CENTER FOR SCALABLE DATA ANALYTICS
AND ARTIFICIAL INTELLIGENCE

NATIONAL RESEARCH DATA MANAGEMENT INFRASTRUCTURE
FOR MICROSCOPY AND BIOIMAGE ANALYSIS

GLOBAL BIOIMAGE
ANALYST'S SOCIETY

Large Language Models for Bio-image Analysis

Robert Haase

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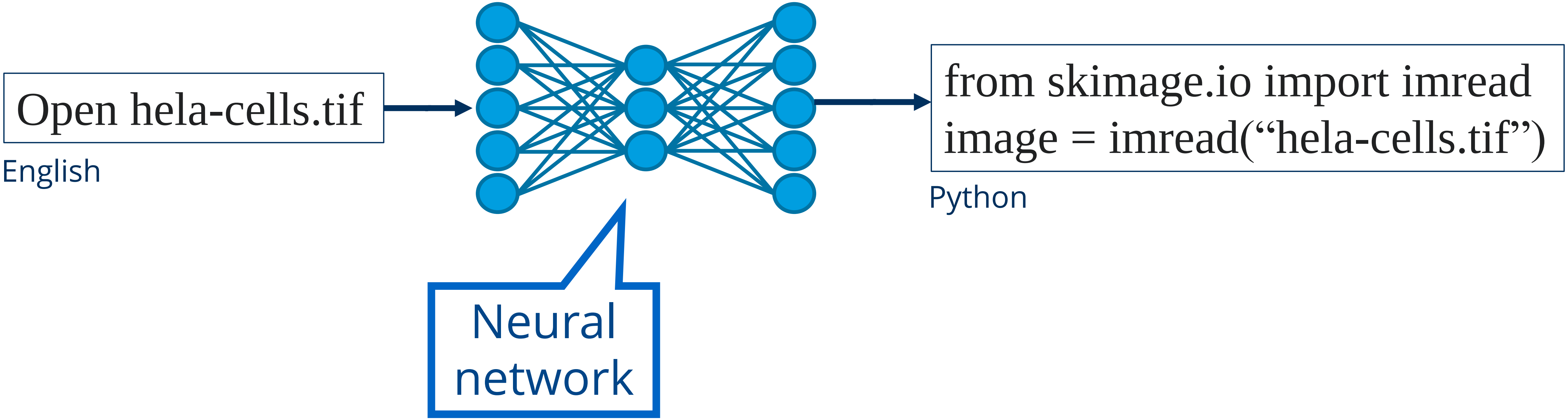
für Bildung
und Forschung

SACHSEN

Diese Maßnahme wird gefördert durch die Bundesregierung aufgrund eines Beschlusses des Deutschen Bundestages. Diese Maßnahme wird mitfinanziert durch Steuermittel auf der Grundlage des von den Abgeordneten des Sächsischen Landtags beschlossenen Haushaltes.

Large Language Models (LLMs)

Text-to-text, translation, code generation



Open hela-cells.tif

English

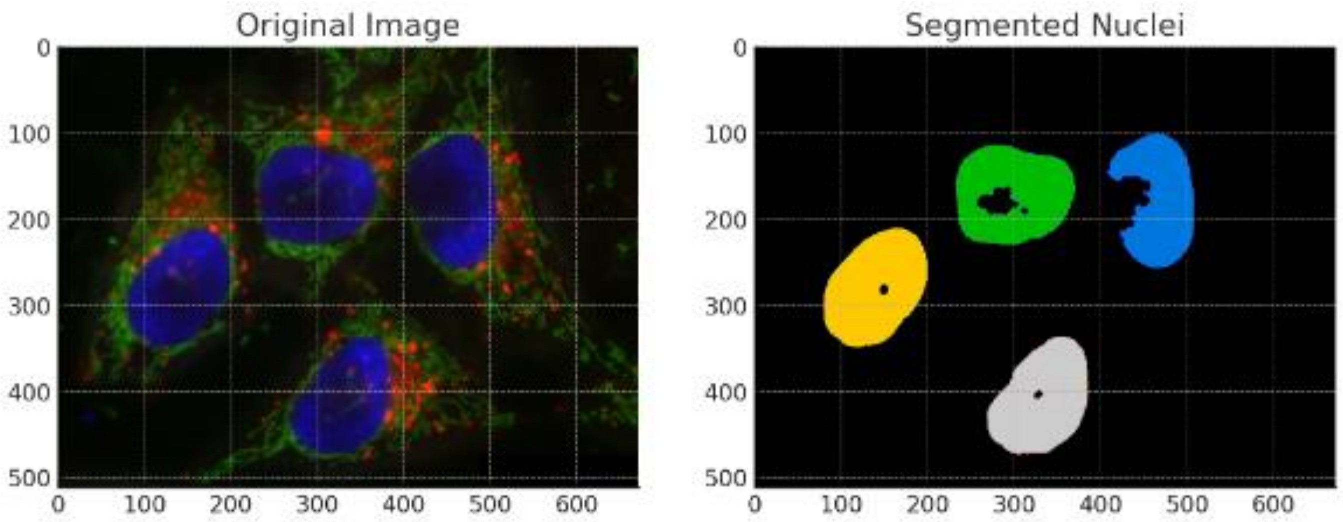
```
from skimage.io import imread
image = imread(“hela-cells.tif”)
```

Python

Neural network

Bio-image Analysis

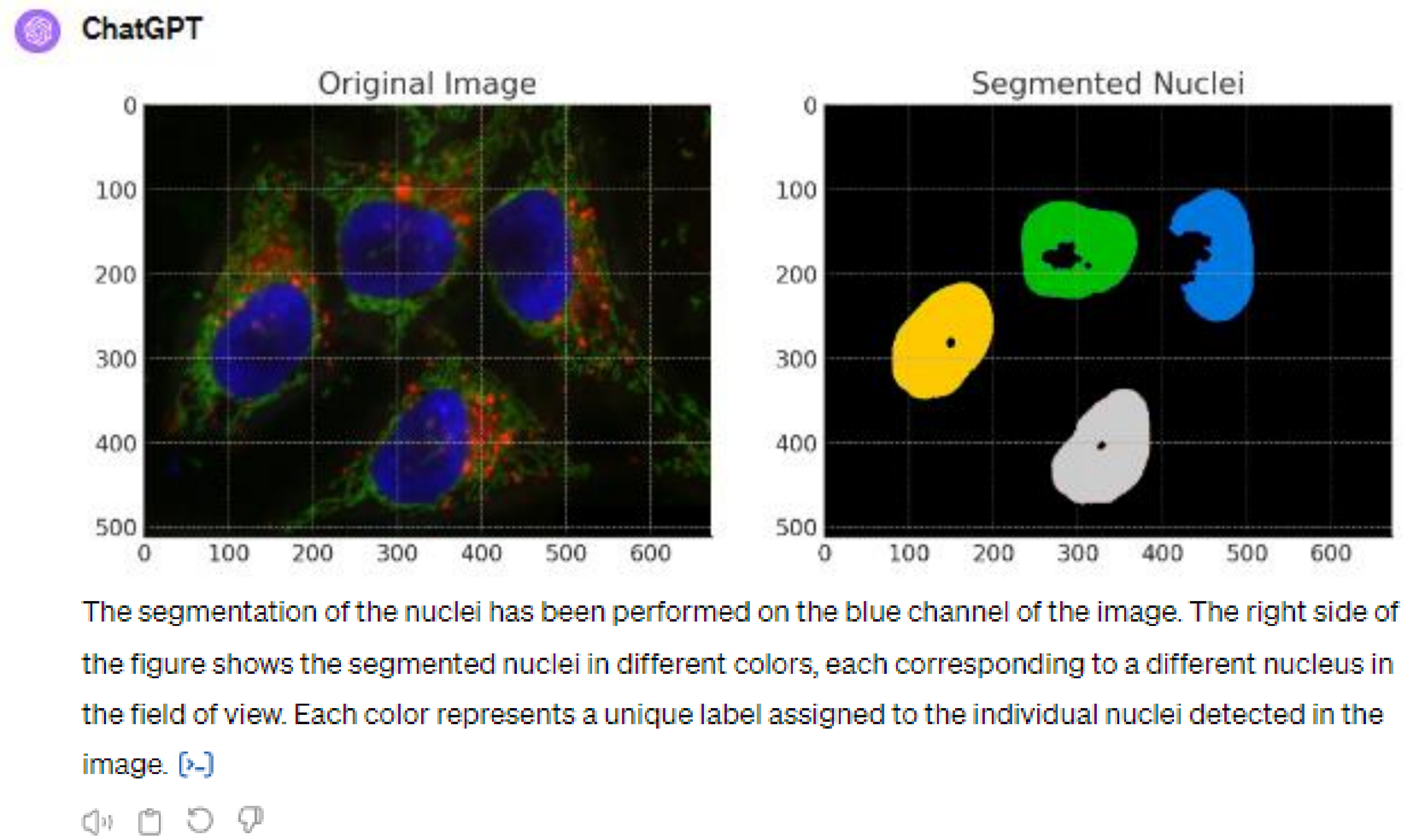
My job …



Bio-image Analysis using Large-Language Models

My job is changing, since we have ChatGPT

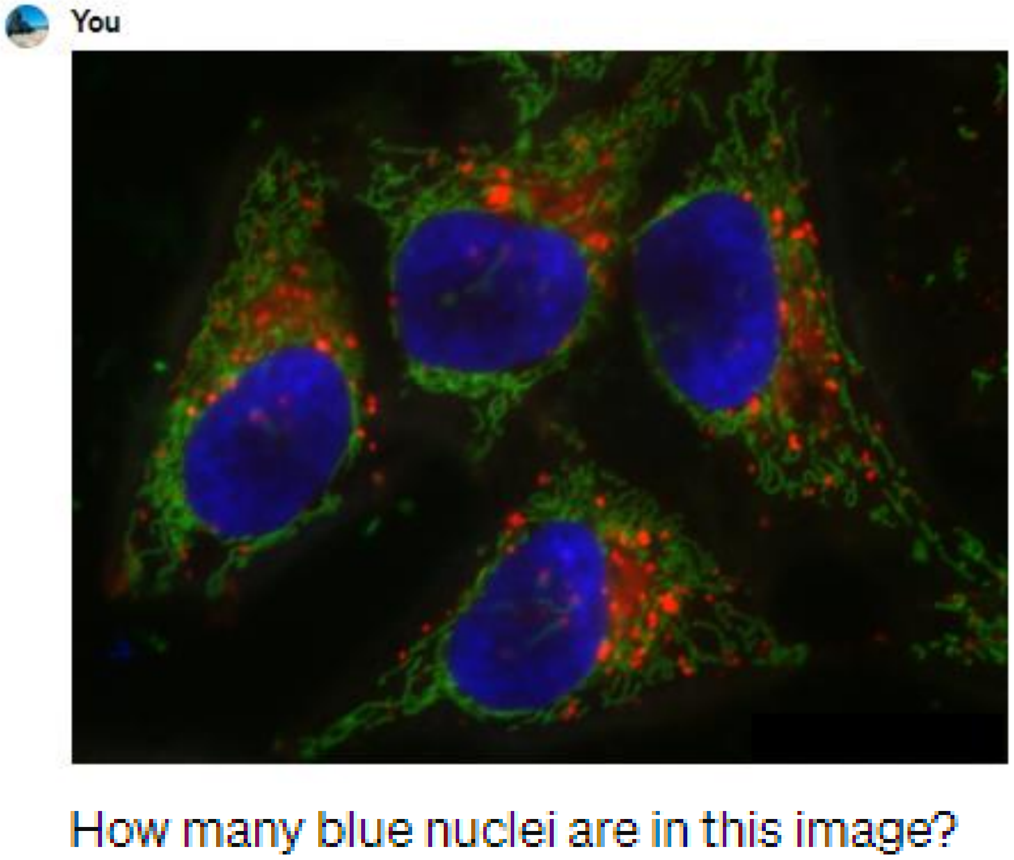
Prompt:
“Please segment the nuclei in the blue channel of the image”



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.

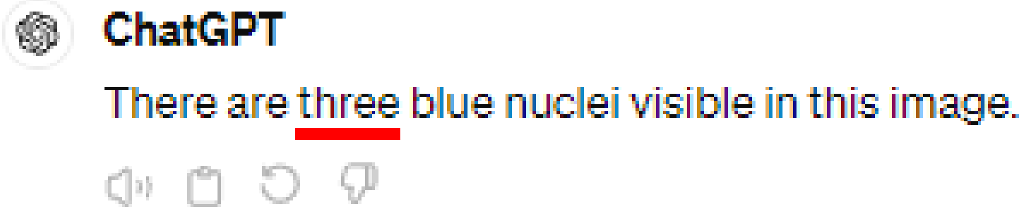
Vision language models for counting objects

LLMs were not exactly built for this use-case…



You

How many blue nuclei are in this image?



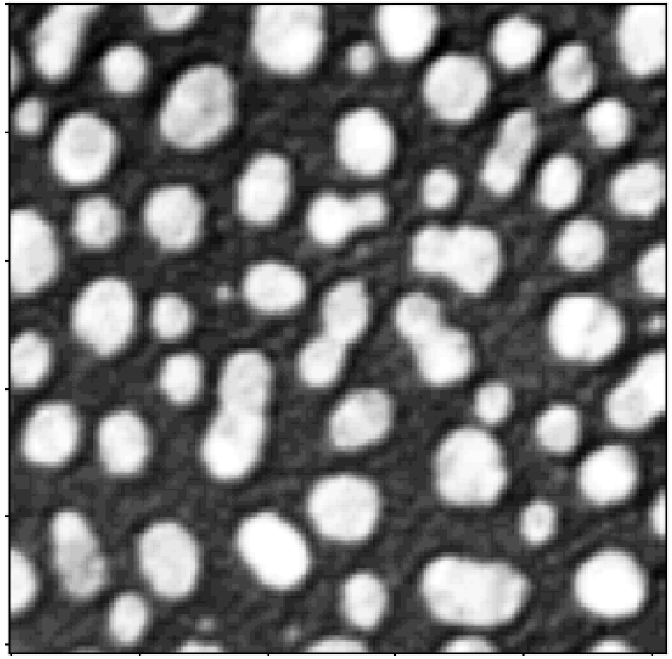
ChatGPT

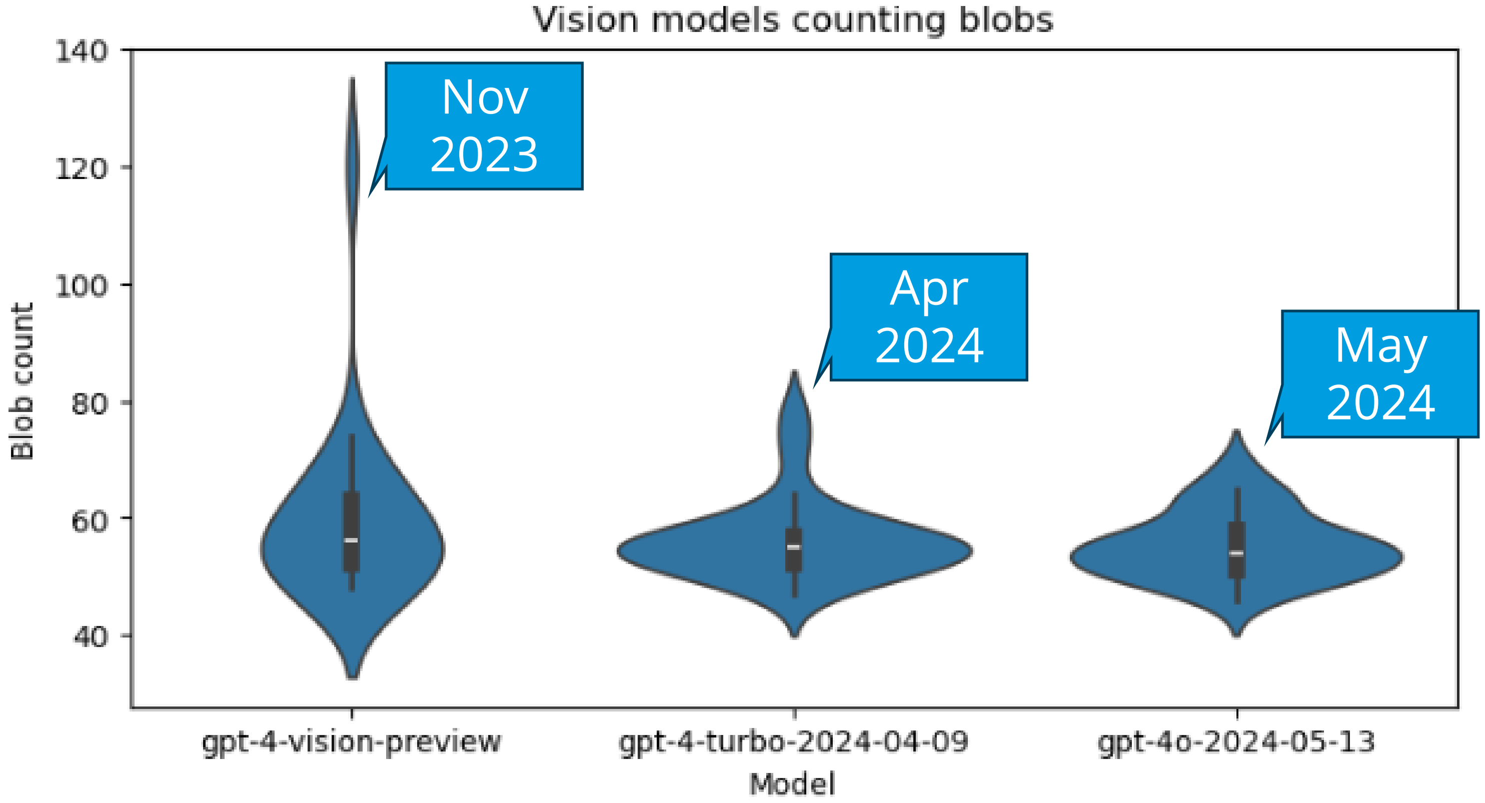
There are three blue nuclei visible in this image.

n=1

Vision language models for counting objects

Prompt: „Analyse the following image by counting the bright blobs. Respond with the number only. “ (n=25)





Nov 2023

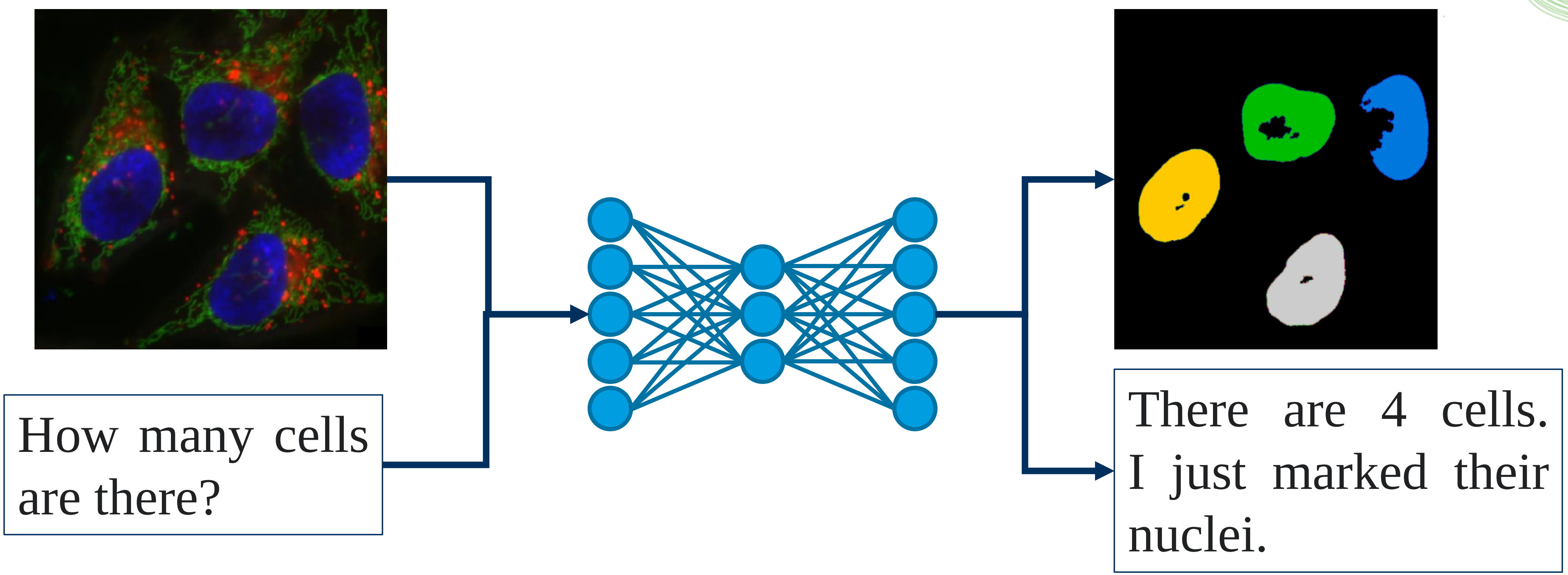
Apr 2024

May 2024

https://haesleinhuepf.github.io/BioImageAnalysisNotebooks/20c_vision_models/vision_models.html

Multi-modal LLMs

Combining image, text and [...] data, to gain new [biological] insights.



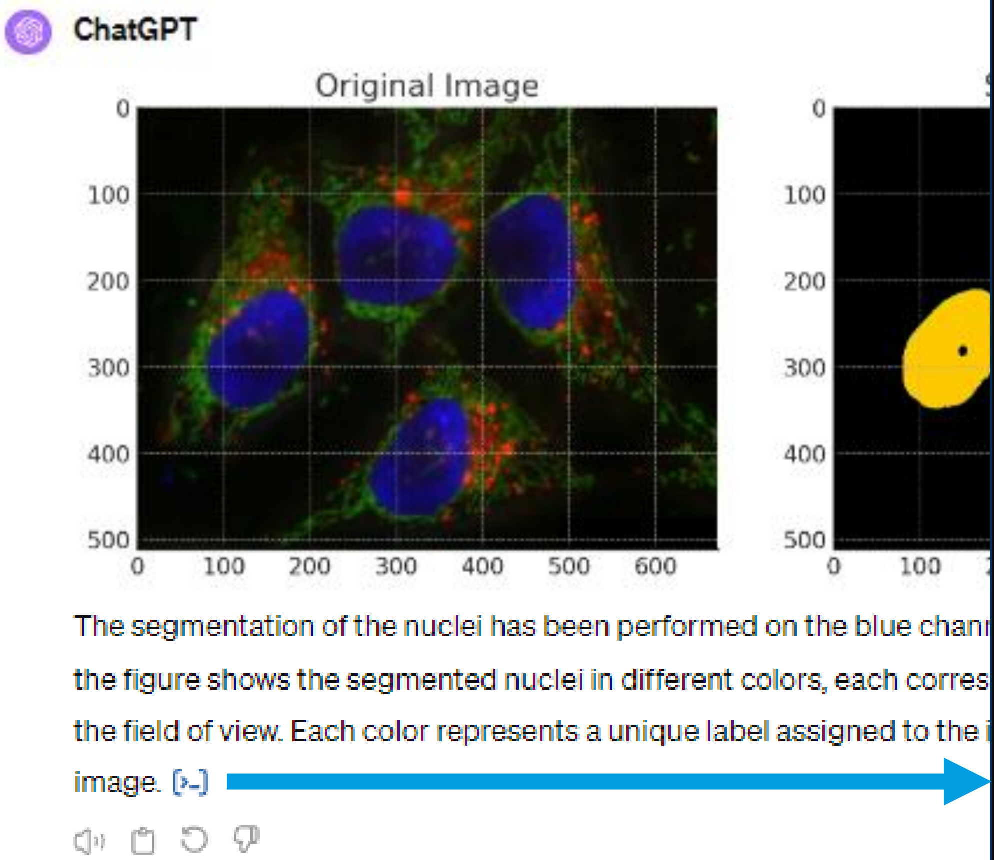
How many cells are there?

There are 4 cells. I just marked their nuclei.

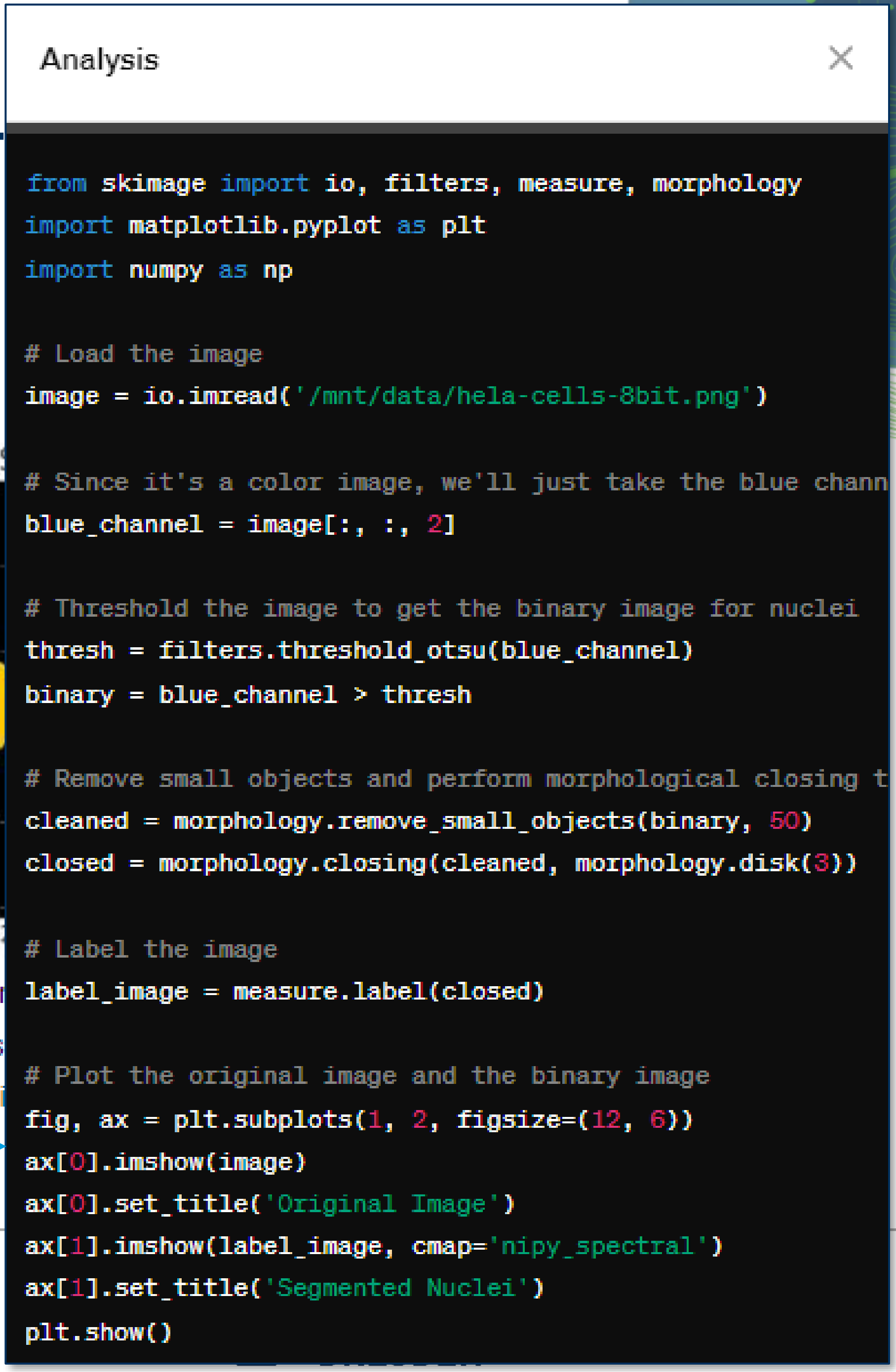
Bio-image Analysis using Large-L

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 chan
the figure shows the segmented nuclei in different colors, each corres
the field of view. Each color represents a unique label assigned to the i
image. [>_]



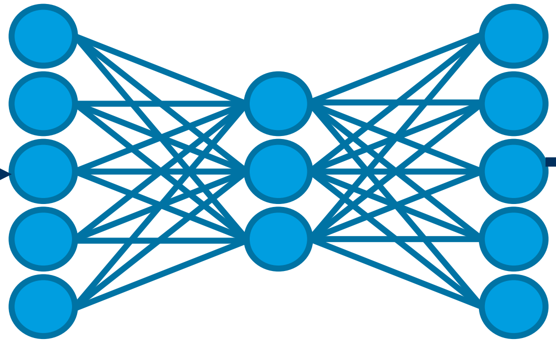
```
from skimage import io, filters, measure, morphology
import matplotlib.pyplot as plt
import numpy as np

# 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()
```

Large Language Models (LLMs)

Text-to-text, translation, code generation

Open blobs.tif

English

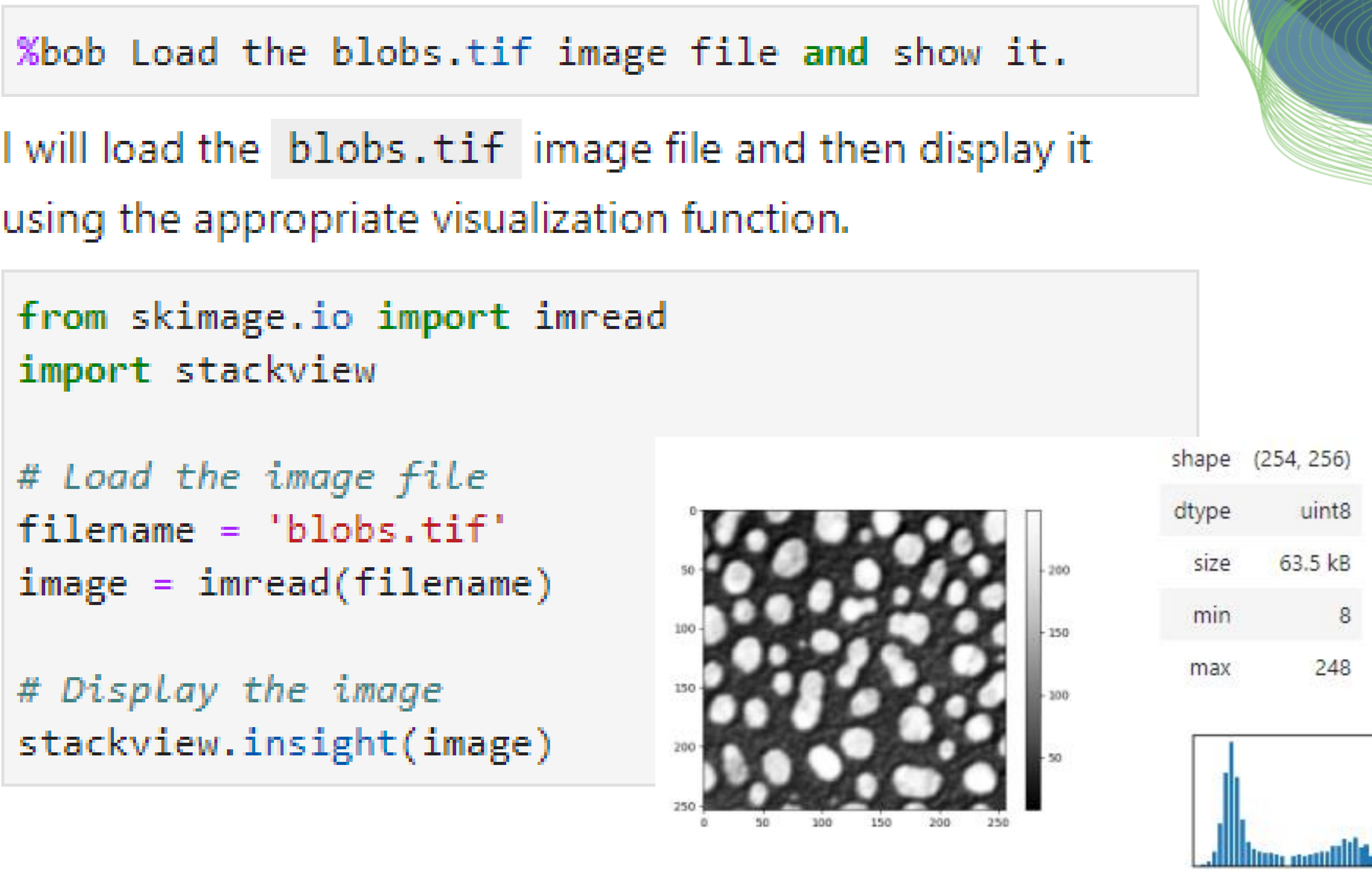


```
from skimage.io import imread
image = imread(“blobs.tif”)
```

Python

Open source assistant: BiA-Bob

- No need to upload your [image] data (-> privacy)
- Multi-agent / -platform capable
- Vision models
- Extensible through plugins
- Integrated in Jupyter



```
%bob Load the blobs.tif image file and show it.
```

I will load the `blobs.tif` image file and then display it using the appropriate visualization function.

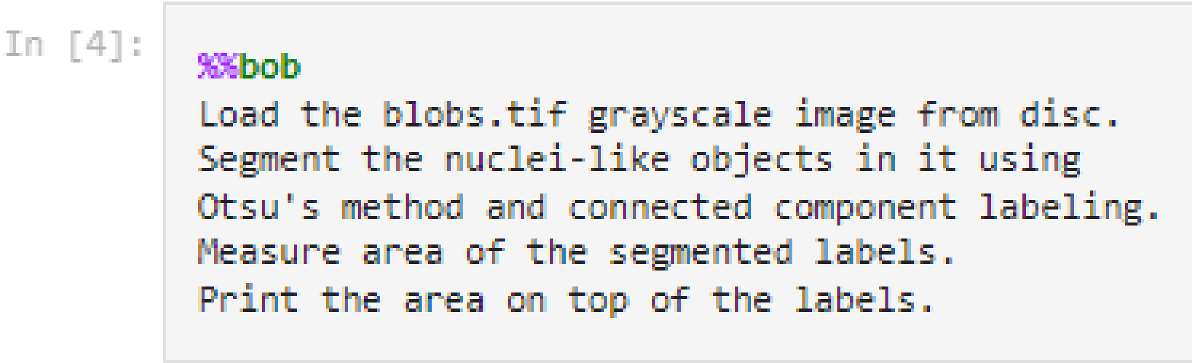
```python
from skimage.io import imread
import stackview

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

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

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

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

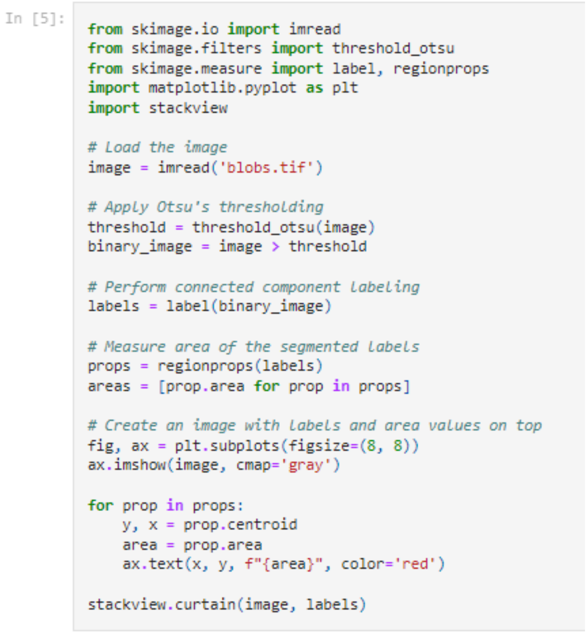
Generating complex code blocks

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



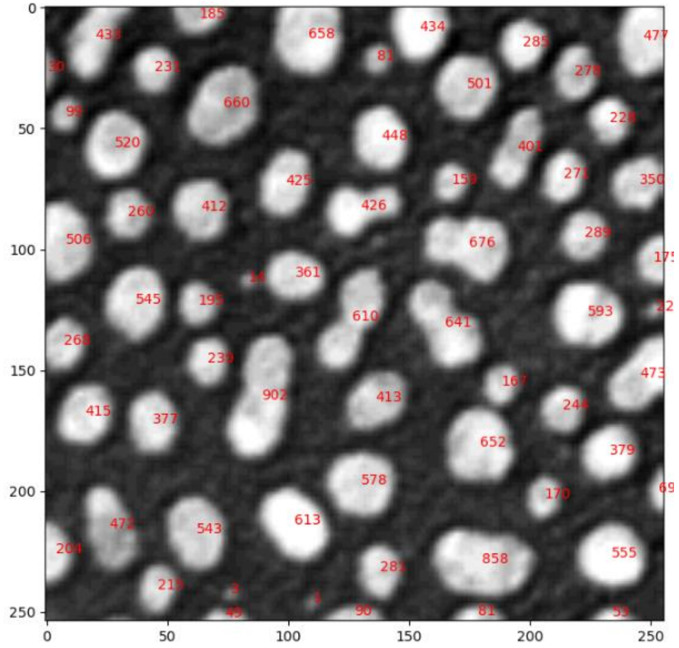
In [4]:

```
%%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]:

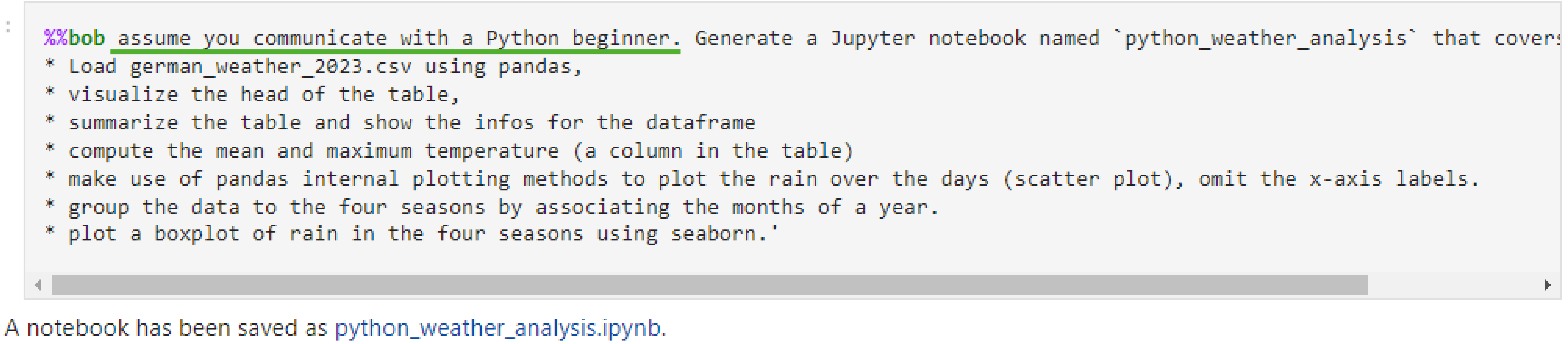
```
from skimage.io import imread
from skimage.filters import threshold_otsu
from skimage.measure import label, regionprops
import matplotlib.pyplot as plt
import stackview

# 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

Generating notebooks

… also great for learning Python



```
%%bob assume you communicate with a Python beginner. Generate a Jupyter notebook named `python_weather_analysis` that cover
* Load german_weather_2023.csv using pandas,
* visualize the head of the table,
* summarize the table and show the infos for the dataframe
* compute the mean and maximum temperature (a column in the table)
* make use of pandas internal plotting methods to plot the rain over the days (scatter plot), omit the x-axis labels.
* group the data to the four seasons by associating the months of a year.
* plot a boxplot of rain in the four seasons using seaborn.'
```

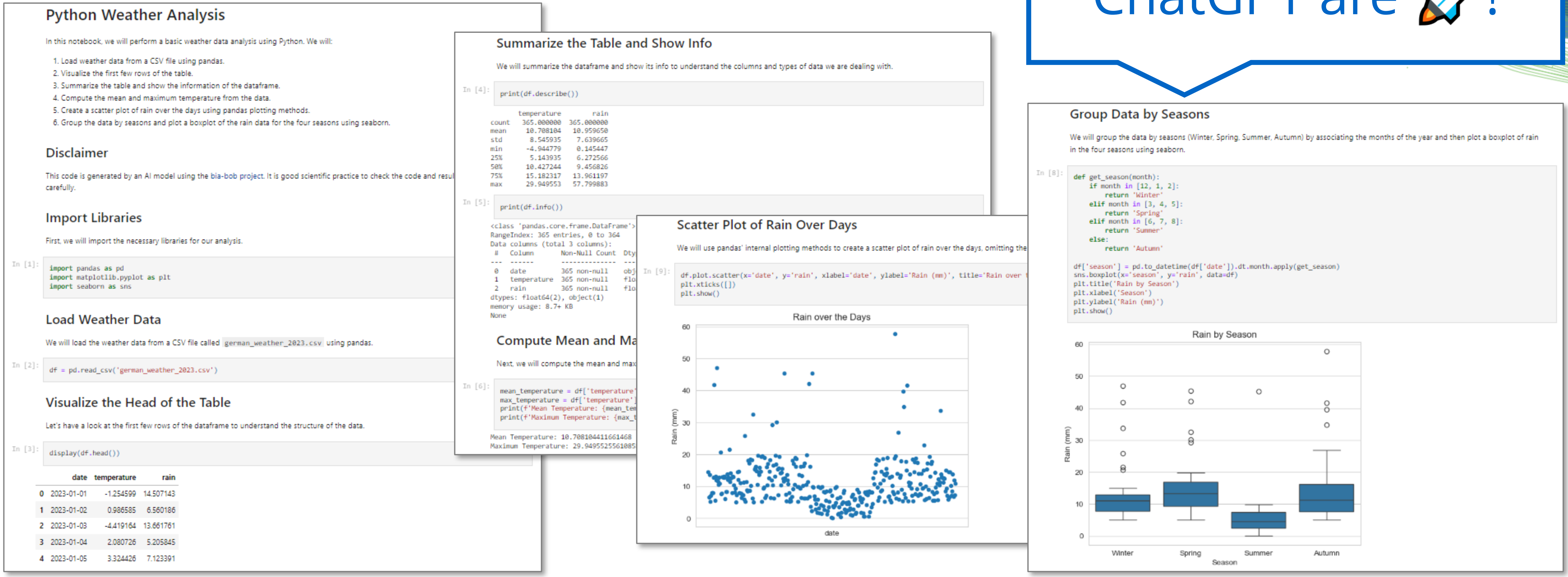
A notebook has been saved as python_weather_analysis.ipynb.

Cropped, licensed CC-BY 4.0 by Matthias Täschner & Robert Haase
https://github.com/ScaDS/Python-training-2024/blob/main/2_tables_plots/python_weather_analysis.ipynb

Generating notebooks

… also great for learning Python

In these kind of tasks, Python and ChatGPT are 🚀!



Python Weather Analysis

In this notebook, we will perform a basic weather data analysis using Python. We will:

1. Load weather data from a CSV file using pandas.
2. Visualize the first few rows of the table.
3. Summarize the table and show the information of the dataframe.
4. Compute the mean and maximum temperature from the data.
5. Create a scatter plot of rain over the days using pandas plotting methods.
6. Group the data by seasons and plot a boxplot of the rain data for the four seasons using seaborn.

Disclaimer

This code is generated by an AI model using the bia-bob project. It is good scientific practice to check the code and resul
carefully.

Import Libraries

First, we will import the necessary libraries for our analysis.

In [1]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

Load Weather Data

We will load the weather data from a CSV file called `german_weather_2023.csv` using pandas.

In [2]:
```
df = pd.read_csv('german_weather_2023.csv')
```

Visualize the Head of the Table

Let's have a look at the first few rows of the dataframe to understand the structure of the data.

In [3]:
```
display(df.head())
```

	date	temperature	rain
0	2023-01-01	-1.254599	14.507143
1	2023-01-02	0.986585	6.560186
2	2023-01-03	-4.419164	13.661761
3	2023-01-04	2.080726	5.205845
4	2023-01-05	3.324426	7.123391

Summarize the Table and Show Info

We will summarize the dataframe and show its info to understand the columns and types of data we are dealing with.

In [4]:
```
print(df.describe())
```

```
       temperature        rain
count   365.000000  365.000000
mean     10.708104   10.959650
std       8.545935    7.639665
min      -4.944779    0.145447
25%       5.143935    6.272566
50%      10.427244    9.456826
75%      15.182317   13.961197
max      29.949553   57.799883
```

In [5]:
```
print(df.info())
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 365 entries, 0 to 364
Data columns (total 3 columns):
 #   Column       Non-Null Count  Dty
---  ------       --------------  ---
 0   date         365 non-null    obj
 1   temperature  365 non-null    flo
 2   rain         365 non-null    flo
dtypes: float64(2), object(1)
memory usage: 8.7+ KB
None
```

Compute Mean and Ma

Next, we will compute the mean and max

In [6]:
```
mean_temperature = df['temperature'
max_temperature = df['temperature']
print(f'Mean Temperature: {mean_tem
print(f'Maximum Temperature: {max_t
```

```
Mean Temperature: 10.708104411661468
Maximum Temperature: 29.9495525561085
```

Scatter Plot of Rain Over Days

We will use pandas' internal plotting methods to create a scatter plot of rain over the days, omitting the

In [9]:
```
df.plot.scatter(x='date', y='rain', xlabel='date', ylabel='Rain (mm)', title='Rain over
plt.xticks([])
plt.show()
```

Group Data by Seasons

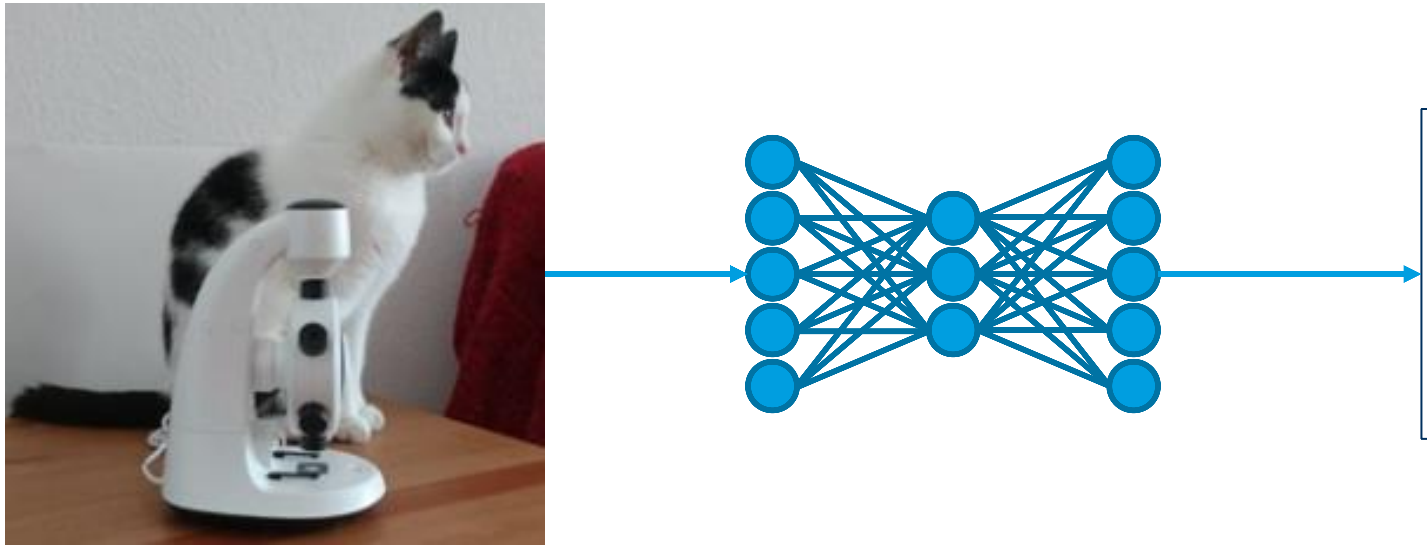
We will group the data by seasons (Winter, Spring, Summer, Autumn) by associating the months of the year and then plot a boxplot of rain in the four seasons using seaborn.

In [8]:
```
def get_season(month):
    if month in [12, 1, 2]:
        return 'Winter'
    elif month in [3, 4, 5]:
        return 'Spring'
    elif month in [6, 7, 8]:
        return 'Summer'
    else:
        return 'Autumn'

df['season'] = pd.to_datetime(df['date']).dt.month.apply(get_season)
sns.boxplot(x='season', y='rain', data=df)
plt.title('Rain by Season')
plt.xlabel('Season')
plt.ylabel('Rain (mm)')
plt.show()
```

Cropped, licensed CC-BY 4.0 by Matthias Täschner & Robert Haase
https://github.com/ScaDS/Python-training-2024/blob/main/2_tables_plots/python_weather_analysis.ipynb

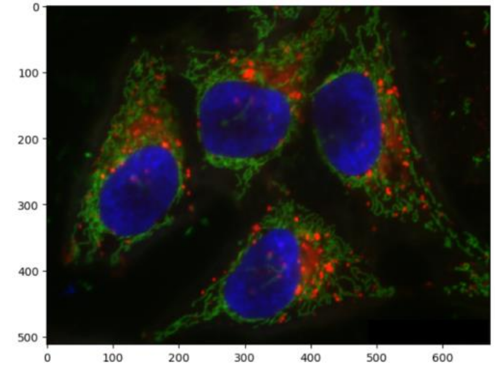
Vision Language Models

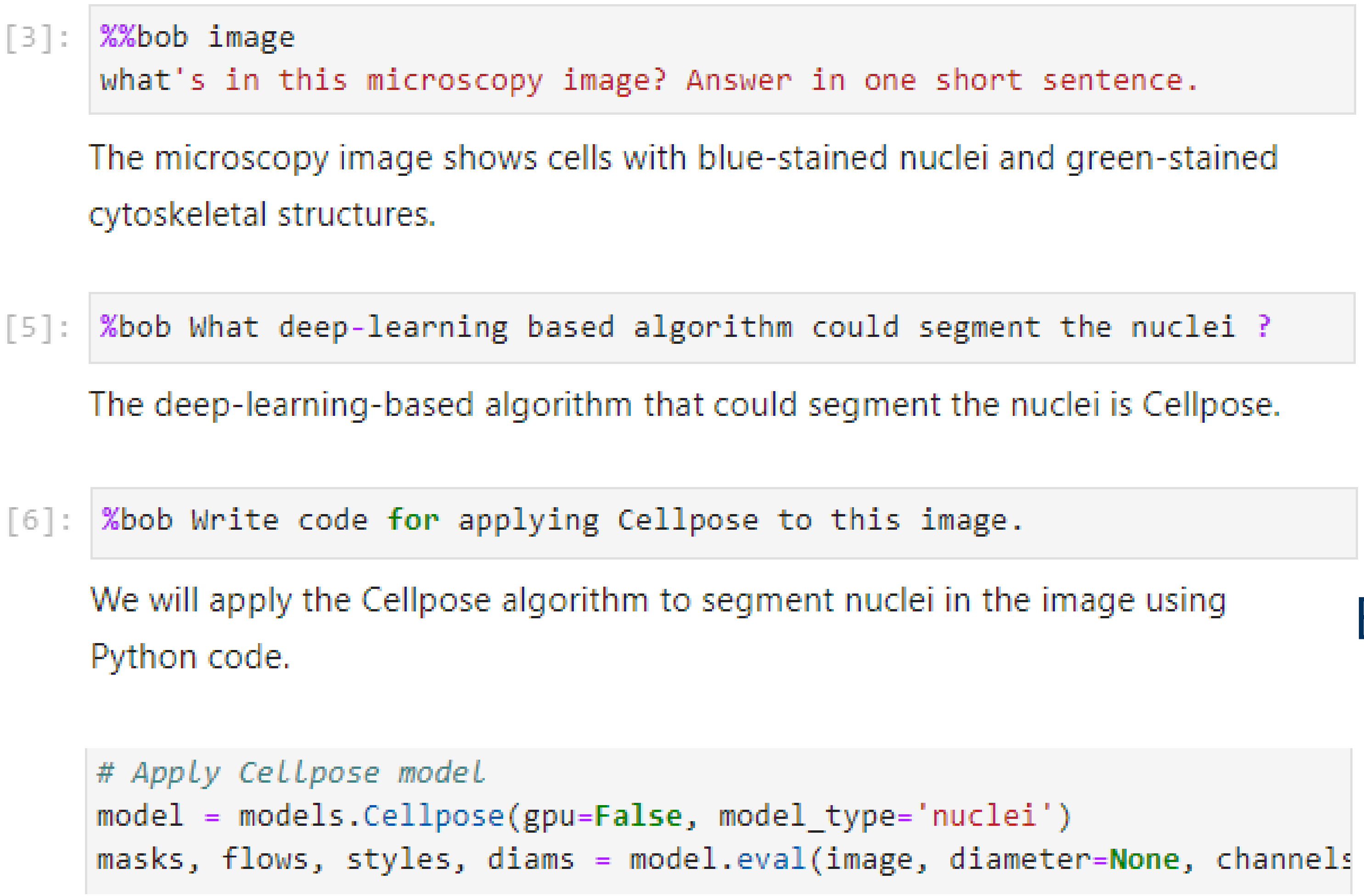
- Classifying images 🥱
- Describing images



A picture of a cat and a microscope

Vision language models





```
[3]: %%bob image
     what's in this microscopy image? Answer in one short sentence.
```

The microscopy image shows cells with blue-stained nuclei and green-stained cytoskeletal structures.

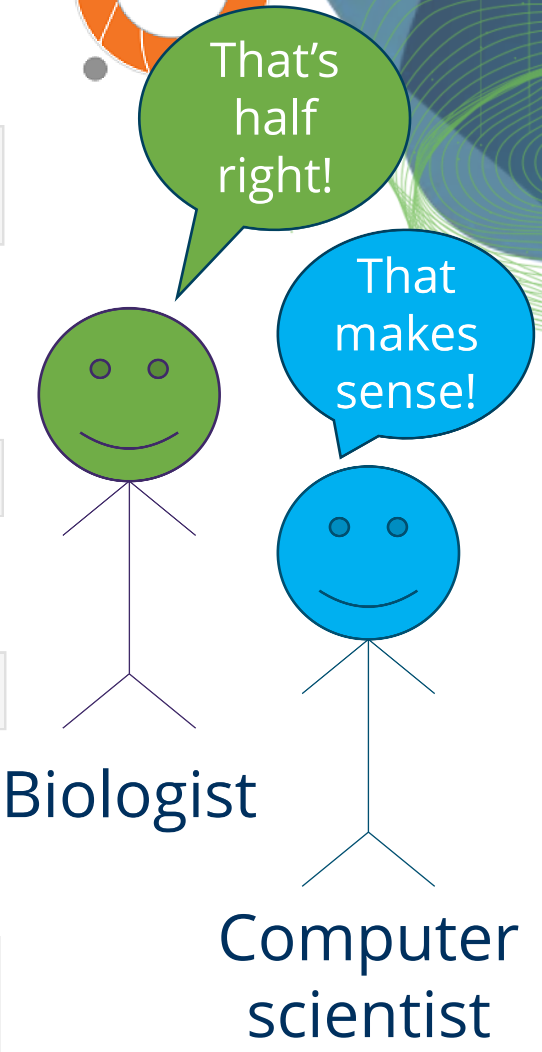
```
[5]: %bob What deep-learning based algorithm could segment the nuclei ?
```

The deep-learning-based algorithm that could segment the nuclei is Cellpose.

```
[6]: %bob Write code for applying Cellpose to this image.
```

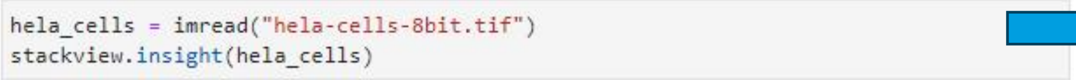
We will apply the Cellpose algorithm to segment nuclei in the image using Python code.

```
# Apply Cellpose model
model = models.Cellpose(gpu=False, model_type='nuclei')
masks, flows, styles, diams = model.eval(image, diameter=None, channels
```

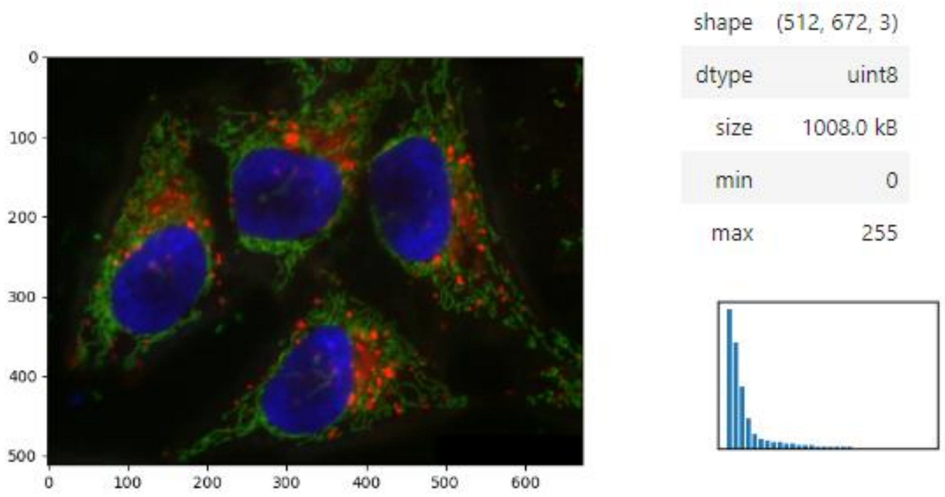


Generating notebooks using vision models

Ask %%bob to generate a Jupyter notebook

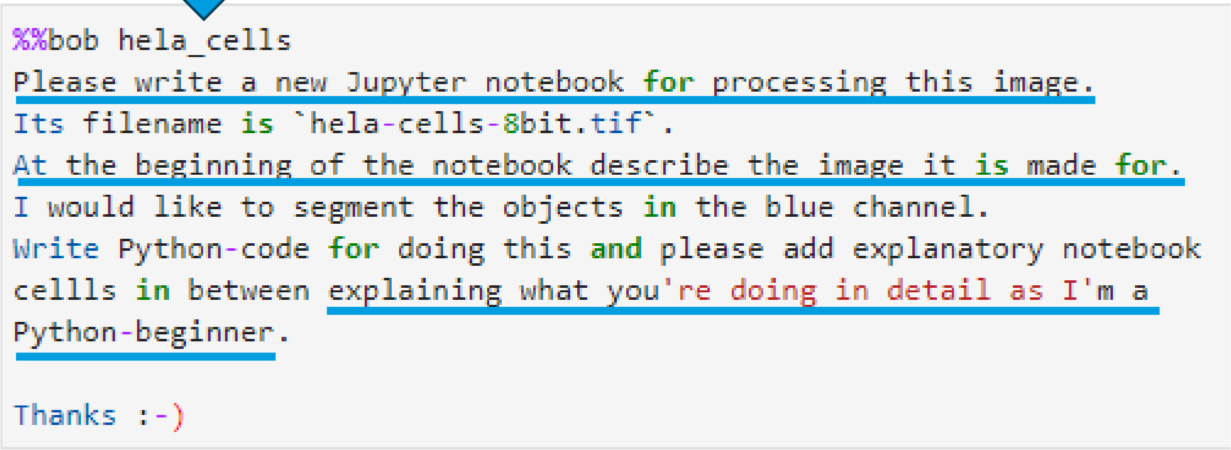


```
hela_cells = imread("hela-cells-8bit.tif")
stackview.insight(hela_cells)
```

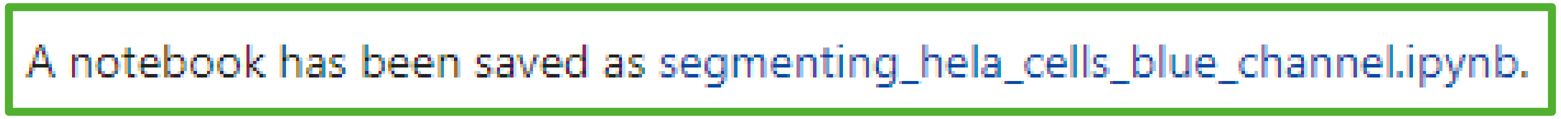


shape	(512, 672, 3)
dtype	uint8
size	1008.0 kB
min	0
max	255

Present Bob an image like this



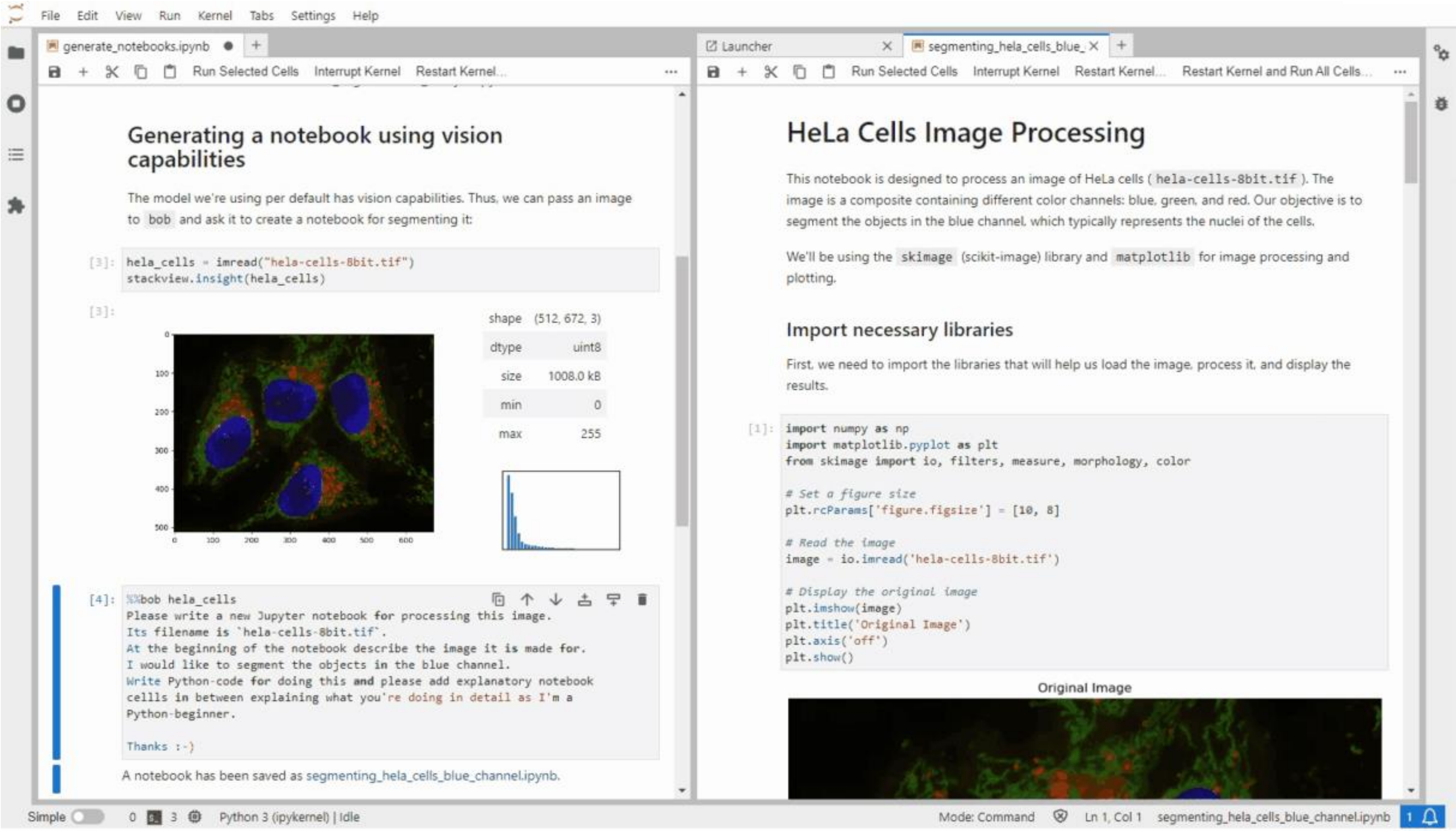
```
%%bob hela_cells
Please write a new Jupyter notebook for processing this image.
Its filename is `hela-cells-8bit.tif`.
At the beginning of the notebook describe the image it is made for.
I would like to segment the objects in the blue channel.
Write Python-code for doing this and please add explanatory notebook
cellls in between explaining what you're doing in detail as I'm a
Python-beginner.

Thanks :-)
```



A notebook has been saved as segmenting_hela_cells_blue_channel.ipynb.

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

Generating notebooks using vision models



Generating a notebook using vision capabilities

The model we're using per default has vision capabilities. Thus, we can pass an image to `bob` and ask it to create a notebook for segmenting it:

```
[3]: hela_cells = imread("hela-cells-8bit.tif")
     stackview.insight(hela_cells)
```

[3]:

shape	(512, 672, 3)
dtype	uint8
size	1008.0 kB
min	0
max	255

```
[4]: %%bob hela_cells
     Please write a new Jupyter notebook for processing this image.
     Its filename is `hela-cells-8bit.tif`.
     At the beginning of the notebook describe the image it is made for.
     I would like to segment the objects in the blue channel.
     Write Python-code for doing this and please add explanatory notebook
     cellls in between explaining what you're doing in detail as I'm a
     Python-beginner.

     Thanks :-)
```

A notebook has been saved as segmenting_hela_cells_blue_channel.ipynb.

HeLa Cells Image Processing

This notebook is designed to process an image of HeLa cells (`hela-cells-8bit.tif`). The image is a composite containing different color channels: blue, green, and red. Our objective is to segment the objects in the blue channel, which typically represents the nuclei of the cells.

We'll be using the `skimage` (scikit-image) library and `matplotlib` for image processing and plotting.

Import necessary libraries

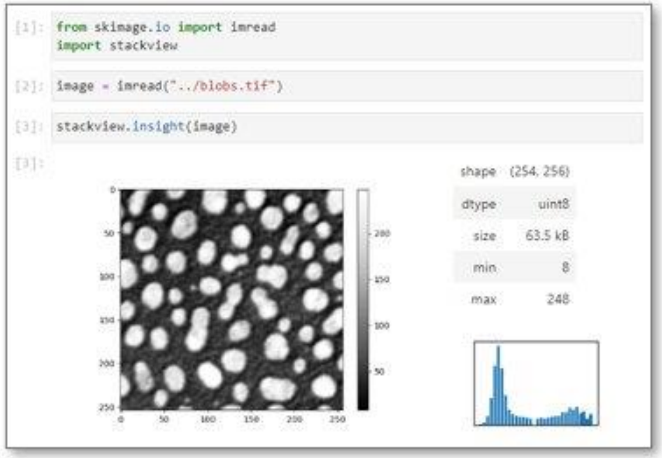
First, we need to import the libraries that will help us load the image, process it, and display the results.

```
[1]: import numpy as np
     import matplotlib.pyplot as plt
     from skimage import io, filters, measure, morphology, color

     # Set a figure size
     plt.rcParams['figure.figsize'] = [10, 8]

     # Read the image
     image = io.imread('hela-cells-8bit.tif')

     # Display the original image
     plt.imshow(image)
     plt.title('Original Image')
     plt.axis('off')
     plt.show()
```

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

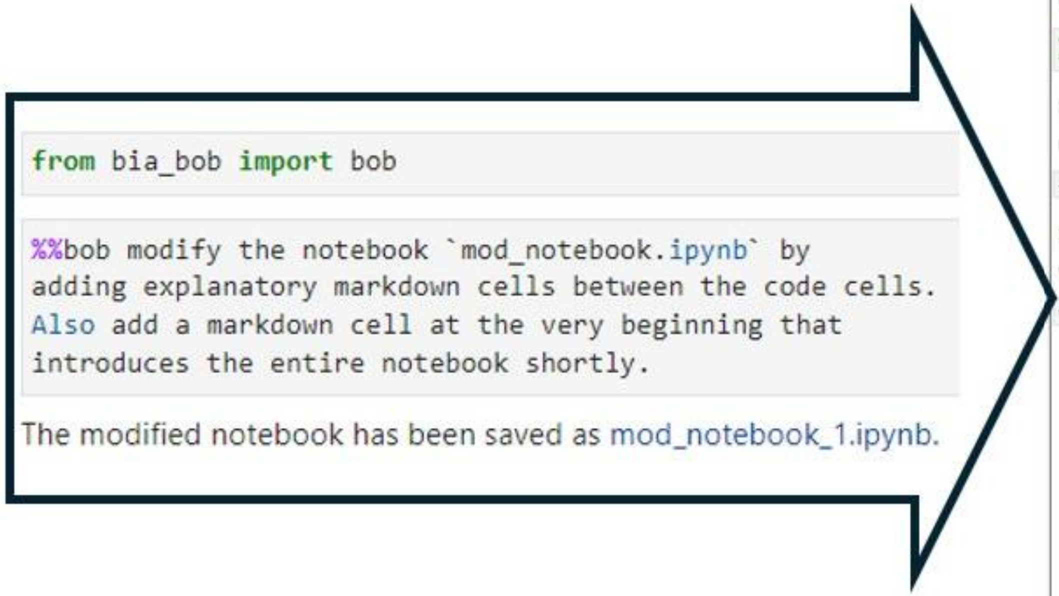
Optimizing documentation

E.g. to make code more readable



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

[2]: image = imread("../blobs.tif")

[3]: stackview.insight(image)

[3]:
```

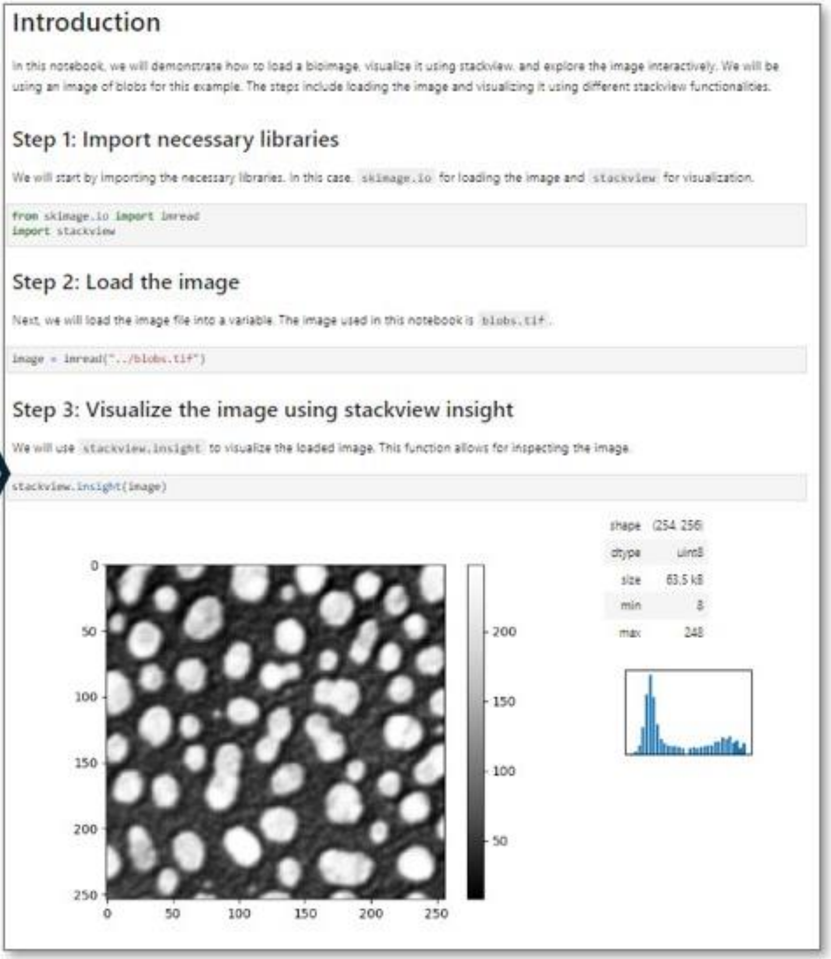
```
shape  (254, 256)
dtype       uint8
size      63.5 kB
min             8
max           248
```



```
from bia_bob import bob
```

```
%%bob modify the notebook `mod_notebook.ipynb` by
adding explanatory markdown cells between the code cells.
Also add a markdown cell at the very beginning that
introduces the entire notebook shortly.
```

The modified notebook has been saved as mod_notebook_1.ipynb.



Introduction

In this notebook, we will demonstrate how to load a bioimage, visualize it using stackview, and explore the image interactively. We will be using an image of blobs for this example. The steps include loading the image and visualizing it using different stackview functionalities.

Step 1: Import necessary libraries

We will start by importing the necessary libraries. In this case, `skimage.io` for loading the image and `stackview` for visualization.

```
from skimage.io import imread
import stackview
```

Step 2: Load the image

Next, we will load the image file into a variable. The image used in this notebook is `blobs.tif`.

```
image = imread("../blobs.tif")
```

Step 3: Visualize the image using stackview insight

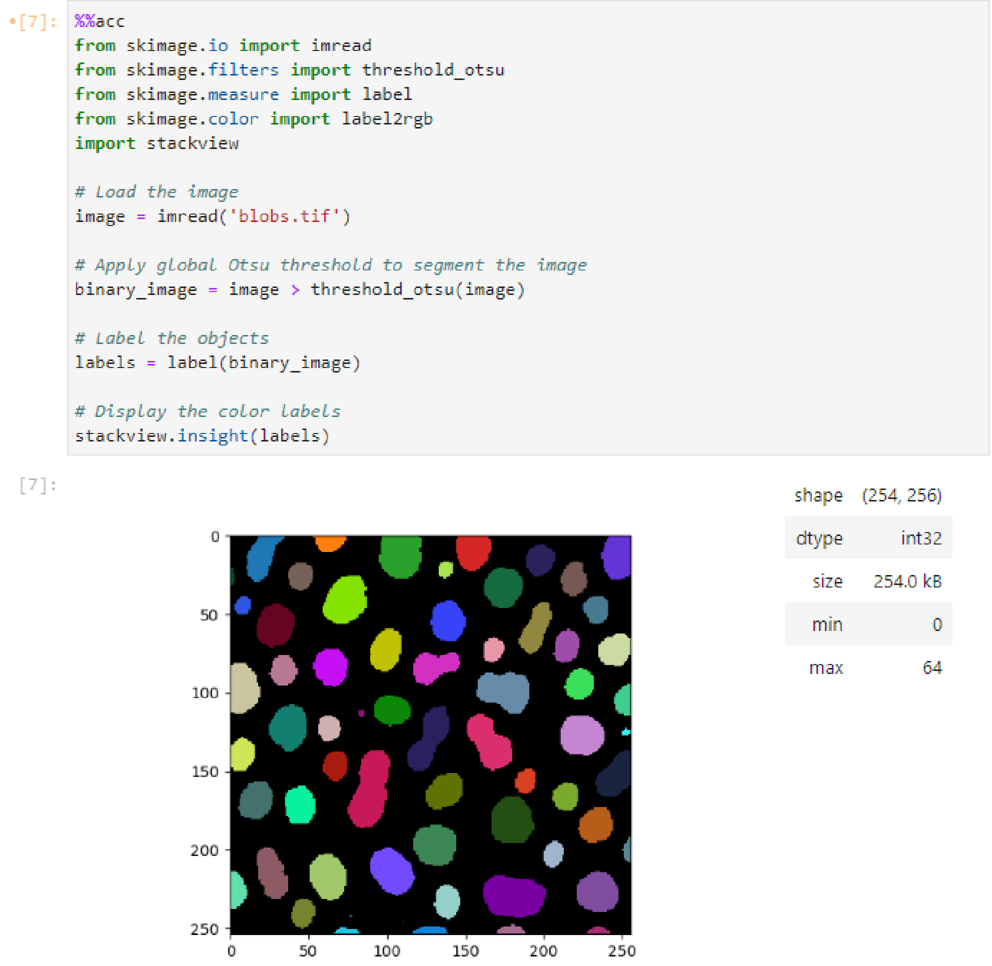
We will use `stackview.insight` to visualize the loaded image. This function allows for inspecting the image.

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

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

GPU-Accelerating code

Original:

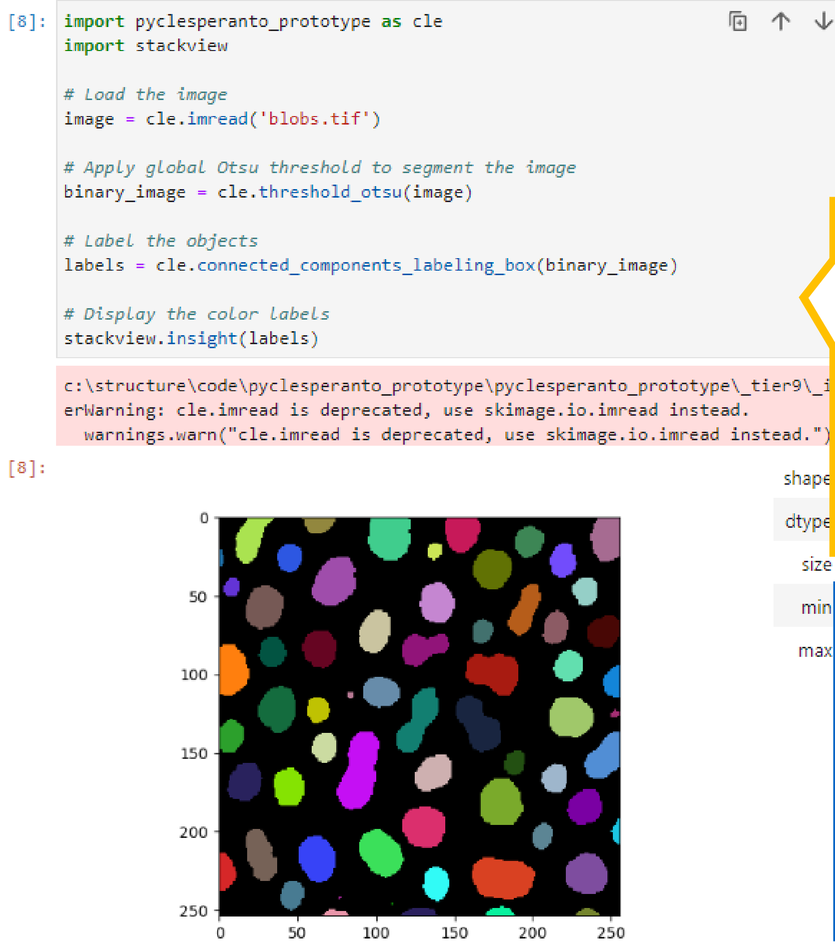


```
•[7]: %%acc
from skimage.io import imread
from skimage.filters import threshold_otsu
from skimage.measure import label
from skimage.color import label2rgb
import stackview

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

# Apply global Otsu threshold to segment the image
binary_image = image > threshold_otsu(image)

# Label the objects
labels = label(binary_image)

# Display the color labels
stackview.insight(labels)
```

[7]:

shape	(254, 256)
dtype	int32
size	254.0 kB
min	0
max	64

Replacement:



```
[8]: import pyclesperanto_prototype as cle
import stackview

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

# Apply global Otsu threshold to segment the image
binary_image = cle.threshold_otsu(image)

# Label the objects
labels = cle.connected_components_labeling_box(binary_image)

# Display the color labels
stackview.insight(labels)
```

```
c:\structure\code\pyclesperanto_prototype\pyclesperanto_prototype\_tier9\_i
erWarning: cle.imread is deprecated, use skimage.io.imread instead.
  warnings.warn("cle.imread is deprecated, use skimage.io.imread instead.")
```

[8]:

shape
dtype
size 254.0 kB
min
max

It‘s our responsibility that results are comparable!

https://link.springer.com/chapter/10.1007/978-3-030-76394-7_5

Under the hood: prompt engineering

Context-dependent system prompt considering

- local variables and functions
- installed python libraries
- chat history

+ your prompt

You are a extremely talented bioimage analyst and you use Python to solve your tasks …

…

Python specific code snippets
If the user asks for those simple tasks, use these code snippets.

* Load an image file from disc and store it in a variable:
```
from skimage.io import imread
image = imread(filename)
```

…

Todos
Answer your response in three sections:

1. Summary: First provide a short summary of the task.
2. Plan: Provide a concise step-by-step plan without any code.
3. Code: Provide the code.

About 6500 tokens (≈words)

Benchmarking LLMs for Bio-image Analysis

Which LLM should I pay for?

Is GPT-4o better than Claude?

Do LLMs introduce bias?

How can we validate LLMs for BiA?

How *good* are LLMs for Bio-image Analysis?

Can LLMs act according to good scientific practice?

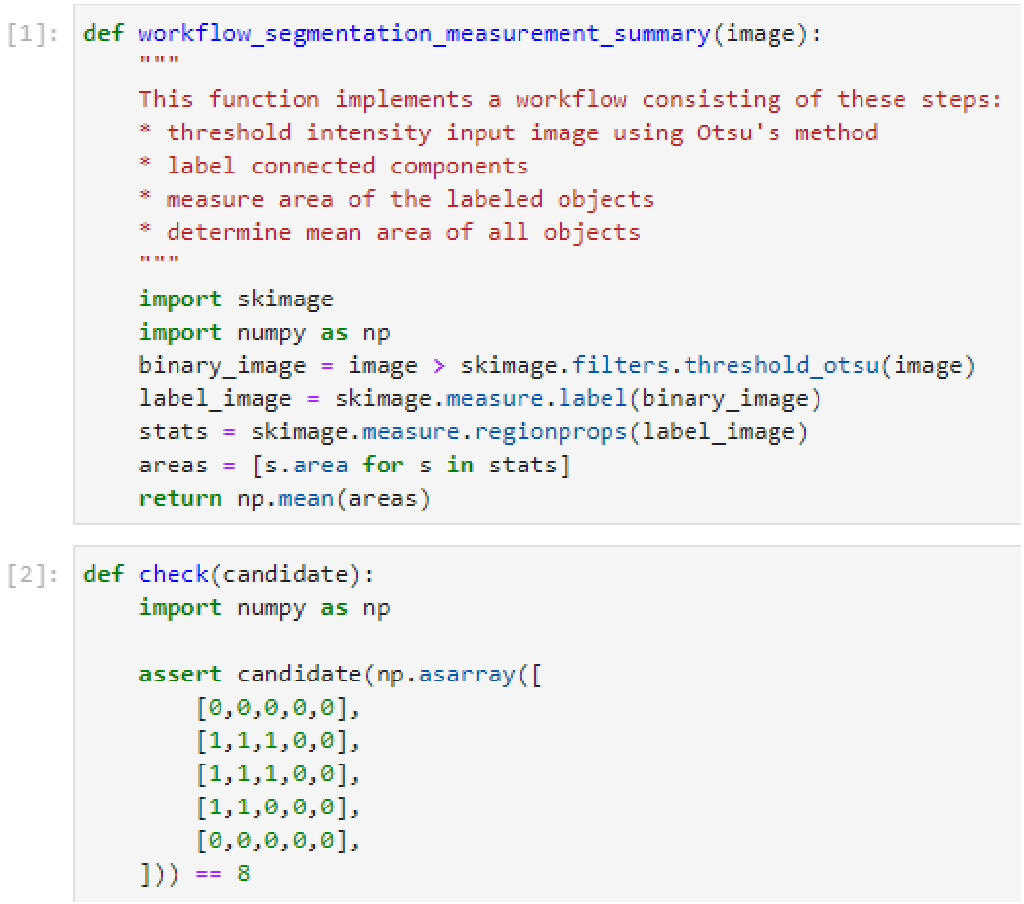
Will we all be replaced by AI anytime soon?

What are the limits of the LLM technology?

How can we validate specific LLM output without ground truth?

Benchmarking LLMs for Bio-image Analysis

Example test-case inspired by HumaEval (Chen et al 2021)



```
[1]: def workflow_segmentation_measurement_summary(image):
         """
         This function implements a workflow consisting of these steps:
         * threshold intensity input image using Otsu's method
         * label connected components
         * measure area of the labeled objects
         * determine mean area of all objects
         """
         import skimage
         import numpy as np
         binary_image = image > skimage.filters.threshold_otsu(image)
         label_image = skimage.measure.label(binary_image)
         stats = skimage.measure.regionprops(label_image)
         areas = [s.area for s in stats]
         return np.mean(areas)
```

```
[2]: def check(candidate):
         import numpy as np

         assert candidate(np.asarray([
             [0,0,0,0,0],
             [1,1,1,0,0],
             [1,1,1,0,0],
             [1,1,0,0,0],
             [0,0,0,0,0],
         ])) == 8
```

Prompt

Reference solution

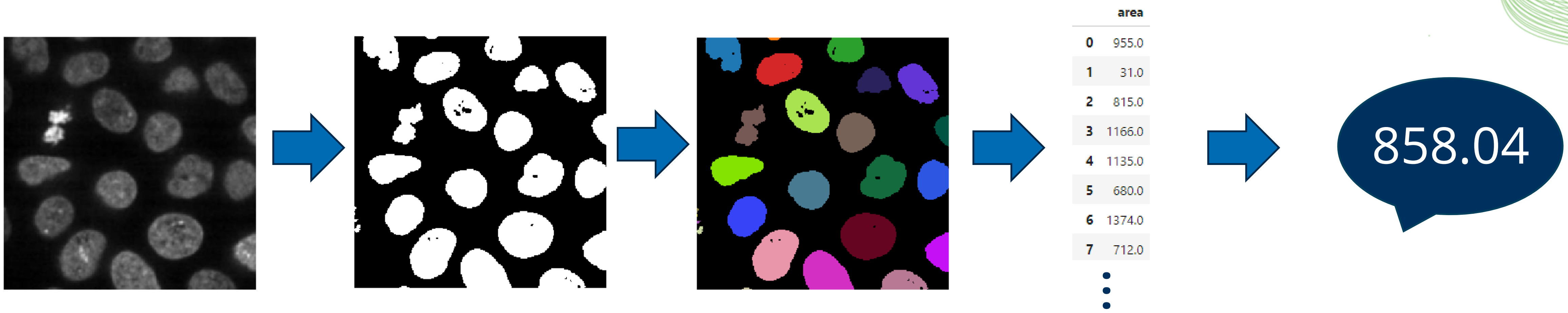
Unit test (excerpt)

We formulated 57 of such test-cases (yet)

Chen at al 2021: https://arxiv.org/abs/2107.03374
https://www.biorxiv.org/content/10.1101/2024.04.19.590278v1
https://github.com/haesleinhuepf/human-eval-bia

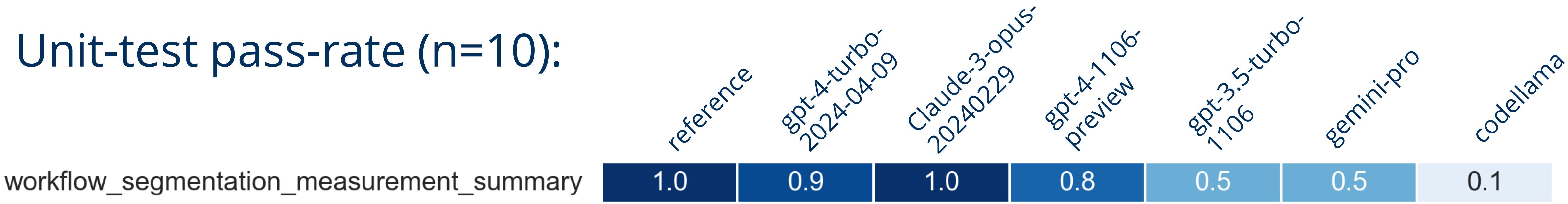
Benchmarking LLMs for Bio-image Analysis

Use case: 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
⋮	

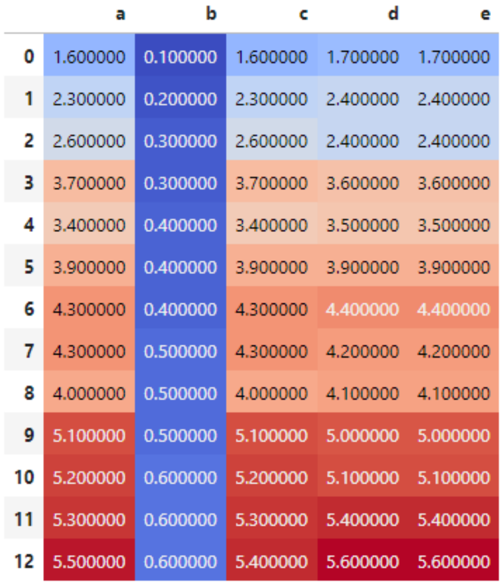
Unit-test pass-rate (n=10):



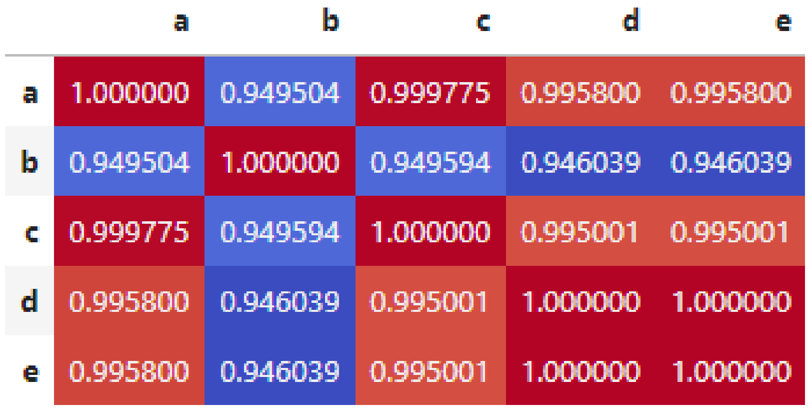
	reference	gpt-4-turbo-2024-04-09	Claude-3-opus-20240229	gpt-4-1106-preview	gpt-3.5-turbo-1106	gemini-pro	codellama
workflow_segmentation_measurement_summary	1.0	0.9	1.0	0.8	0.5	0.5	0.1

Benchmarking LLMs for Bio-image Analysis

Use-case: compute the correlation matrix

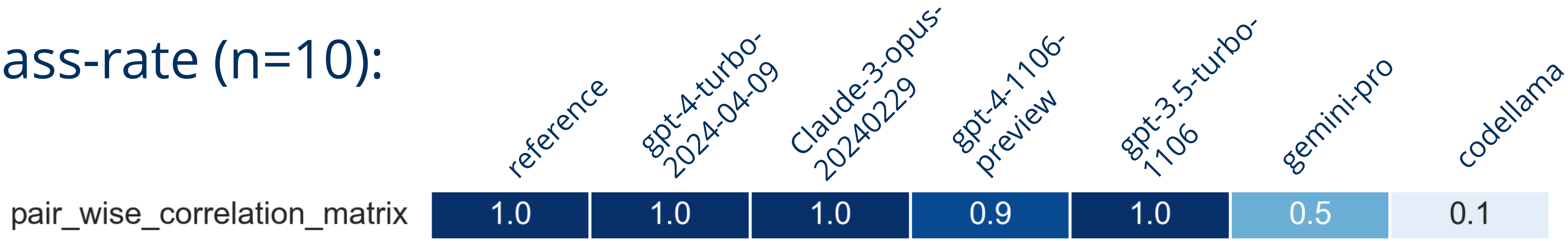


	a	b	c	d	e
0	1.600000	0.100000	1.600000	1.700000	1.700000
1	2.300000	0.200000	2.300000	2.400000	2.400000
2	2.600000	0.300000	2.600000	2.400000	2.400000
3	3.700000	0.300000	3.700000	3.600000	3.600000
4	3.400000	0.400000	3.400000	3.500000	3.500000
5	3.900000	0.400000	3.900000	3.900000	3.900000
6	4.300000	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):

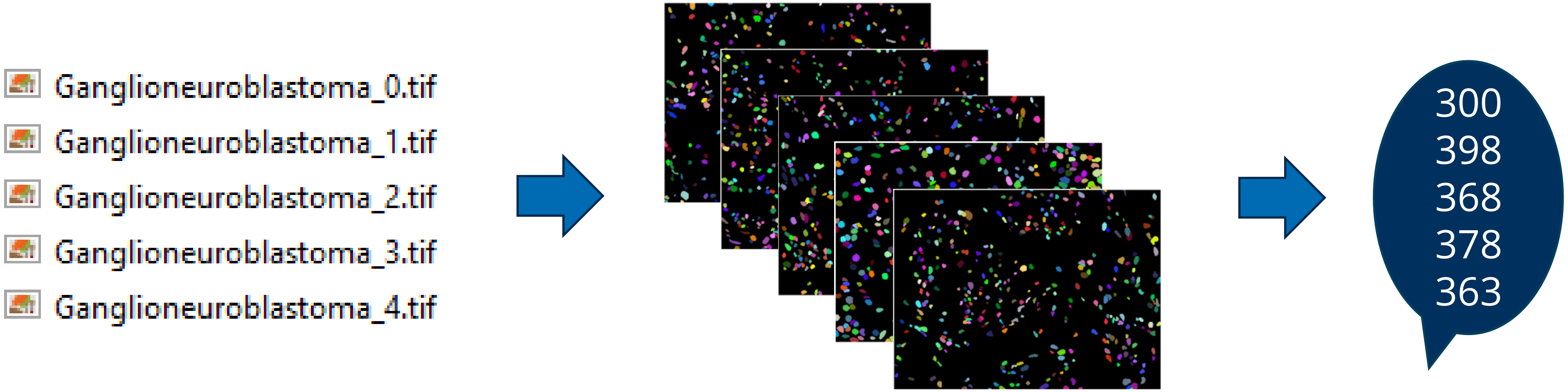


	reference	gpt-4-turbo-2024-04-09	Claude-3-opus-20240229	gpt-4-1106-preview	gpt-3.5-turbo-1106	gemini-pro	codellama
pair_wise_correlation_matrix	1.0	1.0	1.0	0.9	1.0	0.5	0.1

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

Benchmarking LLMs for Bio-image Analysis

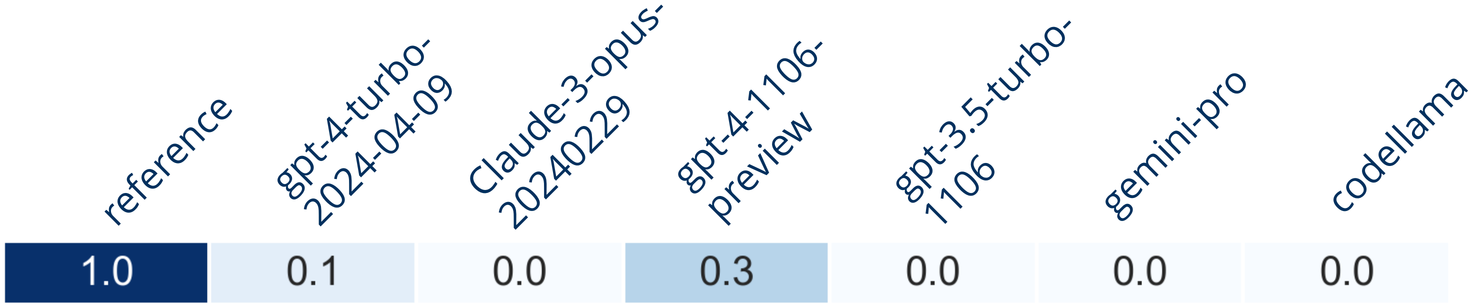
Use case: Count segmented objects in a folder of segmentation results.



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):

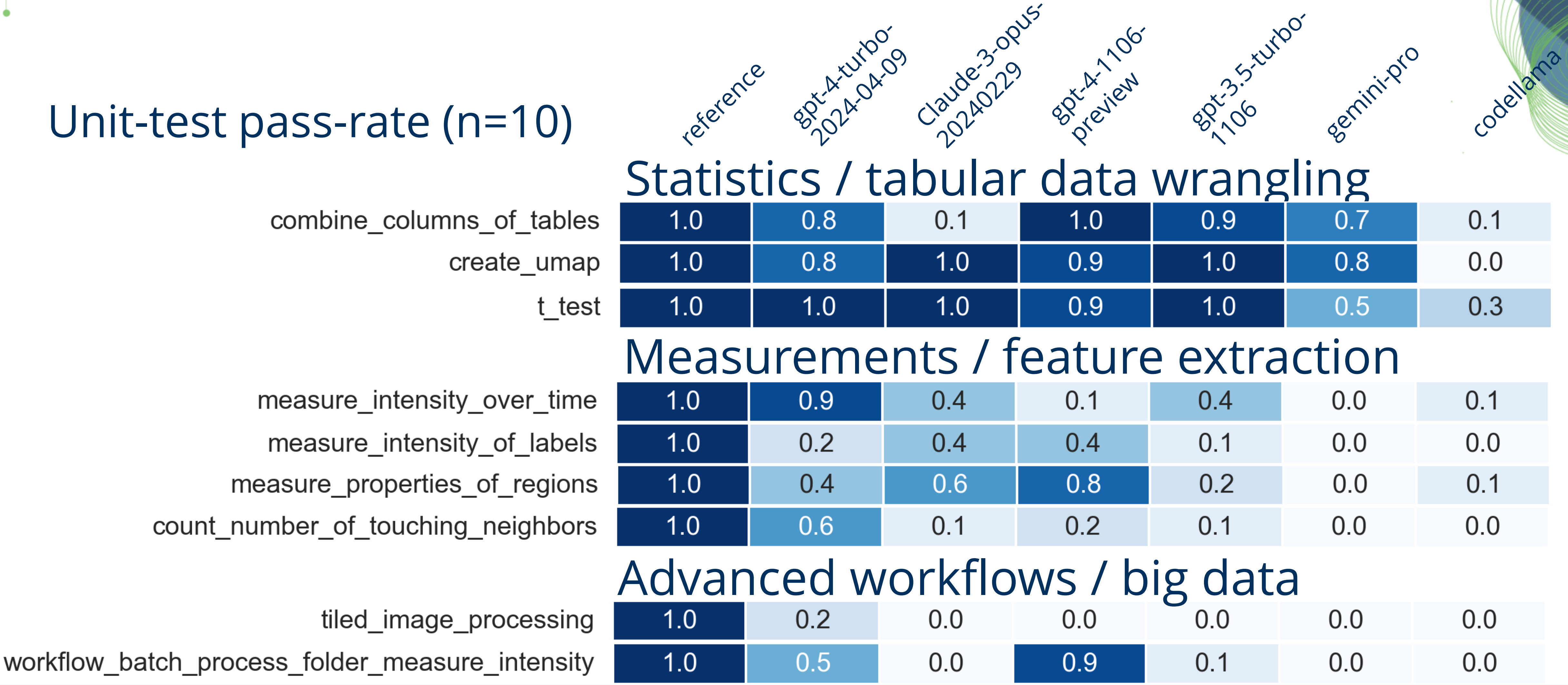


	reference	gpt-4-turbo-2024-04-09	Claude-3-opus-20240229	gpt-4-1106-preview	gpt-3.5-turbo-1106	gemini-pro	codellama
workflow_batch_process_folder_count_labels	1.0	0.1	0.0	0.3	0.0	0.0	0.0

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

Benchmarking LLMs for Bio-image Analysis

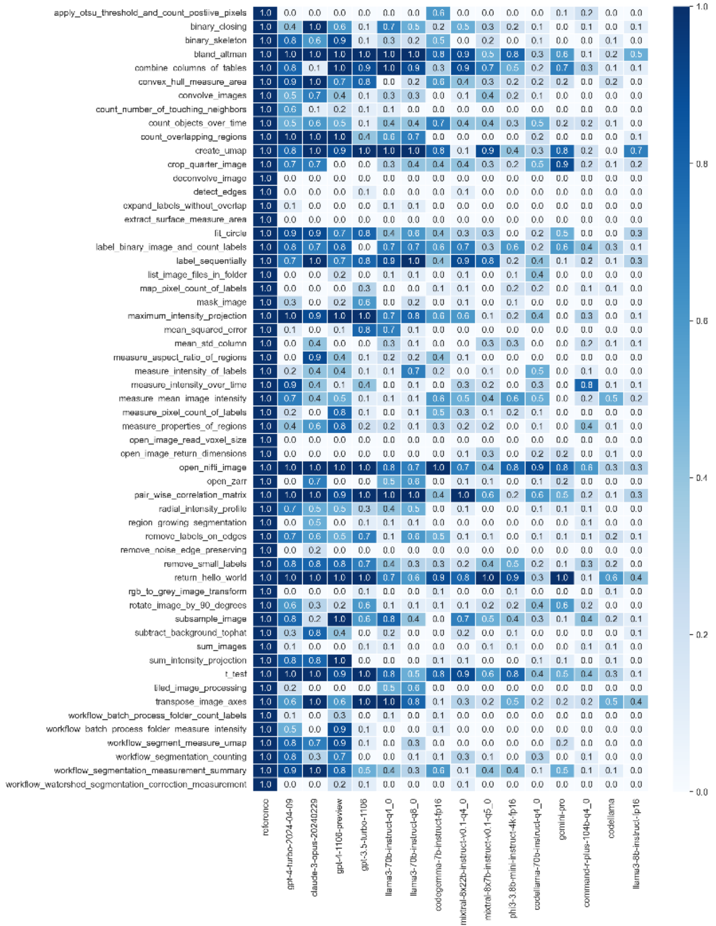
Unit-test pass-rate (n=10)

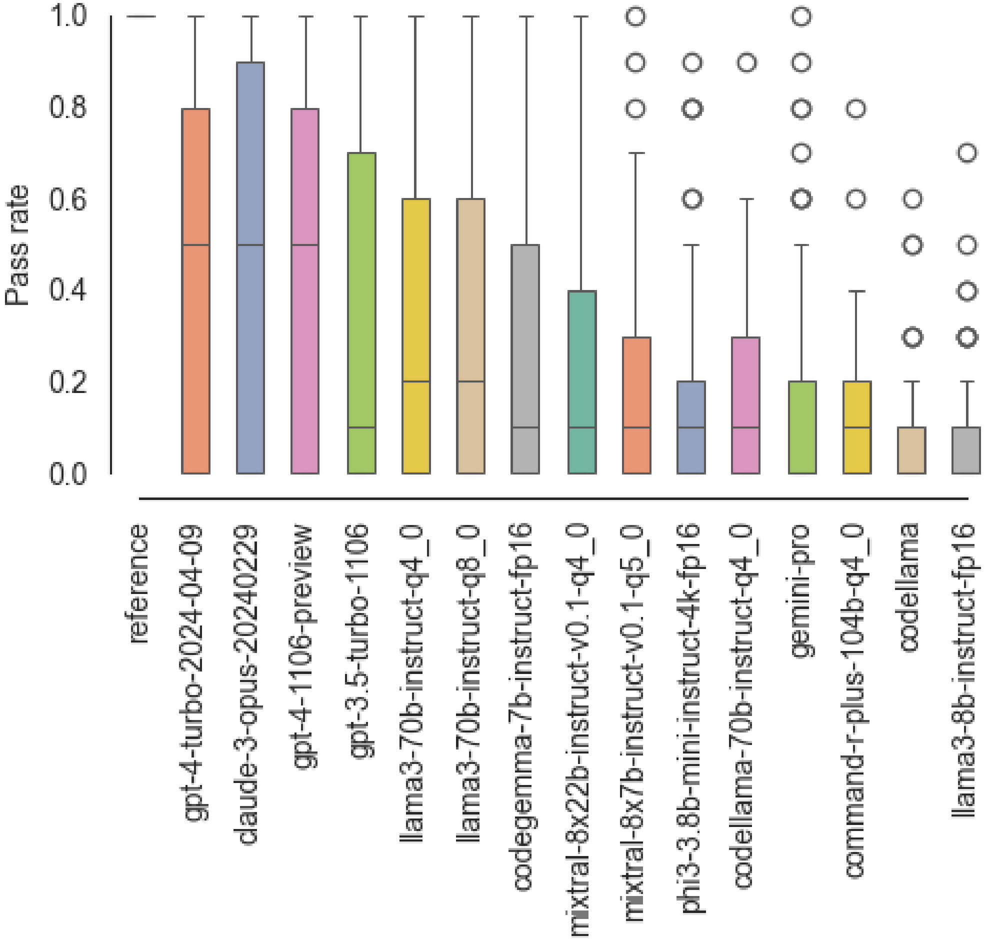


	reference	gpt-4-turbo-2024-04-09	Claude-3-opus-20240229	gpt-4-1106-preview	gpt-3.5-turbo-1106	gemini-pro	codellama
Statistics / tabular data wrangling							
combine_columns_of_tables	1.0	0.8	0.1	1.0	0.9	0.7	0.1
create_umap	1.0	0.8	1.0	0.9	1.0	0.8	0.0
t_test	1.0	1.0	1.0	0.9	1.0	0.5	0.3
Measurements / feature extraction							
measure_intensity_over_time	1.0	0.9	0.4	0.1	0.4	0.0	0.1
measure_intensity_of_labels	1.0	0.2	0.4	0.4	0.1	0.0	0.0
measure_properties_of_regions	1.0	0.4	0.6	0.8	0.2	0.0	0.1
count_number_of_touching_neighbors	1.0	0.6	0.1	0.2	0.1	0.0	0.0
Advanced workflows / big data							
tiled_image_processing	1.0	0.2	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

Benchmarking LLMs for Bio-image Analysis

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

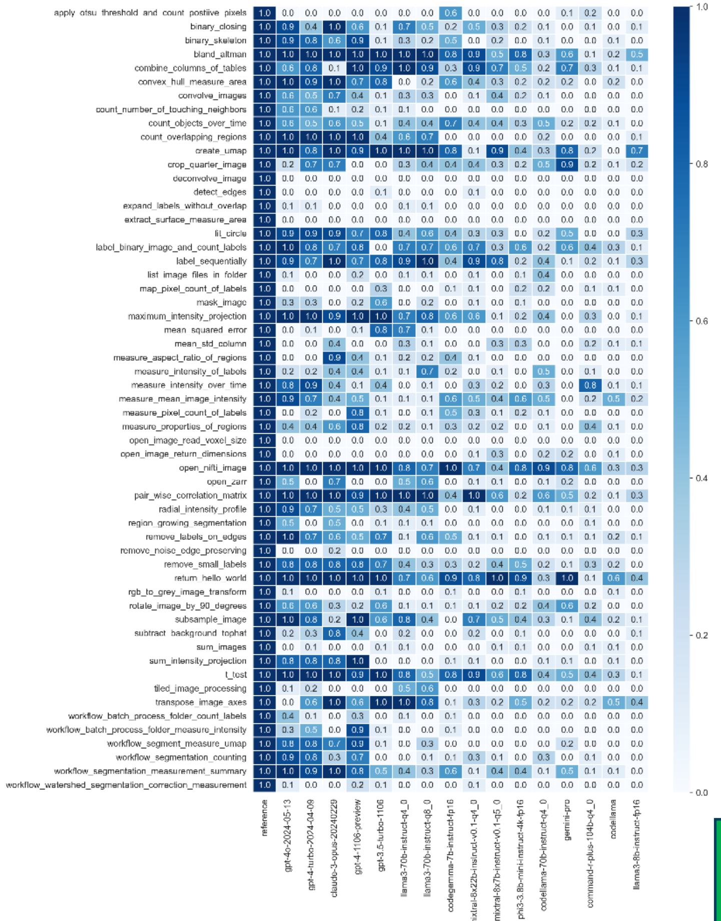




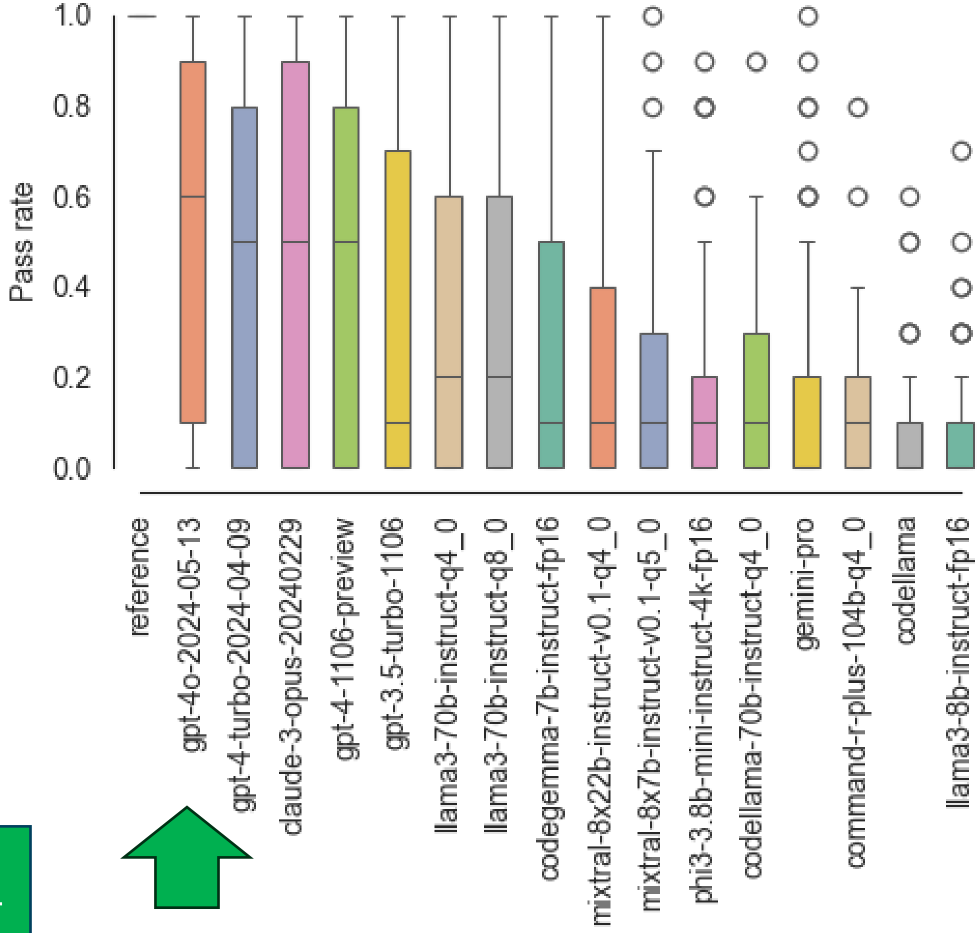
https://www.biorxiv.org/content/10.1101/2024.04.19.590278v1
https://github.com/haesleinhuepf/human-eval-bia

Benchmarking LLMs for Bio-image Analysis

Summary: 57 use-cases (yet), 16 LLMs (yet), n=10



	reference	gpt-4o-2024-05-13	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	0.0	0.6	0.0	0.0	0.0	0.0	0.1	0.2	0.0	0.0
binary_closing	1.0	0.9	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	0.9	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	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	0.6	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	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	0.6	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	0.6	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	0.6	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	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	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	0.2	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	0.0
detect_edges	1.0	0.0	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	0.1	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	0.0
fit_circle	1.0	0.9	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	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	0.9	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	0.1	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	0.0	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	0.3	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	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	0.0	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	0.0	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	0.0	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	0.2	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	0.8	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	0.9	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	0.0	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	0.4	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	0.0
open_image_return_dimensions	1.0	0.0	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	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	0.5	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	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	0.9	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	0.5	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	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	0.0	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	0.8	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	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	0.1	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	0.6	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	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	0.2	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	0.0	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	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	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	0.1	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	0.0	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	0.4	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	0.3	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	0.8	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	0.9	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	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	0.1	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

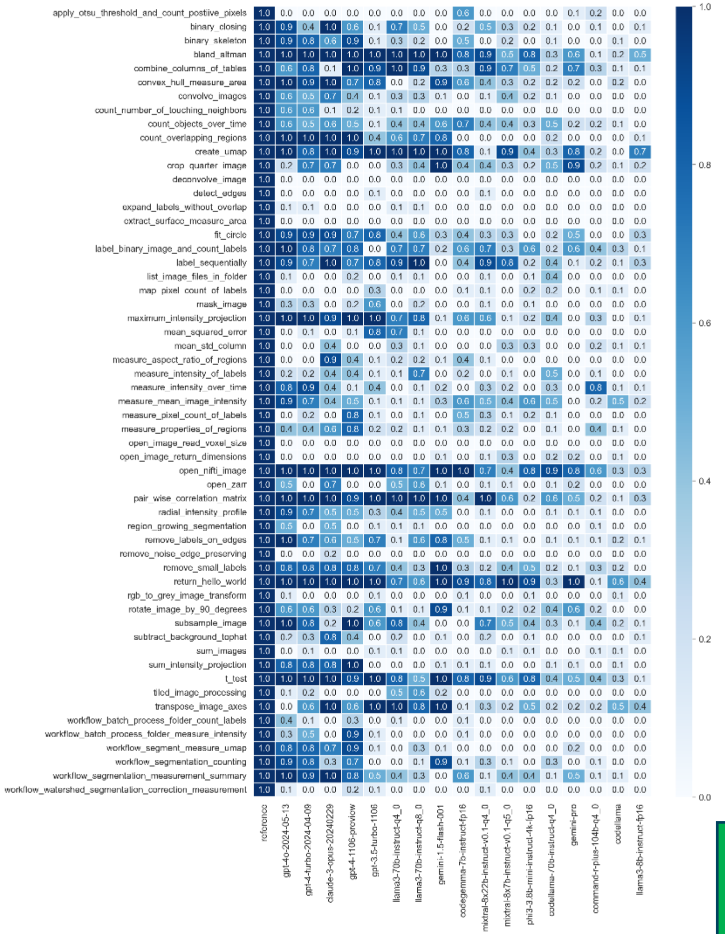


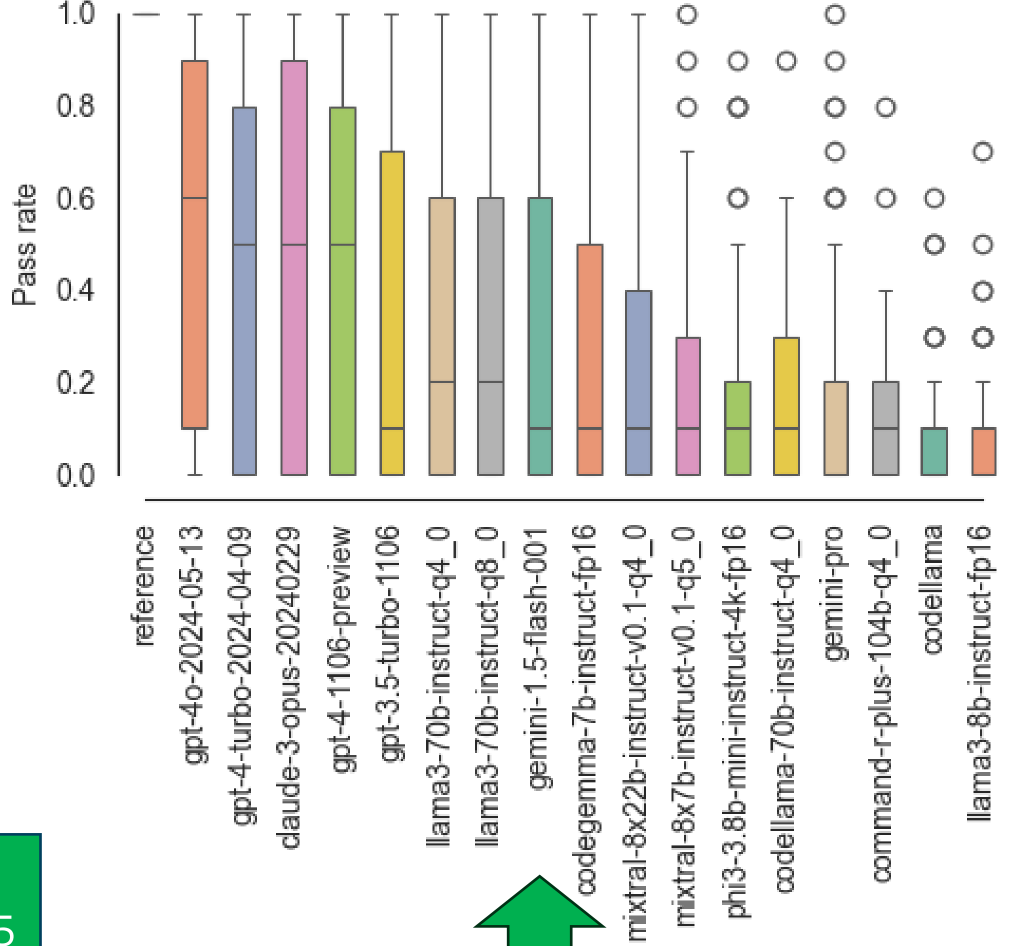
New: gpt4 omni

https://github.com/haesleinhuepf/human-eval-bia/pull/66

Benchmarking LLMs for Bio-image Analysis

Summary: 57 use-cases (yet), 17 LLMs (yet), n=10



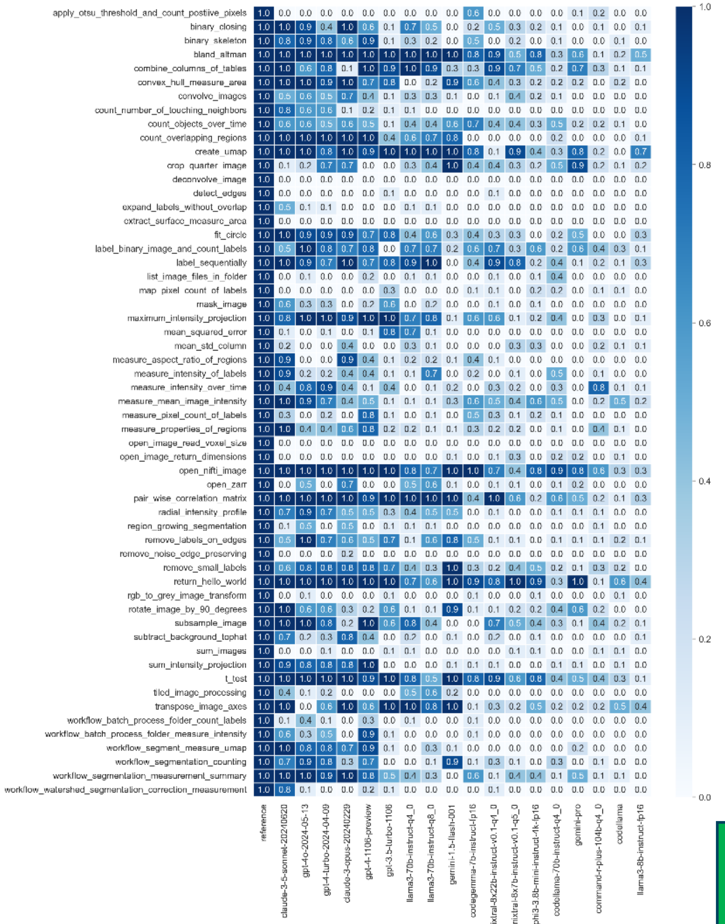


New:
gemini 1.5
flash

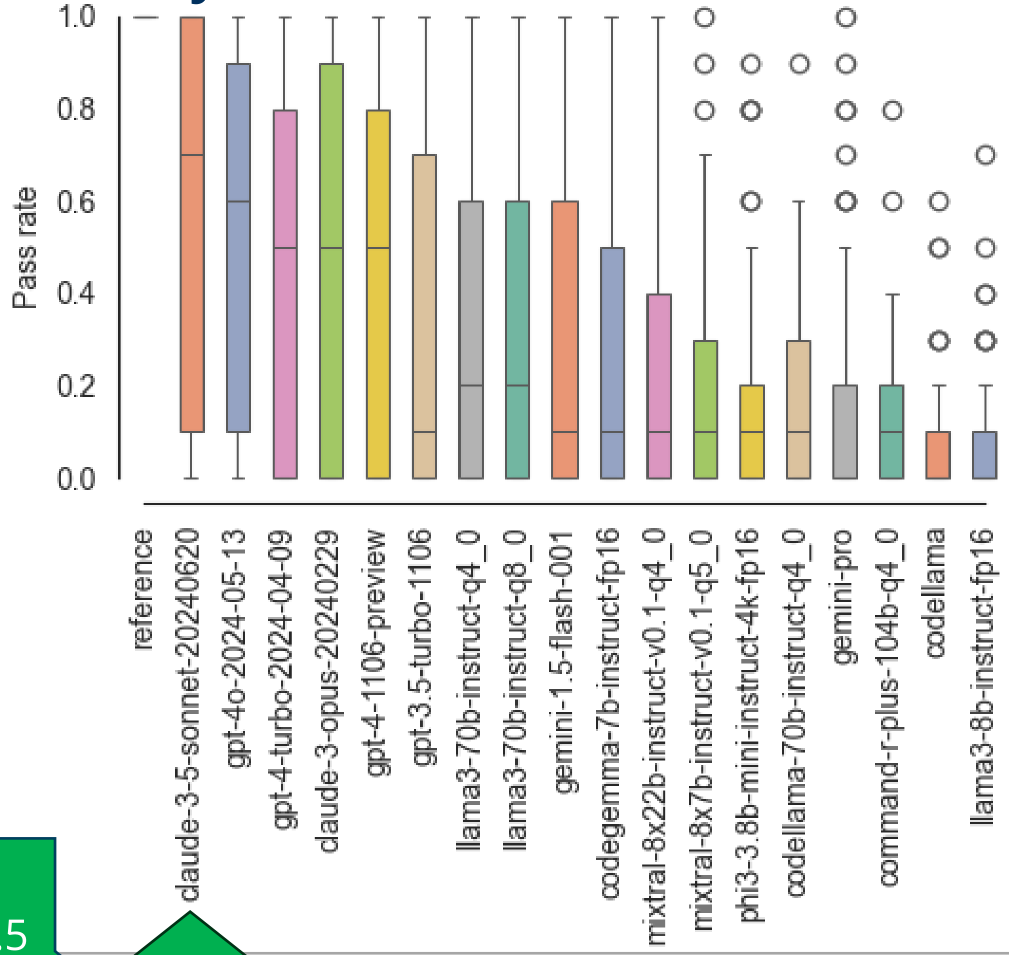
https://github.com/haesleinhuepf/human-eval-bia/pull/67

Benchmarking LLMs for Bio-image Analysis

Summary: 57 use-cases (yet), 18 LLMs (yet), n=10



	reference	claude-3-5-sonnet-20240620	gpt-4o-2024-05-13	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	gemini-1.5-flash-001	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	0.0	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	1.0	0.9	0.4	1.0	0.6	0.1	0.7	0.5	0.0	0.2	0.5	0.3	0.2	0.1	0.0	0.1	0.0	0.1
binary_skeleton	1.0	0.8	0.9	0.8	0.6	0.9	0.1	0.3	0.2	0.0	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	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	1.0	0.6	0.8	0.1	1.0	0.9	1.0	0.9	0.3	0.3	0.9	0.7	0.5	0.2	0.7	0.3	0.1	0.1
convex_hull_measure_area	1.0	1.0	1.0	0.9	1.0	0.7	0.8	0.0	0.2	0.9	0.6	0.4	0.3	0.2	0.2	0.2	0.0	0.2	0.0
convolve_images	1.0	0.5	0.6	0.5	0.7	0.4	0.1	0.3	0.3	0.1	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	0.8	0.6	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	0.0
count_objects_over_time	1.0	0.6	0.6	0.5	0.6	0.5	0.1	0.4	0.4	0.6	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	1.0	1.0	0.4	0.6	0.7	0.8	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.1
create_umap	1.0	1.0	1.0	0.8	1.0	0.9	1.0	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	0.1	0.2	0.7	0.7	0.0	0.0	0.3	0.4	1.0	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	0.0	0.0	0.0
detect_edges	1.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	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	0.5	0.1	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	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	0.0	0.0	0.0
fit_circle	1.0	1.0	0.9	0.9	0.9	0.7	0.8	0.4	0.6	0.3	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	0.5	1.0	0.8	0.7	0.8	0.0	0.7	0.7	0.2	0.6	0.7	0.3	0.6	0.2	0.6	0.4	0.3	0.1
label_sequentially	1.0	1.0	0.9	0.7	1.0	0.7	0.8	0.9	1.0	0.0	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	0.1	0.0	0.0	0.2	0.0	0.1	0.1	0.0	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	0.0	0.0	0.3	0.0	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	0.6	0.3	0.3	0.0	0.2	0.6	0.0	0.2	0.0	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0
maximum_intensity_projection	1.0	0.8	1.0	1.0	0.9	1.0	1.0	0.7	0.8	0.1	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	0.0	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	0.0
mean_std_column	1.0	0.2	0.0	0.0	0.4	0.0	0.0	0.3	0.1	0.0	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	0.9	0.0	0.0	0.9	0.4	0.1	0.2	0.2	0.1	0.4	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
measure_intensity_of_labels	1.0	0.9	0.2	0.2	0.4	0.4	0.1	0.1	0.7	0.0	0.2	0.0	0.1	0.0	0.5	0.0	0.1	0.0	0.0
measure_intensity_over_time	1.0	0.4	0.8	0.9	0.4	0.1	0.4	0.0	0.1	0.2	0.0	0.3	0.2	0.0	0.3	0.0	0.8	0.1	0.1
measure_mean_image_intensity	1.0	1.0	0.9	0.7	0.4	0.5	0.1	0.1	0.1	0.3	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	0.3	0.0	0.2	0.0	0.8	0.1	0.0	0.1	0.0	0.5	0.3	0.1	0.2	0.1	0.0	0.0	0.0	0.0
measure_properties_of_regions	1.0	1.0	0.4	0.4	0.6	0.8	0.2	0.2	0.1	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	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	0.0	0.1	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	1.0	1.0	0.8	0.7	1.0	1.0	0.7	0.4	0.8	0.9	0.8	0.6	0.3	0.3
open_zarr	1.0	0.0	0.5	0.0	0.7	0.0	0.0	0.5	0.6	0.1	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	1.0	1.0	0.9	1.0	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	0.9	0.7	0.5	0.5	0.3	0.4	0.5	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	0.1	0.5	0.0	0.5	0.0	0.1	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0
remove_labels_on_edges	1.0	0.5	1.0	0.7	0.6	0.5	0.7	0.1	0.6	0.8	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	0.0	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	0.0
remove_small_labels	1.0	0.6	0.8	0.8	0.8	0.8	0.7	0.4	0.3	1.0	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	1.0	1.0	0.7	0.6	1.0	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	0.1	0.0	0.0	0.0	0.1	0.0	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	1.0	0.6	0.6	0.3	0.2	0.6	0.1	0.1	0.9	0.1	0.1	0.2	0.2	0.4	0.6	0.2	0.0	0.0
subsample_image	1.0	1.0	1.0	0.8	0.2	1.0	0.6	0.8	0.4	0.0	0.0	0.7	0.5	0.4	0.3	0.1	0.4	0.2	0.1
subtract_background_tophat	1.0	0.7	0.2	0.3	0.8	0.4	0.0	0.2	0.0	0.1	0.0	0.2	0.0	0.1	0.0	0.0	0.0	0.0	0.1
sum_images	1.0	0.0	0.0	0.1	0.0	0.0	0.1	0.1	0.0	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	0.9	0.8	0.8	0.8	1.0	0.0	0.0	0.0	0.1	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	1.0	1.0	0.9	1.0	0.8	0.5	1.0	0.8	0.9	0.6	0.8	0.4	0.5	0.4	0.3	0.1
tiled_image_processing	1.0	0.4	0.1	0.2	0.0	0.0	0.0	0.5	0.6	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
transpose_image_axes	1.0	1.0	0.0	0.6	1.0	0.6	1.0	1.0	0.8	1.0	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	0.4	0.1	0.0	0.3	0.0	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_batch_process_folder_measure_intensity	1.0	0.6	0.3	0.5	0.0	0.9	0.1	0.0	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	1.0	0.8	0.8	0.7	0.9	0.1	0.0	0.3	0.1	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0
workflow_segmentation_counting	1.0	0.7	0.9	0.8	0.3	0.7	0.0	0.0	0.1	0.9	0.1	0.3	0.1	0.0	0.3	0.0	0.1	0.0	0.0
workflow_segmentation_measurement_summary	1.0	1.0	1.0	0.9	1.0	0.8	0.5	0.4	0.3	0.0	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	0.8	0.1	0.0	0.0	0.2	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0

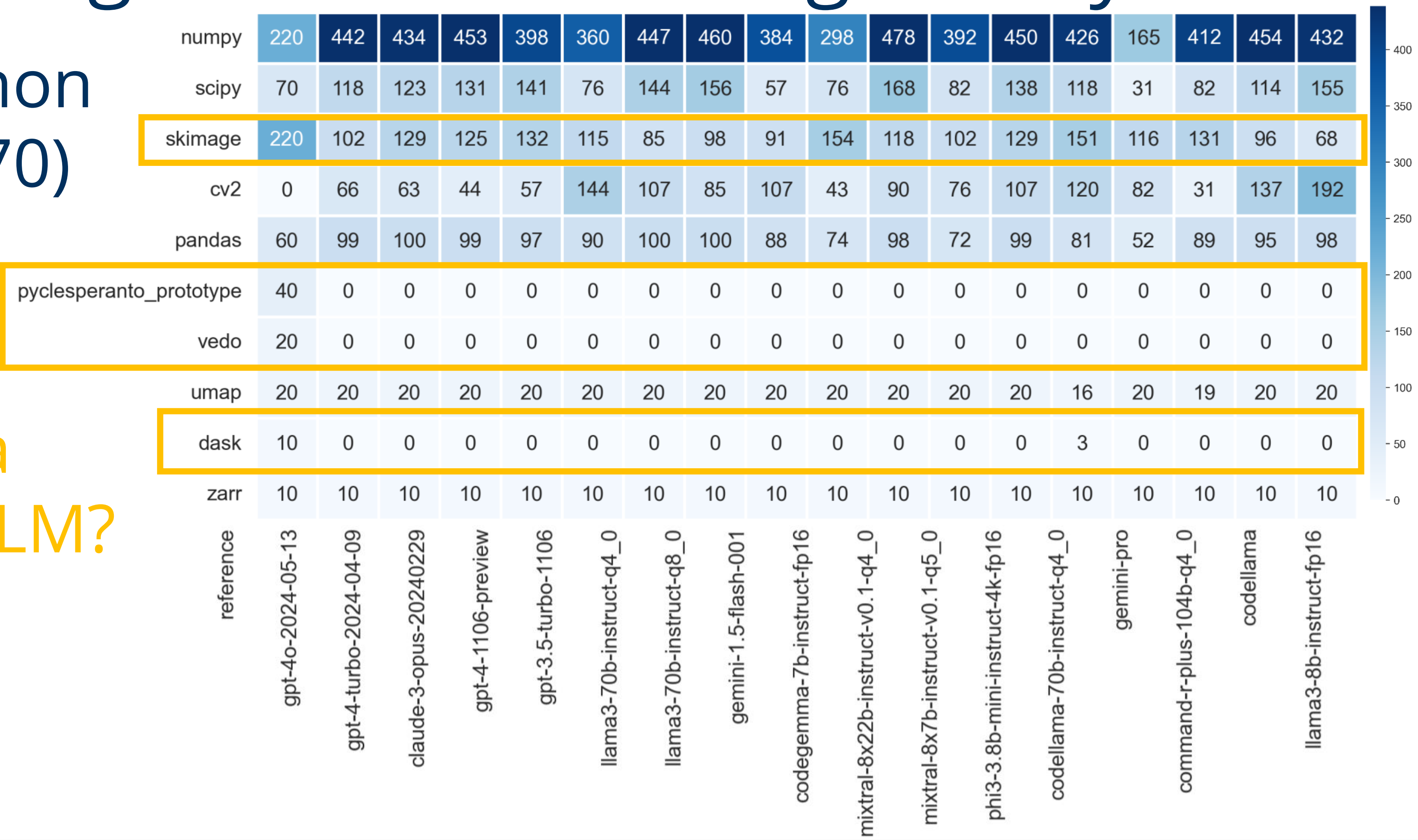


New:
claude 3.5
sonnet!

https://github.com/haesleinhuepf/human-eval-bia/pull/69

Benchmarking LLMs for Bio-image Analysis

Common Python libraries (n=570)



	reference	gpt-4o-2024-05-13	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	gemini-1.5-flash-001	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
numpy	220	442	434	453	398	360	447	460	384	298	478	392	450	426	165	412	454	432
scipy	70	118	123	131	141	76	144	156	57	76	168	82	138	118	31	82	114	155
skimage	220	102	129	125	132	115	85	98	91	154	118	102	129	151	116	131	96	68
cv2	0	66	63	44	57	144	107	85	107	43	90	76	107	120	82	31	137	192
pandas	60	99	100	99	97	90	100	100	88	74	98	72	99	81	52	89	95	98
pyclesperanto_prototype	40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
vedo	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
umap	20	20	20	20	20	20	20	20	20	20	20	20	20	16	20	19	20	20
dask	10	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
zarr	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10

Do we need a BiA-specific LLM?

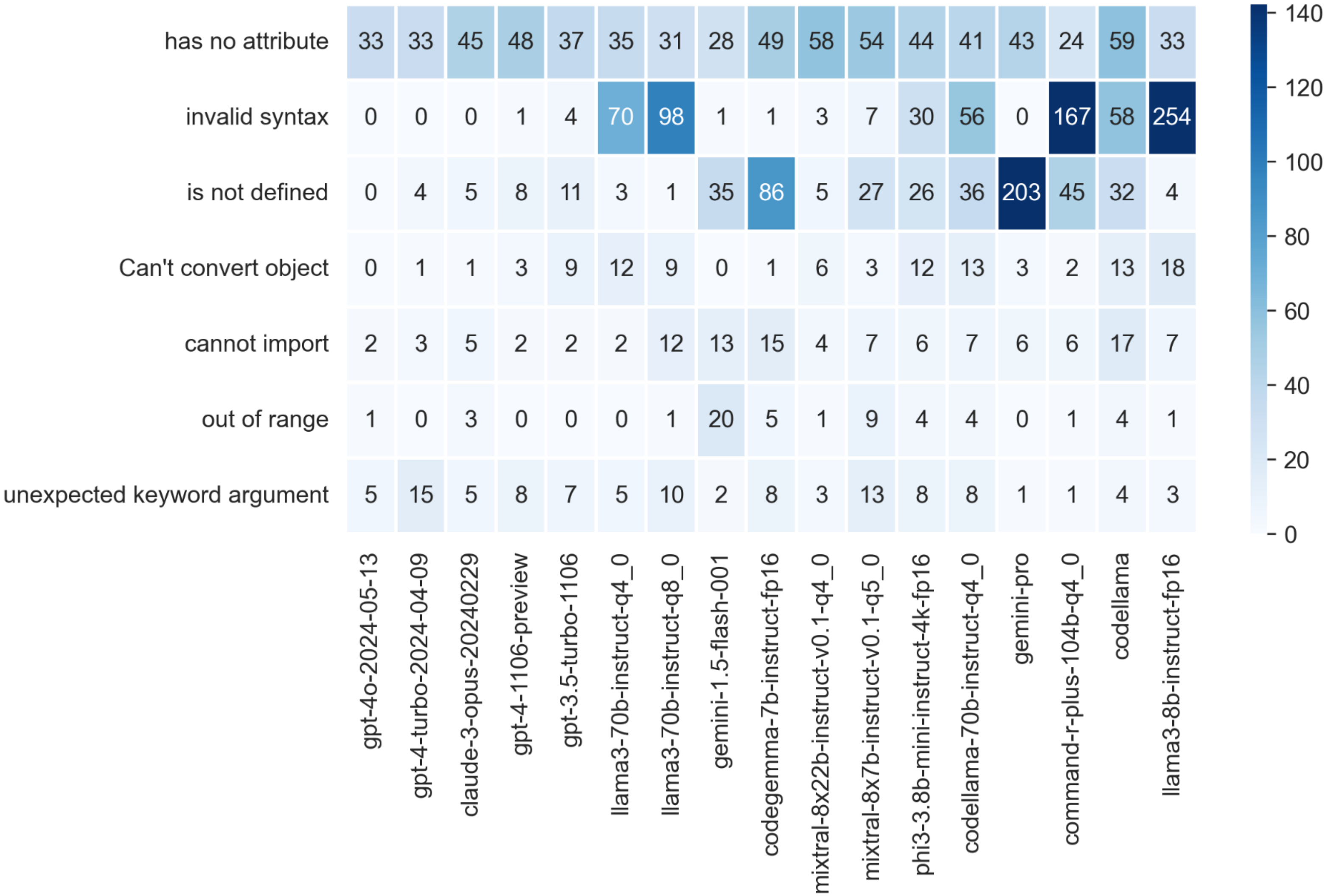
https://www.biorxiv.org/content/10.1101/2024.04.19.590278v1
https://github.com/haesleinhuepf/human-eval-bia

Benchmarking LLMs for Bio-image Analysis

Common error messages (n=570)

Halucinating API?

Forgot import statements?



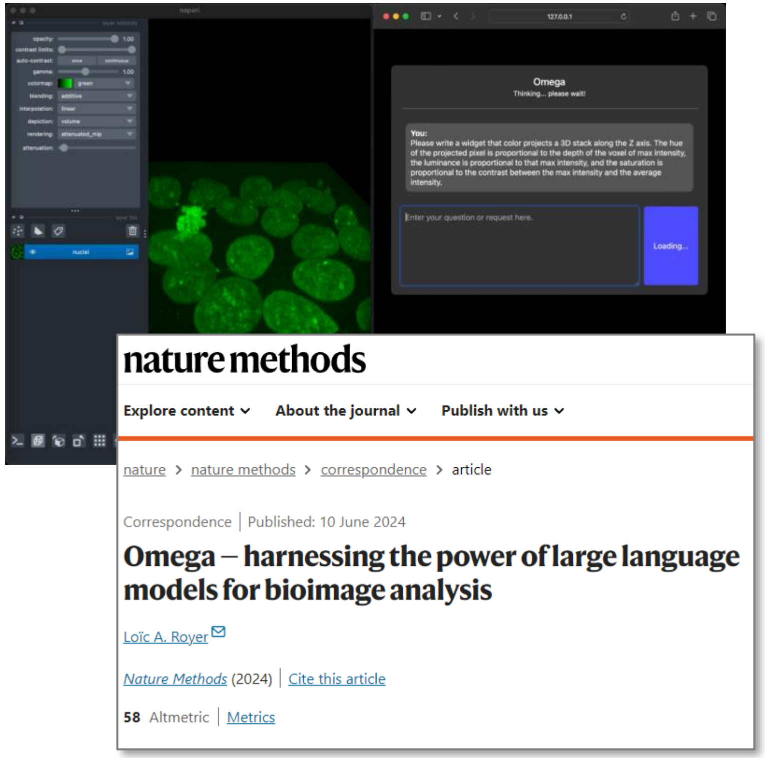
	gpt-4o-2024-05-13	gpt-4-turbo-2024-04-09	claude-3-opus-20240229	gpt-4-1106-preview	gpt-3.5-turbo-1106	llama3-70b-instruct-q4_0	llama3-70b-instruct-q8_0	gemini-1.5-flash-001	codegemma-7b-instruct-fp16	mixtral-8x22b-instruct-v0.1-q4_0	mixtral-8x7b-instruct-v0.1-q5_0	phi3-3.8b-mini-instruct-4k-fp16	codellama-70b-instruct-q4_0	gemini-pro	command-r-plus-104b-q4_0	codellama	llama3-8b-instruct-fp16
has no attribute	33	33	45	48	37	35	31	28	49	58	54	44	41	43	24	59	33
invalid syntax	0	0	0	1	4	70	98	1	1	3	7	30	56	0	167	58	254
is not defined	0	4	5	8	11	3	1	35	86	5	27	26	36	203	45	32	4
Can't convert object	0	1	1	3	9	12	9	0	1	6	3	12	13	3	2	13	18
cannot import	2	3	5	2	2	2	12	13	15	4	7	6	7	6	6	17	7
out of range	1	0	3	0	0	0	1	20	5	1	9	4	4	0	1	4	1
unexpected keyword argument	5	15	5	8	7	5	10	2	8	3	13	8	8	1	1	4	3

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

Similar tools

Bob is not alone… and they are becoming more.

Napari-chatGPT / Omega



You:
Please write a widget that color projects a 3D stack along the Z axis. The hue of the projected pixel is proportional to the depth of the voxel of max intensity, the luminance is proportional to that max intensity, and the saturation is proportional to the contrast between the max intensity and the average intensity.

nature methods

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nature > nature methods > correspondence > article

Correspondence | Published: 10 June 2024

Omega – harnessing the power of large language models for bioimage analysis

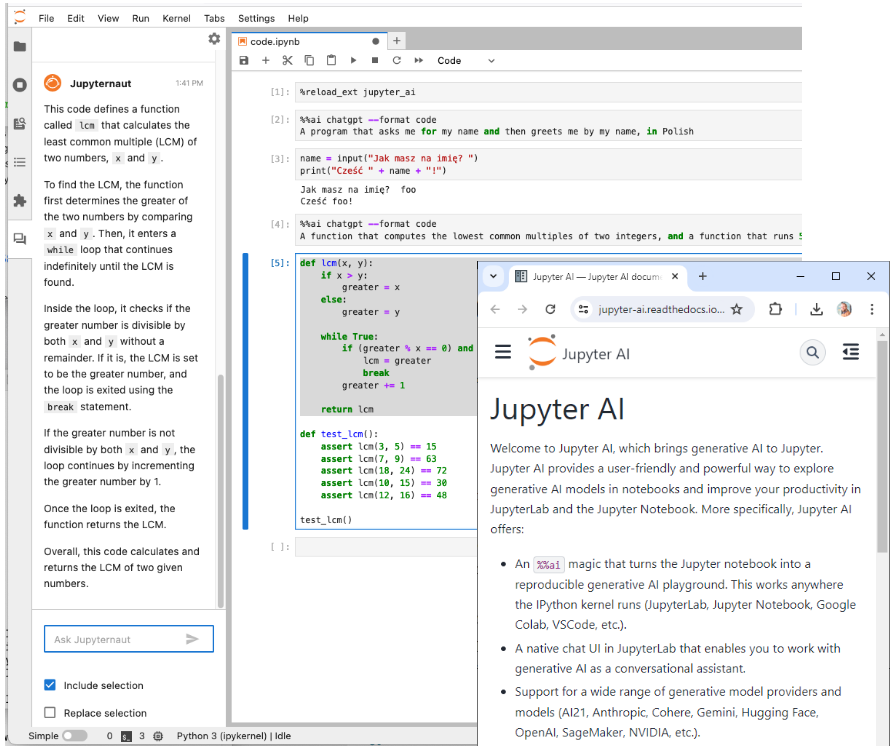
Loïc A. Royer

Nature Methods (2024) | Cite this article

58 Altmetric | Metrics

https://github.com/royerlab/napari-chatgpt
https://www.nature.com/articles/s41592-024-02310-w

Jupyter-AI


File Edit View Run Kernel Tabs Settings Help
code.ipynb
Code
Ask Jupyternaut
Simple
0 3
Python 3 (ipykernel) | Idle
Jupyter AI — Jupyter AI docum
jupyter-ai.readthedocs.io...
Jupyter AI

Jupyternaut 1:41 PM

This code defines a function called `lcm` that calculates the least common multiple (LCM) of two numbers, `x` and `y`.

To find the LCM, the function first determines the greater of the two numbers by comparing `x` and `y`. Then, it enters a `while` loop that continues indefinitely until the LCM is found.

Inside the loop, it checks if the greater number is divisible by both `x` and `y` without a remainder. If it is, the LCM is set to be the greater number, and the loop is exited using the `break` statement.

If the greater number is not divisible by both `x` and `y`, the loop continues by incrementing the greater number by 1.

Once the loop is exited, the function returns the LCM.

Overall, this code calculates and returns the LCM of two given numbers.

☑ Include selection

☐ Replace selection

```
[1]: %reload_ext jupyter_ai

[2]: %%ai chatgpt --format code
     A program that asks me for my name and then greets me by my name, in Polish

[3]: name = input("Jak masz na imię? ")
     print("Cześć " + name + "!")

     Jak masz na imię?  foo
     Cześć foo!

[4]: %%ai chatgpt --format code
     A function that computes the lowest common multiples of two integers, and a function that runs 5

[5]: def lcm(x, y):
         if x > y:
             greater = x
         else:
             greater = y

         while True:
             if (greater % x == 0) and
                 lcm = greater
                 break
             greater += 1

         return lcm

     def test_lcm():
         assert lcm(3, 5) == 15
         assert lcm(7, 9) == 63
         assert lcm(18, 24) == 72
         assert lcm(10, 15) == 30
         assert lcm(12, 16) == 48

     test_lcm()

[ ]:
```

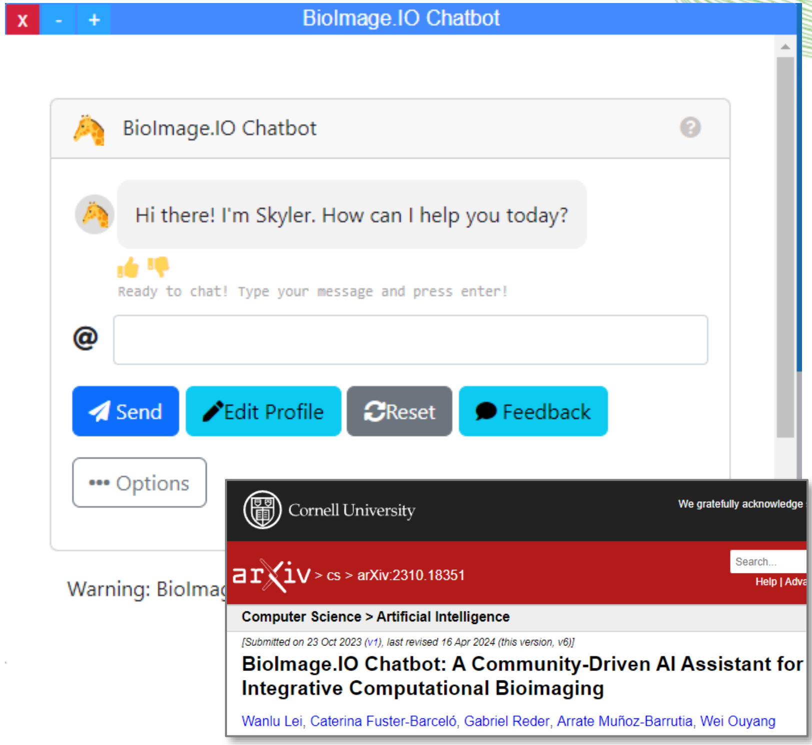
Jupyter AI

Welcome to Jupyter AI, which brings generative AI to Jupyter. Jupyter AI provides a user-friendly and powerful way to explore generative AI models in notebooks and improve your productivity in JupyterLab and the Jupyter Notebook. More specifically, Jupyter AI offers:

- An `%%ai` magic that turns the Jupyter notebook into a reproducible generative AI playground. This works anywhere the IPython kernel runs (JupyterLab, Jupyter Notebook, Google Colab, VSCode, etc.).
- A native chat UI in JupyterLab that enables you to work with generative AI as a conversational assistant.
- Support for a wide range of generative model providers and models (AI21, Anthropic, Cohere, Gemini, Hugging Face, OpenAI, SageMaker, NVIDIA, etc.).

https://jupyter-ai.readthedocs.io/

Bioimage-io ChatBot



Hi there! I'm Skyler. How can I help you today?

Ready to chat! Type your message and press enter!

Warning: BioImag

Computer Science > Artificial Intelligence

[Submitted on 23 Oct 2023 (v1), last revised 16 Apr 2024 (this version, v6)]

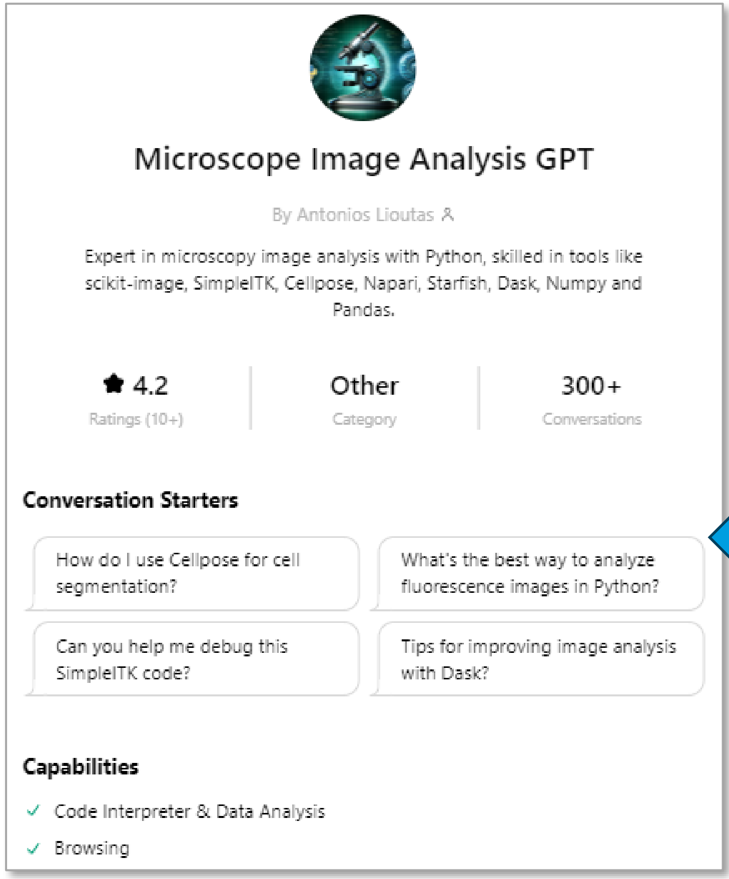
BioImage.IO Chatbot: A Community-Driven AI Assistant for Integrative Computational Bioimaging

Wanlu Lei, Caterina Fuster-Barceló, Gabriel Reder, Arrate Muñoz-Barrutia, Wei Ouyang

https://bioimage.io/#/
https://arxiv.org/abs/2310.18351

Similar tools

Bob is not alone… and they are becoming more.



Microscope Image Analysis GPT

By Antonios Lioutas

Expert in microscopy image analysis with Python, skilled in tools like scikit-image, SimpleITK, Cellpose, Napari, Starfish, Dask, Numpy and Pandas.

★ 4.2	Other	300+
Ratings (10+)	Category	Conversations

Conversation Starters

- How do I use Cellpose for cell segmentation?
- What's the best way to analyze fluorescence images in Python?
- Can you help me debug this SimpleITK code?
- Tips for improving image analysis with Dask?

Capabilities

- ✓ Code Interpreter & Data Analysis
- ✓ Browsing

https://chatgpt.com/g/g-FGdNx7MlI-microscope-image-analysis-gpt

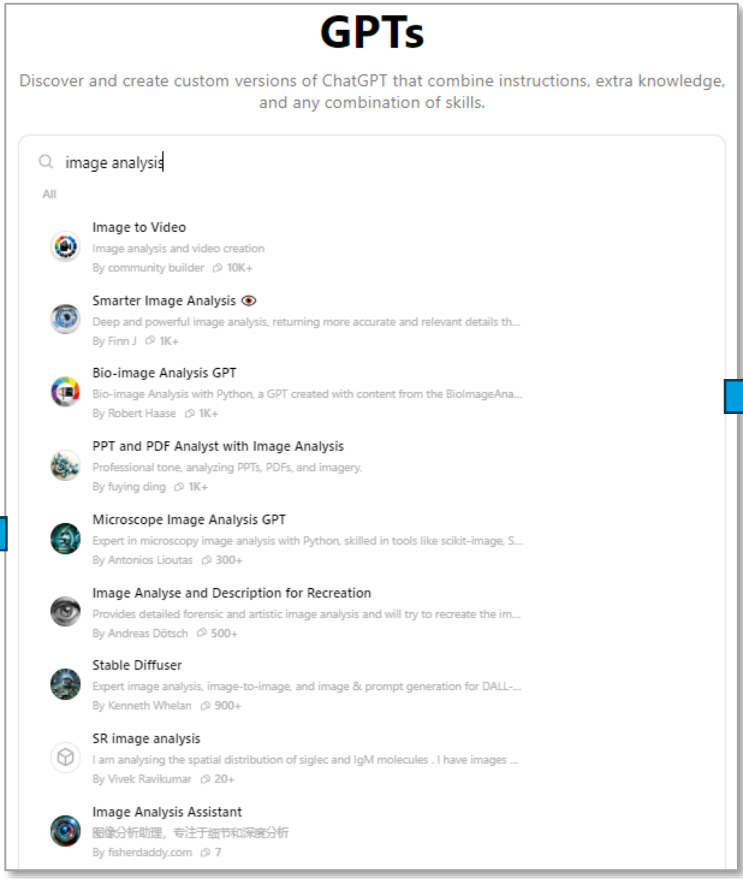


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image analysis

All

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Microscope Image Analysis GPT
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Provides detailed forensic and artistic image analysis and will try to recreate the im...
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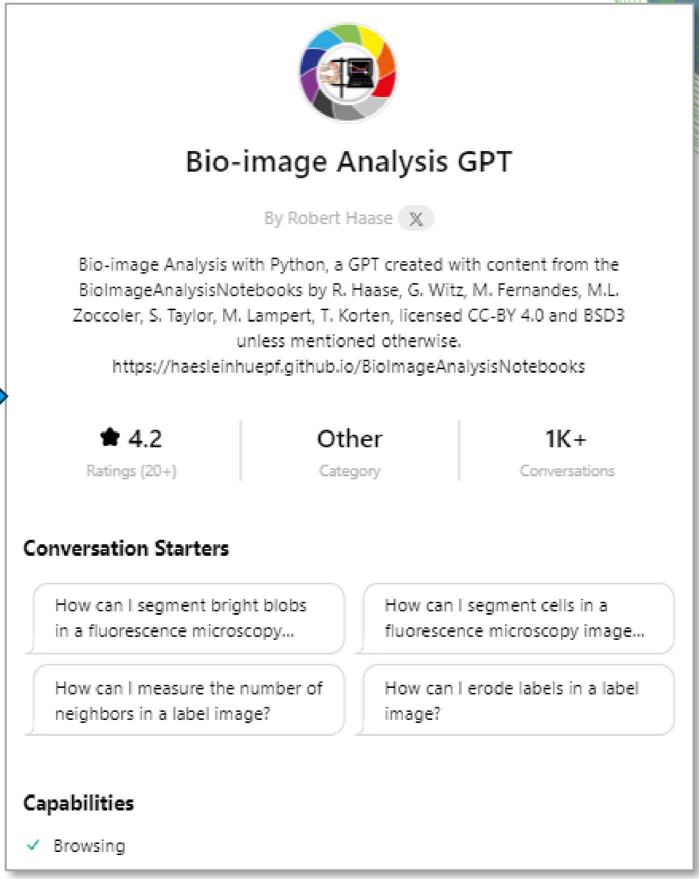
Stable Diffuser
Expert image analysis, image-to-image, and image & prompt generation for DALL-...
By Kenneth Whelan · 900+

SR image analysis
I am analysing the spatial distribution of siglec and IgM molecules . I have images ...
By Vivek Ravikumar · 20+

Image Analysis Assistant
图像分析助理，专注于细节和深度分析
By fisherdaddy.com · 7

http://chat.openai.com/gpts



Bio-image Analysis GPT

By Robert Haase

Bio-image Analysis with Python, a GPT created with content from the BioImageAnalysisNotebooks by R. Haase, G. Witz, M. Fernandes, M.L. Zoccoler, S. Taylor, M. Lampert, T. Korten, licensed CC-BY 4.0 and BSD3 unless mentioned otherwise. https://haesleinhuepf.github.io/BioImageAnalysisNotebooks

★ 4.2	Other	1K+
Ratings (20+)	Category	Conversations

Conversation Starters

- How can I segment bright blobs in a fluorescence microscopy...
- How can I segment cells in a fluorescence microscopy image...
- How can I measure the number of neighbors in a label image?
- How can I erode labels in a label image?

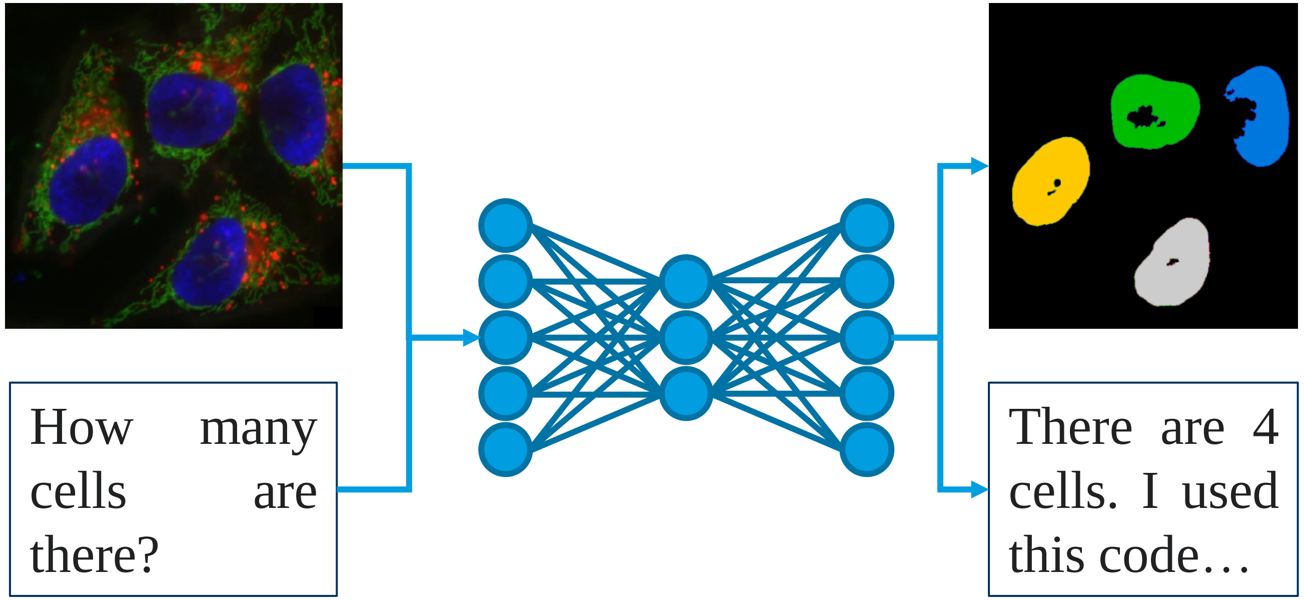
Capabilities

- ✓ Browsing

https://chatgpt.com/g/g-psAohb1OY-bio-image-analysis-gpt

Summary & outlook

- LLMs can generate code to analyze biological microscopy images
- Open-source benchmarks can help targeting further improvement
- Challenges:
  - Identify best strategy (fine-tuning, prompt-engineering, RAGs)
  - Multi-modal / multi-agent approaches
  - Introduce good scientific practice -> trustworthy AI



How many cells are there?

There are 4 cells. I used this code…

Acknowledgements

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PoL
Physics of Life
TU Dresden

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- Marcelo Zoccoler
- Johannes Soltwedel
- Maleeha Hassan
- Stefan Hahmann

Former lab members:

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- Laura Zigutyte
- Mara Lampert
- Allyson Ryan
- Conni Wetzker
- Till Korten
- Somashekhar Kulkarni

Communities & platforms

NFDI4BIOIMAGE

image.sc

German BioImaging
Gesellschaft für Mikroskopie und Bildanalyse

neubias
network of european bioimage analysts

GloBIAS
Global BioImage Analysts' Society

Funding

Bundesministerium
für Bildung
und Forschung

SACHSEN

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Chan
Zuckerberg
Initiative

DFG Deutsche Forschungsgemeinschaft

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