

Note - this is all included in the ReadMe file under 2b

Step-by-Step Manual

Follow these steps to use the pipeline to generate matching slices for all patients or a specific subset:

1. Prepare Image Data: Place .tif image files in the designated folder (e.g., processed_images). Ensure that each patient has images for all three stains (H&E, Melanin, Sox10).
2. Choose Full or Subset Processing:
 - For All Patients: Place all images in the same processed_images directory.
 - For a Subset of Patients: Separate patient image files into their own folders within processed_images (e.g., processed_images/patient1, processed_images/patient2).
3. Run the Pipeline:
 - Run match_pipeline.py. A GUI will prompt you to select the directory containing the images.
 - Open NoahsMatching.ipynb in Jupyter Notebook and execute cells in sequence.
4. Process and Review Matches:
 - Upon execution, the pipeline will preprocess, extract contours, and match images, saving results in the matches folder. Images will be organized by patient, with matched slices grouped in subfolders.