

# Cellpose

In this google document, go to :

File > Make a copy (it will make a copy on your own googleDrive).

When you're done with the homework, go to :

File > Download > pdf

Upload the pdf on moodle

In the document below you will find :

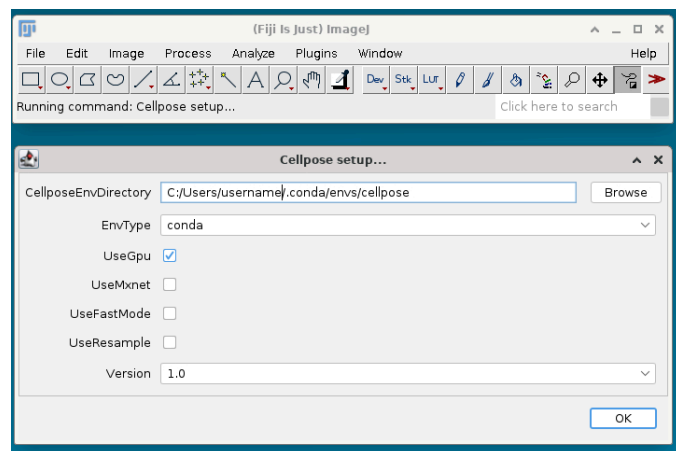
- Underlined text which requires you to type a short answer (40-50 words)

- **Underlined bold text, which requires you to type a thorough answer (80-100 words)**

## I. Configure cellpose

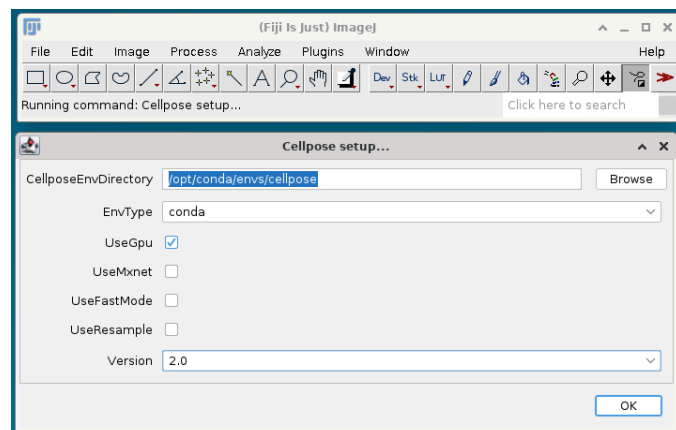
In Fiji

Start **Cellpose setup** ...



Replace **CellposeEnvDirectory**  
with **/opt/conda/envs/cellpose**

Change **version** to **2.0**



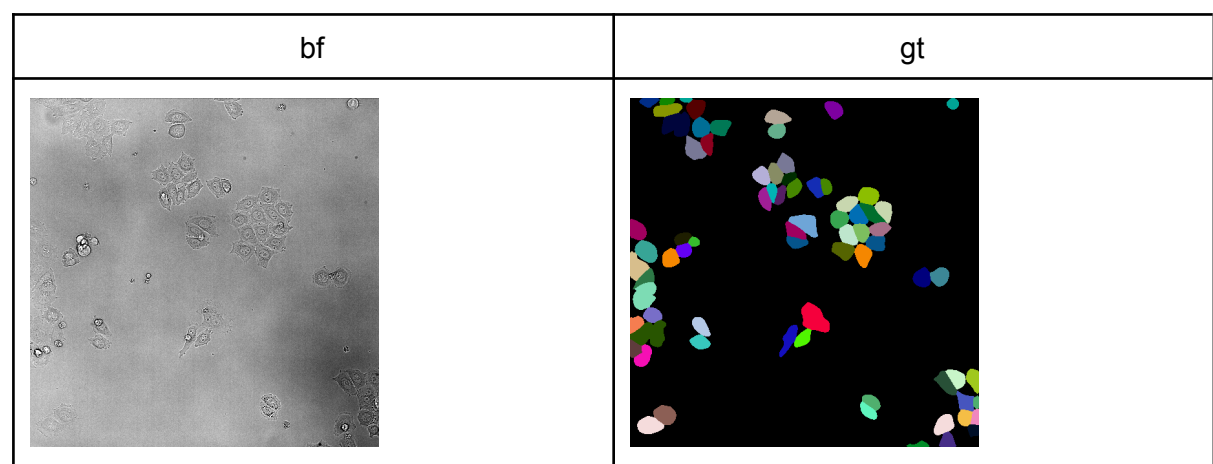
## II. Discover cellpose

- A. File > Open Samples... > Blobs
- B. Plugins > BIOP > Cellpose > Segment Nuclei
- C. Plugins > BIOP > Cellpose > Cellpose Advanced (custom model)
  - 1. select model nuclei
    - a) try with diameter = 17
    - b) try with diameter = 34
    - c) Use Plugins > MiC > Mask instant Comparator
    - d) Please comment on the MiC results
  - 1. select model cyto2
    - a) try with diameter = 30
    - b) try with diameter = 15
    - c) Use Plugins > MiC > Mask instant Comparator
    - d) Please comment on the MiC results

**From the results you obtained can you guess the parameters of the command "Cellpose>Segment Nuclei" ?**

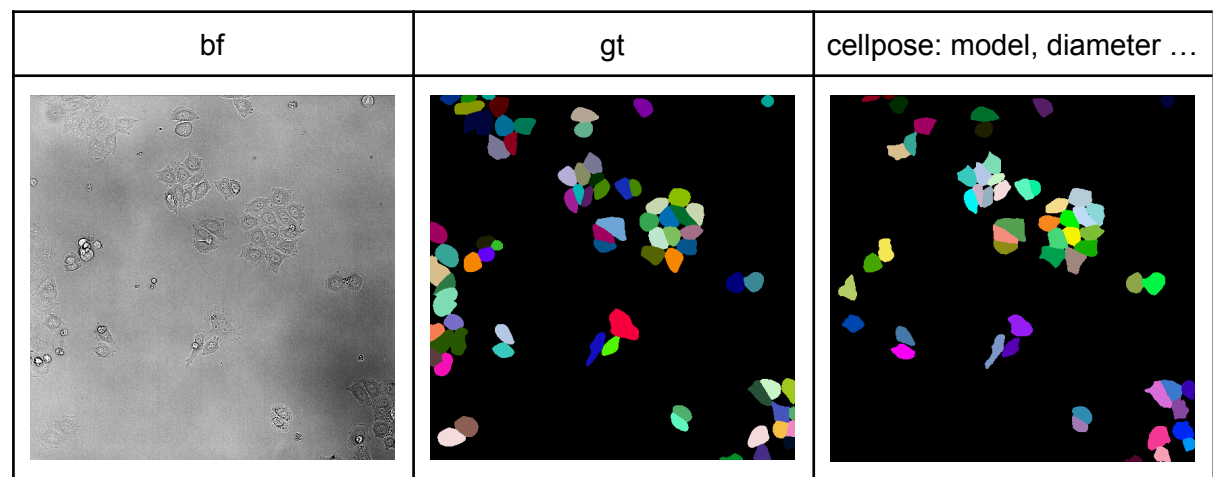
### III. Use cellpose on a real dataset

We have access to a fraction of a test dataset (folder week-11/1-*data/bf*) with the corresponding “Ground truth” (folder week-11/1-*data/gt*).



A. Tweak Cellpose

- a. Define satisfying results
- b. Change suitable cellpose parameters
- c. Find settings to predict cell labels that satisfy the criteria defined in A.a.
- d. Save predicted label images
- e. Comment on the results obtained with MiC plugin



B. Own model

From the same experiment, a “training” dataset was used to train a model (folder : Homework/2-*model/cyto\_from\_bf*)

- a. From Fiji run **Cellpose Advanced (custom model)** , using our own model
  - i. diameter : 30
  - ii. model\_path : browse to the model  
“2-*model/cyto\_from\_bf/verylongfilename*”
  - iii. model : “own model cyto2”

- b. Save predicted label images
- c. **Comment on the results**