Deep Learning Interface
Biomedical Optics Laboratory

Important Note:

This interface has been developed using the 64–bit Windows platform and hence, the installation steps described are only compatible with this platform. If you wish to use this interface on any other platform, please contact us. Kindly refer to the additional notes at the end of this document for more pointers on running the interface.

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Installation Instructions:

- Download the "Deep Learning Interface.zip" file from the link below:
  https://drive.google.com/file/d/1snUVJvzU7HpyE2EKLz1EROJzWzIkkdaG/view?usp=sharing

- Unzip and extract the files from "Deep Learning Interface.zip" into a folder of your choice. It is important to unzip this in the same drive where the rest of the applications would be installed. (the default C drive is recommended)
- From the unzipped folder, install the application "Anaconda3-2019.10-Windows-x86_64". First, right-click on the .exe file to check if your PC has the "Run as administrator" option and click on it to start the installation. If this option isn't shown for you, double-click on the .exe file to run it. Ensure that the "All Users" check box is selected as the installation type.
- Install the application "MCR_R2018b_win64_installer".
- After successfully installing these two applications, open "Anaconda Prompt (Anconda3)" using the start menu.
- In the Anaconda command prompt, copy and press enter to run the below commands one after another. While running them, a few of them will prompt for a yes [y] or no [n] to proceed and you can just enter "y". All the commands will be installing the Python packages required for running the interface. After most of the commands, a successful installation shall be displayed. If it doesn't, there might be an issue in which case, please contact us.

  conda create -n Interface python=3.5.6
  conda activate Interface
  pip install opencv-python
  pip install Keras
  pip install --upgrade tensorflow
  pip install scikit-image
  pip install pandas
  pip install xlrd
  pip install scikit-learn==0.22.1
  pip install jupyterlab
  pip install ipykernel

- After the above installations, change the directory in the Anaconda command prompt to the folder where you have extracted the Deep Learning Interface files. For example, if your unzipped folder "ABC" is saved in your "Downloads folder", type the following in the prompt. ("cd" is used for changing the directory)

  cd Downloads/ABC/Deep Learning Interface

Deep Learning Interface
Biomedical Optics Laboratory

- Once you have Deep Learning Interface as the current directory in the prompt, copy and paste the following one after another:
  cd MATLAB_Files/for_testing
  python setup.py install

- Go back to the Deep Learning Interface directory by entering "*cd..*" twice.
- Now, run the command "*python -m ipykernel install --user --name=Interface*" to finish the installation.
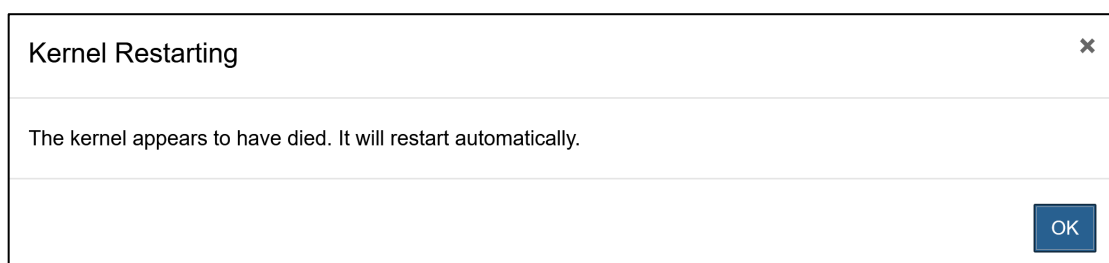
Running the Interface:

- Add the images you want to analyze to the folder "Deep Learning Interface → Input Images → Cells"
- Go to the Anaconda prompt.
- Enter "*conda activate Interface*".
  Enter "*cd Downloads/ABC/Deep Learning Interface*".
- Enter "*jupyter notebook*".
- A new window will open in your internet browser. It can work with any browser. You might be prompted the first time to select the browser if it detects more than one.
- From the list displayed, double-click on "*Main Interface.ipynb*" to open it.
- Confirm that "Interface" is displayed on the right top of the screen below the "Logout" option. If not, click on "Kernel" from the top bar and click on "Change Kernel". Now, you can select the kernel named "Interface".
- Also, to start fresh, click on "Restart and Clear Output" from the Kernel menu drop-down. After pressing on that, you will see "Connected" flashed in the top right corner. This means you are all set.
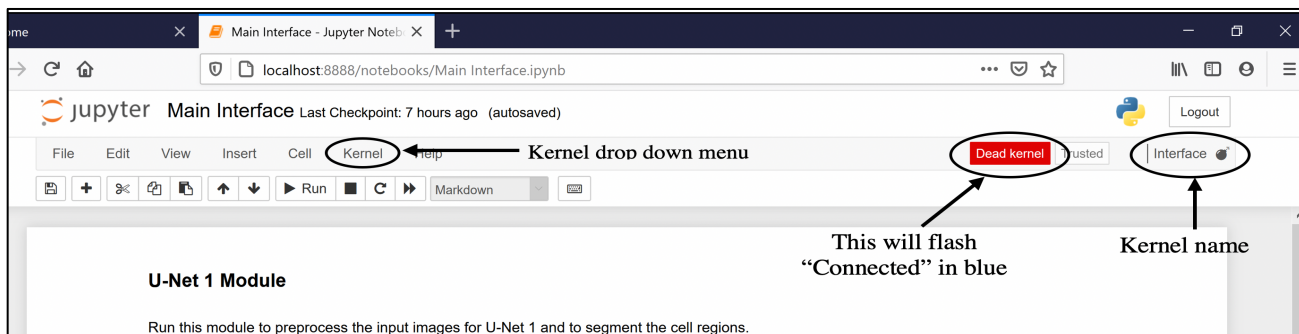
- Now you may execute one cell at a time by clicking on the cell and clicking on the run button available below the top bar. (Cell is each row that has a command starting with %run)

  Note: You will know each cell has run successfully when the message box shown below gets displayed.

Deep Learning Interface
Biomedical Optics Laboratory

Deep Learning Interface Contents:

Zip file contents

Deep Learning Interface	Folder contains all the files and folders required for the interface
Anaconda3-2019.10-Windows-x86_64	Application file to install Python
MCR_R2018b_win64_installer	Application file to install the MATLAB Runtime

Deep Learning Interface folder contents

Cell Segmentation Masks	Folder contains binary segmentation images with white pixels for cell bodies
Cell Segmentation Outlines	Folder contains output images showing segmentation outlines on input images
Input Images	Folder contains "Cells" folder where culture images to be analyzed are added
Markers	Folder contains output images from cell marker detection
MATLAB Files	Folder contains the setup to make MATLAB files run in Python environment
Python Files	Folder contains all the backend Python scripts for the interface
Regions	Folder contains output images from cell region detection
Results Visualization (Cell Number)	Folder contains images with cell segmentation outlines and cell numbers
Results Visualization (Cell Phenotype Probability)	Folder contains images with cell segmentation outlines and RS/SR probabilities
Results Visualization (Cell Phenotype)	Folder contains images with cell segmentation outlines in green (RS) / red (SR)
Sample Input Images	Folder contains samples for day 2 and day 4 culture images
U-Net 1 Postprocessed	Folder contains images obtained after postprocessing U-Net 1 results
U-Net 1 Preprocessed	Folder contains preprocessed images to be used as input for U-Net 1
U-Net 1 Results	Folder contains the prediction results from U-Net 1
U-Net 2 Preprocessed	Folder contains preprocessed images to be used as input for U-Net 2
U-Net 2 Results	Folder contains the prediction results from U-Net 2
Main Interface.ipynb	Main jupyter notebook file to run the interface
MATLAB_Files.prj	Project file contains the backend MATLAB functions

Additional Notes:

- The interface is currently designed to process up to 99 images in one run. Do not add more than 99 images in the folder "Cells" to run the interface correctly.
- The algorithm has been trained with .tif files of dimension 1280 X 1024 pixels acquired using a from phase contrast microscope with 10X objective. The interface will work well only for similar 10X phase contrast images and not brightfield or any other modality. It is recommended that you save the microscope images as .tif files.
- The image size can be different but maintaining the aspect ratio is highly recommended. For clear segmentation, avoid acquiring images of size lesser than 640 X 512 pixels.
- All the image outputs and excel files get stored as you are running the interface in the appropriate folders.
- To run the interface for a new dataset, remove the current images and place the new images you want to analyze inside the "Cells" folder.

Deep Learning Interface
Biomedical Optics Laboratory

- The interface folder also has some sample images for both day 2 and day 4 inside the "Sample Input Images" folder. You can use these to get familiar with the interface.
- Running the interface for new data will overwrite the previous output files, so make sure to copy and save them separately. Do not remove or rename any folders inside the "Deep Learning Interface" folder as the interface won't work in that case. You can only copy/cut/remove the files from the folders.
- If the interface ever seems to be stuck, you can select "Restart and Clear Output" from the Kernel menu drop-down. This won't affect the previously run cells. You can continue from the cell you had to run next.
- The algorithm has been trained only with culture images acquired on day 2 and day 4. It's working with images from other days has not been validated.