CZ BioHub_Take Home Test



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For Associated R&D Engineer

For Each Exercise:

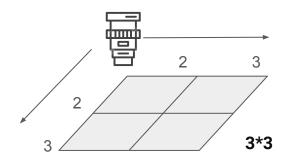
- Work
- Choice Made
- Challenges
- Solution

Exercise 1

Exercise 1 — Explain the Work, Choice Made

Acquiring a multi-dimensional dataset using microscopy simulation

Work Explanation



```
z_step = 0.1
num_z_slices = 12
spacing = 500
channels = ['DAPI', 'FITC']
```

Choice made



- pycromanager complex multi-dimensional acquisition and real-time image processing
- pymmcore-plus lightweight, direct hardware control, without UI or advanced features.

Multi_dimensional_Acq_Events

```
# Step 6: Generate acquisition events, Using multi_d_acquisition_events
events = multi_d_acquisition_events(
    num_time_points=1,  # Set as 1, acquisit once at each event
    z_start=0, z_end=z_step*(num_z_slices-1.5), z_step=z_step, #Bas
    channels=channels,
    xy_positions=positions,
    order='tpcz'  # Acquisition order: time, position, chan
)
```

Exercise 1 — Challenges and solutions

Challenges

· Connect With the Micro-Manager

Data Acquisition on Micro-Manager

- **Solutions**
- → Look into the Official Document
- Connect to port 4827
- pip install pycromanager
- import pycromanager
- → Official Document

Dealing multi-dimensional data

- → Two Method:
 - 1. events = multi_d_acquisition_events()
 - 2. Loop in the Acquisition Function

Exercise 1 — Verification Code to Check the Shape

```
def verify z step(acquisition script path, expected z step):
   Verify that the z-step defined in the acquisition script matches the expected z-step.
    :param acquisition_script_path: The path to the acquisition script.
    :param expected z step: The expected z-step in micrometers.
    :return: None
   # This is a simplified example and assumes you have a way to extract the z step from the script.
   # In reality, you may need to parse the script or otherwise determine the z step.
   z_step_defined_in_script = 0.1 # Example value
   if np.isclose(z_step_defined_in_script, expected_z_step):
       print("Z-step check passed.")
    else:
       print(f"Z-step mismatch: Expected {expected_z_step} um, got {z_step_defined_in_script} um")
# Load the dataset
path to dataset = r'C:\Users\chanq\Desktop\2024 AssocRDEng TakeHome\Exercise1\my acquisition 6\my acquisition NDTiffStack.tif'
images = tiff.imread(path to dataset)
print(images.shape)
# Example usage:
expected_dims = (9, 12, 512, 512) # Adjust based on actual expected dimensions
expected channels = ['DAPI', 'FITC']
expected_z_step = 0.1 # in micrometers
# Verify dimensions
if images.shape[:] != expected_dims[:]:
   print(f"Dimension mismatch: Expected {expected dims[:]}, got {images.shape[:]}")
else:
   print(images.shape[1:])
   print("Dimension check passed.")
```

```
events = multi_d_acquisition_events(
    z_start=0,
    z_end=z_step*(num_z_slices-1.5),
    z_step=z_step,
)

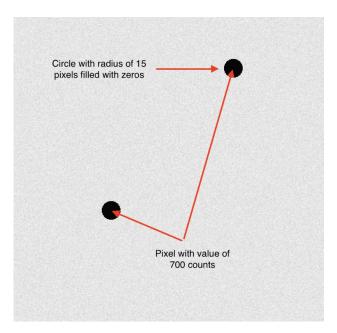
# Based on the verification adjustment,
# '-1.5' could give in 12 slices
```

Exercise 2

Exercise 2 — Explain the Work, Choice Made

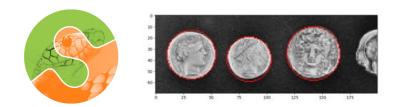
Modifying images in real-time during acquisition based on pixel value

Work Explanation



Choice made

Skimage.draw.disk



Process Image After Acquisition → image_process_fn

```
def img_process_fn(image, metadata):
    ### send image and metadata somewhere ###

# this acquisition won't show a viewer or save data
with Acquisition(image_process_fn=img_process_fn) as acq:
    ### acquire some stuff ###
```

Exercise 2 — Challenges and solutions

Challenges

- Cannot do disk drawing in Acquisition Function()
 - Acquisition Func() can only do event acquiring

- Data Type event , image wrong
 - image should be 'numpy.array' but show 'dict'
 - event should be dict but show 'numpy.array' or 'queue'

Solutions

- → Have to use image_process_fn to call out def()
- Define two function
 - o process_image(image)
 - Draw disk when image =700
 - o image_process_fn(image, metadata)
 - Processing modified image (Save pics)
 - metadata is the event in this function
- → 1. Print in each process to see its 'type', 'shape'
 - 2. Look into official document for function usage
 - 3. Ask for micro-manager community
- image_process_fn(image, metadata)
 - has strict order for sending back value
- The event in image_process_fn() called metadata

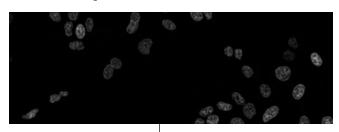


Exercise 3

Exercise 3 — Explain the Work, Choice Made

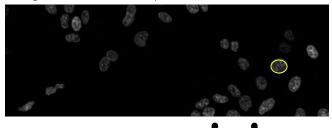
Segmenting cell nuclei and measuring their shape deviations

Work Explanation



Segmentation

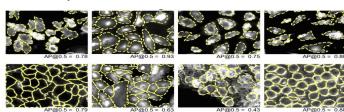
Eccentricities



Choice made

Segmentation - Cellpose:

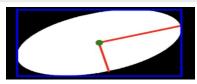
- easy to access and specific to cell
- model()



Eccentricities - Skimage:



measure.regionprops(mask).eccentricity



Exercise 3 — Challenges and solutions

Challenges

The images cannot be processed directly

 The data including 17 images, all of the images have multiple dimension

masks = model.eval()

```
python

Process the images with Cellpose
masks = model.eval(images, diameter=None, flow_threshold=None, channels=[0,0])
```

'list' object has no attribute 'ndim'

Solutions

- → To ensure 'image' was type: 'numpy array'
- using io in scikit-image to read the TIFF.
- → 1. Using 'for' loop to go over each images
 - 2. Ensure images is the list of 2D arrays
 - Only take first channel for processing

```
# Ensure images is a list of 2D arrays
if images.ndim == 3:
    ## If the image is 3D (multiple channels or Z-stacks), select
    images = [img[0] if img.ndim == 3 else img for img in images]
```

- → model eval()
 - model eval() must send back 4 variables
 - masks, flows, styles, diams = model.eval()

What I have learned

- Learning the automation of microscopy from scratch
- Ask 'Official Document' and 'Community' for help
- Seeking for multiple tools to try more in different angles

Thanks!