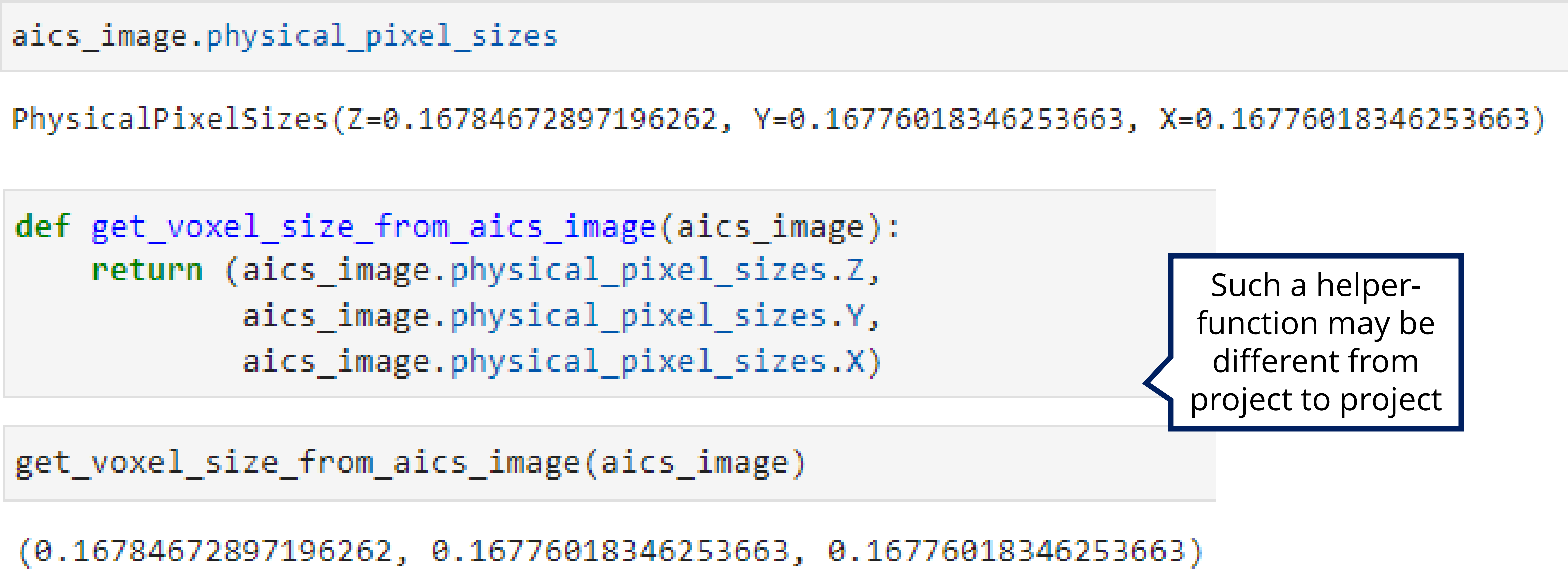


```
np_image = aics_image.get_image_data("ZYX", T=0)
np_image.shape
```

```
(256, 256, 256)
```

Loading domain-specific file formats

Aicsimageio supports dimension names and physical voxel sizes.



```
aics_image.physical_pixel_sizes
```

```
PhysicalPixelSizes(Z=0.16784672897196262, Y=0.16776018346253663, X=0.16776018346253663)
```

```
def get_voxel_size_from_aics_image(aics_image):
    return (aics_image.physical_pixel_sizes.Z,
            aics_image.physical_pixel_sizes.Y,
            aics_image.physical_pixel_sizes.X)
```

```
get_voxel_size_from_aics_image(aics_image)
```

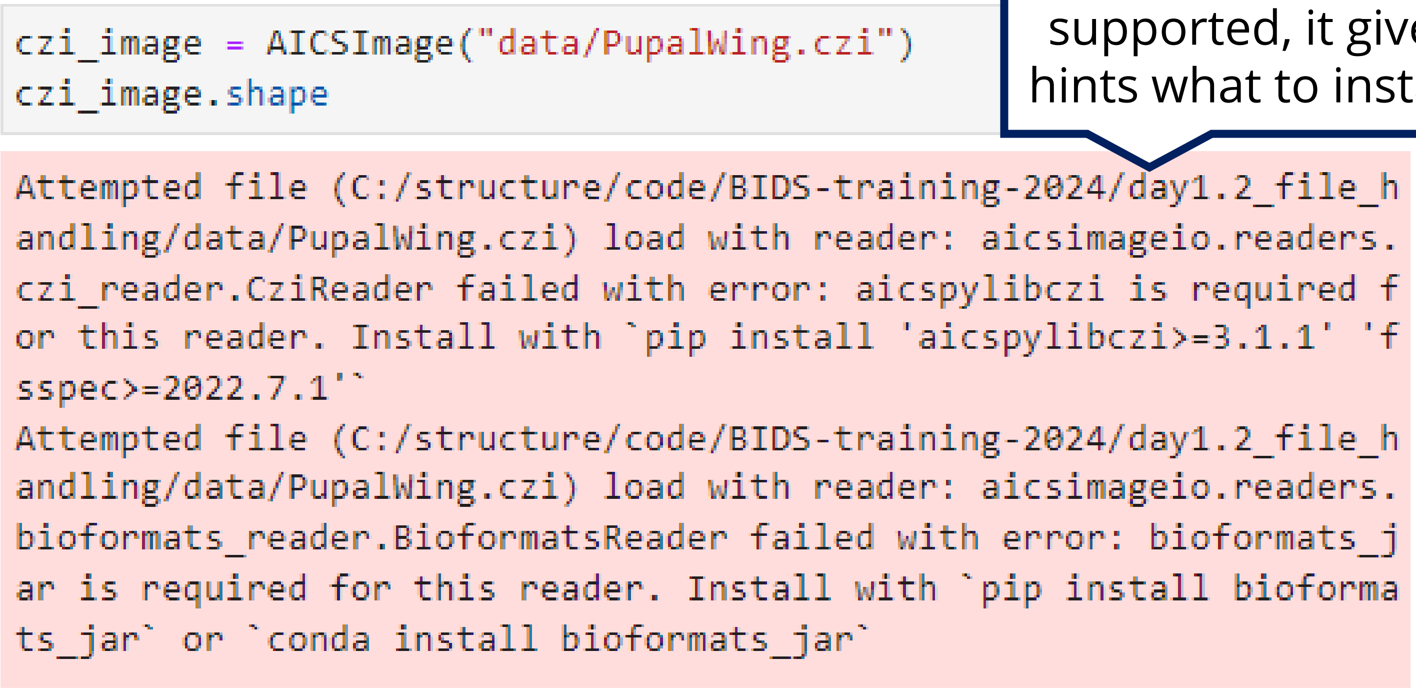
```
(0.16784672897196262, 0.16776018346253663, 0.16776018346253663)
```

Such a helper-function may be different from project to project

Loading domain-specific file formats

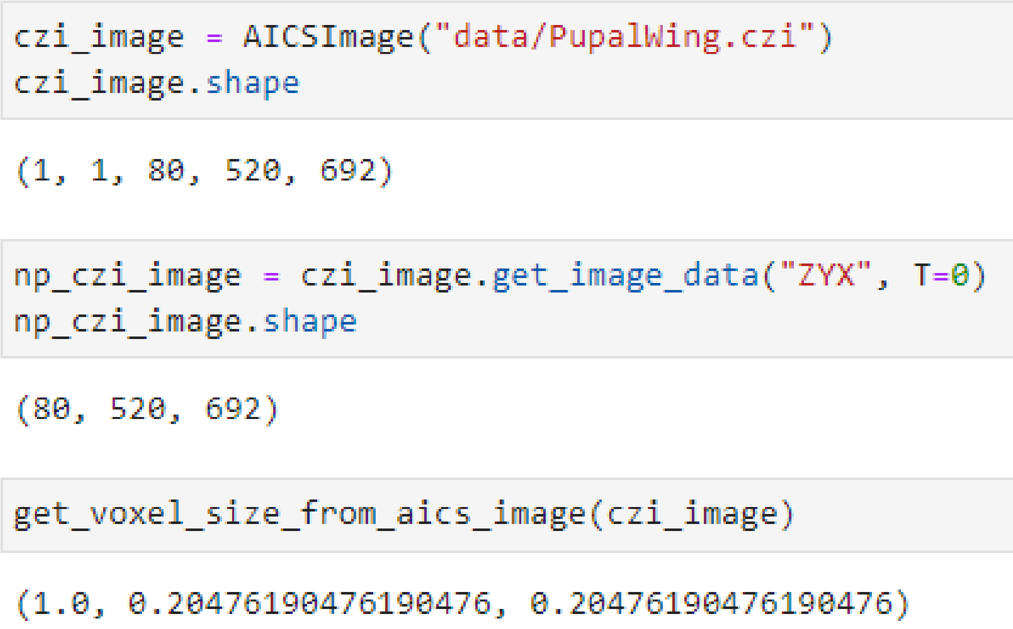
Common Python libraries cannot open file formats such as OME-TIF, CZI, LIF, ND2… Solution: aicsimageio

In case your file format is not supported, it gives hints what to install.



```
czi_image = AICSImage("data/PupalWing.czi")
czi_image.shape
```

```
Attempted file (C:/structure/code/BIDS-training-2024/day1.2_file_h
andling/data/PupalWing.czi) load with reader: aicsimageio.readers.
czi_reader.CziReader failed with error: aicspylibczi is required f
or this reader. Install with `pip install 'aicspylibczi>=3.1.1' 'f
sspec>=2022.7.1'`
Attempted file (C:/structure/code/BIDS-training-2024/day1.2_file_h
andling/data/PupalWing.czi) load with reader: aicsimageio.readers.
bioformats_reader.BioformatsReader failed with error: bioformats_j
ar is required for this reader. Install with `pip install bioforma
ts_jar` or `conda install bioformats_jar`
```



```
czi_image = AICSImage("data/PupalWing.czi")
czi_image.shape
```

```
(1, 1, 80, 520, 692)
```

```
np_czi_image = czi_image.get_image_data("ZYX", T=0)
np_czi_image.shape
```

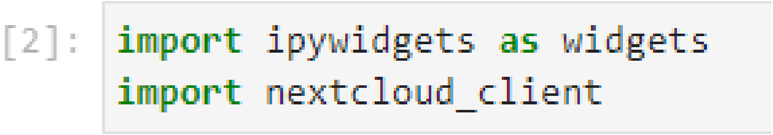
```
(80, 520, 692)
```

```
get_voxel_size_from_aics_image(czi_image)
```

```
(1.0, 0.20476190476190476, 0.20476190476190476)
```

Working with files in the cloud

Example nextcloud / owncloud

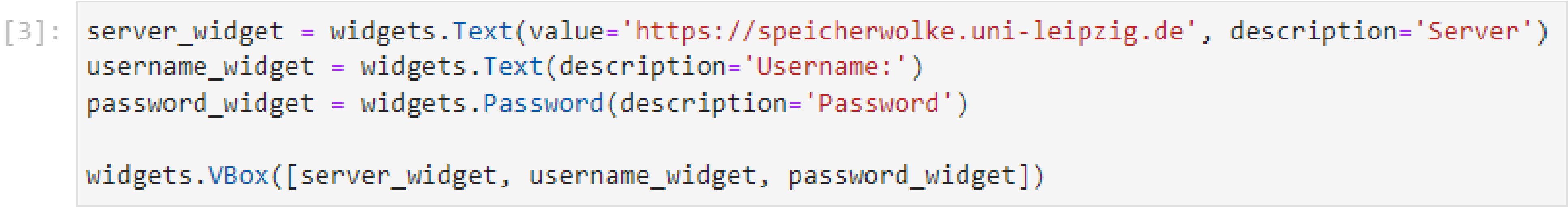


```
[2]: import ipywidgets as widgets
     import nextcloud_client
```

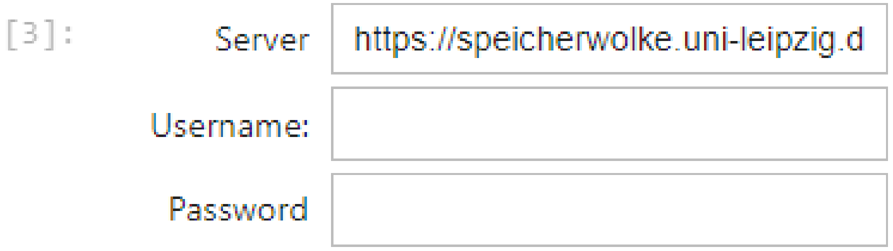
Install another Python library into your environment

```
conda activate devbio-napari-env
pip install pyncclient
```

Login-form



```
[3]: server_widget = widgets.Text(value='https://speicherwolke.uni-leipzig.de', description='Server')
     username_widget = widgets.Text(description='Username:')
     password_widget = widgets.Password(description='Password')

     widgets.VBox([server_widget, username_widget, password_widget])
```



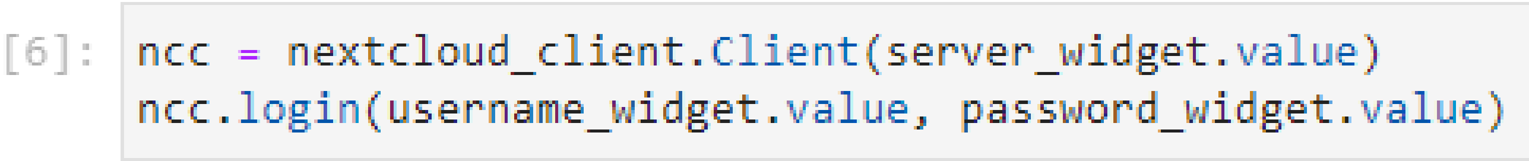
[3]:

Server https://speicherwolke.uni-leipzig.d

Username:

Password

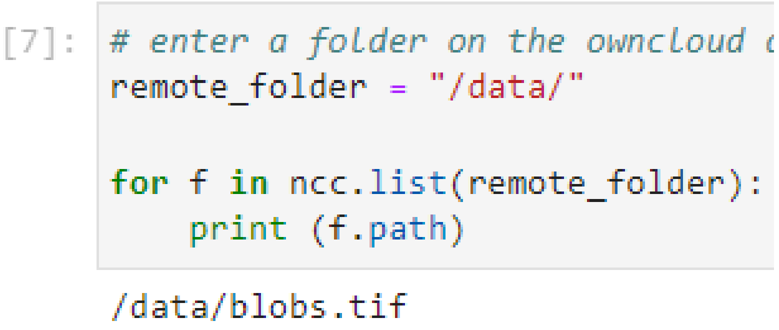
Actually logging in



```
[6]: ncc = nextcloud_client.Client(server_widget.value)
     ncc.login(username_widget.value, password_widget.value)
```

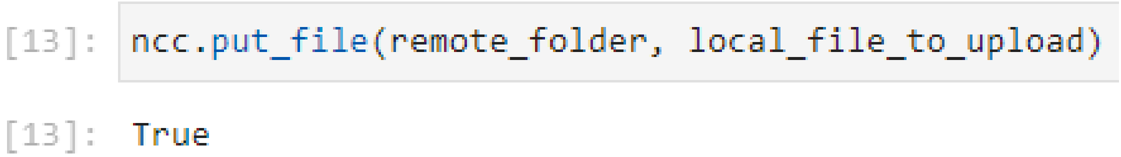
Working with files in the cloud

Listing files in a remote folder



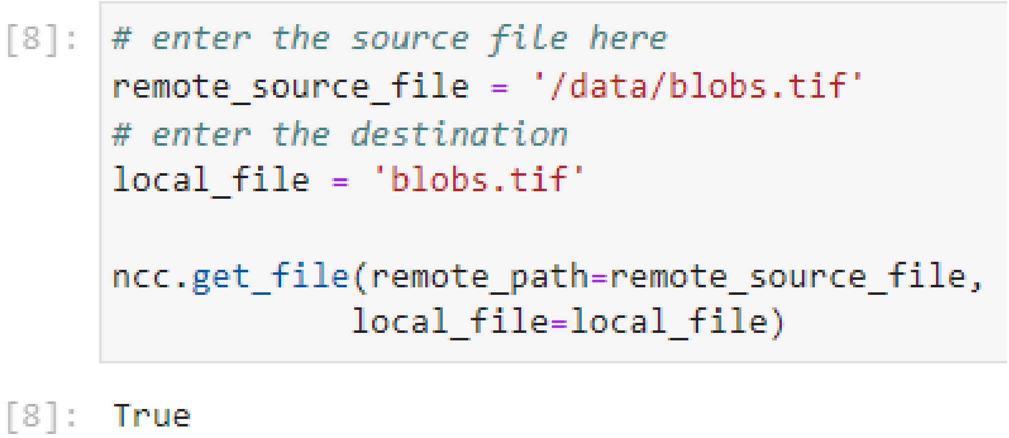
```
[7]: # enter a folder on the owncloud
     remote_folder = "/data/"

     for f in ncc.list(remote_folder):
         print (f.path)

     /data/blobs.tif
```

Uploading a file



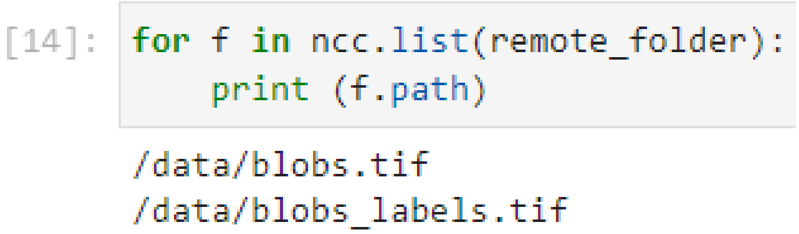
```
[13]: ncc.put_file(remote_folder, local_file_to_upload)

[13]: True
```

Downloading a file



```
[8]: # enter the source file here
     remote_source_file = '/data/blobs.tif'
     # enter the destination
     local_file = 'blobs.tif'

     ncc.get_file(remote_path=remote_source_file,
                  local_file=local_file)

[8]: True
```

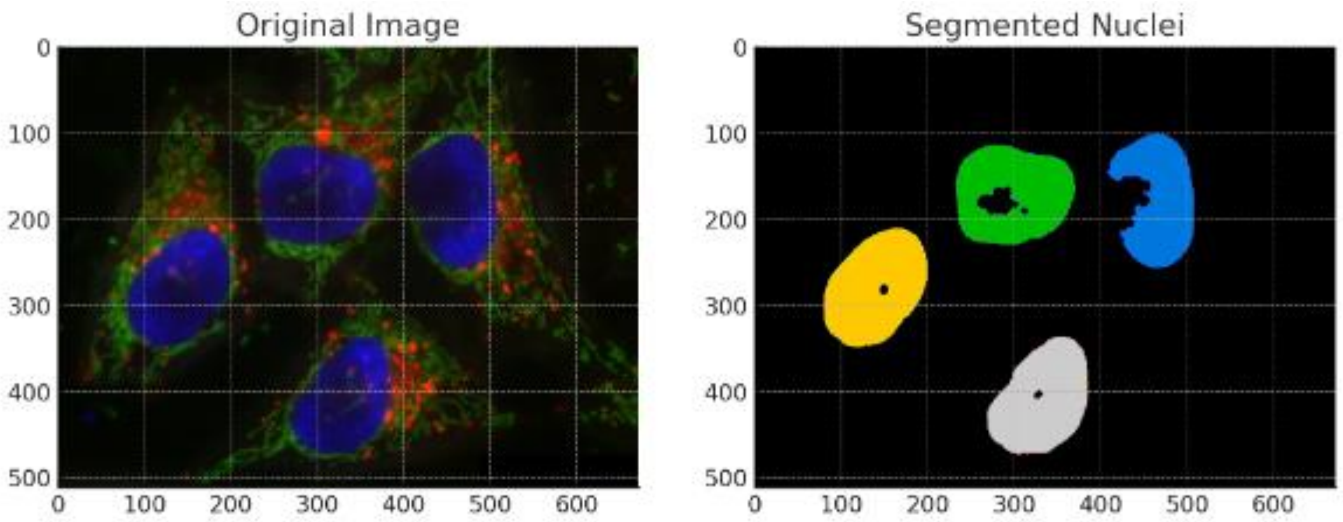
Listing files again



```
[14]: for f in ncc.list(remote_folder):
          print (f.path)

      /data/blobs.tif
      /data/blobs_labels.tif
```

Bio-image Analysis

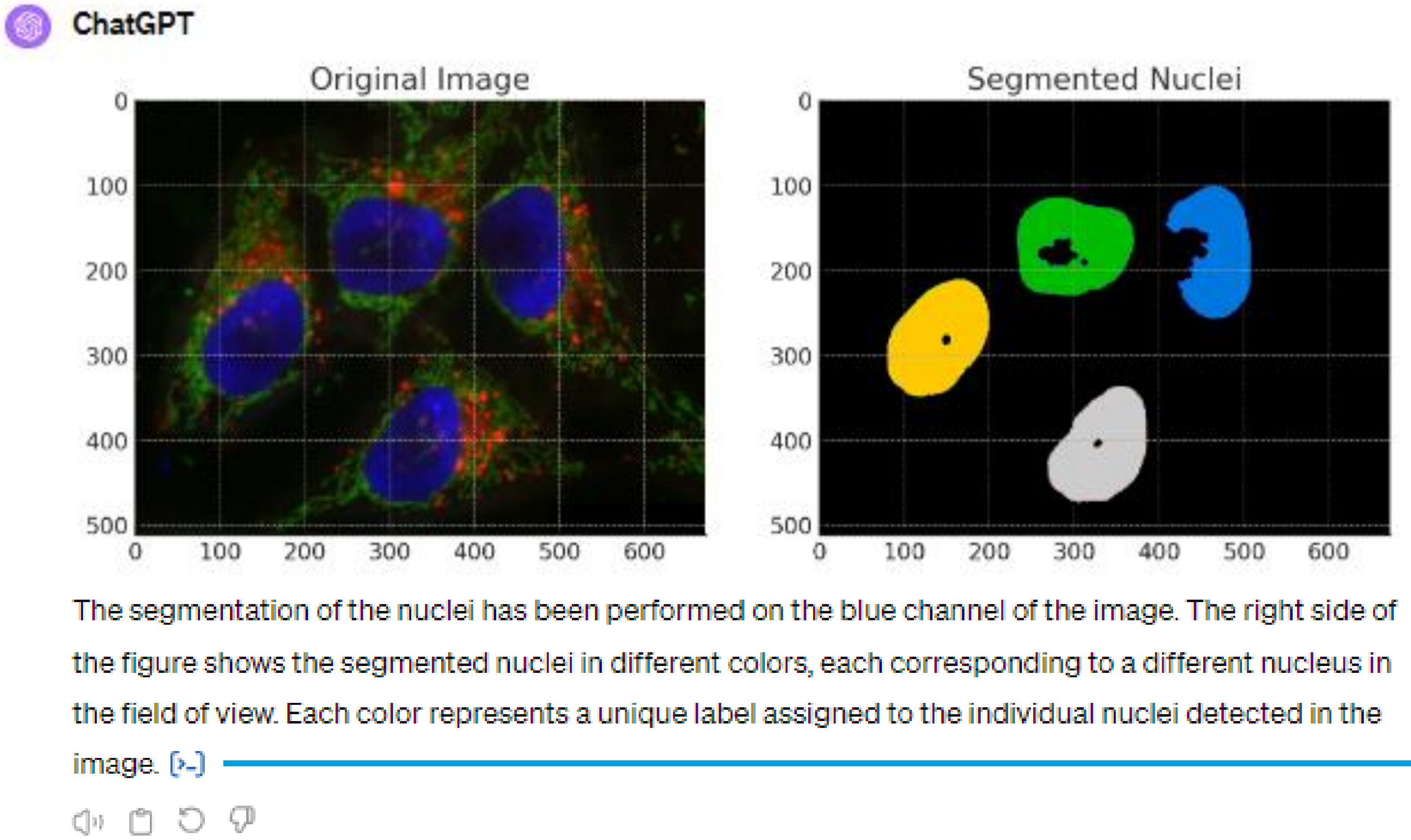
My job …



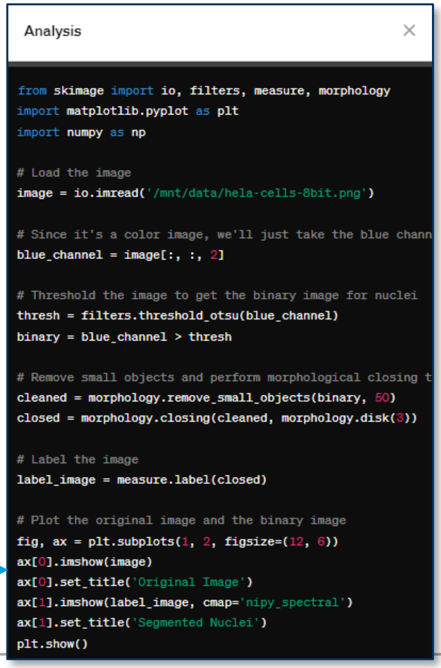
Bio-image Analysis using Large-Language Models

My job is changing, since we have ChatGPT

Prompt:
“Please segment the nuclei in the blue channel of the image”



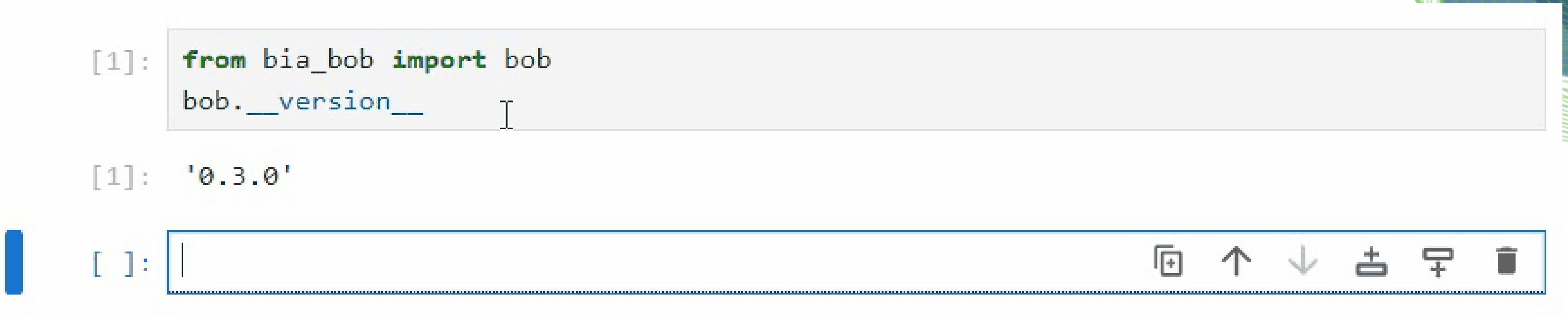
The segmentation of the nuclei has been performed on the blue channel of the image. The right side of the figure shows the segmented nuclei in different colors, each corresponding to a different nucleus in the field of view. Each color represents a unique label assigned to the individual nuclei detected in the image. [>_]



```
from skimage import io, filters, measure, morphology
import matplotlib.pyplot as plt
import numpy as np

# Load the image
image = io.imread('/mnt/data/hela-cells-8bit.png')

# Since it's a color image, we'll just take the blue chann
blue_channel = image[:, :, 2]

# Threshold the image to get the binary image for nuclei
thresh = filters.threshold_otsu(blue_channel)
binary = blue_channel > thresh

# Remove small objects and perform morphological closing t
cleaned = morphology.remove_small_objects(binary, 50)
closed = morphology.closing(cleaned, morphology.disk(3))

# Label the image
label_image = measure.label(closed)

# Plot the original image and the binary image
fig, ax = plt.subplots(1, 2, figsize=(12, 6))
ax[0].imshow(image)
ax[0].set_title('Original Image')
ax[1].imshow(label_image, cmap='nipy_spectral')
ax[1].set_title('Segmented Nuclei')
plt.show()
```

Coding assistance: BiA-Bob

- Open-source alternative to OpenAI's Data Analyst
- No need to upload your [image] data
- Extensible through plugins



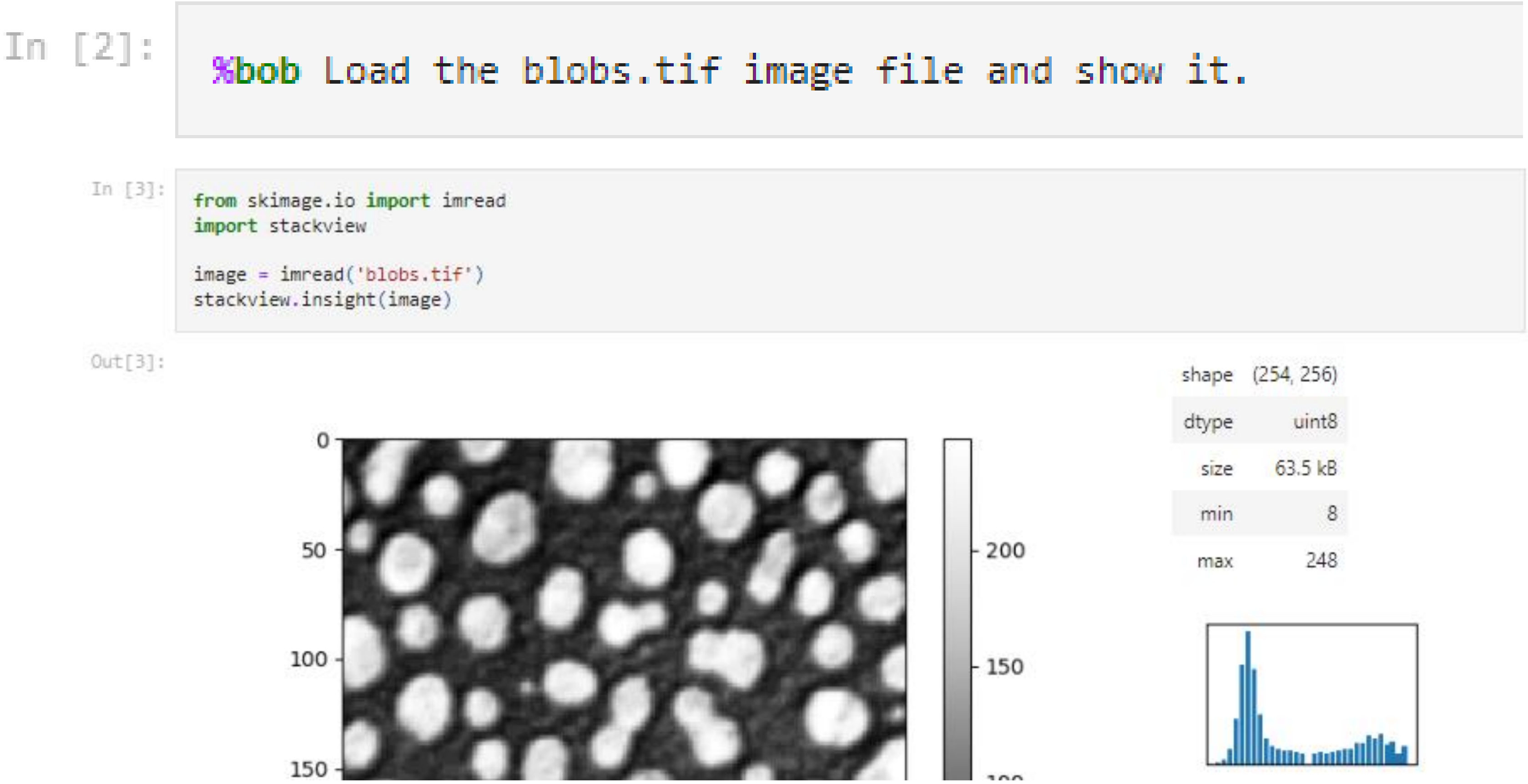
```
[1]: from bia_bob import bob
     bob.__version__

[1]: '0.3.0'

[ ]:
```

With Christian Tischer (EMBL Heidelberg) @tischitischer

https://github.com/haesleinhuepf/bia-bob

Coding assistance: BiA-Bob

Use the `%bob` … syntax to ask for small things.



```
In [2]: %bob Load the blobs.tif image file and show it.
```

```
In [3]: from skimage.io import imread
        import stackview

        image = imread('blobs.tif')
        stackview.insight(image)
```

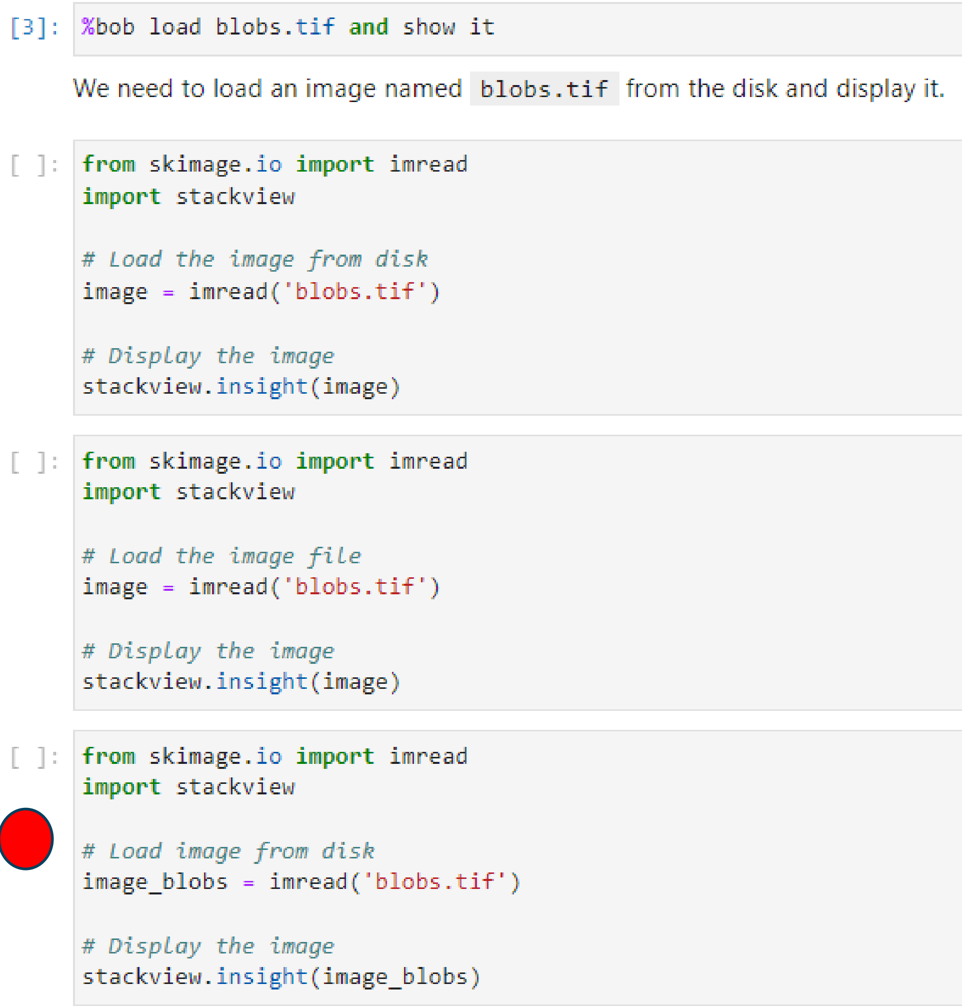
```
Out[3]:
shape   (254, 256)
dtype        uint8
size       63.5 kB
min              8
max            248
```

https://github.com/haesleinhuepf/bia-bob/blob/main/demo/basic_demo.ipynb

Coding assistance: BiA-Bob

- Bob adds a new cell to your code. If you ask it 3 times, it will make 3 cells.

- Clean up from time to time!



```
[3]: %bob load blobs.tif and show it
```

We need to load an image named `blobs.tif` from the disk and display it.

```
[ ]: from skimage.io import imread
     import stackview

     # Load the image from disk
     image = imread('blobs.tif')

     # Display the image
     stackview.insight(image)
```

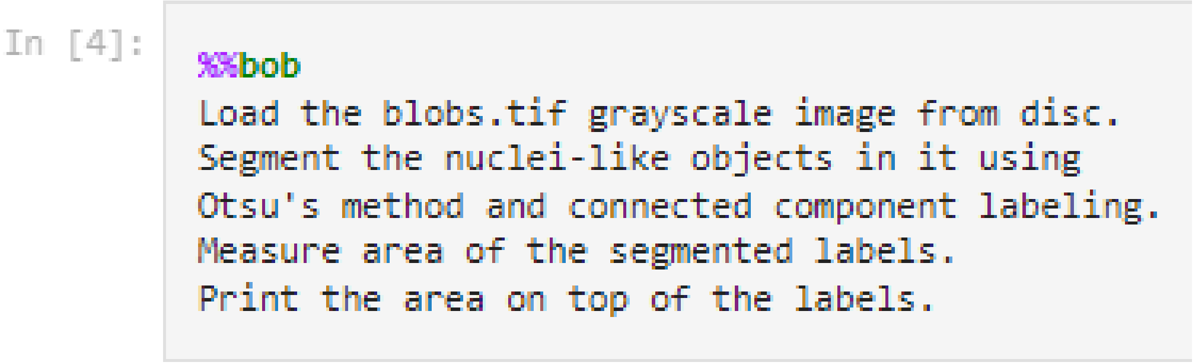
```
[ ]: from skimage.io import imread
     import stackview

     # Load the image file
     image = imread('blobs.tif')

     # Display the image
     stackview.insight(image)
```

```
[ ]: from skimage.io import imread
     import stackview

     # Load image from disk
     image_blobs = imread('blobs.tif')

     # Display the image
     stackview.insight(image_blobs)
```

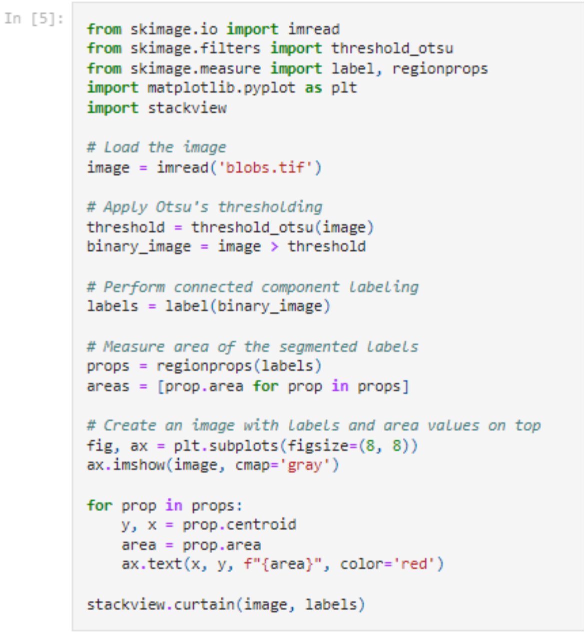
Click on the bar here and enter **dd**

Coding assistance: BiA-Bob

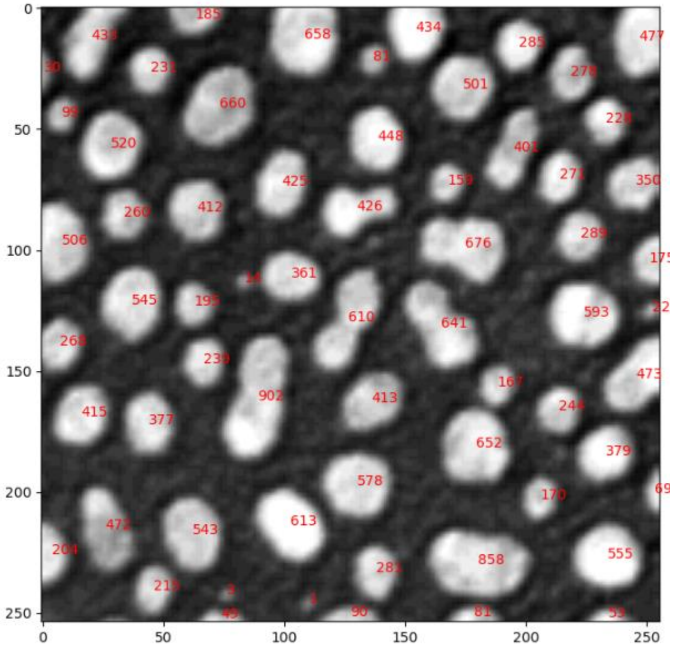
Use the `%%bob` … syntax to ask for complex analysis tasks.



```
In [4]:
%%bob
Load the blobs.tif grayscale image from disc.
Segment the nuclei-like objects in it using
Otsu's method and connected component labeling.
Measure area of the segmented labels.
Print the area on top of the labels.
```



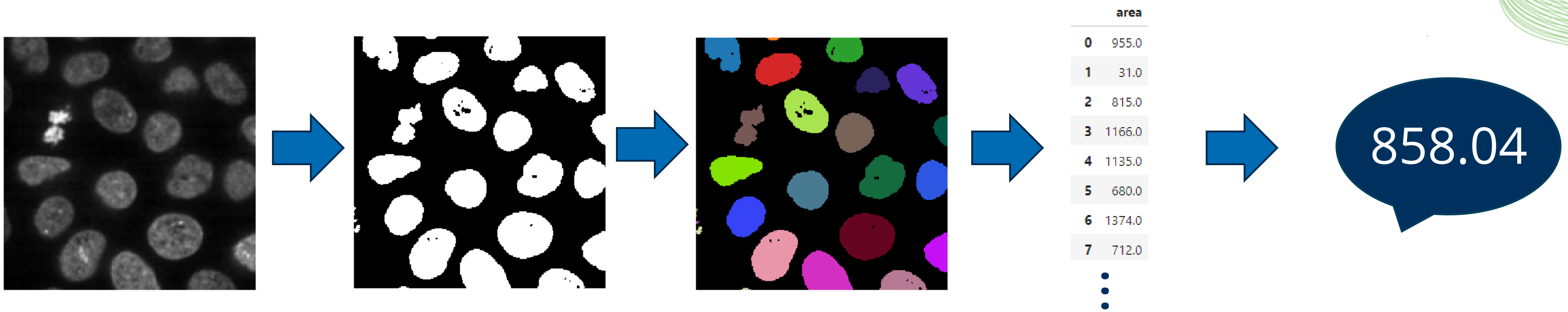
```
In [5]:
from skimage.io import imread
from skimage.filters import threshold_otsu
from skimage.measure import label, regionprops
import matplotlib.pyplot as plt
import stackview

# Load the image
image = imread('blobs.tif')

# Apply Otsu's thresholding
threshold = threshold_otsu(image)
binary_image = image > threshold

# Perform connected component labeling
labels = label(binary_image)

# Measure area of the segmented labels
props = regionprops(labels)
areas = [prop.area for prop in props]

# Create an image with labels and area values on top
fig, ax = plt.subplots(figsize=(8, 8))
ax.imshow(image, cmap='gray')

for prop in props:
    y, x = prop.centroid
    area = prop.area
    ax.text(x, y, f"{area}", color='red')

stackview.curtain(image, labels)
```



https://github.com/haesleinhuepf/bia-bob/blob/main/demo/basic_demo.ipynb

Benchmarking LLMs for Bio-image Analysis

Use case: segment the image and measure the average area of objects.



	area
0	955.0
1	31.0
2	815.0
3	1166.0
4	1135.0
5	680.0
6	1374.0
7	712.0
⋮	

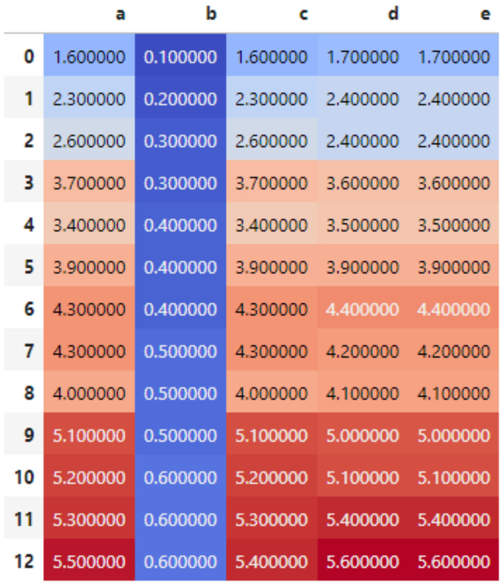
Unit-test pass-rate (n=10):

	reference	**gpt-4-turbo-2024-04-09**	Claude-3-opus-20240229	gpt-4-1106-preview	gpt-3.5-turbo-1106	gemini-pro	codellama
workflow_segmentation_measurement_summary	1.0	0.9	1.0	0.8	0.5	0.5	0.1

https://www.biorxiv.org/content/10.1101/2024.04.19.590278v1
https://github.com/haesleinhuepf/human-eval-bia

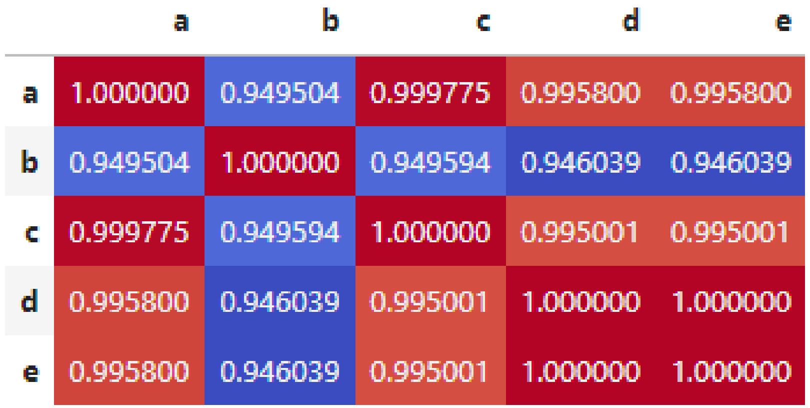
Benchmarking LLMs for Bio-image Analysis

Use-case: correlation matrix



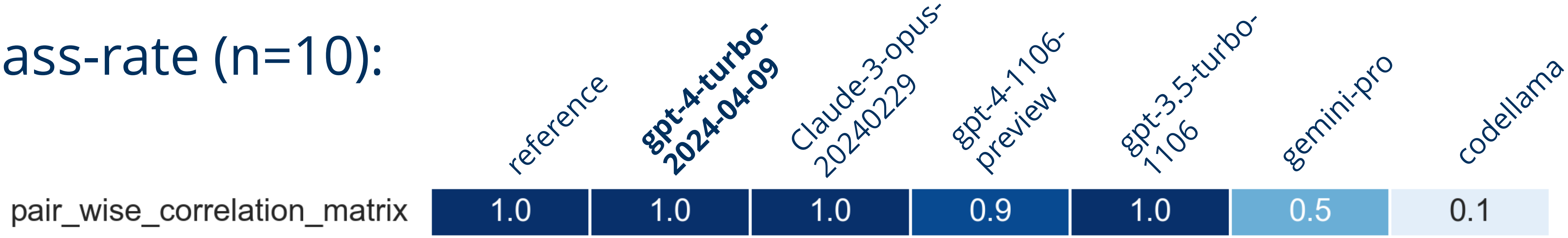
	a	b	c	d	e
0	1.600000	0.100000	1.600000	1.700000	1.700000
1	2.300000	0.200000	2.300000	2.400000	2.400000
2	2.600000	0.300000	2.600000	2.400000	2.400000
3	3.700000	0.300000	3.700000	3.600000	3.600000
4	3.400000	0.400000	3.400000	3.500000	3.500000
5	3.900000	0.400000	3.900000	3.900000	3.900000
6	4.300000	0.400000	4.300000	4.400000	4.400000
7	4.300000	0.500000	4.300000	4.200000	4.200000
8	4.000000	0.500000	4.000000	4.100000	4.100000
9	5.100000	0.500000	5.100000	5.000000	5.000000
10	5.200000	0.600000	5.200000	5.100000	5.100000
11	5.300000	0.600000	5.300000	5.400000	5.400000
12	5.500000	0.600000	5.400000	5.600000	5.600000

→



	a	b	c	d	e
a	1.000000	0.949504	0.999775	0.995800	0.995800
b	0.949504	1.000000	0.949594	0.946039	0.946039
c	0.999775	0.949594	1.000000	0.995001	0.995001
d	0.995800	0.946039	0.995001	1.000000	1.000000
e	0.995800	0.946039	0.995001	1.000000	1.000000

Unit-test pass-rate (n=10):

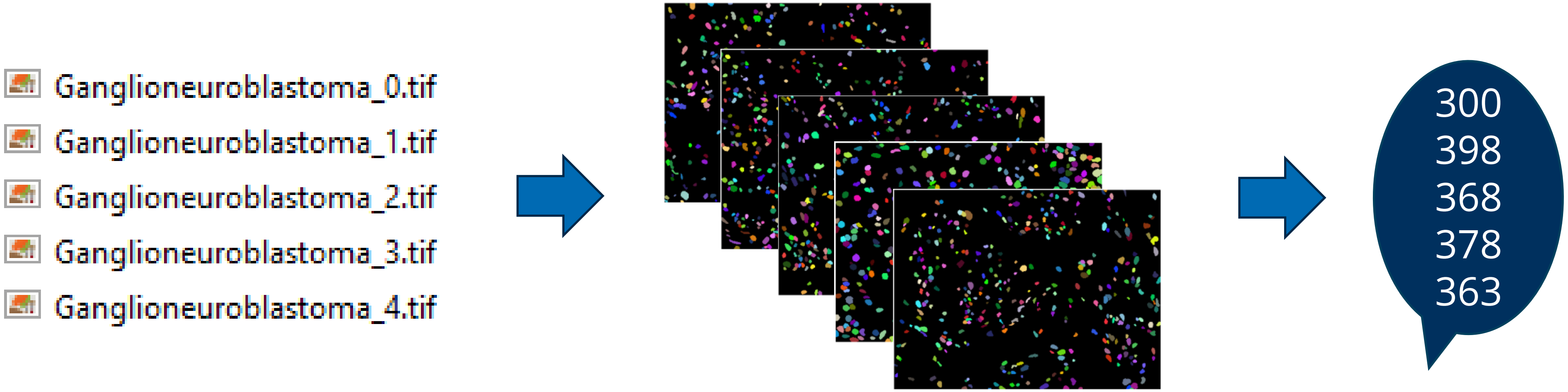


	reference	**gpt-4-turbo-2024-04-09**	Claude-3-opus-20240229	gpt-4-1106-preview	gpt-3.5-turbo-1106	gemini-pro	codellama
pair_wise_correlation_matrix	1.0	1.0	1.0	0.9	1.0	0.5	0.1

https://www.biorxiv.org/content/10.1101/2024.04.19.590278v1
https://github.com/haesleinhuepf/human-eval-bia

Benchmarking LLMs for Bio-image Analysis

Use case: Count segmented objects in a folder of segmentation results.



Ganglioneuroblastoma_0.tif
Ganglioneuroblastoma_1.tif
Ganglioneuroblastoma_2.tif
Ganglioneuroblastoma_3.tif
Ganglioneuroblastoma_4.tif

300
398
368
378
363

Unit-test pass-rate (n=10):

	reference	gpt-4-turbo-2024-04-09	Claude-3-opus-20240229	gpt-4-1106-preview	gpt-3.5-turbo-1106	gemini-pro	codellama
workflow_batch_process_folder_count_labels	1.0	0.1	0.0	0.3	0.0	0.0	0.0

https://www.biorxiv.org/content/10.1101/2024.04.19.590278v1
https://github.com/haesleinhuepf/human-eval-bia
Data Source: https://www.ebi.ac.uk/bioimage-archive/galleries/S-BIAD634-ai.html

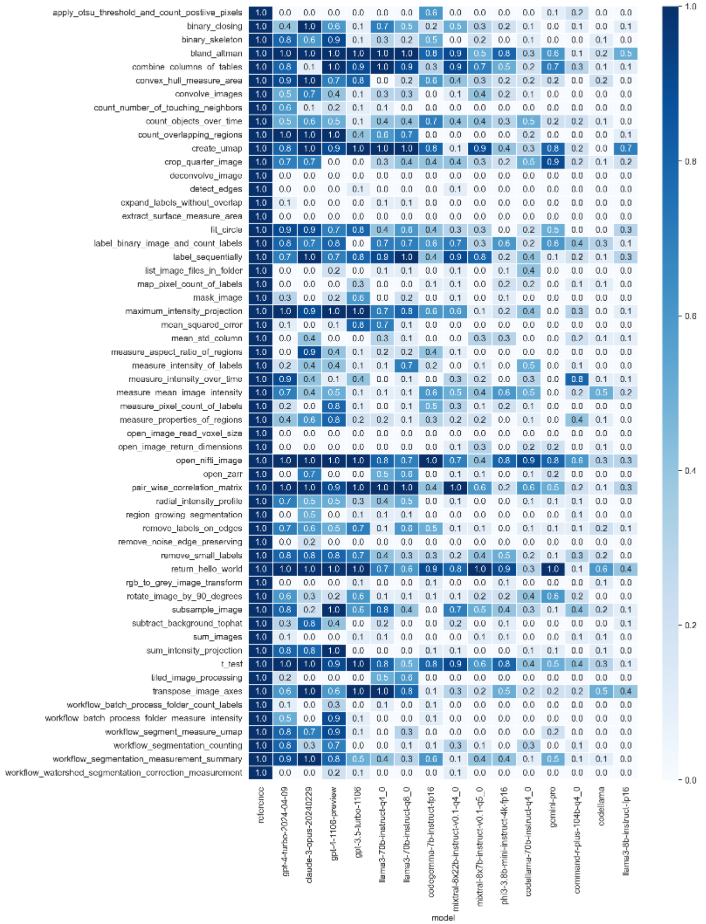
Coding assistance: BiA-Bob

Keep your feed on the ground with *Bob*. Bob can do crazy things, but you are responsible for what it does with your data.

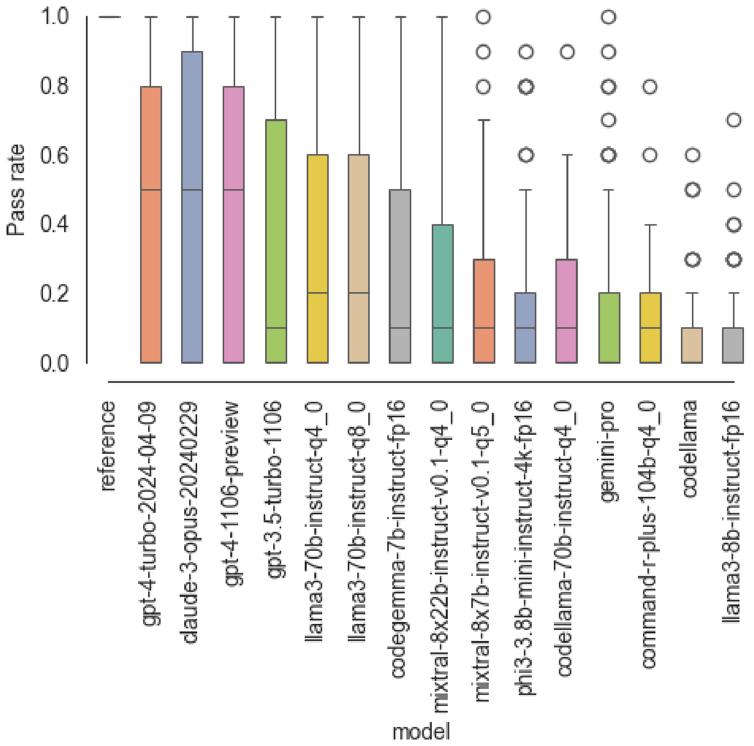
Do not enter personal / private information. What you enter will be sent to the server of an american company.

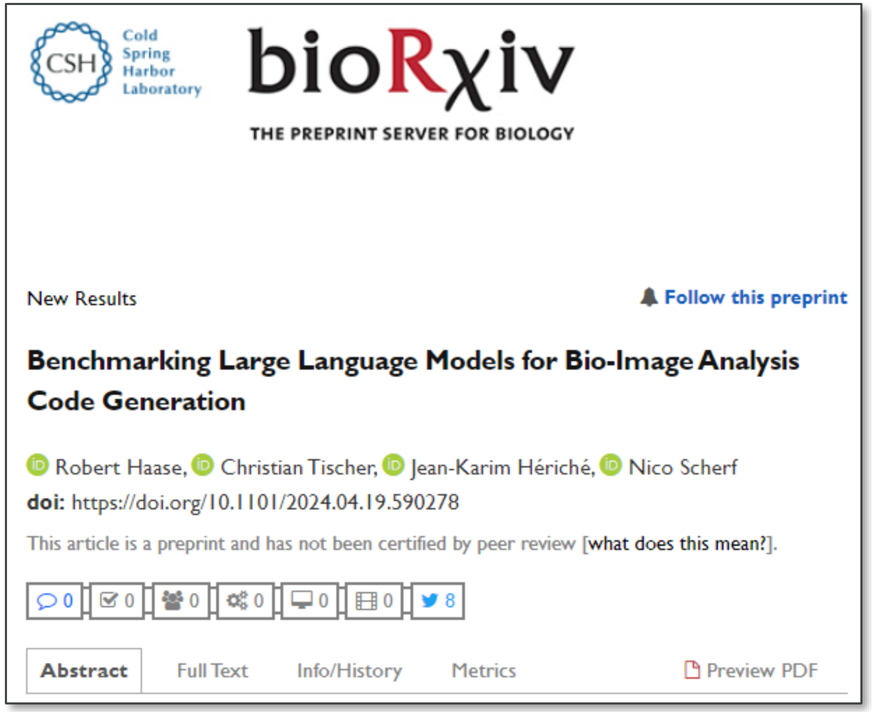
Benchmarking LLMs for Bio-image Analysis

Summary: 57 use-cases (yet), 15 LLMs (yet), n=10



	reference	gpt-4-turbo-2024-04-09	claude-3-opus-20240229	gpt-4-1106-preview	gpt-3.5-turbo-1106	llama3-70b-instruct-q4_0	llama3-70b-instruct-q8_0	codegemma-7b-instruct-fp16	mixtral-8x22b-instruct-v0.1-q4_0	mixtral-8x7b-instruct-v0.1-q5_0	phi3-3.8b-mini-instruct-4k-fp16	codellama-70b-instruct-q4_0	gemini-pro	command-r-plus-104b-q4_0	codellama	llama3-8b-instruct-fp16
apply_otsu_threshold_and_count_postiive_pixels	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.6	0.0	0.0	0.0	0.0	0.1	0.2	0.0	0.0
binary_closing	1.0	0.4	1.0	0.6	0.1	0.7	0.5	0.2	0.5	0.3	0.2	0.1	0.0	0.1	0.0	0.1
binary_skeleton	1.0	0.8	0.6	0.9	0.1	0.3	0.2	0.5	0.0	0.2	0.0	0.1	0.0	0.0	0.1	0.0
bland_altman	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.8	0.9	0.5	0.8	0.3	0.6	0.1	0.2	0.5
combine_columns_of_tables	1.0	0.8	0.1	1.0	0.9	1.0	0.9	0.3	0.9	0.7	0.5	0.2	0.7	0.3	0.1	0.1
convex_hull_measure_area	1.0	0.9	1.0	0.7	0.8	0.0	0.2	0.6	0.4	0.3	0.2	0.2	0.2	0.0	0.2	0.0
convolve_images	1.0	0.5	0.7	0.4	0.1	0.3	0.3	0.0	0.1	0.4	0.2	0.1	0.0	0.0	0.0	0.0
count_number_of_touching_neighbors	1.0	0.6	0.1	0.2	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
count_objects_over_time	1.0	0.5	0.6	0.5	0.1	0.4	0.4	0.7	0.4	0.4	0.3	0.5	0.2	0.2	0.1	0.0
count_overlapping_regions	1.0	1.0	1.0	1.0	0.4	0.6	0.7	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.1
create_umap	1.0	0.8	1.0	0.9	1.0	1.0	1.0	0.8	0.1	0.9	0.4	0.3	0.8	0.2	0.0	0.7
crop_quarter_image	1.0	0.7	0.7	0.0	0.0	0.3	0.4	0.4	0.4	0.3	0.2	0.5	0.9	0.2	0.1	0.2
deconvolve_image	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
detect_edges	1.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
expand_labels_without_overlap	1.0	0.1	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
extract_surface_measure_area	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
fill_circle	1.0	0.9	0.9	0.7	0.8	0.4	0.6	0.4	0.3	0.3	0.0	0.2	0.5	0.0	0.0	0.3
label_binary_image_and_count_labels	1.0	0.8	0.7	0.8	0.0	0.7	0.7	0.6	0.7	0.3	0.6	0.2	0.6	0.4	0.3	0.1
label_sequentially	1.0	0.7	1.0	0.7	0.8	0.9	1.0	0.4	0.9	0.8	0.2	0.4	0.1	0.2	0.1	0.3
list_image_files_in_folder	1.0	0.0	0.0	0.2	0.0	0.1	0.1	0.0	0.1	0.0	0.1	0.4	0.0	0.0	0.0	0.0
map_pixel_count_of_labels	1.0	0.0	0.0	0.0	0.3	0.0	0.0	0.1	0.1	0.0	0.2	0.2	0.0	0.1	0.1	0.0
mask_image	1.0	0.3	0.0	0.2	0.6	0.0	0.2	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0
maximum_intensity_projection	1.0	1.0	0.9	1.0	1.0	0.7	0.8	0.6	0.6	0.1	0.2	0.4	0.0	0.3	0.0	0.1
mean_squared_error	1.0	0.1	0.0	0.1	0.8	0.7	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
mean_std_column	1.0	0.0	0.4	0.0	0.0	0.3	0.1	0.0	0.0	0.3	0.3	0.0	0.0	0.2	0.1	0.1
measure_aspect_ratio_of_regions	1.0	0.0	0.9	0.4	0.1	0.2	0.2	0.4	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
measure_intensity_of_labels	1.0	0.2	0.4	0.4	0.1	0.1	0.7	0.2	0.0	0.1	0.0	0.5	0.0	0.1	0.0	0.0
measure_intensity_over_time	1.0	0.9	0.4	0.1	0.4	0.0	0.1	0.0	0.3	0.2	0.0	0.3	0.0	0.8	0.1	0.1
measure_mean_image_intensity	1.0	0.7	0.4	0.5	0.1	0.1	0.1	0.6	0.5	0.4	0.6	0.5	0.0	0.2	0.5	0.2
measure_pixel_count_of_labels	1.0	0.2	0.0	0.8	0.1	0.0	0.1	0.5	0.3	0.1	0.2	0.1	0.0	0.0	0.0	0.0
measure_properties_of_regions	1.0	0.4	0.6	0.8	0.2	0.2	0.1	0.3	0.2	0.2	0.0	0.1	0.0	0.4	0.1	0.0
open_image_read_voxel_size	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
open_image_return_dimensions	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.3	0.0	0.2	0.2	0.0	0.1	0.0
open_nifti_image	1.0	1.0	1.0	1.0	1.0	0.8	0.7	1.0	0.7	0.4	0.8	0.9	0.8	0.6	0.3	0.3
open_zarr	1.0	0.0	0.7	0.0	0.0	0.5	0.6	0.0	0.1	0.1	0.0	0.1	0.2	0.0	0.0	0.0
pair_wise_correlation_matrix	1.0	1.0	1.0	0.9	1.0	1.0	1.0	0.4	1.0	0.6	0.2	0.6	0.5	0.2	0.1	0.3
radial_intensity_profile	1.0	0.7	0.5	0.5	0.3	0.4	0.5	0.0	0.1	0.0	0.0	0.1	0.1	0.1	0.0	0.0
region_growing_segmentation	1.0	0.0	0.5	0.0	0.1	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0
remove_labels_on_edges	1.0	0.7	0.6	0.5	0.7	0.1	0.6	0.5	0.1	0.1	0.0	0.1	0.1	0.1	0.2	0.1
remove_noise_edge_preserving	1.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
remove_small_labels	1.0	0.8	0.8	0.8	0.7	0.4	0.3	0.3	0.2	0.4	0.5	0.2	0.1	0.3	0.2	0.0
return_hello_world	1.0	1.0	1.0	1.0	1.0	0.7	0.6	0.9	0.8	1.0	0.9	0.3	1.0	0.1	0.6	0.4
rgb_to_grey_image_transform	1.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.0
rotate_image_by_90_degrees	1.0	0.6	0.3	0.2	0.6	0.1	0.1	0.1	0.1	0.2	0.2	0.4	0.6	0.2	0.0	0.0
subsample_image	1.0	0.8	0.2	1.0	0.6	0.8	0.4	0.0	0.7	0.5	0.4	0.3	0.1	0.4	0.2	0.1
subtract_background_tophat	1.0	0.3	0.8	0.4	0.0	0.2	0.0	0.0	0.2	0.0	0.1	0.0	0.0	0.0	0.0	0.1
sum_images	1.0	0.1	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.1	0.0
sum_intensity_projection	1.0	0.8	0.8	1.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.1	0.0	0.1	0.0
t_test	1.0	1.0	1.0	0.9	1.0	0.8	0.5	0.8	0.9	0.6	0.8	0.4	0.5	0.4	0.3	0.1
tiled_image_processing	1.0	0.2	0.0	0.0	0.0	0.5	0.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
transpose_image_axes	1.0	0.6	1.0	0.6	1.0	1.0	0.8	0.1	0.3	0.2	0.5	0.2	0.2	0.2	0.5	0.4
workflow_batch_process_folder_count_labels	1.0	0.1	0.0	0.3	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
workflow_batch_process_folder_measure_intensity	1.0	0.5	0.0	0.9	0.1	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
workflow_segment_measure_umap	1.0	0.8	0.7	0.9	0.1	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0
workflow_segmentation_counting	1.0	0.8	0.3	0.7	0.0	0.0	0.1	0.1	0.3	0.1	0.0	0.3	0.0	0.1	0.0	0.0
workflow_segmentation_measurement_summary	1.0	0.9	1.0	0.8	0.5	0.4	0.3	0.6	0.1	0.4	0.4	0.1	0.5	0.1	0.1	0.0
workflow_watershed_segmentation_correction_measurement	1.0	0.0	0.0	0.2	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0





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Benchmarking Large Language Models for Bio-Image Analysis Code Generation

Robert Haase, Christian Tischer, Jean-Karim Hériché, Nico Scherf

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https://github.com/haesleinhuepf/human-eval-bia

ScaDS.AI
DRESDEN LEIPZIG
CENTER FOR SCALABLE DATA ANALYTICS AND ARTIFICIAL INTELLIGENCE

Exercises

Robert Haase

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SACHSEN

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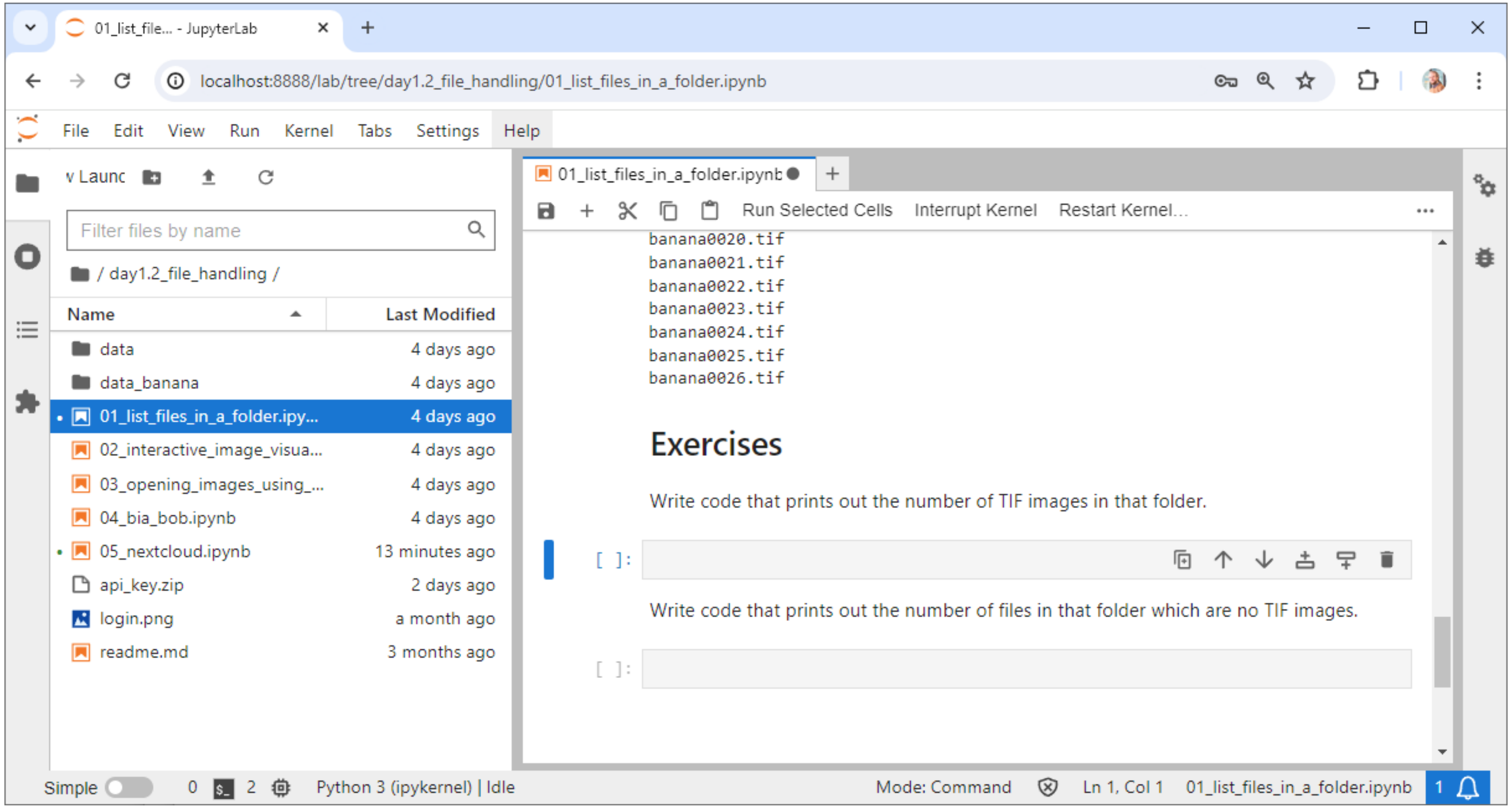
https://doi.org/10.5281/zenodo.10841765

Exercise: File lists and folder

Apply your knowledge about Python lists to list of files.



```
banana0020.tif
banana0021.tif
banana0022.tif
banana0023.tif
banana0024.tif
banana0025.tif
banana0026.tif
```

Exercises

Write code that prints out the number of TIF images in that folder.

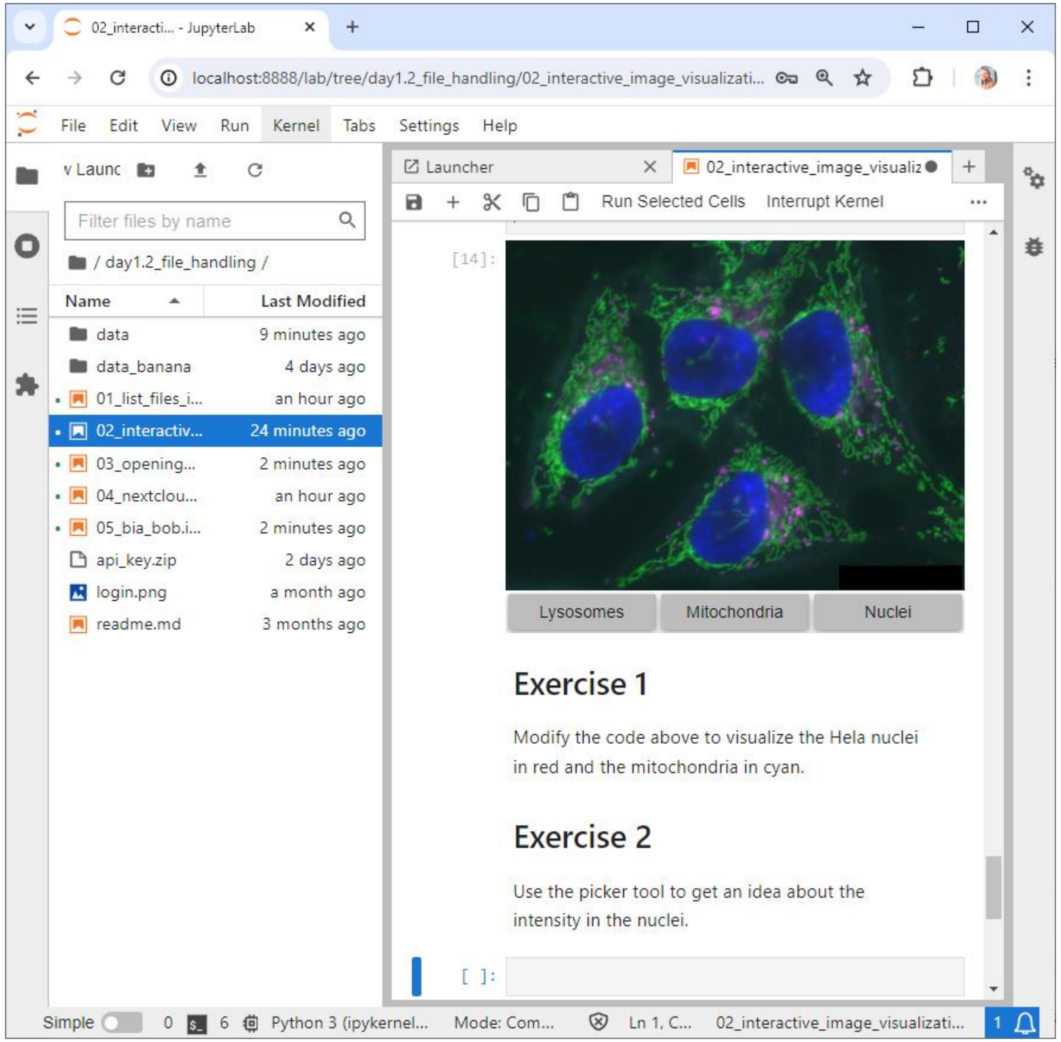
[ ]:

Write code that prints out the number of files in that folder which are no TIF images.

[ ]:

Prompt Eng. for Bio-image Analysis
Monash Advanced Microscopy Sem.
Robert Haase @haesleinhuepf
March 13th 2024

Exercise: Loading and visualizing image files



Name	Last Modified
data	9 minutes ago
data_banana	4 days ago
01_list_files_i...	an hour ago
02_interactiv...	24 minutes ago
03_opening...	2 minutes ago
04_nextclou...	an hour ago
05_bia_bob.i...	2 minutes ago
api_key.zip	2 days ago
login.png	a month ago
readme.md	3 months ago

```
[14]:
```

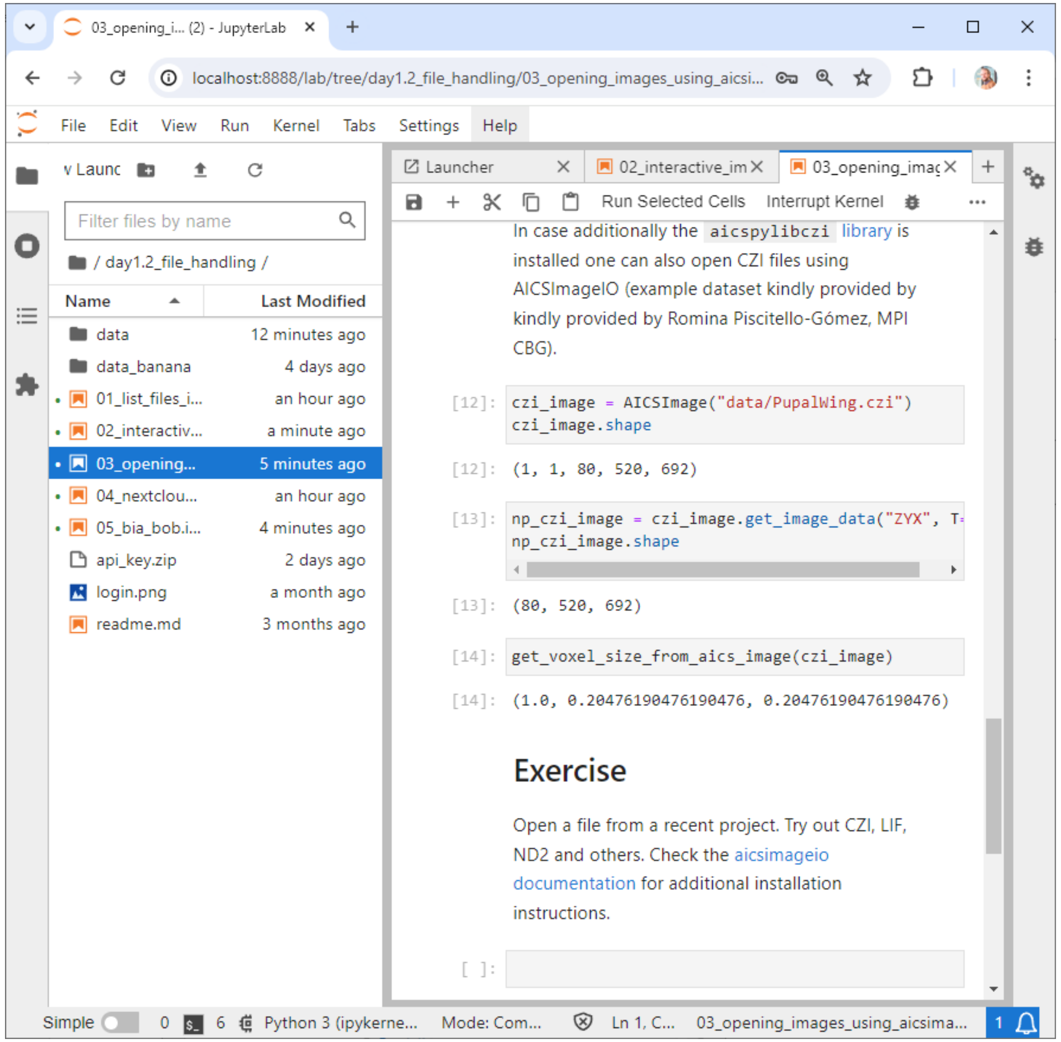
Exercise 1

Modify the code above to visualize the Hela nuclei in red and the mitochondria in cyan.

Exercise 2

Use the picker tool to get an idea about the intensity in the nuclei.

```
[ ]:
```



Name	Last Modified
data	12 minutes ago
data_banana	4 days ago
01_list_files_i...	an hour ago
02_interactiv...	a minute ago
03_opening...	5 minutes ago
04_nextclou...	an hour ago
05_bia_bob.i...	4 minutes ago
api_key.zip	2 days ago
login.png	a month ago
readme.md	3 months ago

In case additionally the `aicspylibczi` library is installed one can also open CZI files using AICSImageIO (example dataset kindly provided by kindly provided by Romina Piscitello-Gómez, MPI CBG).

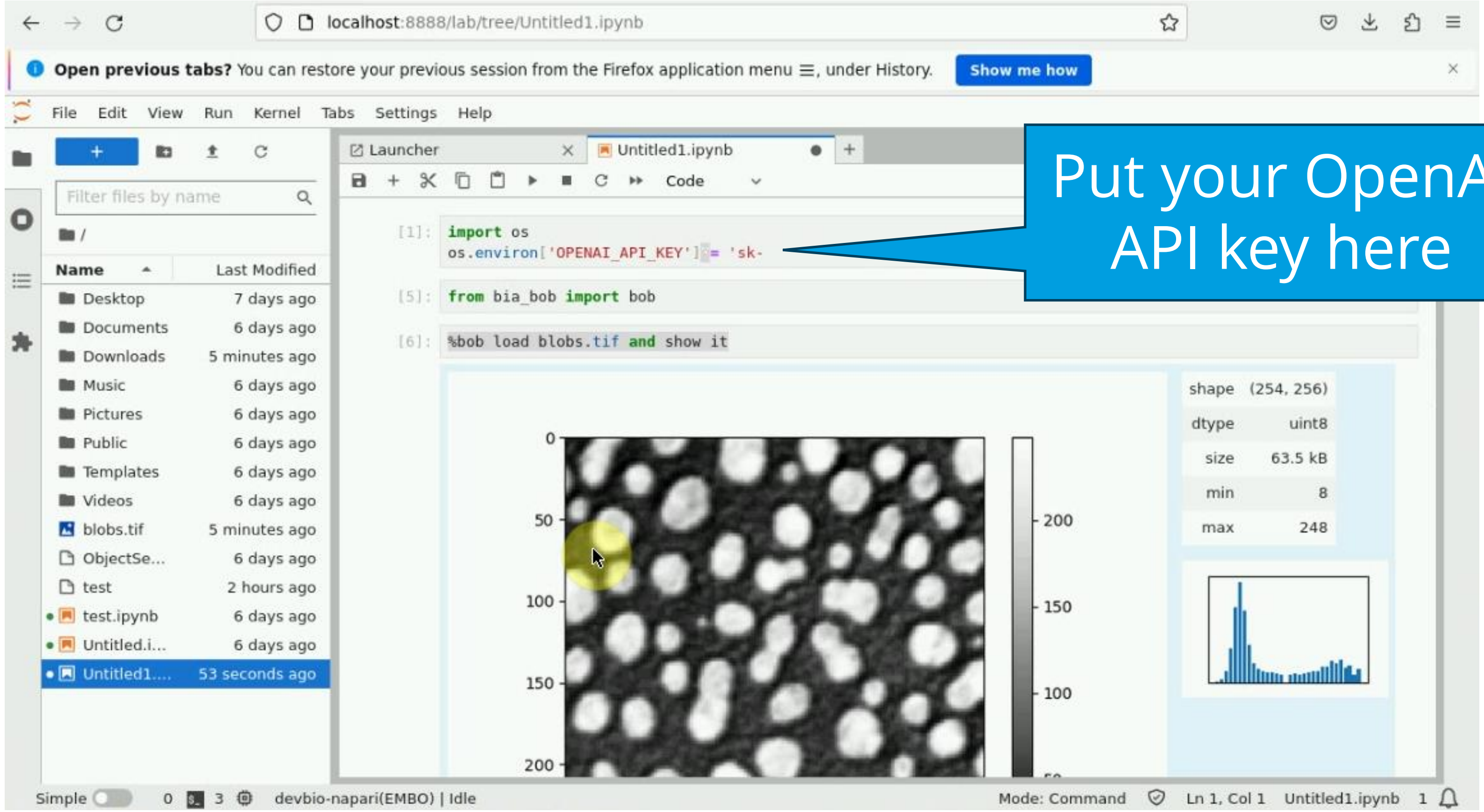
```
[12]: czi_image = AICSImage("data/PupalWing.czi")
      czi_image.shape

[12]: (1, 1, 80, 520, 692)

[13]: np_czi_image = czi_image.get_image_data("ZYX", T=
      np_czi_image.shape

[13]: (80, 520, 692)

[14]: get_voxel_size_from_aics_image(czi_image)

[14]: (1.0, 0.20476190476190476, 0.20476190476190476)
```

Exercise

Open a file from a recent project. Try out CZI, LIF, ND2 and others. Check the aicsimageio documentation for additional installation instructions.

```
[ ]:
```

Optional exercise: BiA-Bob



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Name	Last Modified
Desktop	7 days ago
Documents	6 days ago
Downloads	5 minutes ago
Music	6 days ago
Pictures	6 days ago
Public	6 days ago
Templates	6 days ago
Videos	6 days ago
blobs.tif	5 minutes ago
ObjectSe...	6 days ago
test	2 hours ago
test.ipynb	6 days ago
Untitled.i...	6 days ago
Untitled1....	53 seconds ago

```
[1]: import os
     os.environ['OPENAI_API_KEY'] = 'sk-

[5]: from bia_bob import bob

[6]: %bob load blobs.tif and show it
```

shape	(254, 256)
dtype	uint8
size	63.5 kB
min	8
max	248

Put your OpenAI API key here