# Brief overview

* Create a folder containing all HDAB images you wish to process
* Select a representative image, interactively obtain HDAB color vectors using MATLAB script
* Run each of the 6 methods on a dataset
  + Alsubaie (ICA) MATLAB script
  + Macenko (PCA) python script
  + Xu (SNMF) python script
  + QuPath (Ruifrok) groovy script in QuPath
  + HistomicsTK (Ruifrok) python script
  + Zaidi (Ruifrok) MATLAB script
* Run batch normalization MATLAB
  + If running on Xu or Macenko, need to enable variable in MATLAB script
* Merge all 6 deconvolution images and original RGB image into an ometiff using groovy script in QuPath
* Run QuPath script to set channel names and display ranges
* Run QuPath script to perform Stardist nucleus segmentation using QuPath hematoxylin (may need to modify for high DAB nuclei
  + Need to build a script to visualize nuclear to cytoplasm Hx ratio, probably in MATLAB to keep things simple
* Need to build a script to perform watershed segmentation and compare binary masks of detected nuclei in each method, against that of a pathologist scores (similar to what’s done in CODEX project)
* Performance (speed) comparisons also need to be done