Deep learning-based high-throughput detection of in vitro germination to assess pollen viability from microscopic images (https://doi.org/10.1093/jxb/erad315)

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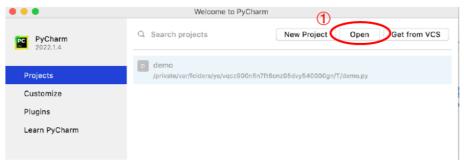
⚠The software versions are crucial, please check them carefully.

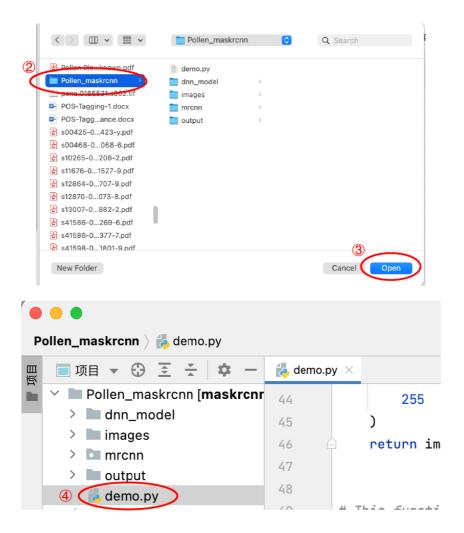
(The guidance's schematics are based on the macOS operating system, but all the steps are generic for Windows system. Mac with the Apple M1 chip is not compatible with this guidance because of the different versions of the required packages.)

1. Download "Pycharm Community Version 2022.1.4" with the link below and install.

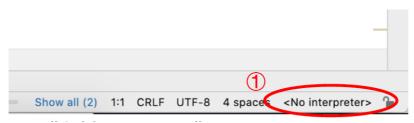
https://www.jetbrains.com/pycharm/download/other.html

- 2. Download "Python 3.8.X" with the link below and install. Choose the appropriate link to download depending on your computer. (macOS) https://www.python.org/downloads/macos/ (Windows) https://www.python.org/downloads/windows/
- 3. Download "Pollen_maskrcnn.zip" with the link below. https://github.com/Nihon-snail/Pollen_germination_detection
- 4. Download the weight file with the link below. Then place it in the "Pollen_maskrcnn/dnn_model" folder. https://drive.google.com/drive/folders/1QZzJZ8bLtDNEZZ_DBupGNNiHj8eB_JBN? usp=drive_link
- 5. Open the folder "Pollen_maskrcnn" in Pycharm. Double-click to open file "demo.py".

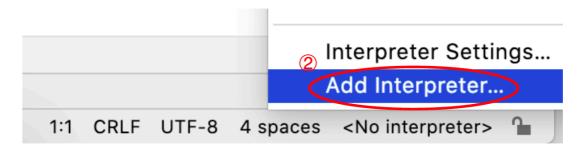




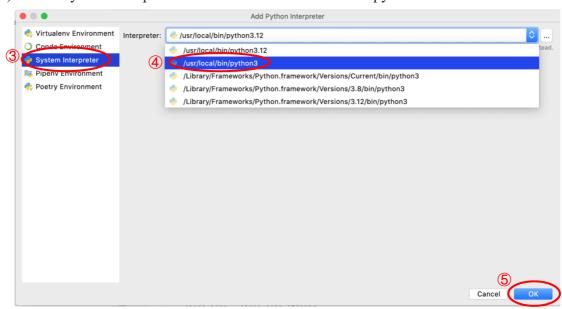
- 6. Set python 3.8 as the interpreter.
- 1) At the beginning, "No interpreter" is displayed in the bottom right corner of the Pycharm interface.



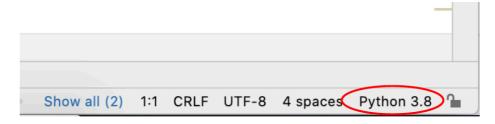
2) Click <No interpreter> then choose "Add Interpreter"



3) Click "System Interpreter" then choose "/user/local/bin/python3"



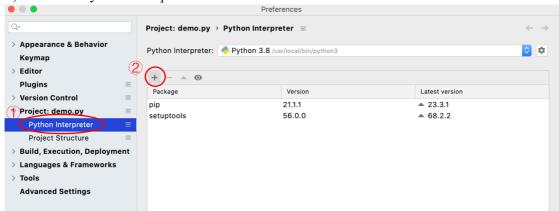
4) Now the interpreter was added successful.



- 7. Packages installation
- 1) Click "Python 3.8" then choose "Interpreter Settings".

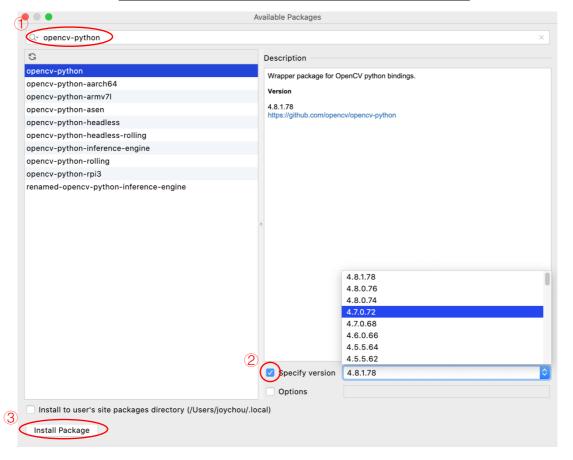


2) Choose "Python Interpreter" and click "+".

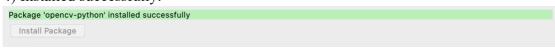


3) Enter the name of the installation package and select the specified version. Install the listed packages one by one.

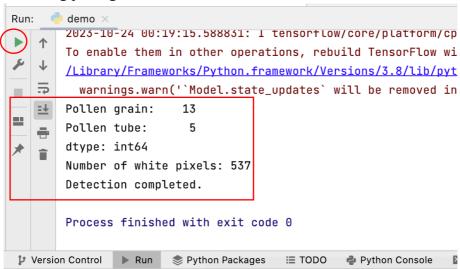
Package	Version
opency-python	4.7.0.72
tensorflow	2.5.0
pandas	1.4.4
numpy	1.19.5
scipy	1.9.1
scikit-image	0.19.2
diplib	3.1.0
matplotlib	3.5.2



4) Installed successfully.



8. Click "Run" to launch the demo.py after all packages have been installed. The number of pollen grains, tubes, and total pollen tube pixels are shown below based on the "template" image. The output images are saved in "Pollen_maskrcnn/output". Check the version information in the file "Pollen_maskrcnn/requirements" if there are any other missing packages.



9. When detecting your own image, place the pollen microscopic image (in JPG or PNG format) in the "Pollen_maskrcnn/images" folder. Remember to change the name of the image in the demo.py script on line 12 (path = "images/the name of your own file").