Assignment 3 Software Guide

Working on LTS Macs

The LTS Macs have all of the necessary software packages already installed. Boot up the Terminal and get started! To run Python, you need to type python3.9 on LTS machines.

Working on your own machine

This assumes that you are working on macOS, Linux, or WSL on Windows.

1. Download and unzip the assignment from the course website: http://web.stanford.edu/class/cs279/index.html#hw
2. Activate your conda environment: `conda activate cs279`
    a. If you do not have conda installed or have not created a conda environment, set that up by following the directions on the Assignment 2 Software Guide, which creates an environment called `cs279`.
    b. Run `conda activate cs279` every time you open a new terminal. With the environment active, type `python` exactly as the assignment shows. If the `python` command does not exist, see Common problems in the Assignment 2 Software Guide.
3. Install the Python packages required for the assignment:
    a. `pip install matplotlib numpy scipy imageio`
4. Install celltool with the following commands:
    a. `pip install scikit-image`
    b. `pip install git+https://github.com/maschka/celltool` (a deprecation warning during this step is normal and can be ignored)
5. You should now be able to run `celltool -h` in the terminal and see a help document printed.

Challenge question 1: segmenting nuclei

You only need this section if you attempt Challenge 1. The starter code, `challenge_problem.py`, needs Pillow, matplotlib, and numpy. The commands below also install scipy, scikit-image, and OpenCV, which the challenge suggests you may find useful.

On the LTS Macs: in the terminal, go to the folder with `challenge_problem.py` and the .tif files, then run these two lines:

```
python3.9 -m pip install Pillow scipy scikit-image opencv-python
python3.9 challenge_problem.py nucleus_10x_img1.tif
```

On your own computer: in the terminal, go to the same folder, then run these three lines:

```
conda activate cs279
pip install Pillow scipy scikit-image opencv-python
```

```
python challenge_problem.py nucleus_10x_img1.tif
```

Either way, the last line should open the first image in a matplotlib window.

Using the packages in your code: the name you import is not always the name you installed. Copy the lines you need to the top of `challenge_problem.py`:

```
from PIL import Image          # Pillow (already in the starter code)
from scipy import ndimage      # scipy
from skimage import filters, segmentation, measure   # scikit-image
import cv2                     # opencv-python
```

To browse the images outside Python, you can also use ImageJ or any other program for scientific images; this is optional.

Challenge question 2: interpreting segmentation-based measurements

Nothing to install. Challenge 2 uses the Allen Institute's Cell Feature Explorer, which runs in your web browser at `cfe.allencell.org`.