

# Experience Roadmap

## 1. Plugin Development

The programming of simple routines in Java.  
Open the package with pointwise.zip plugins and images.  
Easy access to image pixels: ImageAccess class.

Name	Description	Example
ImageAccess(nx, ny)	Constructor: Creates a Image of size [nx,ny]	ImageAccess im = new ImageAccess (nx, ny);
getPixel(x, y)	Returns the value of the pixel in the position (x, y)	value = im.getPixel(x, y);
putPixel(x, y, value)	Assigns value to the pixel at (x, y)	im.putPixel(x, y, value);
getWidth() getHeight()	Returns the width of a image Returns the height of an image	int nx = im.getWidth(); int ny = im.getHeight();
getMaximum()	Returns the maximum of an image	double max = im.getMaximum();
getMinimum()	Returns the minimum of an image	double min = im.getMinimum();

## 1. The point transformation to improve visualization.

### 1.1. Understanding: contrast inversion.

Understand the inverse() routine, it changes the pixel values of the image  $f(x, y)$  to  $g(x, y) = 255 - f(x, y)$ .

Apply the routine to the image microtubules.tif calling the plugin "Inverse".  
Look at the histogram.

## 1.2. Stretching and normalizing contrast.

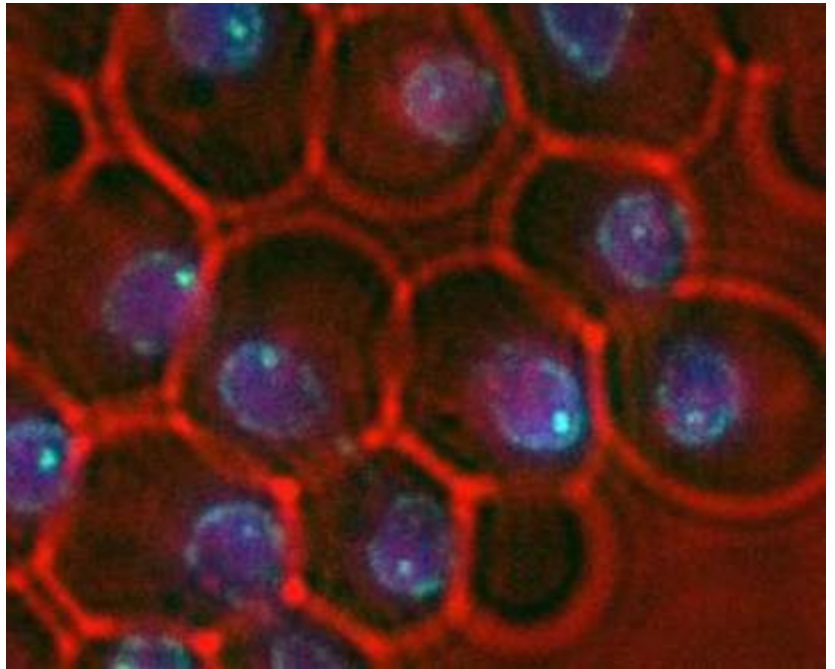
Write the `rescale()` routine that changes the pixel value of the image  $f(x, y)$  to:

$$g(x,y) = \alpha (f(x,y) - \beta)$$

$$\beta = \min(f(x,y))$$

$$\alpha = 255 / (\max(f(x,y)) - \min(f(x,y)))$$

Reescalone  $g(x, y)$  a  $[0,255]$ .



Apply the routine to the image of `microtubules.tif` calling the "Rescale" plugin. Look at the histogram.

## 1.3. Application: Saturates a medical image.

Write the `saturate()` routine that puts pixels to 10000 when the input value is greater than 10000. So call the routine `rescale()`.

Apply the routine in `HRCT.tif` calling the plugin "Saturate". Look at the histogram.

## 2. Threshold segmentation: "thresholding".

### 2.1 Contando partículas.

Using the "Threshold" command of ImageJ, you try to segment the images: `yeast1`, `yeast2`, `yeast3`, and `yeast4` to get 25 objects in the ImageJ particle analyzer (Analyzes -> Analyzes Particles). If you can't find a suitable threshold, explain why in the report file.doc.

## 3. "Z-Stack" projection.

### 3.1. Maximum intensity projection.

Write the `zprojectMaximum()` routine that generates the maximum intensity projection image of an image stack.

Apply the routine to the `yeard_stack.tif` by calling the ZMIP plugin.

### 3.2. Projection of mean intensity.

Write the `zprojectMean()` routine that generates the average image from a stack of images.

Apply the routine to the `yeard_stack.tif` by calling the ZMean plugin.

### 3.3. Presentation of z-stack images.

Use two plugins beforehand, the command "Brightness + Contrast", the command "Image Calculator" → "Color Merge" of ImageJ in an attempt to obtain a composite image of color where we can clearly distinguish the yeast cell, the GFP-tagged nucleus and the GFP-tagged telomere (stain).

The source is a z-stack of fluorescent images called `yeast_stack.tif` and the phase image is `yeast_phase.tif`. In the image above is an example of what we can expect. Place the resulting image in the `report.doc` file.