

HOW TO USE MOMENTMACRO WITH NIH IMAGE

A.DOWNLOAD NIH Image 1.62 from <http://rsb.info.nih.gov/nih-image> if necessary. Start up.

B.OPEN OR IMPORT your image ("File: Open" or "Import")

C.SET OPTIONS IN NIH IMAGE (first time use only)

Click on Analyze:Options. Then:

1. Make sure that only the following are checked off:
 - a. Area
 - b. Mean Density
 - c. Std. Dev.
 - d. X-Y Center
 - e. Perimeter/Length
 - f. Ellipse Major Axis
 - g. Ellipse Minor Axis
 - h. Angle
 - i. Min/Max
 - j. User1
 - k. User2

(note: these are not the actual properties calculated, but this creates enough spaces in the internal storage array to temporarily store cross-sectional properties that are calculated)

2. Change "Field Width" to 9. (Other field widths are fine, but 9 works best with the macro)
3. Change "Number of digits right of decimal point" to 2 (or however many you want).
4. Click OK, then click on File:Record Preferences. You need to follow this step(4) any time you change an option under the Analyze menu. (The above will remain as defaults even after you quit the program.)

(Note : If you want to change the units and scale in the displayed image, go to Analyze/Set scale, set units and #pixels/unit, using known distance and information displayed in "Info" window below image. Note that this does **not** affect the macro and calculation of properties, though - that scale must be set separately as described below.)

D. SET APPROPRIATE BONE THRESHOLDS

1. Click on Options:Density Slice
2. (Note: these directions are for a black bone on white background image. For a white bone on a black background these will need to be reversed.) A red area (bar) in the LUT window to the left will be displayed, overlapping a black area corresponding to the black area in the image. The top of the red bar is the lower threshold (in arbitrary units) and the bottom is the upper threshold. You can move the thresholds up or down using the crossed arrow tool above "A" to the right of the LUT.
3. To fill in the bone image with red, click the eyedropper tool on the red in the LUT, click on the bucket tool, and then click within the boundaries of the bone in the image. Adjust the upper and lower thresholds (LUT window) up or down until the red area completely fills (but doesn't overflow) the bone area. You can practice with the washer image supplied, but you should also do some tests with phantoms or cut sections of your material with known properties to establish the most accurate thresholds.

IMPORTANT: Note the threshold values of the red in your image (displayed under "Info" window in bottom left as you move the crossed arrow tool over the LUT window, or by clicking with the tool).

If your image is black on white, make sure that you set the lower threshold (you'll be prompted for it later) at the lower threshold of the red in your image. The higher threshold can be set at the maximum (255) unless you have something of higher density (e.g., metal, matrix) in the image that you want to leave out.

If your image is white on black, make sure that you set the higher threshold (you'll be prompted for it later) as high as the higher threshold of the red in your image. The lower threshold can be set at 0.

For other types of images (i.e., not all black or white) you will need to experiment with these limits.

E. LOAD THE MACRO: click on Special:Load Macro, find "momentmacro" wherever it's saved and double-click on it.

F. SET SCALE FOR MACRO

1. Using the tools, determine the length, in pixels, between 2 landmarks whose distance apart is known in real units.
2. From this determine the # of pixels/unit unit (for the washer image, this is 12.2 pixels/mm).
3. Click on Special:Set Units
4. Type in name of desired unit (e.g., mm).
5. Type in the # of pixels.

G. EXECUTING THE MACRO:

1. Using the wand tool, click inside the outer edge of the bone image (image should have flashing dotted line around it).
2. click on Special: Moment Calculation
3. When prompted for the name, enter the name of that image.
4. Enter appropriate thresholds as described above.

H. DISPLAY AND SAVING OF RESULTS:

A line of data will be displayed in the Measurement Results window. These are:

TA:	Total subperiosteal area
CA:	Cortical area
Xbar:	x coordinate of centroid
Ybar:	y coordinate of centroid
Ix:	Second moment of area about x axis
Iy:	Second moment of area about y axis
Imax:	Maximum second moment of area
Imin:	Minimum second moment of area
Theta:	Angle from M-L axis counterclockwise to major axis
Zx:	Section modulus about x axis ($I_x/\text{max y radius}$)
Zy:	Section modulus about y axis ($I_y/\text{max x radius}$)
Max x radius:	X distance from centroid to outermost fiber (used in calculating Zy)
Max y radius:	Y distance from centroid to outermost fiber (used in calculating Zx)

These can be cut and pasted into, e.g., an Excel file. Note that each time the macro is run, this window will be erased and replaced with the new data, so copy data off before you analyze another section. Also, NIH Image will only allow you to do a certain number of sections in one session, after which you'll need to re-start the program to collect more data.

A "Max and Min Radii" window will also appear, showing the maximum and minimum radii in x and y directions. These can be used to calculate an average radius in each direction, or the diameters.

J, the polar second moment of area, can be derived as $I_x + I_y$ (or $I_{\text{max}} + I_{\text{min}}$). The polar section modulus, Z_p , can be derived as J divided by the average or maximum overall radius. Empirical tests indicate that the former will be closer to the mean of (twice) Z_x and Z_y .

When quitting the program, you'll be asked whether to "save changes" in the image files you analyzed. Click "no" unless you edited them during the analysis and want to save those edits.