1. Preprocessing: reduce noise, turn to grayscale image, crop a single sperm image from the original image. (I cannot find the code for this part for now, but follow these steps, you can finish preparing the sample:
   1. For a raw image, use matlab function contour, we can get the contour matrix, use the function contourdata.m in the package to obtain the boundaries, then we have all the contour in one figure
   2. Cropping the single object: use the histeq function to equalize the image. For each contour, calculate the coordinate of center of the image, squared-crop that part of image and save as the single sample, the resulting image should be like the images as the ones in the folder)
2. Training data: use save\_to\_dataset.m to obtain the sperm’s contours which specialist judged to be normal, or you can use create\_ground\_truth.m, change some of the parameters inside it should work, then use run\_training.m to train the optimal prior, you will obtain training\_data.mat, and prior file. (you need to adjust the index)
3. Segmentation: load the testing images as test\_image\_snips.mat, use run\_segmentation.m to obtain the segmentation. First, try to make the procedure work, and then try to change the options in the setting.
4. The calculation of the sperm parameters. Use get\_feature.m for the obtained one single image. It will help you calculate the features.