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#Python pseudo code outlining the image analysis process

#Required Data:
#irSpectra - 2D data array with shape (number of spectra, number of points
in each spectrum)
#irImage - 2D IR image with shape (x,y) where x*y = number of spectra

import numpy as np
from scipy import ndimage
import pymorph

#median filter to remove noise (3x3 pixel filter in this case)

fltImage = ndimage.filters.median_filter(irImage, size=3)

#set background pixels to zero (0.03 used as minimum signal value here)

fltImage[fltImage<0.03] =0

#determine regional maxima locations (fltImage must be converted to bytes
for pymorph package, not shown here)

rmax = pymorph.regmax(fltImage)

#label each regional maximum

seeds,nr_nuclei = ndimage.label(rmax)

#use the regional maxima as seeds for the watershed

labels = pymorph.cwatershed(-fltImage, seeds)

#calulate mean spectra per labelled cell

meanSpectra = np.zeros([labels.max()+1,irSpectra.shape[1]])

for i in range(0,labels.max()+1):

      #determine which pixels are in the cell and which spectra they
correspond to
      inCell =labels.reshape(irSpectra.shape[0])==i

      #average all the spectra in the cell
      meanSpectra[i,:]=irSpectra[inCell,:].mean(axis=0)

#meanSpectra now contains all the average spectra for each of the isolated
cells
#meanSpectra[i,:] is the average spectrum corresponding to the image labels
== i
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