*# Step 1: Load the user's Bash configuration file*

source ~/.bashrc

*# Applies all environment variables and alias configurations from the .bashrc file.*

*# Step 2: Change to the working directory containing MATLAB scripts*

cd /home/jingyifei/Desktop/Li\_8well/2025-MATLAB-nucleorm

*# Navigate to the directory where MATLAB scripts are stored in preparation for execution.*

*# Step 3: Run the MATLAB script for preprocessing*

matlab -batch Pre\_cellpose

*# Executes the MATLAB script `Pre\_cellpose` in non-interactive mode to generate images for further processing.*

*# Step 4: Move the generated images to the folder named "temp"*

# (This step is performed manually or using the `mv` command)

# Example: mv generated\_images\_folder/\* temp/

*# Organizes the generated images into the specified folder for the next steps.*

*# Step 5: Navigate back to the parent directory*

cd ..

*# Switch to the parent directory to set up the next processing environment.*

*# Step 6: Activate the specified Conda environment*

conda activate /home/jingyifei/miniconda3/envs/cellpose

*# Activates the Conda environment that includes Cellpose to ensure the required dependencies are available.*

*# Step 7: Use Cellpose for image segmentation*

nohup cellpose --dir mask\_4/temp --pretrained\_model 8well\_dapi\_model/20230802\_Li\_8well\_dapi \

--chan 3 --chan2 0 --save\_png --no\_npy --look\_one\_level\_down --verbose --diameter 110.927

*# Processes images in the specified directory:*

*# --dir: Specifies the input image directory.*

*# --pretrained\_model: Uses a specific pretrained model for segmentation.*

*# --chan: Specifies the primary channel (3 = third channel).*

*# --chan2: Specifies the secondary channel (0 = none).*

*# --save\_png: Saves the segmented masks in PNG format.*

*# --no\_npy: Does not save masks in NPY format.*

*# --look\_one\_level\_down: Scans subfolders in the input directory.*

*# --verbose: Outputs detailed processing logs.*

*# --diameter: Sets the average object diameter for segmentation.*

# Note: The `nohup` command can be used to run the process in the background and log the output to a file.

# Example: nohup cellpose ... > output.log &

# Step 8: Move the generated masks from "temp" to the original folders

# (This step is performed manually or using the `mv` command)

# Example: mv temp/masks/\* original\_folder/

# Step 9: Return to the MATLAB scripts directory

cd 2025-MATLAB-nucleorm

# Navigate back to the directory containing the MATLAB scripts for further operations.

# Step 10: Run the MATLAB script for postprocessing

matlab -batch Post\_cellpose

# Executes the MATLAB script `Post\_cellpose` in non-interactive mode for postprocessing and result analysis.